

Piecing Together Pollutant Profiles: Combining High-Resolution MS From Multiple Ionization Modes With Multidimensional GC for Petroleum Forensics and Environmental Analyses

Christina Kelly, Joe Binkley, John Hayes | LECO Corporation, St. Joseph, MI, USA

Introduction

Complex mixtures create challenges for calculating risk exposure and determining environmental remediation, necessitating streamlined analytical workflows for detailed compositional identification.

Analysis of heavy fuel oil (HFO) and a mixture of common persistent organic pollutants (POP) was performed by comprehensive two-dimensional gas chromatography (GCxGC) combined with high-resolution time-of-flight mass spectrometry (HRTOFMS) in multiple ionization modes: electron ionization (EI), positive chemical ionization (PCI), and electron capture negative chemical ionization (ECNI). Deconvoluted EI spectra from individual chromatographic peaks were matched to commercial libraries, with hits ranked by an identification grading system based on criteria including mass accuracy of both molecular ions when present and chemically possible fragment ions. Complementary information from PCI and ECNI were used to further confirm molecular formula of individual compounds and leverage scaled mass defect plots to target chromatographic areas of interest.

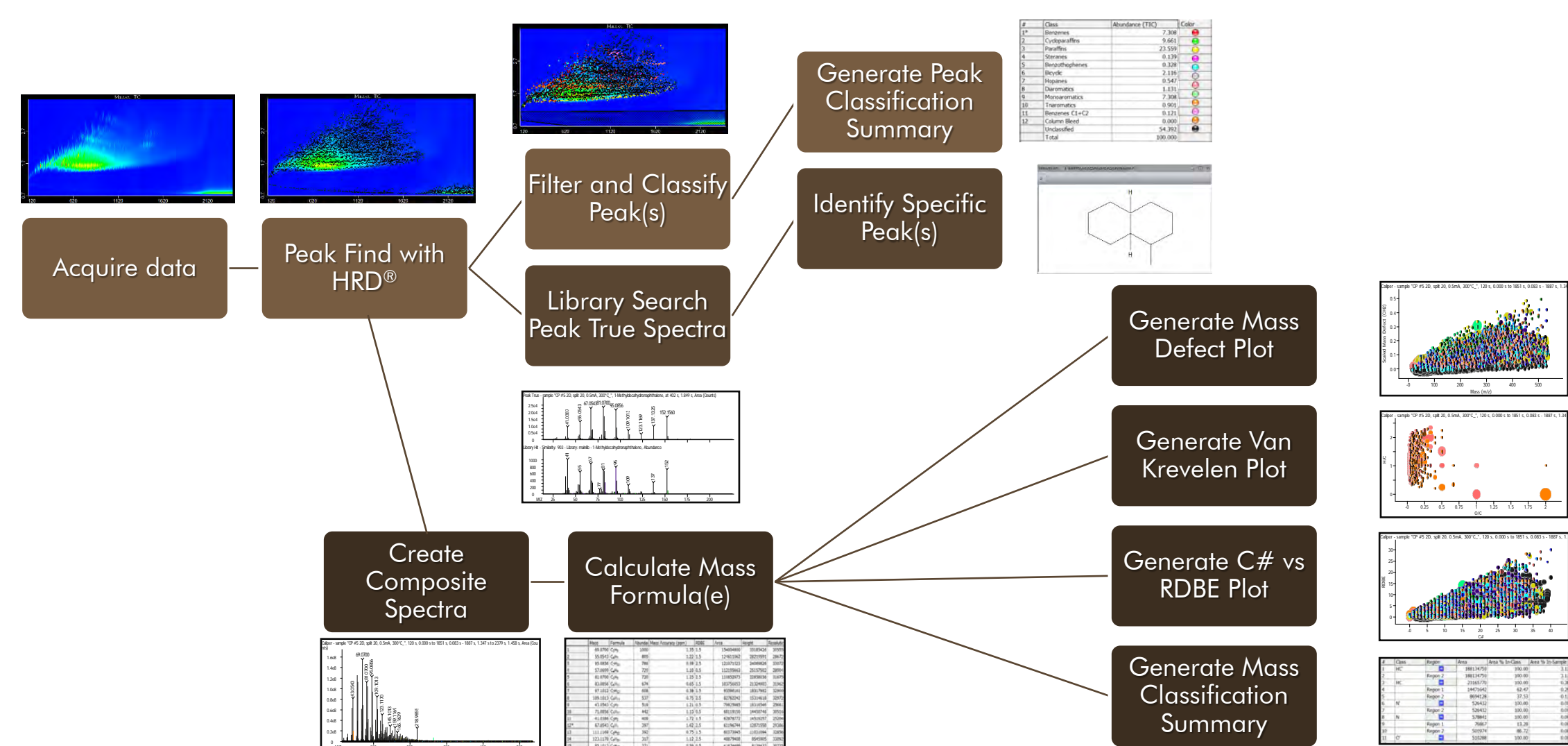


Figure 1: Generalized workflow for working through GCxGC High-Resolution Data.



Figure 2: Pegasus® HRT•4D with Multi-Mode Ionization source, which provides ability to analyze samples in EI, PCI, and ECNI modes without venting or other manual hardware changes, preserving chromatographic correlation between modes.

Petroleum Forensics

Goals: Identify biomarkers and thermal maturity markers such as hopanes, steranes, and dibenzothiophenes, whose ratios assist in tracing source of heavy fuel oils.

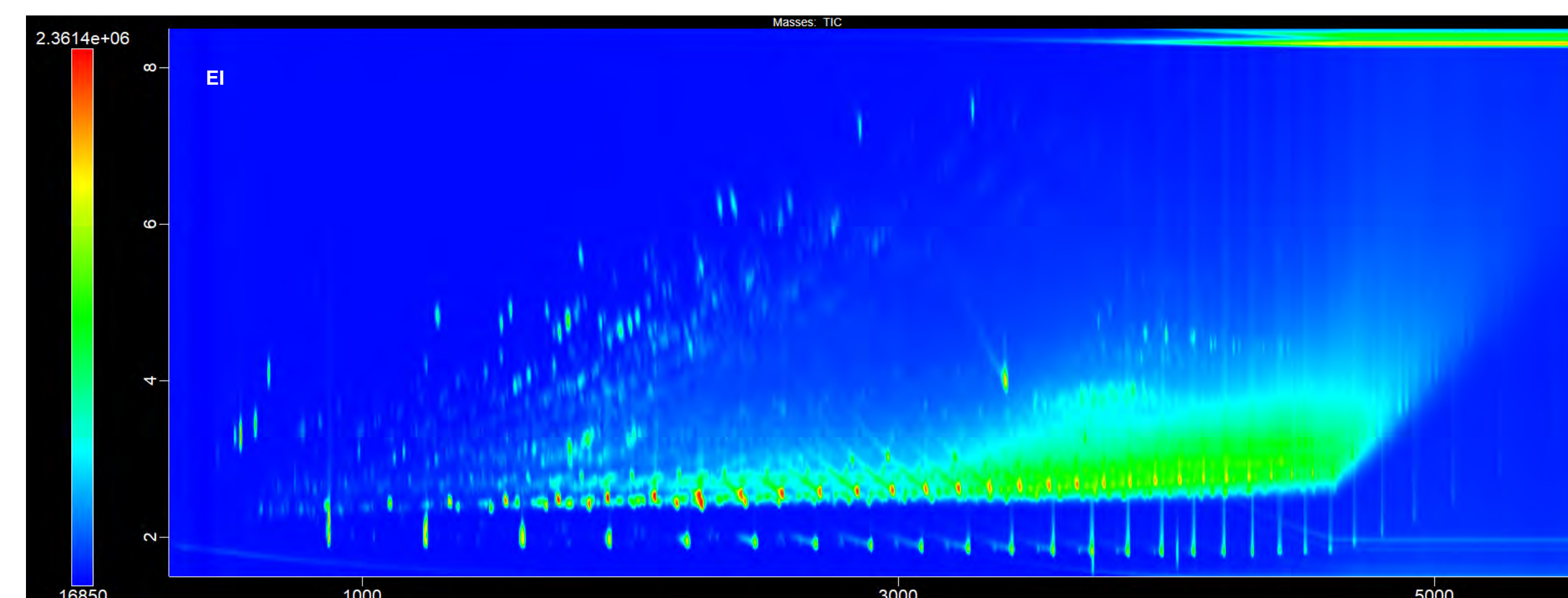


Figure 3: Total Ion Chromatogram of heavy fuel oil illustrates the complexity of the matrix and the benefits of multidimensional chromatography for class separation of peaks.

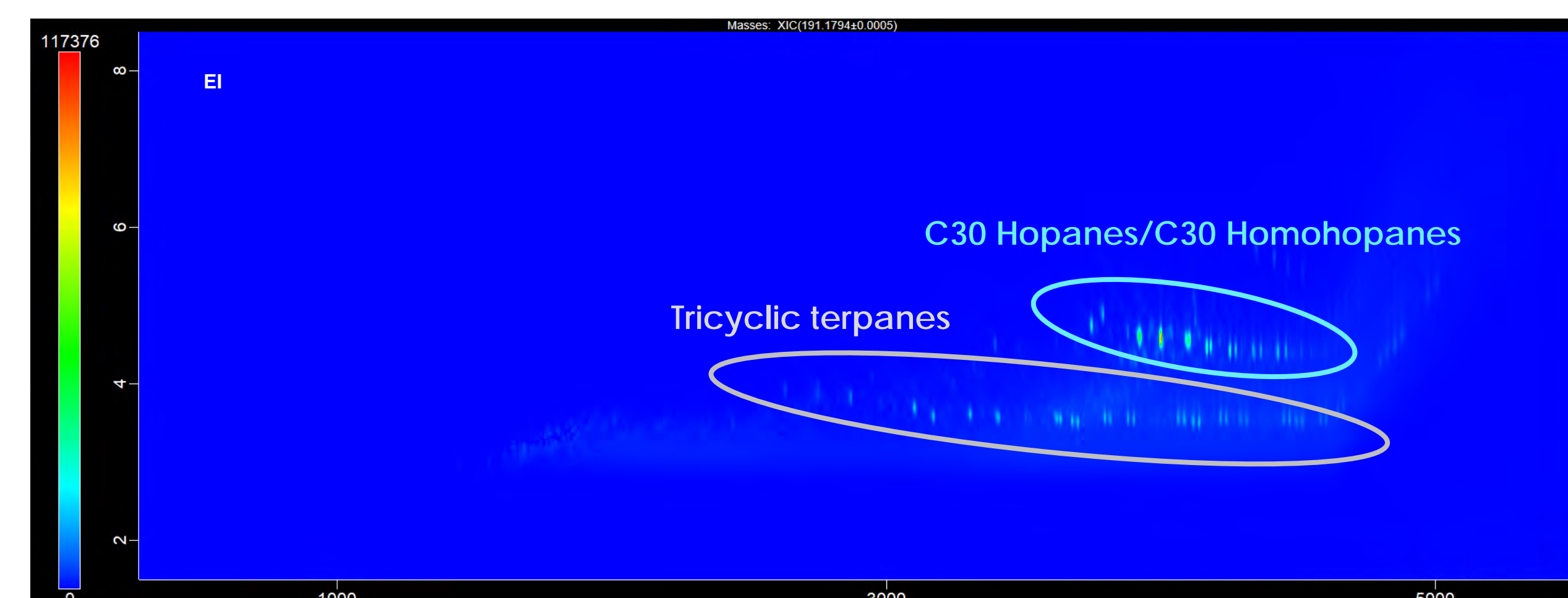


Figure 4: Extracted Ion Chromatogram of heavy fuel oil plotting characteristic mass fragment for hopanes and steranes reveals regions of interest for these biomarkers.

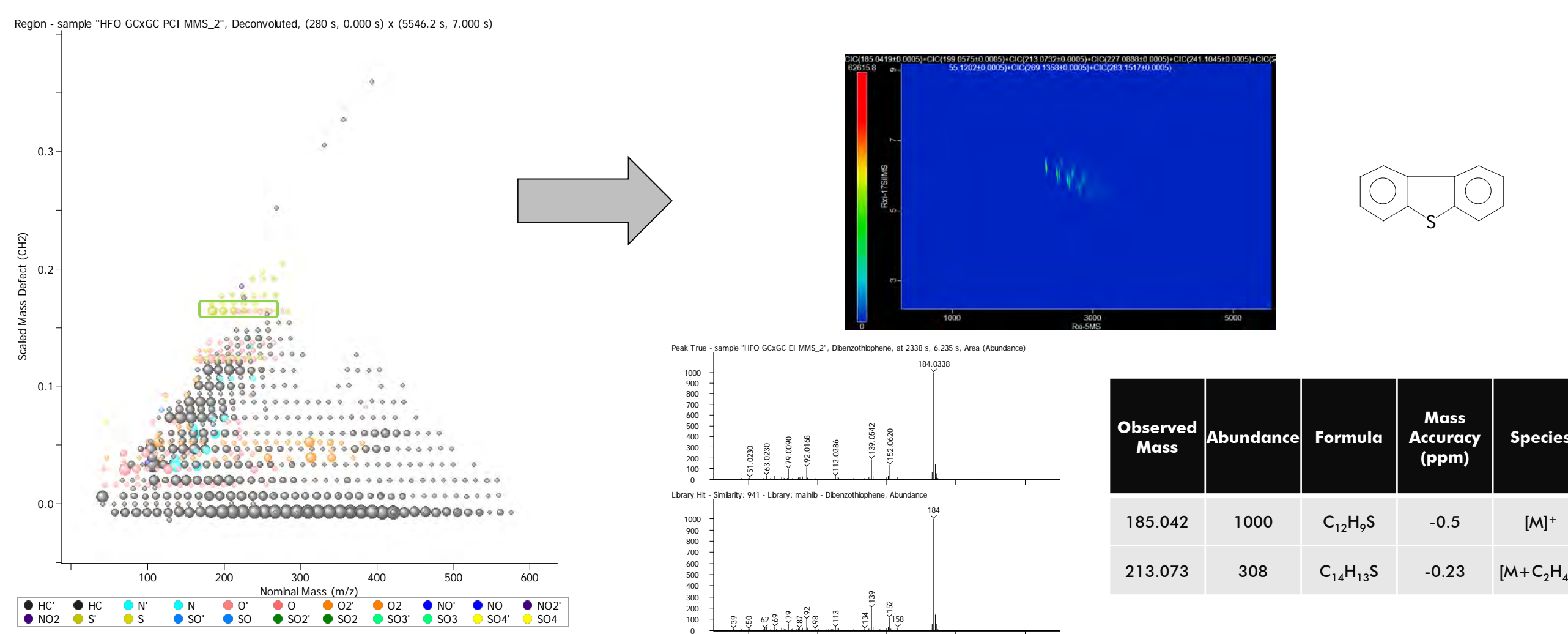


Figure 5: Colorized mass defect plot of the PCI data from heavy fuel oil allows for quick identification of peaks with heteroatomic species of interest, such as S-containing compounds. Plotting the masses of interest (in the green box) onto the contour plot allowed for identification of C0-C5 series of dibenzothiophenes.

Environmental Analyses

Goals: Leverage ECNI to identify and created targeted methods for organic pollutants of interest.

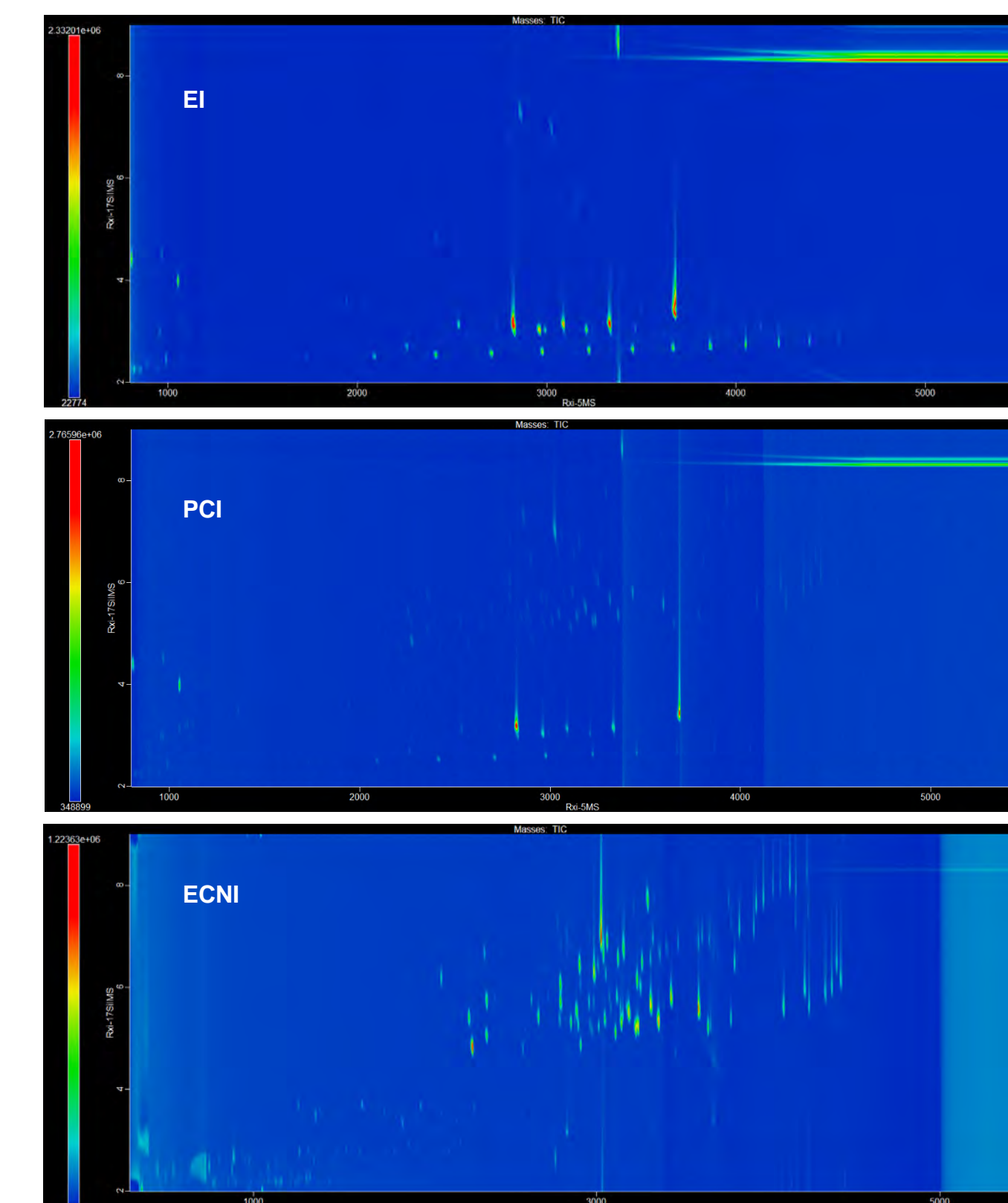


Figure 6: Total Ion Chromatograms of environmental mixture shows the power of the complementary modes of ionization, especially with the high selectivity of ECNI for the low-level halogenated species that could be missed by EI analysis alone.

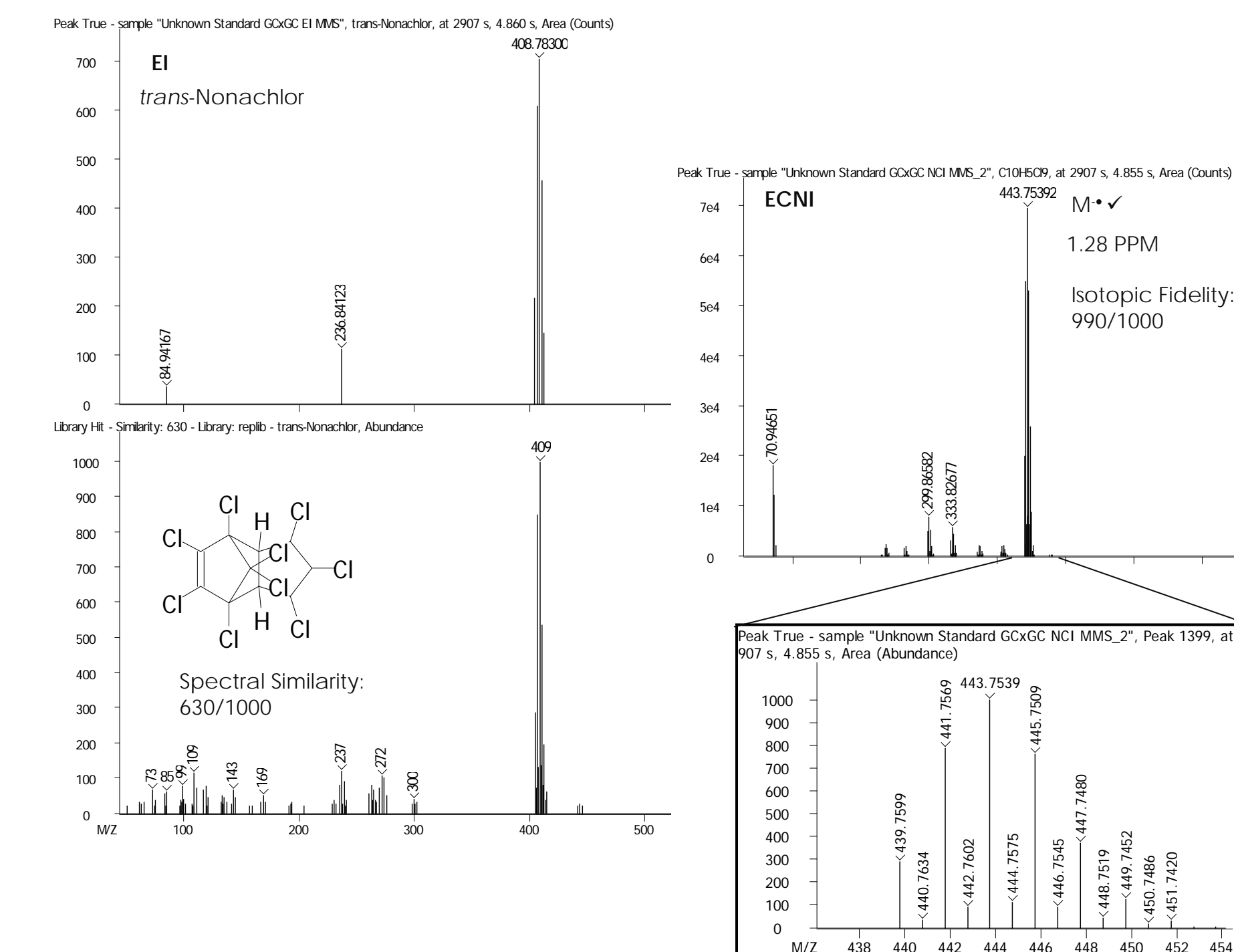


Figure 7: Confirming identity of trans-nonachlor using combination of EI fragmentation and ECNI molecular ion with high isotopic fidelity; where EI match to library did not provide either molecular ion or high enough confidence in spectral similarity score, the corresponding ECNI peak shows a clear molecular ion with excellent isotopic fidelity for the putative formula.

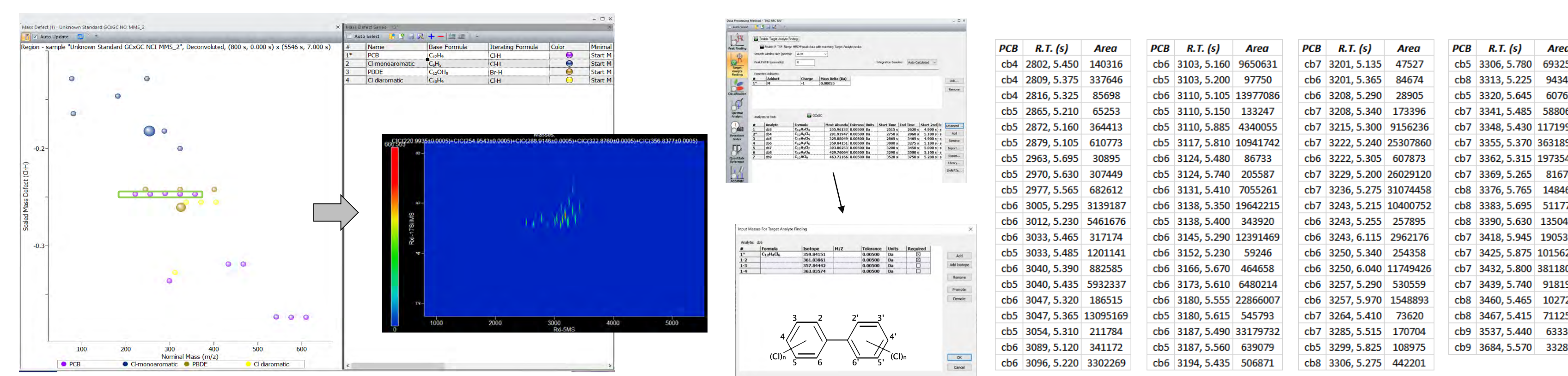


Figure 8: Mass defect plot generated from ECNI data allows for targeting groups of compounds like these PCB congeners displayed onto the contour plot. Regions of interest can then be targeted to find specific analytes using the highlighted masses; table reflects resulting PCB congeners identified with a S/N of greater than 20.

Conclusion

Many pieces of the identification puzzle were provided by the combination of GCxGC with multiple modes of HRTOFMS ionization—GCxGC offered not only enhanced chromatographic resolution and cleaner mass spectra for more accurate deconvolution, but also structural information based on regions of elution, while the HRTOFMS supplied full-mass range spectra and confident calculation of chemical formulae in addition to the ability to leverage scaled mass defect plots for heteroatom determination. This poster highlights the power of combining all these contributions into one workflow with streamlined tools within one software package that allows for more confident identification of both targeted and nontarget species of interest.