Electronic Supplementary Information
– Automated 3D sampling and imaging of uneven sample surfaces with LA-REIMS

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Supplementary Information S1 – Optimization of the functioning of the 3D MS Scanner

The optimization of the performance of the 3D MS Scanner consists of three parts: 1) Optimization of the relevant settings, 2) Improving the speed of the whole process, and 3) Alignment of the analog laser trigger and raw TIC chromatogram.

Optimization of settings of the 3D MS Scanner

Height between laser probe and sample surface

The distance between the laser probe and the sample surface is important for the amount of smoke that is aspirated into the mass spectrometer, as the increasing distance is expected to result in decreasing signal. Although no distance between the laser probe and the sample surface would result in the highest signal intensities, this is not preferred because of cross-contamination between sampling points. Besides, because of the shape of the laser probe (see Supplementary Figure S2C), small distances between the laser probe and the sample surface can result in unwanted collisions between the laser probe and the sample.

Seven distances between the laser probe and the sample surface were compared; 0.5 mm, 1.0 mm, 1.5 mm, 2.0 mm, 3.0 mm, 4.0 mm, and 10.0 mm. Fifty points were measured on an apple with a laser power of 2.5 J (CW, 25 W, 0.1 s) per pulse using the 3D MS Scanner for each distance. (Except for a distance of 3.0 mm, as the first 3 points were not recorded in the mass spectrometer due to an issue with aspiration.) The different distances were compared based on the overall intensity and the intensity of nine m/z values specific for the apple signal defined over the measured mass range. The overall signal intensity was determined by 1) the maximum total ion current (TIC) peak value in the chromatogram trace of the measurement, and 2) the area of the TIC peak in the chromatogram trace of the measurement. The maximum of each of the TIC peaks corresponding to measurement points were determined to obtain the maximum TIC peak values. The TIC peak per measurement point was integrated to calculate the area of the TIC peak. The intensities of nine selected m/z values were compared using the areas of the extracted ion chromatograms (EICs). The areas under the peaks corresponding to measurement points in the EICs for the m/z values were calculated using integration.

Results are represented as average ± standard deviation (SD) and coefficient of variance (CV, %). The overall signal intensity decreases with an increasing height between the laser probe and the sample surface, which was as expected and can be seen from the peak TIC value (see Supplementary Figure S4A) and the TIC peak area (see Supplementary Figure S4B). In addition, the CVs show an upward trend with increasing height, which indicates a raising variation between TIC peaks in the
chromatogram occur the further away the laser probe is from the sample surface. The most pronounced result is the big drop (almost 90% between 2.0 mm and 3.0 mm) in peak area for m/z value 833.5 from 3.0 mm onwards for the nine selected m/z values (see Supplementary Figure S4C). The peak areas show a drop for the bigger heights for the other m/z values (3.0, 4.0, and 10.0 mm). In general an increasing trend can be seen with increasing distance between the laser probe and sample surface for the CVs of the different m/z values. Large CVs can be noted for m/z 133.0 in comparison to other m/z values. The CVs for the distances 0.5, 1.0, 1.5, and 2.0 mm are in the acceptable range (<25 %) for all m/z values except m/z 133.0, as they vary from 9.47 to 22.72 %. In addition, the absolute intensities of all m/z values decrease with increasing height and five of the m/z values show a big drop in absolute intensity for heights from 3.0 mm onwards (data not shown).

To conclude, the optimal height between the laser probe and the sample surface is 2.0 mm to avoid collision between the laser probe and sample surface while maintaining good signal intensities over the measured mass range.

Waiting time after laser shot and before sample movement

The waiting time between the laser shot and the start of the sample movement to the next measurement point might affect the amount of aspirated smoke, as when the sample movement is too quick the created smoke might be disturbed before it is aspirated to the mass spectrometer. It is important to keep this waiting time as short as possible to reduce the overall speed of the acquisition of the mass spectra for each measurement point.

Seven waiting times between the laser shot and sample movement were compared; 0.1 s, 0.3 s, 0.5 s, 0.7 s, 1.0 s, 1.5 s, and 2.0 s. Twenty points were measured on an apple with a laser power of 2.5 J (CW, 25 W, 0.1 s) per pulse using the 3D MS Scanner for each waiting time. The different waiting times were compared based on the overall intensity and the intensity of nine m/z values specific for the apple signal defined over the measured mass range. The overall signal intensity was determined by 1) the maximum total ion current (TIC) peak value in the chromatogram trace of the measurement, and 2) the area of the TIC peak in the chromatogram trace of the measurement. The maximum of each of the TIC peaks corresponding to measurement points were determined to obtain the maximum TIC peak values. The TIC peak per measurement point was integrated to calculate the area of the TIC peak. The intensities of nine selected m/z values were compared using the areas of the EICs. The areas under the peaks corresponding to measurement points in the EICs for the m/z values were calculated using integration. Results are represented as average ± standard deviation (SD) and coefficient of variance (CV, %).

No decreasing trend for the overall signal intensity was observed with decreasing the waiting time between the laser shot and the sample movement, as can be seen from the peak TIC value (see
Supplementary Figure S5A) and the TIC peak area (see Supplementary Figure S5B). The overall signal intensity is even the highest for the shortest waiting time of 0.1 s, contradicting the expectations. The CVs for the TIC peak values and TIC peak areas show no clear trend with decreasing waiting time, indicating the variations in overall signal intensity vary between measurements, but are not dependent on the waiting time. No general trends can be seen in the peak areas for the nine selected m/z values (see Supplementary Figure S5C), although the peak areas are quite stable or show a slightly decreasing trend for 2.0 s to 0.3 s for most m/z values. The waiting time of 0.1 s resulted in the highest peak area for m/z values 279.2, 301.0, 697.5, 721.5, 745.5, and 833.5, and is among the highest normalized intensities for m/z values 415.2 and 455.4 in comparison to the other waiting times. Only for m/z 133.0, the peak areas is among the lowest values for all waiting times. No trends can be seen for the CVs of the different m/z values. Nevertheless, the CVs of the different m/z values is the lowest for 0.1 s for 6 of the 9 m/z values. m/z 133.0 shows a larger variation between measurement points even within one measurement than the other m/z values. The CVs for a waiting time of 0.1s are in the acceptable range (<20 %) for all m/z values except 133.0 and 301.0. In addition, for the absolute intensities of all the m/z values except 133.0, the waiting time of 0.1 s resulted in the highest intensity with an almost twofold increase for 0.1 s in comparison to the other waiting times (data not shown).

To conclude, the optimal waiting time between the laser shot and the sample movement is 0.1 s, as this allows for fast acquisition speeds and results in both a high signal intensity without disturbance of the smoke before aspiration.

**Speed of the whole process of the 3D MS Scanner**

The whole process of the 3D MS Scanner consists of multiple steps, namely homing the axes, performing the height scan, and performing the mass spectrometry measurement (see Materials and methods). Each of the steps has been optimized to ensure the whole process is as quickly as possible. In general, the performance of the three stepper motors of the translational axes and the rotary driver of the rotational axis were optimized in terms of acceleration, deceleration, and maintaining position. The height scan consists of two phases: 1) a quick scan of the surface and a spline is fitted through the points, and 2) optimization of the motor positions at each measurement point. In the first step, twice as many points as the number of measurement points are quickly scanned to determine the distance for each of these points without the use of the rotational axis. A spline is fitted through these points to calculate the coordinates of each measurement and to correct for any inaccuracies or unexpected height differences. Based on these points, the motor positions are optimized for each measurement point by determining the distance for each point by movement to these points with the application of the rotational axis. After the height scan, the user can check the obtained topography for any unexpected height differences or other potential issues before the mass spectrometry analysis. For
the mass spectrometry measurement, two different aspects define the speed of the measurement, namely how fast the sample can be moved to the next measurement point and how fast the mass spectrometry acquisition is performed. To reduce the required time to move to the next measurement point a snake pattern was implemented and the performance of all motors was optimized (as indicated before). For the mass spectrometry acquisition, the limiting factor is the aspiration of the created smoke to the mass spectrometer, as this will always take a few seconds. In relation, the peak created in the TIC chromatogram is always a few seconds wide, as not all the molecules in the smoke are aspirated at the same speed. The smoke arrives more quickly at the mass spectrometer and the peaks in the TIC chromatogram are smaller by using small tubing for the aspiration than in comparison to the broader tubing. The measurement time required per point is 4 s when allowing the system to go back to the baseline background intensity after a measurement peak, but can be shorter when allowing overlap between measurement peaks in the TIC chromatogram.

The homing of the axes takes less than one minute, the height scan takes 5.1 s per measurement point, and the mass spectrometry acquisition takes 5 s per measurement point. For a measurement of 300 points, the whole process would take around 60 minutes, where 300 measurement points correspond to an area of 22.04 cm$^2$ with a spatial resolution of 2 mm.

Alignment between the laser trigger and raw TIC chromatogram

Alignment between the laser shots and the measurement points is important for the conversion of the data for 3D visualization, as only with the correct alignment between the 3D coordinates with the correct peak in the TIC chromatogram is the visualization representative of the sample surface. The registration of an analog signal together with a TIC chromatogram was used to achieve this. In the analog signal, peaks are recorded that corresponds to the trigger given to the CO$_2$ laser to fire per measurement point. In case a measurement point gives no signal, the misalignment between measurement points and coordinates can be prevented by using the alignment between the analog signal and the TIC chromatogram. Another added value is ensuring that no measurement points are missed during longer periods of only background signal in case the acquisition times vary between measurement points, despite the snake pattern that is implemented.

An example of the overlay between the analog signal and the TIC chromatogram can be seen in Supplementary Figure S1A. The overlay shows that the TIC peak is recorded slightly after the peak in the analog signal representing the laser trigger. This can be explained by the time required for the smoke to be aspirated to the mass spectrometer. Each of the TIC peaks fits nicely between two peaks of the analog signal. Nevertheless, over time an increasing shift occurs between the analog signal and the TIC chromatogram (see Supplementary Figure S1B). A comparison between the overlays of the start and the end of the measurement shows that the delay between the laser trigger and the TIC peak
is increased. A possible explanation can be the difference in the registration of both signals, as the analog signal is acquired using an eSAT/IN module and TIC chromatogram is acquired by the mass spectrometer. Therefore, the maximum number of measurement points that can be acquired using this approach will be around 350 points (or half an hour acquisition time for the mass spectrometer) to prevent the falling edge of the TIC peak from occurring after the analog peak of the next measurement point.
Supplementary Figure S1: Overlay between analog laser signal and TIC chromatogram. A) Overlay of the analog signal (green) and TIC chromatogram (red) at the start of a measurement of 300 points. B) Overlay of the analog signal (green) and TIC chromatogram (red) at the end of a measurement of 300 points.
**Supplementary Figure S2: Details of the 3D MS Scanner set-up**

A) Overview of the set-up in the lab. The 3D MS Scanner is placed in the biosafety cabinet. The control box and the Windows Surface Pro, control the 3D MS Scanner and send the triggers to the laser, the mass spectrometer, and the eSAT/IN module. These are placed outside of the biosafety cabinet. The smoke created by the laser is aspirated.
through the tubing towards the mass spectrometer with the REIMS source. B) Close up picture of the sample holder with a (frozen) femoral head. C) Close up picture of the laser probe and aspiration tube.
Supplementary Figure S3 – PCA plots displaying the variation in the automated and manual acquisitions

Supplementary Figure S3: PCA plots displaying the variation in the automated and manual acquisitions. Principle component analysis (PCA) plots of the automated and manual acquisitions for the different samples, which display the variation between measurement points. These PCA plots can be related to the variation between measurement points, as the closer the different measurement points (represented by spheres) are together the lower the variance in between them and vice versa. A) PCA plot for the apple acquisitions with PC1, PC2, and PC 3 explaining 75.3%, 8.96%, and 2.94% of the variance, respectively. B) PCA plot for the bone acquisitions with PC1, PC 2, and PC3 explaining 49.26%, 28.57%, and 9.53% of the variance, respectively. C) PCA plot for the femoral head 1 acquisitions with PC1, PC2, and PC3 explaining 58.07%, 20.67%, and 5.22% of the variance, respectively. D) PCA plot for the femoral head 2 acquisitions with PC1, PC2, and PC3 explaining 55.10%,
26.24%, and 4.40% of the variance, respectively. E) PCA plot for the femoral head 3 acquisitions with PC1, PC2, and PC3 explaining 65.65%, 23.86%, and 1.64% of the variance, respectively. F) PCA plot for the femoral head 4 acquisitions with PC1, PC2, and PC3 explaining 74.96%, 7.63%, and 3.86% of the variance, respectively. G) PCA plot for the femoral head 5 acquisitions with PC1, PC2, and PC3 explaining 63.17%, 19.64%, and 4.14% of the variance, respectively.
Supplementary Figure S4: Comparison of heights between the laser probe and sample surface. Comparison of signal intensity between seven different distances between the laser probe and the sample surface, namely 0.5 mm, 1.0 mm, 1.5 mm, 2.0 mm, 3.0 mm, 4.0 mm, and 10.0 mm. A) The average of the peak TIC values in the chromatogram per measurement point with the standard deviation. In addition, the coefficient of variation (CV) is provided as a percentage in the table underneath. B) The average of the areas under the TIC peaks in the chromatogram determined with integration. Average with the standard deviation as well as the coefficient of variation (CV, %) are provided. C) The average of the areas under the extracted ion chromatogram peaks for nine selected m/z values. The m/z values were selected based on their specificity for the sample and to cover the measured mass range as much as possible. For each m/z value, the average area with standard deviation and the coefficient of variance (CV, %) are provided.
Supplementary Figure S5: Comparison of waiting times between laser shot and sample movement.

Comparison of signal intensity between seven different waiting times between the laser shot and the sample movement, namely 2.0 s, 1.5 s, 1.0 s, 0.7 s, 0.5 s, 0.3 s, and 0.1 s. A) The average of the peak TIC values in the chromatogram per measurement point with the standard deviation. In addition, the coefficient of variation (CV) is provided as a percentage in the table underneath. B) The average of the areas under the TIC peaks in the chromatogram determined with integration. Average with the standard deviation as well as the coefficient of variation (CV, %) are provided. C) The average of the areas under the extracted ion chromatogram peaks for nine selected m/z values. The m/z values were selected based on their specificity for the sample and to cover the measured mass range as much as possible. For each m/z value, the average area with standard deviation and the coefficient of variance (CV, %) are provided.
Supplementary Table S1 – Comparison of selected \( m/z \) values between automated and manual experiments

**Supplementary Table S1:** Comparison of selected \( m/z \) values between automated and manual experiments. For the different samples, apple, marrowbone, and five femoral heads, a comparison of signal intensity is provided between automated and manual experiments. This comparison is based on the average of the areas under the extracted ion chromatogram peaks with the standard deviation (STD) for 10 selected \( m/z \) values as well as the coefficient of variance (CV, %). The \( m/z \) values were selected based on their specificity for the sample and to cover the measured mass range as much as possible.

### Apple

| \( m/z \) | Automated measurements | Manual measurements |
|-----------|------------------------|---------------------|
|           | Average | STD | CV | Average | STD | CV |
| 147.0     | 89800   | 48091 | 53.55 | 70643 | 18123 | 25.65 |
| 279.2     | 309842  | 57597 | 18.59 | 444828 | 89840 | 20.20 |
| 301.0     | 828577  | 156155 | 18.85 | 1016699 | 214975 | 21.14 |
| 415.2     | 85173   | 14814 | 17.39 | 118220 | 25323 | 21.42 |
| 455.4     | 24671   | 4793 | 19.43 | 37554 | 7702 | 20.51 |
| 671.5     | 26194   | 5123 | 19.56 | 41958 | 10998 | 26.21 |
| 721.5     | 189082  | 35126 | 18.58 | 293713 | 64804 | 22.06 |
| 745.5     | 226378  | 41144 | 18.17 | 308987 | 69024 | 22.34 |
| 833.5     | 91428   | 17535 | 19.18 | 118533 | 29316 | 24.73 |
| 861.6     | 64850   | 13086 | 20.18 | 78707 | 20898 | 26.55 |

### Marrowbone

| \( m/z \) | Automated measurements | Manual measurements |
|-----------|------------------------|---------------------|
|           | Average | STD | CV | Average | STD | CV |
| 140.0     | 25279   | 11082 | 43.84 | 66666 | 5270 | 79.07 |
| 185.0     | 12057   | 3366 | 27.92 | 2619   | 1605 | 61.29 |
| 221.9     | 8901    | 1933 | 21.72 | 738     | 630 | 85.32 |
| 237.9     | 10202   | 3118 | 30.57 | 731     | 639 | 87.48 |
| 362.2     | 633     | 954 | 150.84 | 252     | 376 | 149.38 |
| 585.5     | 402     | 1087 | 270.06 | 488     | 1585 | 324.85 |
| 744.6     | 182     | 274 | 150.58 | 98      | 211 | 216.37 |
| 867.7     | 285     | 369 | 129.41 | 108     | 152 | 141.33 |
| 893.7     | 1026    | 1615 | 157.42 | 336     | 579 | 172.05 |
| 921.8     | 513     | 691 | 134.81 | 177     | 244 | 137.97 |
| m/z   | Automated measurements | Manual measurements |
|-------|------------------------|---------------------|
|       | Average  | STD    | CV   | Average  | STD    | CV  |
| 128.0 | 3040     | 1281   | 42.15| 1283     | 725    | 56.49|
| 189.9 | 553      | 776    | 140.16| 113      | 373    | 329.49|
| 281.2 | 71       | 28     | 39.04| 1721     | 2193   | 127.42|
| 303.2 | 1244     | 1217   | 97.83| 633      | 809    | 127.89|
| 559.5 | 1929     | 2053   | 106.45| 186      | 465    | 250.60|
| 642.5 | 853      | 226    | 26.52| 625      | 286    | 45.76 |
| 687.5 | 1477     | 629    | 42.63| 1170     | 695    | 59.45 |
| 744.5 | 913      | 434    | 47.60| 563      | 263    | 46.73 |
| 893.7 | 486      | 313    | 64.54| 124      | 76     | 61.56 |
| 1008.7| 291      | 62     | 21.38| 194      | 81     | 41.81 |

| m/z   | Automated measurements | Manual measurements |
|-------|------------------------|---------------------|
|       | Average  | STD    | CV   | Average  | STD    | CV  |
| 128.0 | 2513     | 431    | 17.15| 1048     | 567    | 54.15|
| 189.9 | 563      | 570    | 101.26| 46       | 77     | 167.15|
| 281.2 | 19100    | 17277  | 90.46| 1429     | 843    | 59.01 |
| 303.2 | 1119     | 622    | 55.57| 691      | 344    | 49.84 |
| 572.5 | 1404     | 1018   | 72.52| 1003     | 406    | 40.46 |
| 642.5 | 773      | 839    | 108.56| 45       | 15     | 32.45 |
| 687.5 | 2155     | 3157   | 146.52| 1744     | 921    | 52.79 |
| 744.5 | 831      | 600    | 72.23| 689      | 346    | 50.23 |
| 893.7 | 1283     | 764    | 59.57| 632      | 393    | 62.22 |
| 919.7 | 1001     | 602    | 60.13| 514      | 325    | 63.11 |

| m/z   | Automated measurements | Manual measurements |
|-------|------------------------|---------------------|
|       | Average  | STD    | CV   | Average  | STD    | CV  |
| 128.0 | 1576     | 446    | 28.29| 803      | 273    | 33.94|
| 186.0 | 332      | 74     | 22.41| 113      | 68     | 60.43 |
| 281.3 | 13638    | 8251   | 60.50| 1823     | 2025   | 111.04|
| 303.2 | 651      | 260    | 39.97| 450      | 416    | 92.45 |
| 572.5 | 2302     | 2281   | 99.06| 2389     | 2233   | 93.46 |
| 642.5 | 1518     | 1450   | 95.52| 1524     | 1649   | 108.19|
| 687.6 | 4002     | 4383   | 109.54| 4310     | 5100   | 118.33|
| 797.7 | 682      | 592    | 86.72| 672      | 663    | 98.55 |
| 893.7 | 744      | 344    | 46.17| 217      | 136    | 62.57 |
| 919.8 | 576      | 243    | 42.12| 184      | 120    | 65.08 |
| Femoral head 4 | Area under extracted ion chromatogram peaks | Automated measurements | Manual measurements |
|---------------|---------------------------------|------------------------|---------------------|
| m/z           | Average | STD  | CV   | Average | STD  | CV   |
| 128.0         | 2918    | 519  | 17.77| 2423    | 734  | 30.30|
| 189.9         | 247     | 130  | 52.75| 103     | 63   | 61.06|
| 281.3         | 18190   | 14891| 81.86| 11872   | 8208 | 69.14|
| 303.2         | 611     | 213  | 34.90| 537     | 172  | 32.10|
| 572.5         | 1103    | 437  | 39.60| 939     | 409  | 43.53|
| 642.5         | 355     | 102  | 28.75| 339     | 127  | 37.45|
| 687.6         | 650     | 302  | 46.56| 622     | 226  | 36.29|
| 744.6         | 324     | 109  | 33.81| 316     | 150  | 47.53|
| 893.8         | 1024    | 458  | 44.71| 684     | 515  | 75.20|
| 919.8         | 894     | 392  | 43.84| 600     | 418  | 69.64|

| Femoral head 5 | Area under extracted ion chromatogram peaks | Automated measurements | Manual measurements |
|---------------|---------------------------------|------------------------|---------------------|
| m/z           | Average | STD  | CV   | Average | STD  | CV   |
| 128.0         | 2866    | 750  | 26.17| 1450    | 677  | 46.68|
| 166.1         | 1586    | 292  | 18.40| 911     | 283  | 31.05|
| 281.2         | 14087   | 12702| 90.16| 6293    | 6373 | 101.27|
| 303.2         | 1067    | 613  | 57.47| 570     | 277  | 48.62|
| 572.5         | 2085    | 528  | 25.32| 1691    | 476  | 28.18|
| 642.5         | 893     | 230  | 25.69| 700     | 161  | 23.03|
| 687.5         | 2189    | 617  | 28.19| 1870    | 504  | 26.96|
| 744.6         | 788     | 353  | 44.82| 542     | 233  | 43.03|
| 893.7         | 1277    | 672  | 52.67| 503     | 356  | 70.80|
| 919.8         | 865     | 452  | 52.25| 361     | 251  | 69.61|
**Supplementary Table S2 – Assignments of m/z values of 3D visualization of molecular distributions**

**Supplementary Table S2: Assignments of m/z values of 3D visualization of molecular distributions.** Identifications of the m/z values that are presented in the 3D visualization of molecular distributions of apple (Figure 2), marrowbone (Figure 3), and femoral head (Figure 4). Identifications are based on MS/MS in combination with the m/z value. For each identification, the experimental m/z value, the assignment, the detected ion, the ppm error, and level of identification are provided. The data of the femoral head acquisition was recalibrated in mMass.

**Apple (Figure 2)**

| m/z   | Assignment     | Ion       | ppm error | Level of identification |
|-------|----------------|-----------|-----------|-------------------------|
| 455.352 | Ursolic acid   | [M-H]     | -2.41     | MS                      |
| 671.467 | PA 16:0_18:2   | [M-H]     | 1.89      | MS/MS                   |
| 846.552 | PS 36:2        | [M+CH$_3$COO]$^-$ | 2.13      | MS                      |

**Marrowbone (Figure 3)**

| m/z   | Assignment     | Ion       | ppm error | Level of identification |
|-------|----------------|-----------|-----------|-------------------------|
| 128.035 | C$_5$H$_7$NO$_3$ | [M-H]     | -2.34     | MS                      |
| 279.233 | FA 18:2        | [M-H]     | -3.58     | MS                      |
| 419.255 | cLPA 18:0      | [M-H]     | -4.29     | MS/MS                   |
| 585.486 | DG O-35:5      | [M-H]     | -4.84     | MS                      |
| 744.557 | PE 36:1        | [M-H]     | 2.82      | MS                      |
| 865.753 | TG 48:0        | [M-H]     | 3.24      | MS                      |

**Femoral head (Figure 4)**

| m/z   | Assignment     | Ion       | ppm error | Level of identification |
|-------|----------------|-----------|-----------|-------------------------|
| 205.899 |                | [M-H]     | -2.55     | MS                      |
| 274.119 | C$_{14}$H$_{17}$N$_3$O$_3$ | [M-H]     | -2.13     | MS/MS                   |
| 281.248 | FA 18:1        | [M-H]     | 1.87      | MS                      |
| 642.488 | CerP 36:2;O2   | [M-H]     | 0.15      | MS                      |
| 682.591 | Cer 42:2;O2    | [M+Cl]$^-$ | 1.21      | MS                      |
| 699.498 | PA 36:2        | [M-H]     | 1.43      | MS                      |
| 744.554 | PE 36:1        | [M-H]     | -1.98     | MS                      |
| 1008.684 | Hex3Cer 34:0;O | [M-H]     | -1.98     | MS                      |
| 1081.011 |                |           |           |                         |