

SUPPORTING INFORMATION TO:

In-vitro metabolites characterization of 1,3-diphenylguanidine and 1,3-di-o-tolylguanidine by high-resolution mass spectrometry and urinary profiling

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Text S1. Analytical methodology for compound identification in urine

Instrumental analyses were carried out in an Agilent 1260 Infinity II LC equipped with a quaternary solvent pump, a thermostatted LC column compartment, and a sample manager. The U(H)PLC system was interfaced to an Agilent 6495 LC/QqQ triple quadrupole mass spectrometer. Chromatographic separation was performed under the same conditions as for the LC-QTOF methodology shown in Section 2.4 and the injection volume was set at 10 μL . To prevent system contamination, an InfinityLab PFC Delay Column (4.6 x 30mm) from Agilent was placed before the injector.

A Jet Stream electrospray ionization (ESI) source operating in positive mode was the interface between the LC system and the 6495 LC/QqQ triple quadrupole mass spectrometer at a fixed capillary and nozzle voltage of 2.5 and 0.5 kV, respectively. Nitrogen was used as sheath gas at 12 L min^{-1} and 400 $^{\circ}\text{C}$ and also as desolvation gas at 15 L min^{-1} and 215 $^{\circ}\text{C}$.

Analyses were performed by MS/MS in selected reaction monitoring (SRM) mode using 166 V as fragmentor voltage. Table S1 summarizes the SRM transitions (Q_n), ratios between the transitions, retention times (RT) and optimal collision energies (CE) for the target chemicals and the internal standard (Ib-d4). As no commercial standard of the metabolic products was available, the sample sets submitted to *in-vitro* metabolism, where metabolites were positive, were used to optimize the MS/MS parameters.

Table S1. Compound name, retention time (RT), transitions (Q_n) used for quantification (Q_1), and confirmation (Q_2 and Q_3), ratio between the transitions, optimal collision energy (CE) values for target chemicals and compound used as internal standards (IS).

Compound	RT (min)	Q_1 (m/z)	CE (eV)	Q_2 (m/z)	CE (eV)	Q_2/Q_1	Q_3 (m/z)	CE (eV)	Q_3/Q_1
DPG	10.1	212.0 -> 94.0	19	212.0 -> 119.0	25	1.1	212.0 -> 195.0	20	0.70
DPG-225	7.3	226.0 -> 108.0	19	226.0 -> 119.0	25	0.72	-	-	-
DPG-227	7.3	228.0 -> 135.0	25	228.0 -> 110.0	19	0.79	228.0 -> 211.0	19	0.42
DPG-387	6.0	388.0 -> 212.0	14	388.0 -> 270.0	15	0.27	-	-	-
DPG-403	6.2	404.0 -> 211.0	13	404.0 -> 212.0	13	1.3	404.0 -> 228.0	9	0.066
DTG	13.0	240.0 -> 133.0	17	240.0 -> 108.0	19	0.95	240.0 -> 223.0	25	0.45
DTG-253	14.1	254.0 -> 77.0	73	254.0 -> 106.0	44	0.18	254.0 -> 112.0	21	0.020
DTG-255	10.2	256.0 -> 124.0	25	256.0 -> 149.0	25	0.97	256.0 -> 221.0	21	0.40
DTG-415	9.5	416.0 -> 240.0	21	416.0 -> 284.0	19	0.30	-	-	-
DTG-431 (1)	6.5	432.0 -> 256.0	25	432.0 -> 149.0	44	0.12	432.0 -> 89.0	98	0.026
DTG-431 (2)	10.5	432.0 -> 256.0	25	432.0 -> 89.0	98	0.13	432.0 -> 149.0	44	0.030
lb-d4	18.4	433.0 -> 211.0	24	433.0 -> 195.0	24	0.28	-	-	-

Table S2. Suspect list for DPG

Name	Chemical Formulae	Monoisotopic Mass	Source ^a
DPG	C ₁₃ H ₁₃ N ₃	211.1109	-
DPG-135	C ₇ H ₉ N ₃	135.0796	QSAR
DPG-93	C ₆ H ₇ N	93.0578	QSAR
DPG-269	C ₁₂ H ₁₅ NO ₆	269.0899	Self-proposal
DPG-173	C ₆ H ₇ NO ₃ S	173.0147	Self-proposal
DPG-311	C ₁₃ H ₁₇ N ₃ O ₆	311.1117	Self-proposal
DPG-215	C ₇ H ₉ N ₃ O ₃ S	215.0365	Self-proposal
DPG-227	C ₁₃ H ₁₃ N ₃ O	227.1059	Sieira et al., 2020 / Clement et al., 1993
DPG-387	C ₁₉ H ₂₁ O ₆ N ₃	387.1430	GloryX
DPG-291	C ₁₃ H ₁₃ N ₃ O ₃ S	291.0678	Self-proposal
DPG-212	C ₁₃ H ₁₂ N ₂ O	212.0950	QSAR
DPG-228	C ₁₃ H ₁₂ N ₂ O ₂	228.0899	QSAR
DPG-244	C ₁₃ H ₁₂ N ₂ O ₃	244.0848	Self-proposal
DPG-243	C ₁₃ H ₁₃ N ₃ O ₂	243.1008	Biotransformer
DPG-136	C ₇ H ₈ N ₂ O	136.0637	QSAR
DPG-312	C ₁₃ H ₁₆ N ₂ O ₇	312.0958	Self-proposal
DPG-232	C ₇ H ₈ N ₂ SO ₅	232.0154	Self-proposal
DPG-209	C ₁₃ H ₁₁ N ₃	209.0953	Self-proposal
DPG-225	C ₁₃ H ₁₁ N ₃ O	225.0902	Sieira et al., 2020
DPG-241	C ₁₃ H ₁₁ N ₃ O ₂	241.0851	Self-proposal
DPG-403	C ₁₉ H ₂₁ N ₃ O ₇	403.1380	QSAR
DPG-401	C ₁₉ H ₁₉ N ₃ O ₇	401.1223	Self-proposal
DPG-305	C ₁₃ H ₁₁ N ₃ O ₄ S	305.0470	Self-proposal
DPG-289	C ₁₃ H ₁₁ N ₃ O ₃ S	289.0521	Self-proposal
DPG-243	C ₁₃ H ₁₃ N ₃ O ₂	243.1008	Sieira et al., 2020
DPG-259	C ₁₃ H ₁₃ N ₃ O ₃	259.0957	Biotransformer
DPG-247	C ₁₂ H ₁₃ N ₃ O ₃	247.0957	Self-proposal

*Sieira BJ, Montes R, Touffet A, Rodil R, Cela R, Gallard H, et al. Chlorination and bromination of 1,3-diphenylguanidine and 1,3-di-o-tolylguanidine: Kinetics, transformation products and toxicity assessment. *Journal of Hazardous Materials* 2020; 385: 121590.

*B. Clement, T. Kunze, In vitro oxygenation of N,N'-diphenylguanidines, *Xenobiotica*, 23 (1993) 155-167.

*QSAR Toolbox. "QSAR Toolbox webpage." Retrieved October 2023, from <https://qsartoolbox.org/>.

*GLORYx Predicting Phase I and Phase II Metabolites. Stork C, Embruch G, Šícho M, de Bruyn Kops C, Chen Y, Svozil D, et al. *NERDD: a web portal providing access to in silico tools for drug discovery*.

*Bioinformatics 2019; 36: 1291-1292

Biotransformer. "Biotransformer 3.0 webpage." Retrieved October 2023, from <https://biotransformer.ca/>.

Table S3. Suspect list for DTG

Name	Chemical Formulae	Monoisotopic Mass	Source ^a
DTG	C ₁₅ H ₁₇ N ₃	239.1422	-
DTG-149	C ₈ H ₁₁ N ₃	149.0953	Sieira et al., 2020
DTG-165	C ₈ H ₁₁ N ₃ O	165.0902	Self-proposal
DTG-163	C ₈ H ₉ N ₃ O	163.0746	Self-proposal
DTG-179	C ₈ H ₉ N ₃ O ₂	179.0695	Self-proposal
DTG-107	C ₇ H ₉ N	107.0735	QSAR
DTG-123	C ₇ H ₉ NO	123.0684	Self-proposal
DTG-121	C ₇ H ₇ NO	121.0528	Self-proposal
DTG-137	C ₇ H ₇ NO ₂	137.0477	Self-proposal
DTG-283	C ₁₃ H ₁₇ NO ₆	283.1056	Self-proposal
DTG-187	C ₇ H ₉ NO ₃ S	187.0303	Self-proposal
DTG-325	C ₁₄ H ₁₉ N ₃ O ₆	325.1274	Self-proposal
DTG-229	C ₈ H ₁₁ N ₃ O ₃ S	229.0521	Self-proposal
DTG-255	C ₁₅ H ₁₇ N ₃ O	255.1371	Sieira et al., 2020
DTG-415	C ₂₁ H ₂₅ O ₆ N ₃	415.1743	GloryX
DTG-319	C ₁₅ H ₁₇ N ₃ O ₃ S	319.0991	Self-proposal
DTG-253	C ₁₅ H ₁₅ N ₃ O	253.1215	QSAR
DTG-269	C ₁₅ H ₁₅ N ₃ O ₂	269.1164	GloryX
DTG-240	C ₁₅ H ₁₆ N ₂ OS	240.1263	QSAR
DTG-256	C ₁₅ H ₁₆ N ₂ O ₂	256.1212	QSAR
DTF-254	C ₁₅ H ₁₄ N ₂ O ₂	254.1055	QSAR
DTG-270	C ₁₅ H ₁₄ N ₂ O ₃	270.1004	QSAR
DTG-272	C ₁₅ H ₁₆ N ₂ O ₃	272.1161	Self-proposal
DTG-286	C ₁₅ H ₁₄ N ₂ O ₄	286.0954	Self-proposal
DTG-300	C ₁₅ H ₁₂ N ₂ O ₅	300.0746	Self-proposal
DTG-271	C ₁₅ H ₁₇ N ₃ O ₂	271.1321	QSAR
DTG-269	C ₁₅ H ₁₅ N ₃ O ₂	269.1164	QSAR
DTG-285	C ₁₅ H ₁₅ N ₃ O ₃	285.1113	Self-proposal
DTG-267	C ₁₅ H ₁₃ N ₃ O ₂	267.1008	Self-proposal
DTG-299	C ₁₅ H ₁₃ N ₃ O ₄	299.0906	Self-proposal
DTG-150	C ₈ H ₁₀ N ₂ O	150.0793	QSAR
DTG-166	C ₈ H ₁₀ N ₂ O ₂	166.0742	Self-proposal
DTG-180	C ₈ H ₈ N ₂ O ₃	180.0535	Self-proposal
DTG-196	C ₈ H ₈ N ₂ O ₄	196.0484	Self-proposal
DTG-342	C ₁₄ H ₁₈ N ₂ O ₈	342.1063	Self-proposal
DTG-246	C ₈ H ₁₀ N ₂ SO ₅	246.0310	Self-proposal
DTG-237	C ₁₅ H ₁₅ N ₃	237.1266	Sieira et al., 2020
DTG-253	C ₁₅ H ₁₅ N ₃ O	253.1215	Sieira et al., 2020
DTG-269	C ₁₅ H ₁₅ N ₃ O ₂	269.1164	Self-proposal
DTG-283	C ₁₅ H ₁₃ N ₃ O ₃	283.0957	Self-proposal
DTG-267	C ₁₅ H ₁₃ N ₃ O ₂	267.1008	Self-proposal
DTG-431	C ₂₁ H ₂₅ N ₃ O ₇	431.1693	Self-proposal
DTG-271	C ₁₅ H ₁₇ N ₃ O ₂	271.1321	Self-proposal
DTG-431	C ₂₁ H ₂₅ N ₃ O ₇	431.1693	Self-proposal
DTG-447	C ₂₁ H ₂₅ N ₃ O ₈	447.1642	Self-proposal
DTG-312	C ₁₅ H ₁₇ N ₃ O ₃	312.0958	Biotransformer

* Sieira BJ, Montes R, Touffet A, Rodil R, Cela R, Gallard H, et al. Chlorination and bromination of 1,3-diphenylguanidine and 1,3-di-o-tolylguanidine: Kinetics, transformation products and toxicity assessment. *Journal of Hazardous Materials* 2020; 385: 121590.

*QSAR Toolbox. "QSAR Toolbox webpage." Retrieved October 2023, from <https://qsartoolbox.org/>.

*GLORYx Predicting Phase I and Phase II Metabolites. Stork C, Embruch G, Šicho M, de Bruyn Kops C, Chen Y, Svozil D, et al. NERDD: a web portal providing access to in silico tools for drug discovery. *Bioinformatics* 2019; 36: 1291-1292

*Biotransformer. "Biotransformer 3.0 webpage." Retrieved October 2023, from <https://biotransformer>

Figure S1. Overview of quality controls employed during the Phase I in-vitro human liver metabolism assay

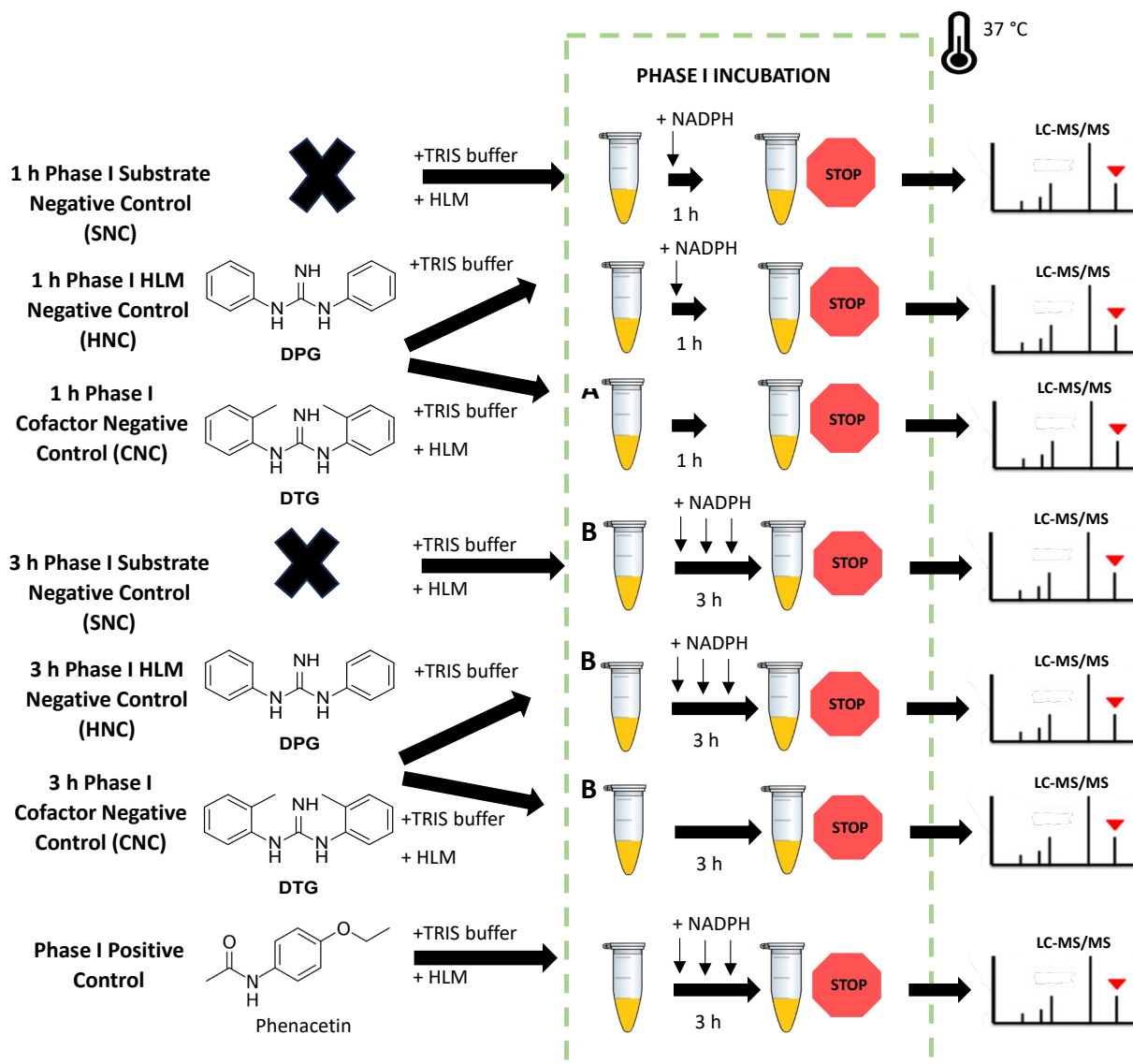


Figure S2. Overview of quality controls employed during the Phase II in-vitro human liver metabolism assay

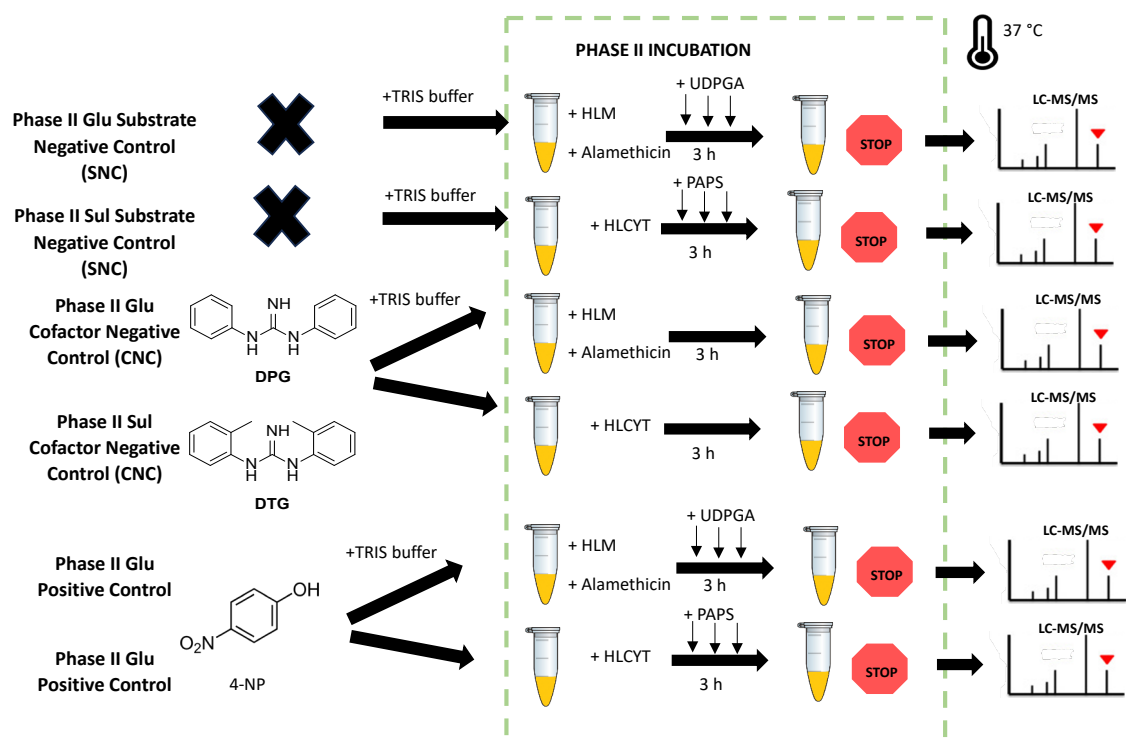
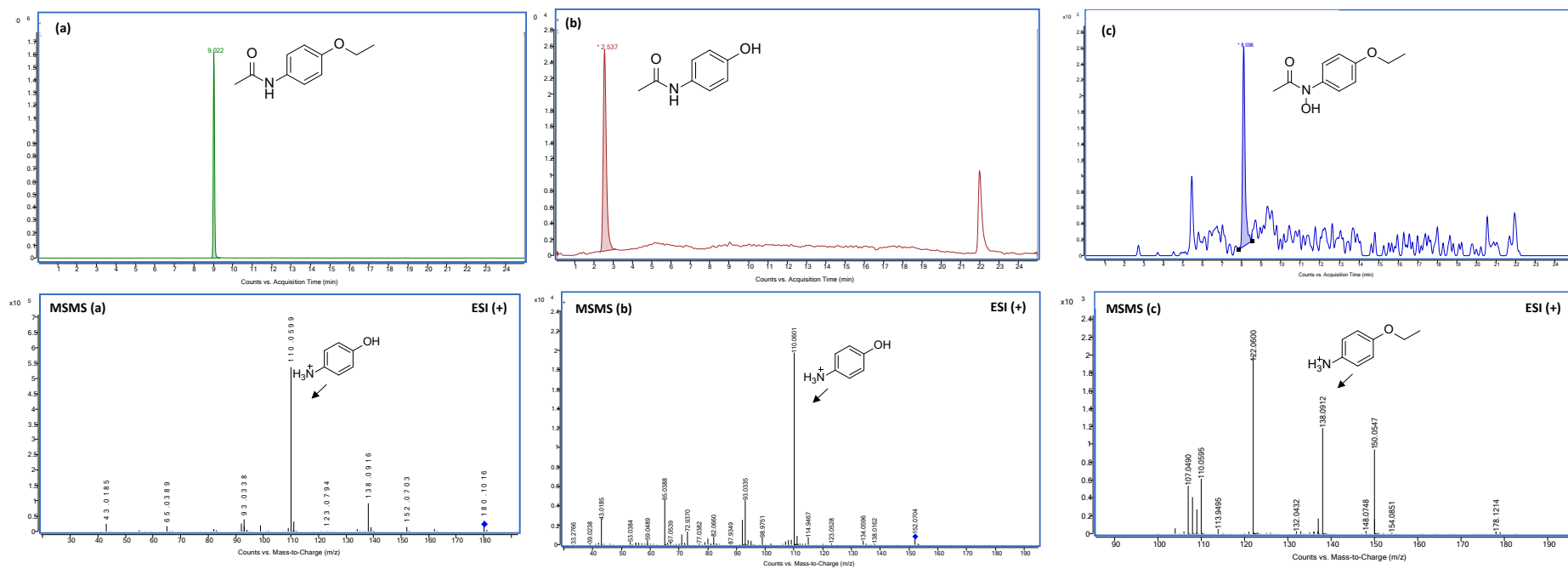


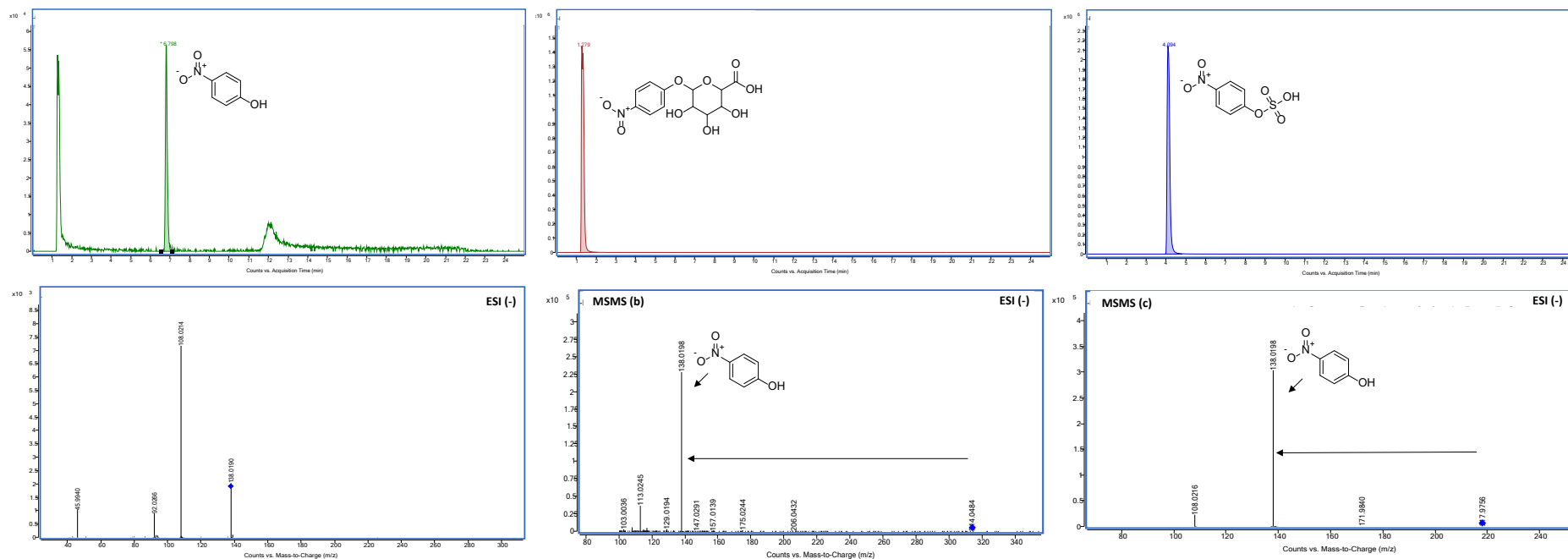
Figure S3. Extracted ion chromatogram, molecular structure and MS/MS spectrum at 20 V in positive mode of (a) phenacetin, (b) P-M1 and (c) P-M2



References:

- [1] J. A. Hinson, Environ Health Perspect 1983 Vol. 49 Pages 71-9, Accession Number: 6339229 PMID: PMC1569121 DOI: 10.1289/ehp.834971
- [2] C. Christia, K. M. da Silva, G. Poma, A. L. N. van Nuijs and A. Covaci Toxicology Letters 2022 Vol. 356 Pages 33-40 DOI: <https://doi.org/10.1016/j.toxlet.2021.12.005>

Figure S4. Extracted ion chromatogram, molecular structure and MS/MS spectrum at 20 V of (a) 4-nitrophenol, (b) 4NP-G and (c) 4NP-S.



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- [1] R. H. Tukey and C. P. Strassburg , *Annu Rev Pharmacol Toxicol* 2000 Vol. 40 Pages 581-616 Accession Number: 10836148 DOI: 10.1146/annurev.pharmtox.40.1.581
- [2] N. Gamage, A. Barnett, N. Hempel, R. G. Duggleby, K. F. Windmill, J. L. Martin, et al. *Toxicological Sciences* 2006 Vol. 90 Issue 1 Pages 5-22 DOI: 10.1093/toxsci/kfj061

Figure S5. Volcano plots of m/z values measured in ESI (+) and ESI (-) modes in Phase I samples for DPG. Features statistically significant are represented in green color (p -value < 0.05 and a \log_{10} FC > 1).

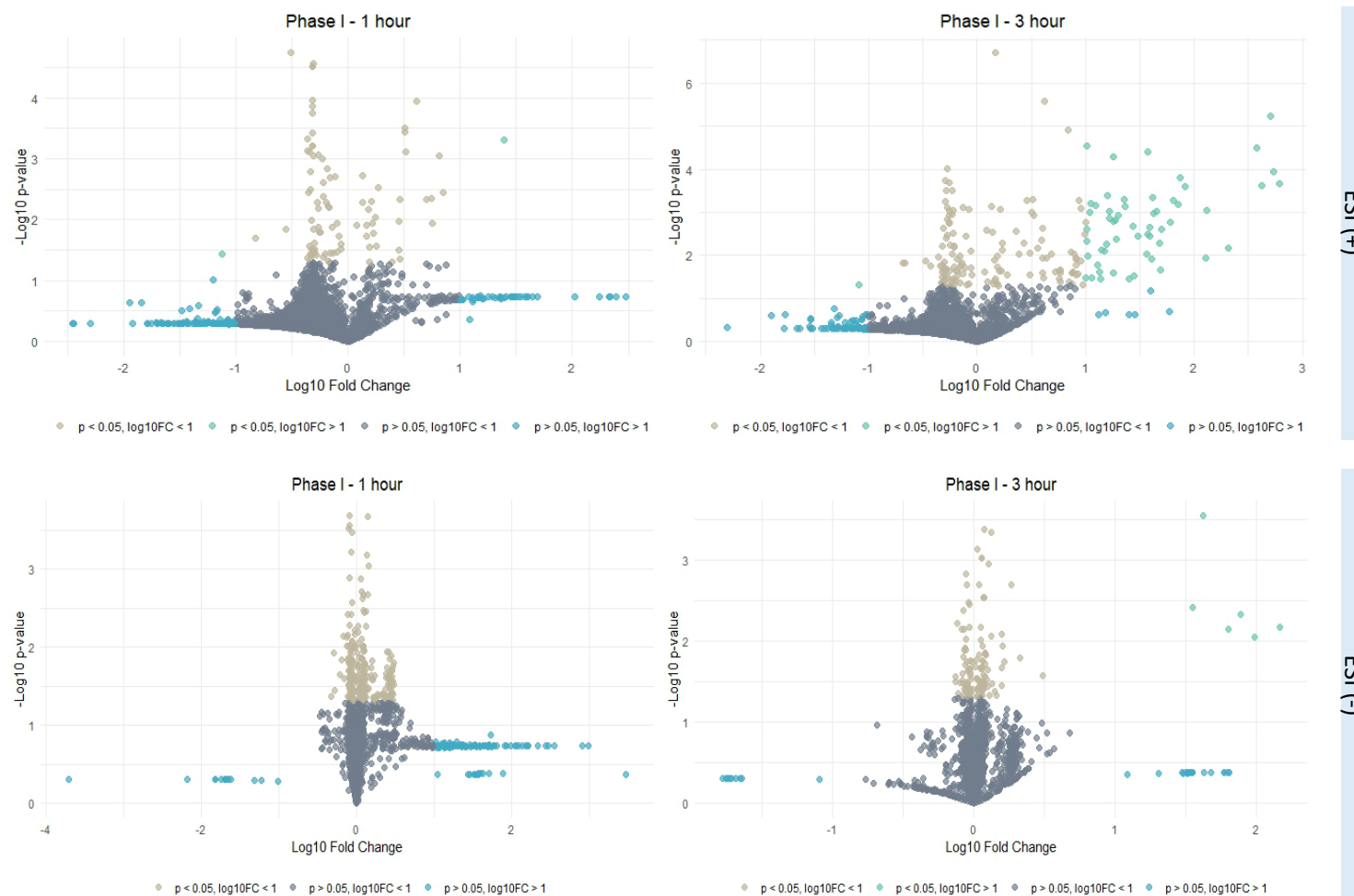


Figure S6. Volcano plots of m/z values measured in ESI (+) and ESI (-) modes in Phase I samples for DTG. Features statistically significant are represented in green color (p -value < 0.05 and a \log_{10} FC > 1).

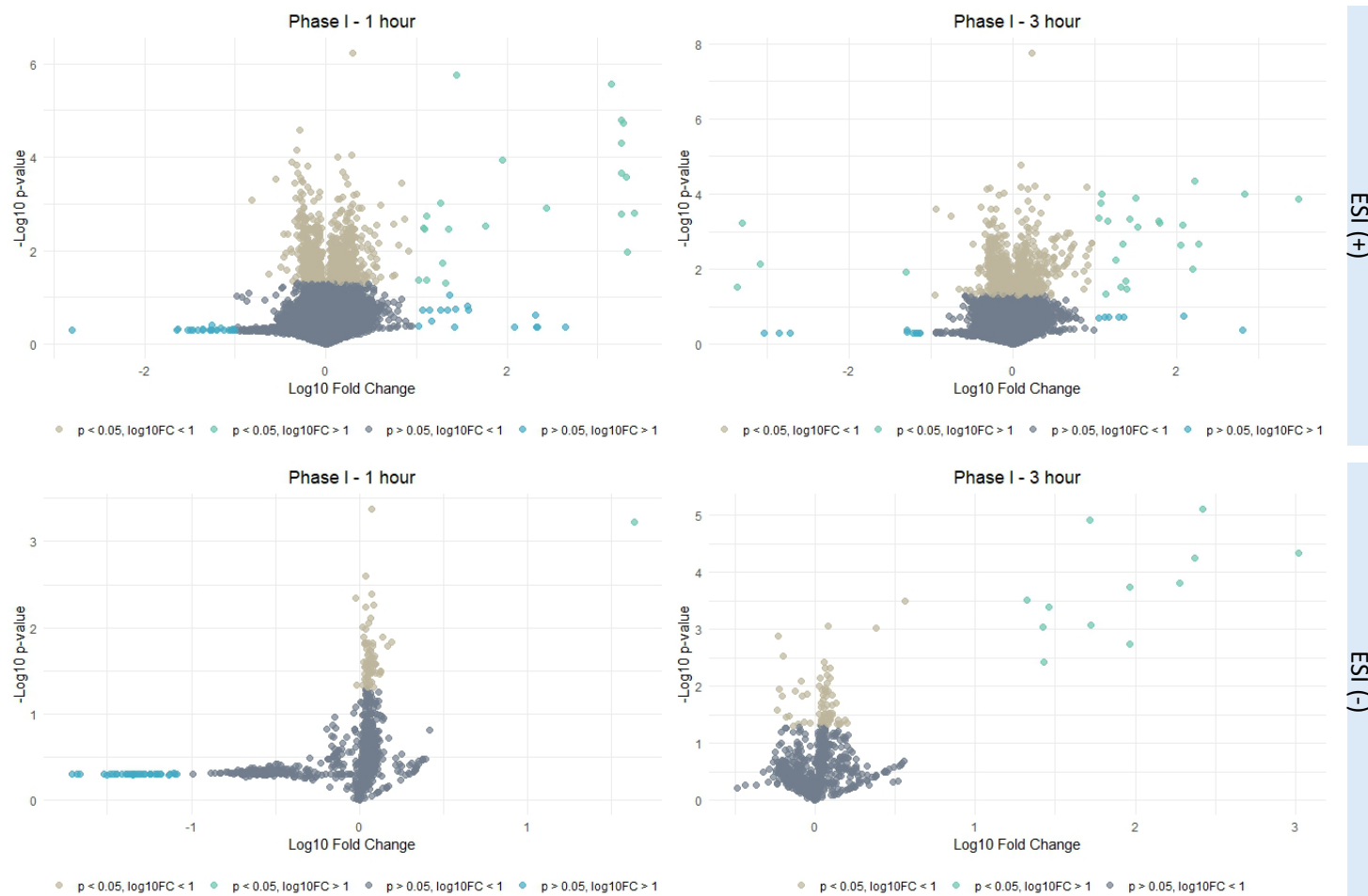


Figure S7. Volcano plots of m/z values measured in ESI (+) and ESI (-) modes in Phase II samples for DPG. Features statistically significant are represented in green color (p -value < 0.05 and a \log_{10} FC > 1).

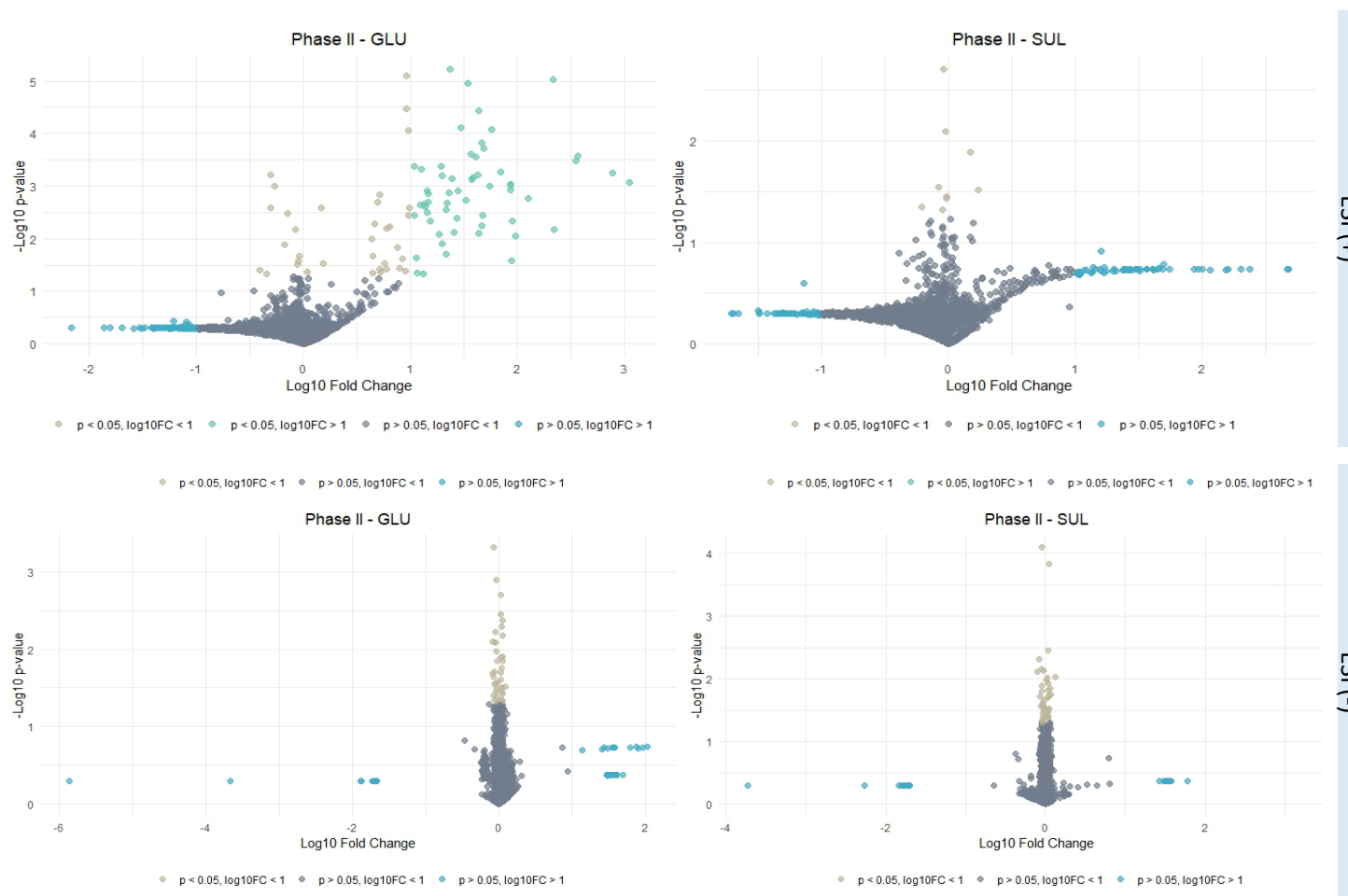


Figure S8. Volcano plots of m/z values measured in ESI (+) and ESI (-) modes in Phase II samples for DTG. Features statistically significant are represented in green color (p -value < 0.05 and a \log_{10} FC > 1).



Figure S9. Extracted ion chromatogram (a) MS/MS spectrum at 20 V in positive (b) and negative mode (c) and fragmentation pathway (d) of DPG.

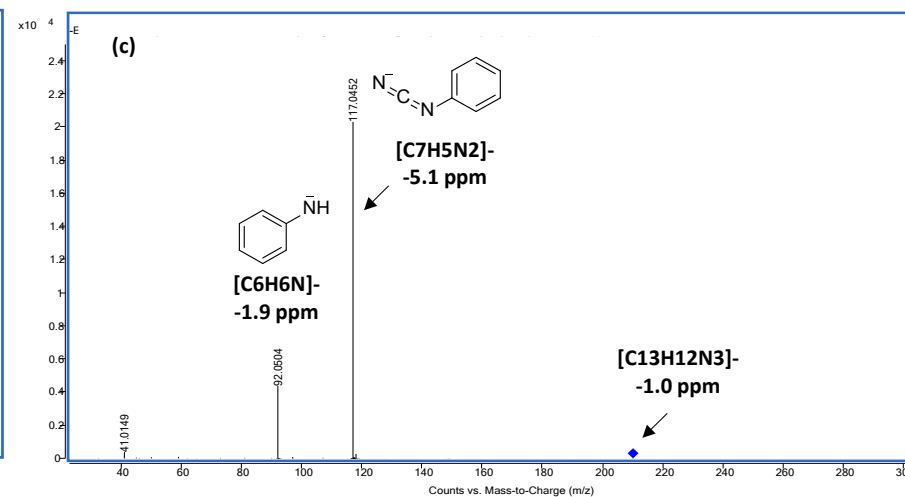
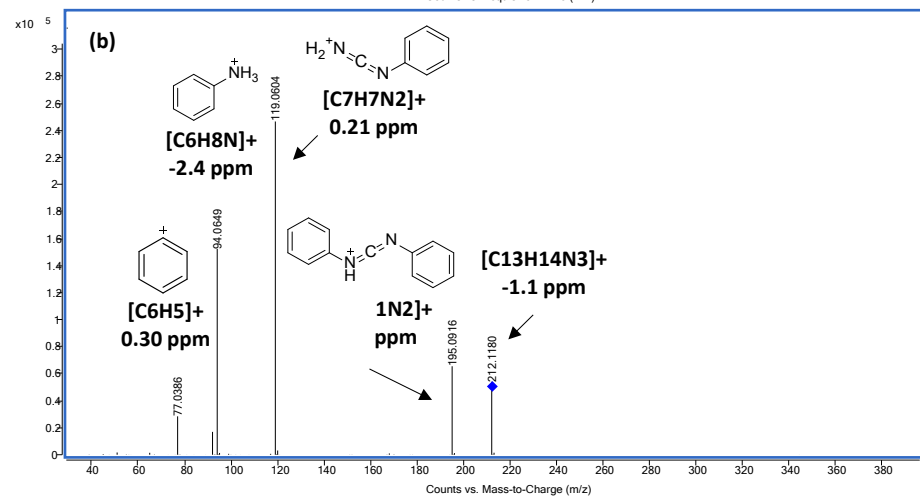
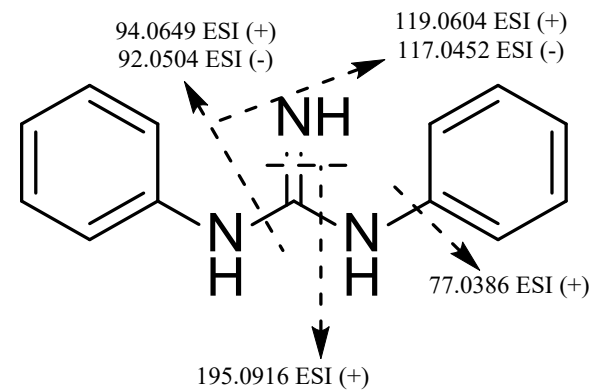
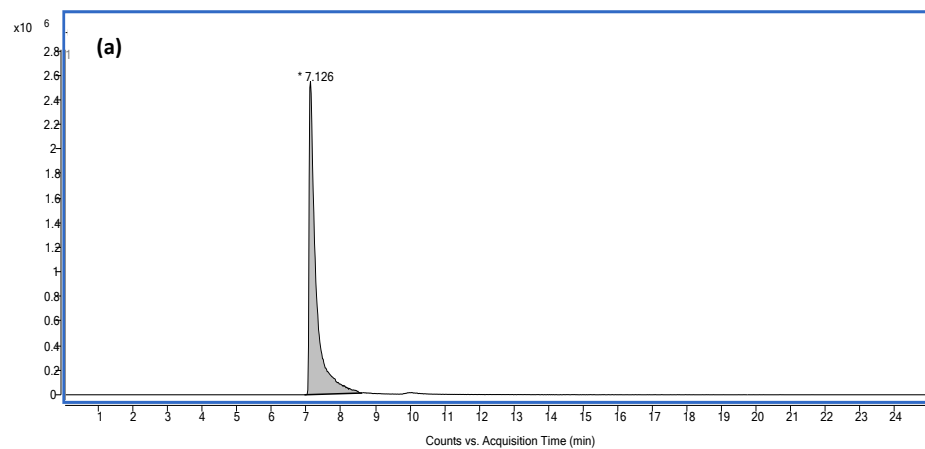


Figure S10. Extracted ion chromatogram (a), MS/MS spectrum at 20 V in positive (b) and negative mode (c) and fragmentation pathway (d) of DTG.

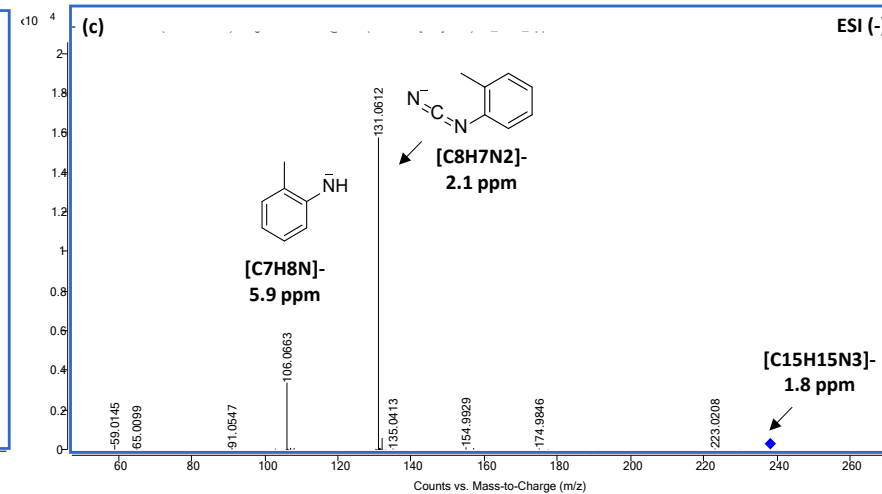
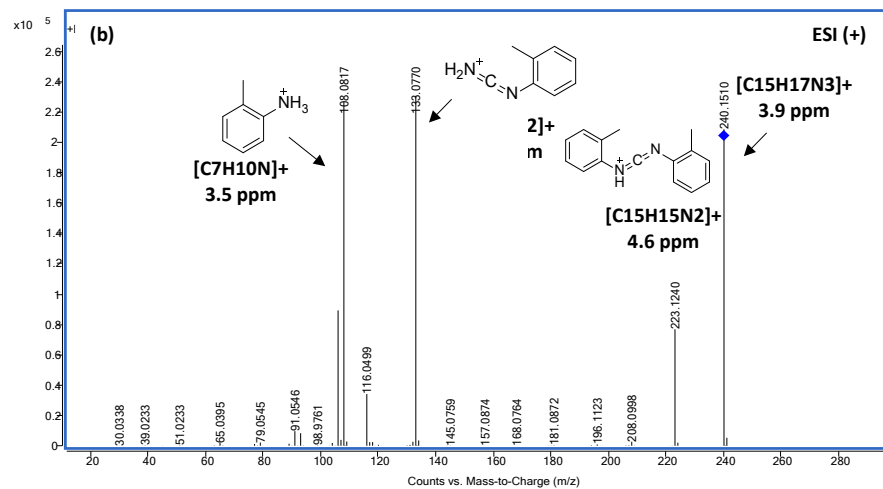
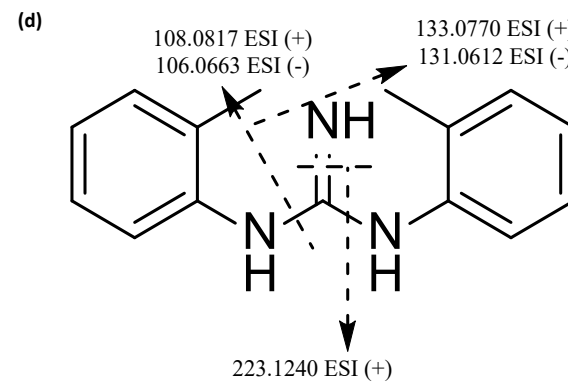
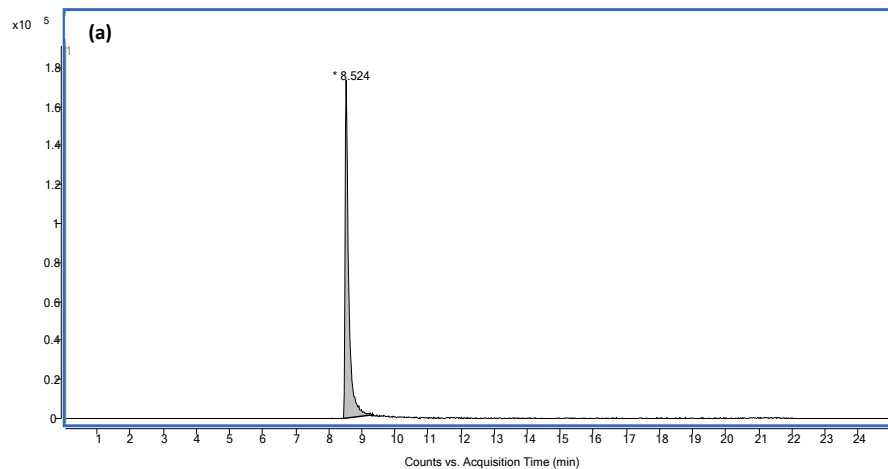


Figure S11.a Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DPG-225.

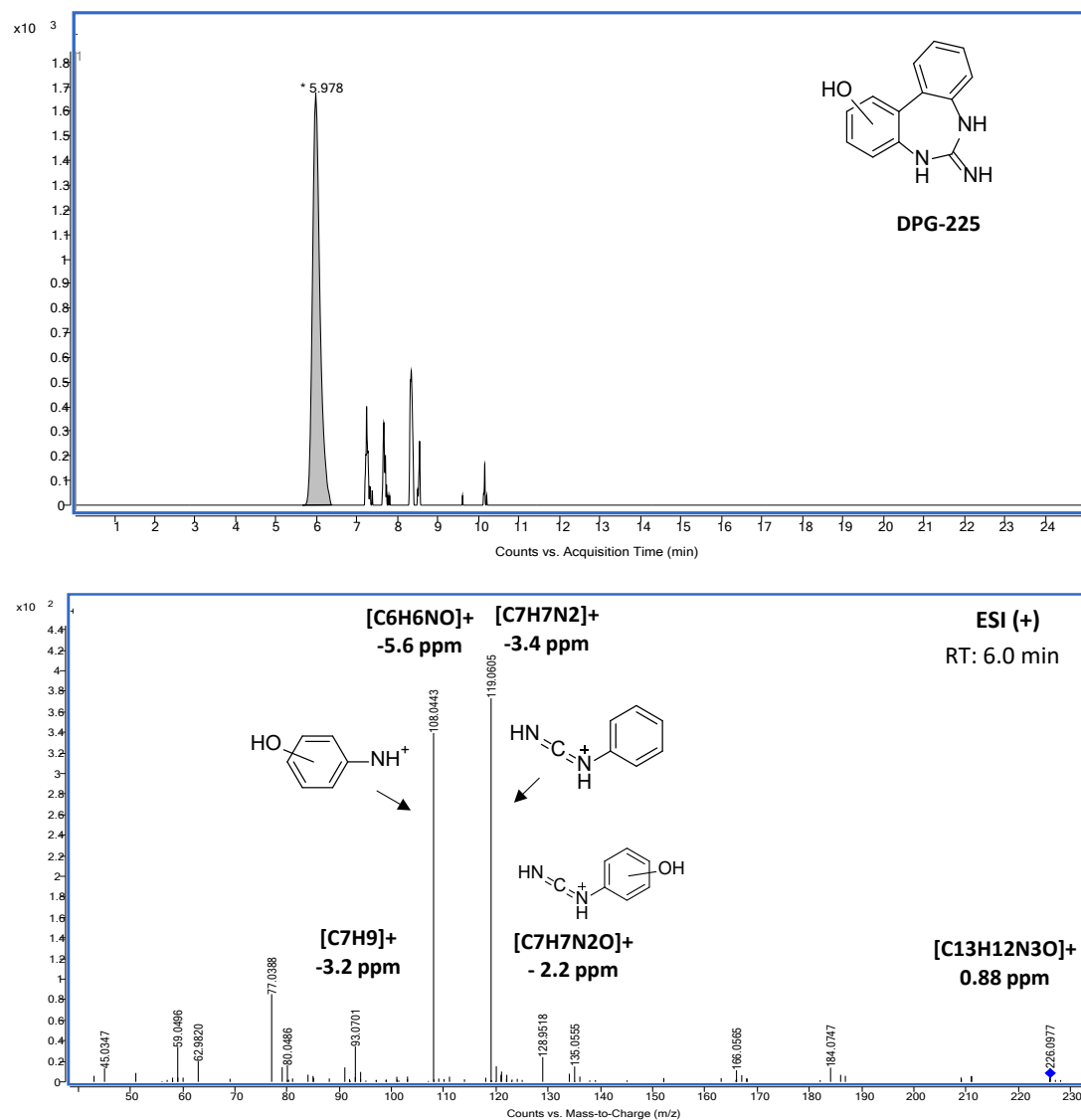


Figure S11.b Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DPG-227.

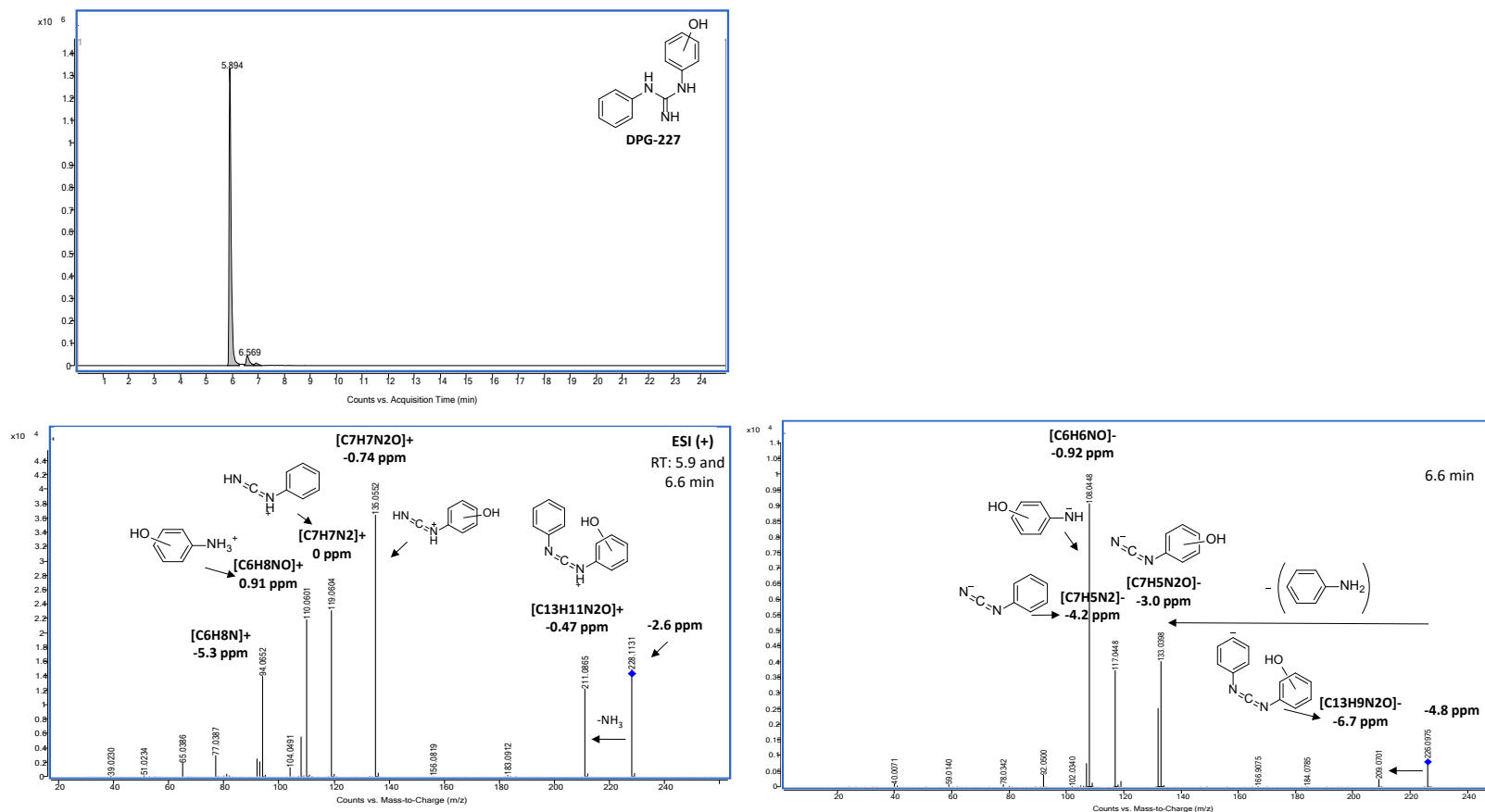


Figure S11.c Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DPG-228.

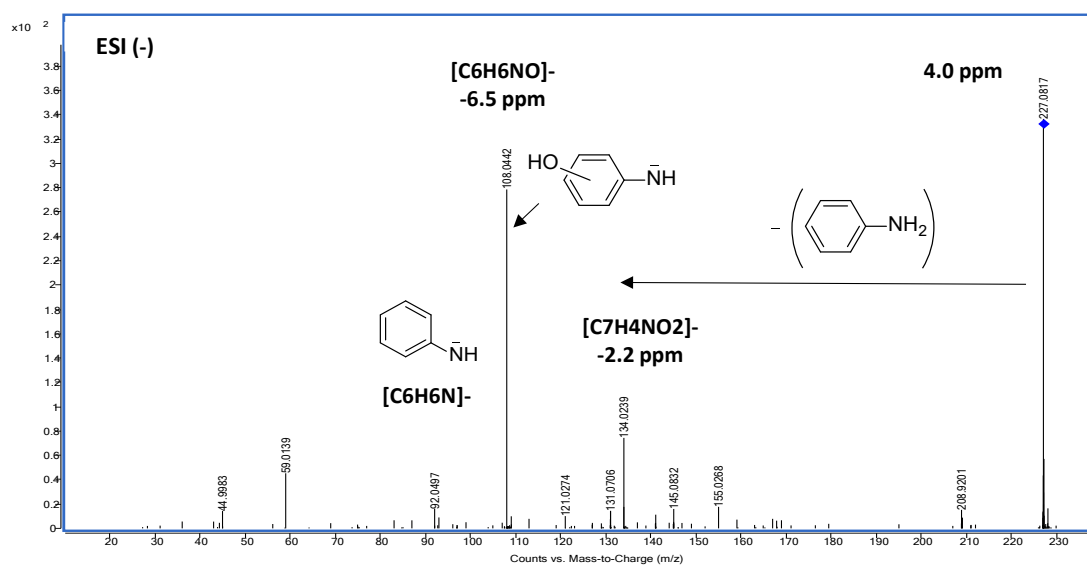
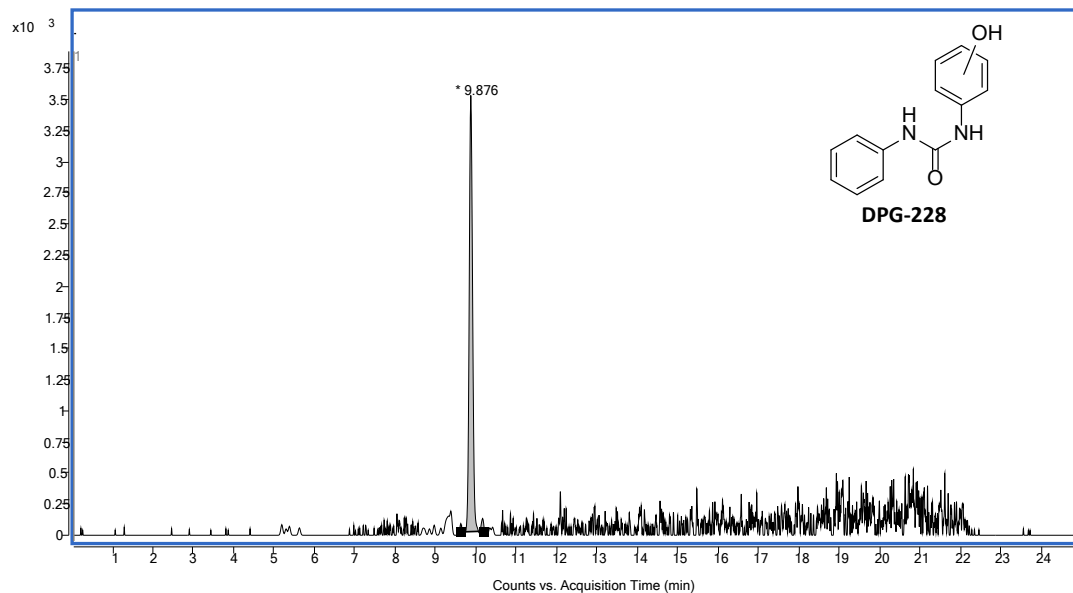


Figure S11.d Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DPG-243.

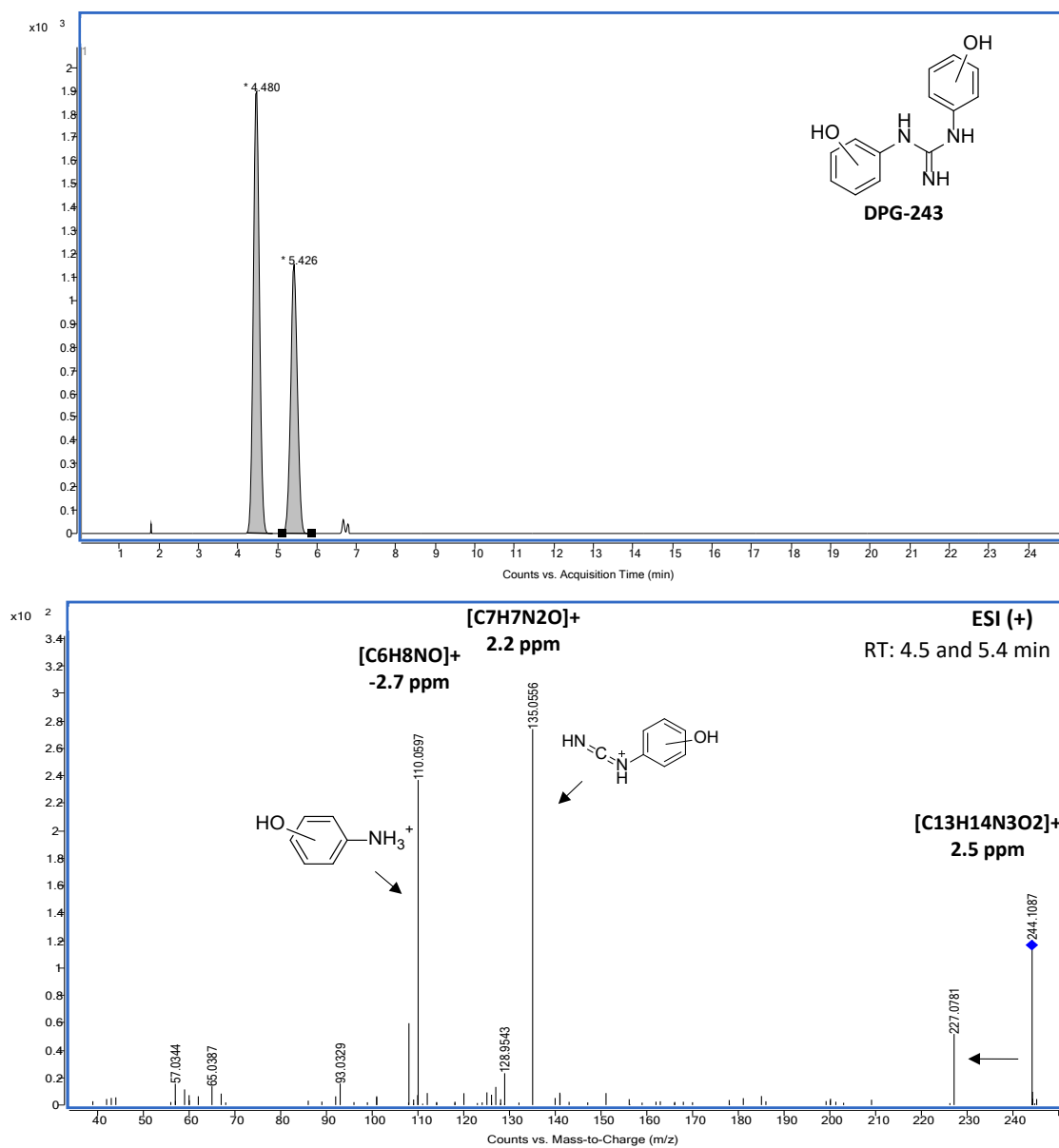


Figure S12.a Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DTG-253.

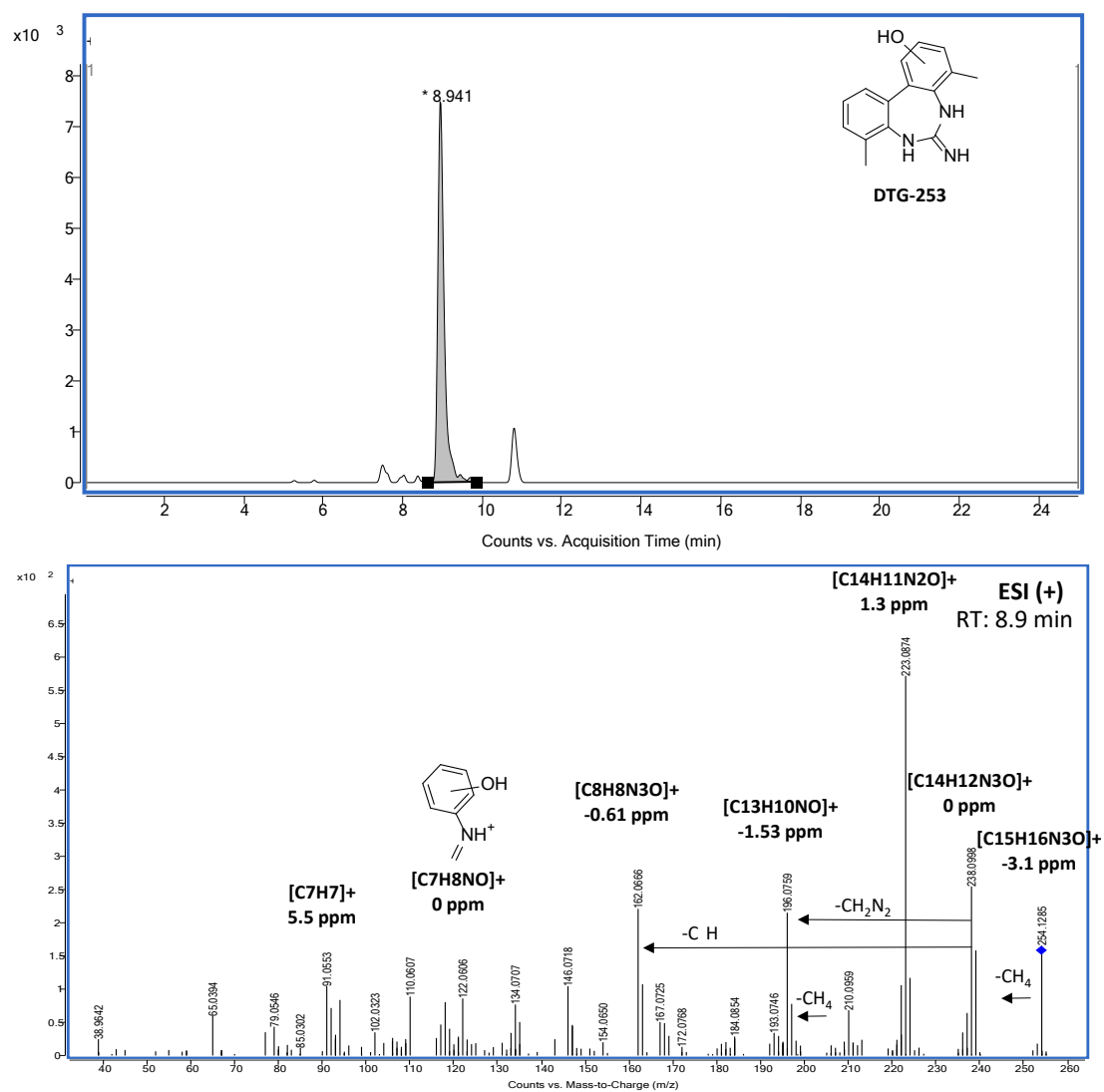


Figure S12.b Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DTG-256.

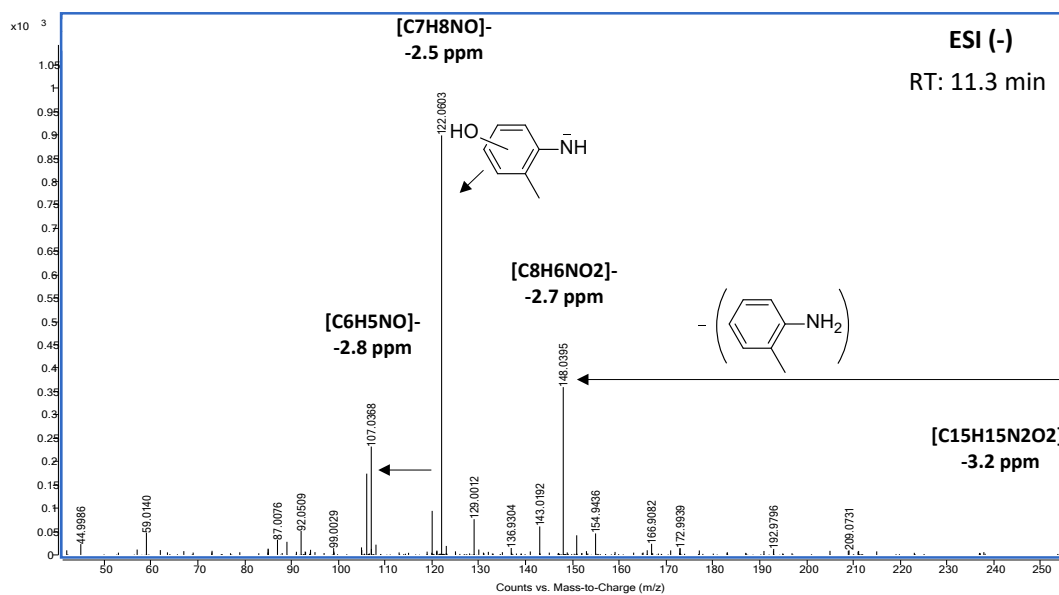
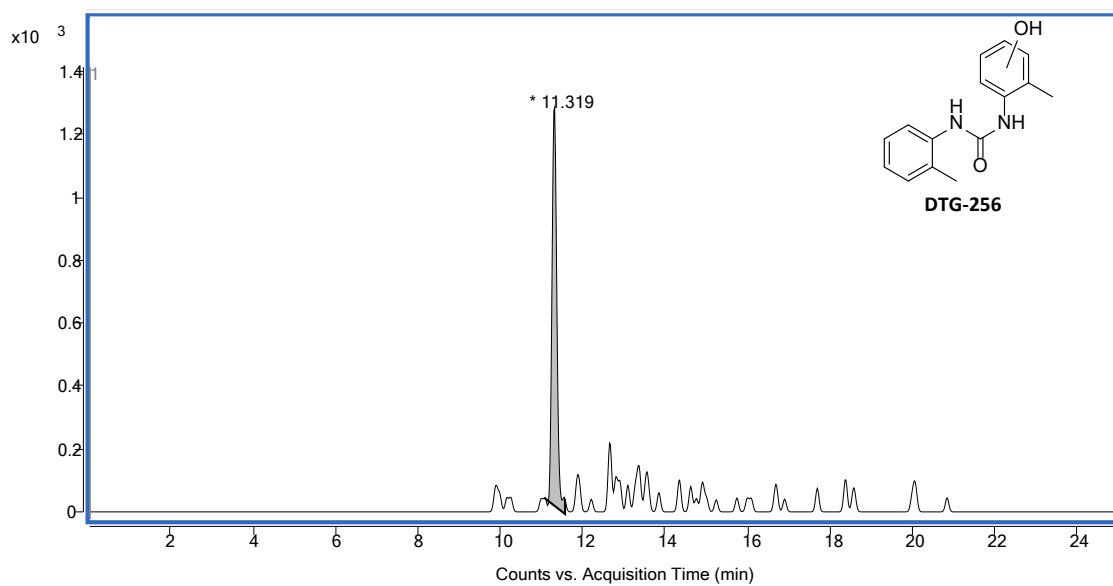


Figure S12.c Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DTG-271.

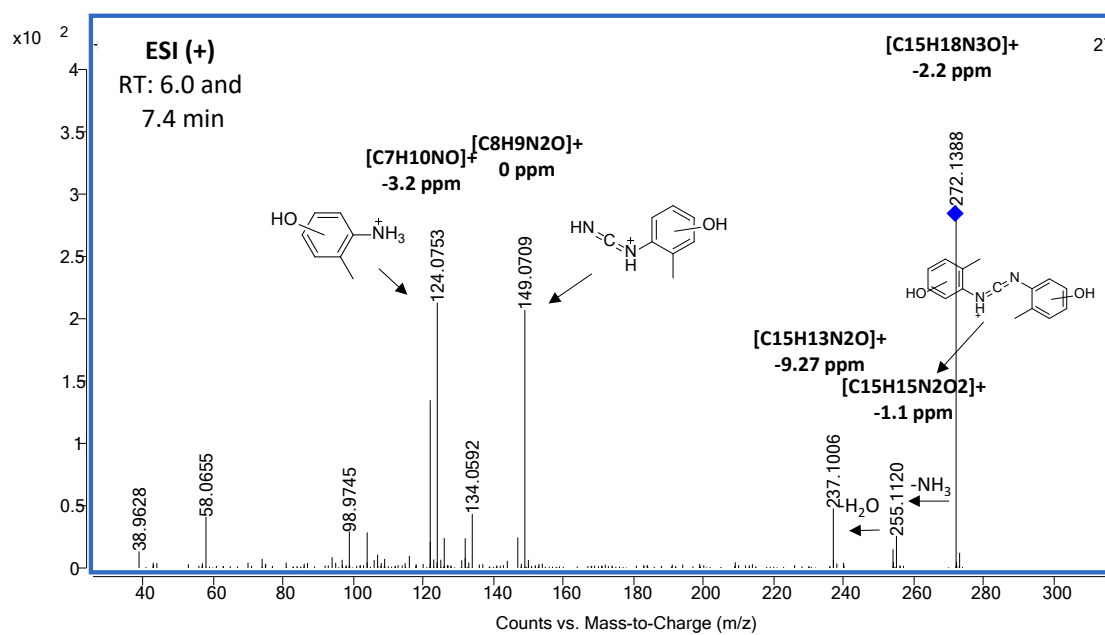
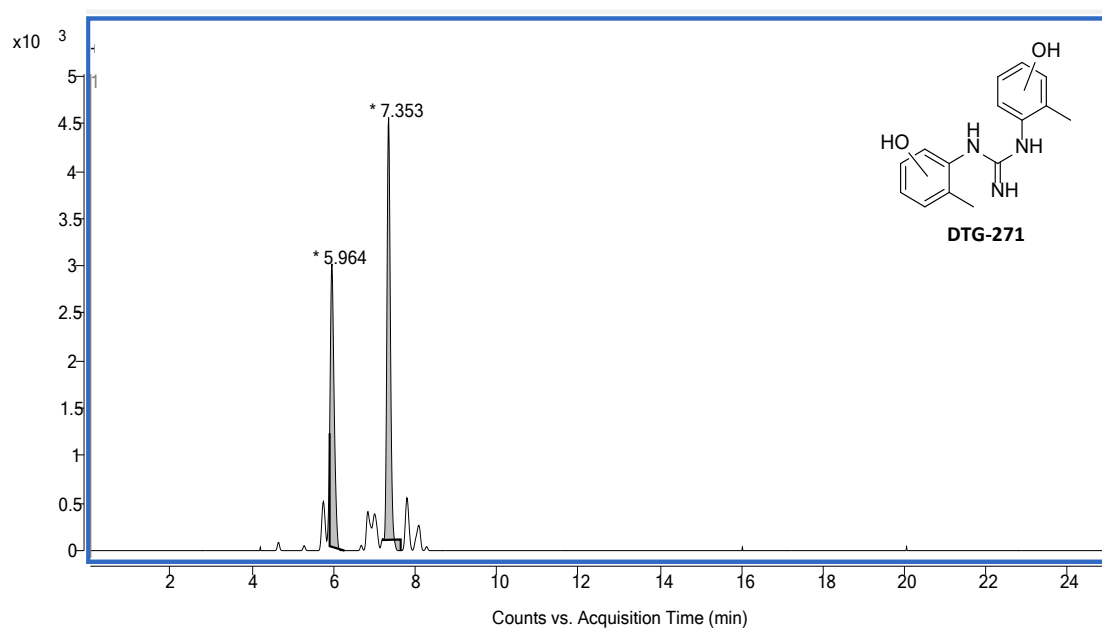


Figure S13.a Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DPG-387.

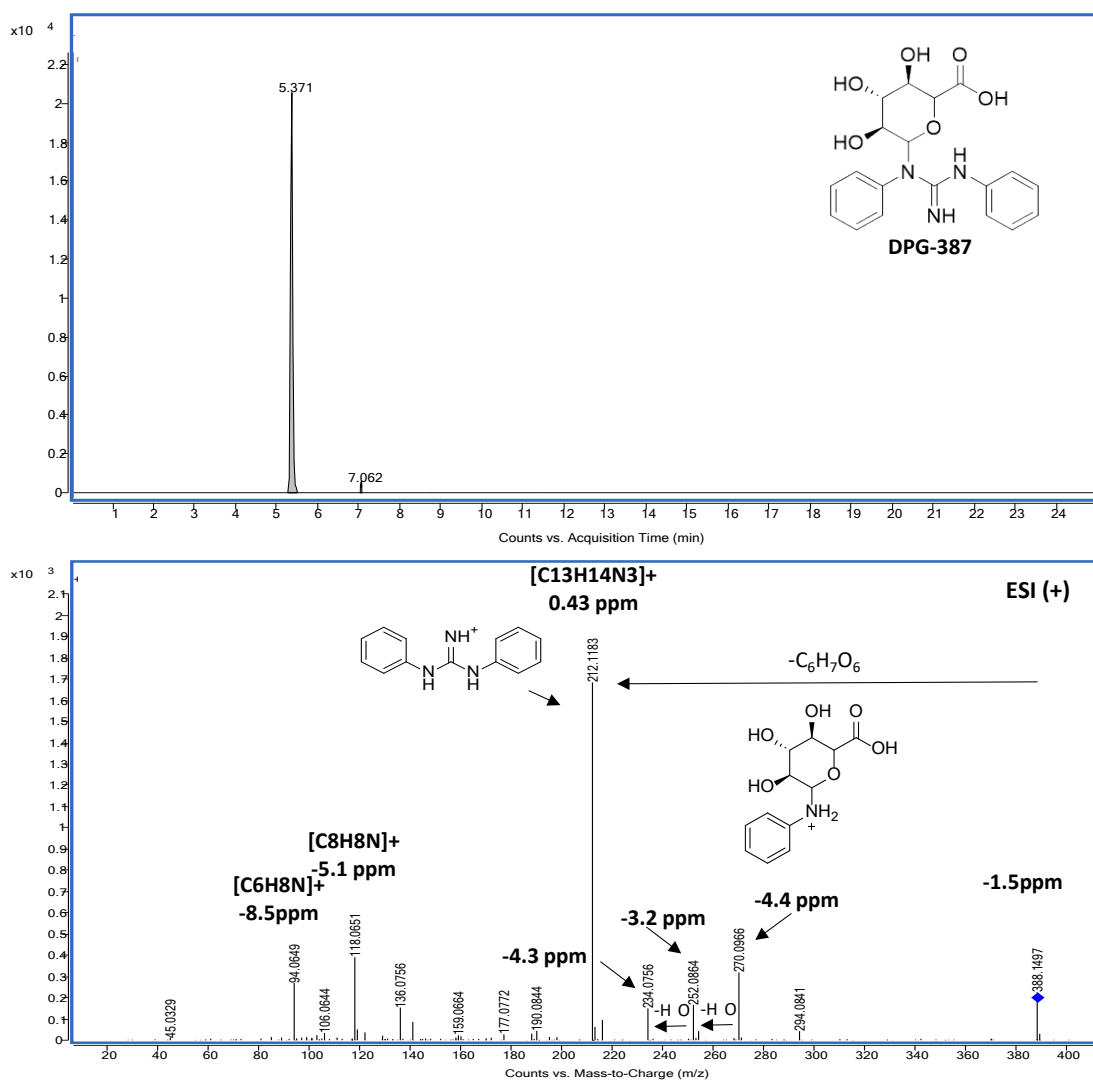


Figure S13.b Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DPG-403.

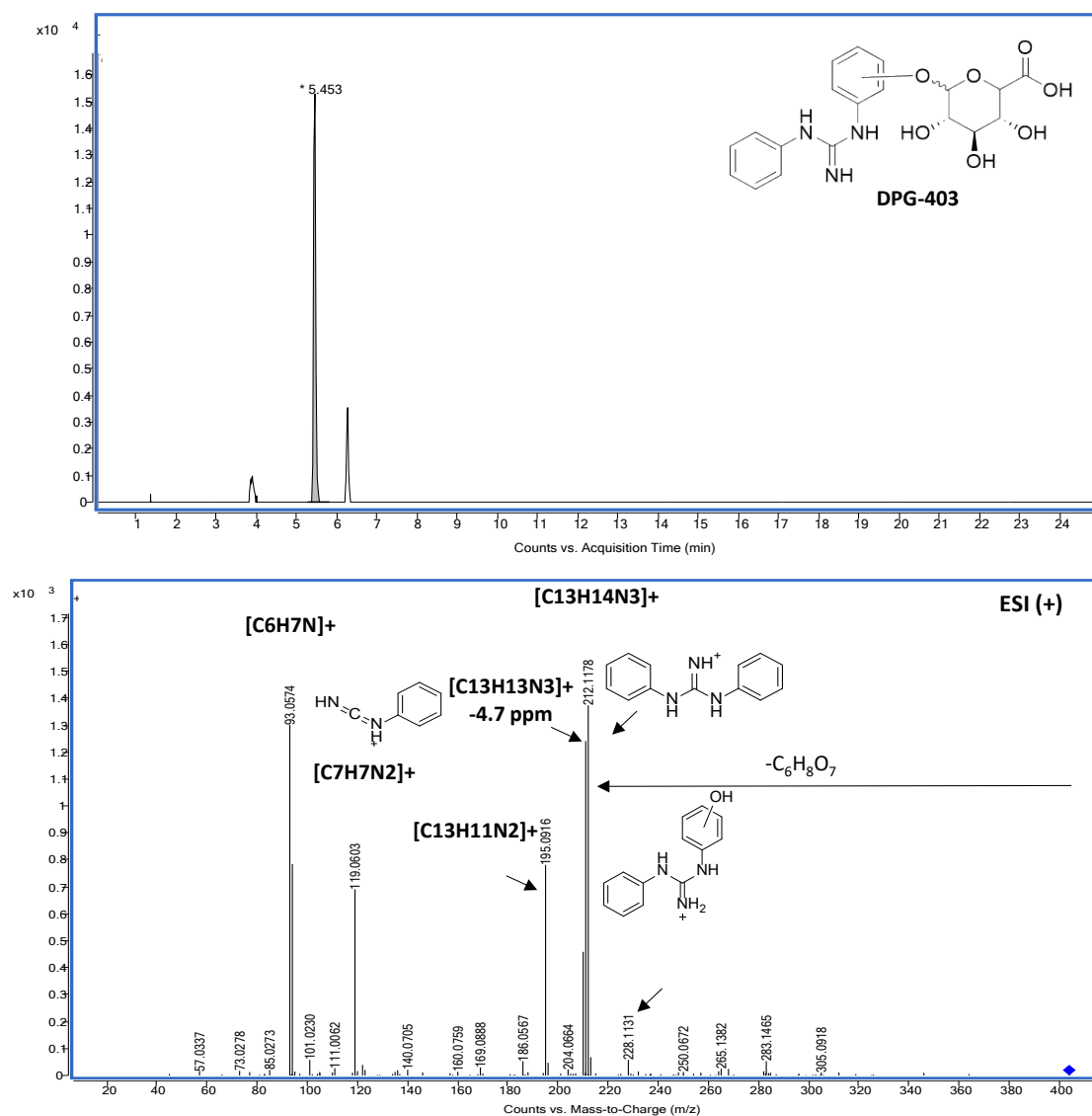


Figure S14. Extracted ion chromatogram and MS/MS spectrum at 20 V with proposed fragmentation pattern for DTG-415.

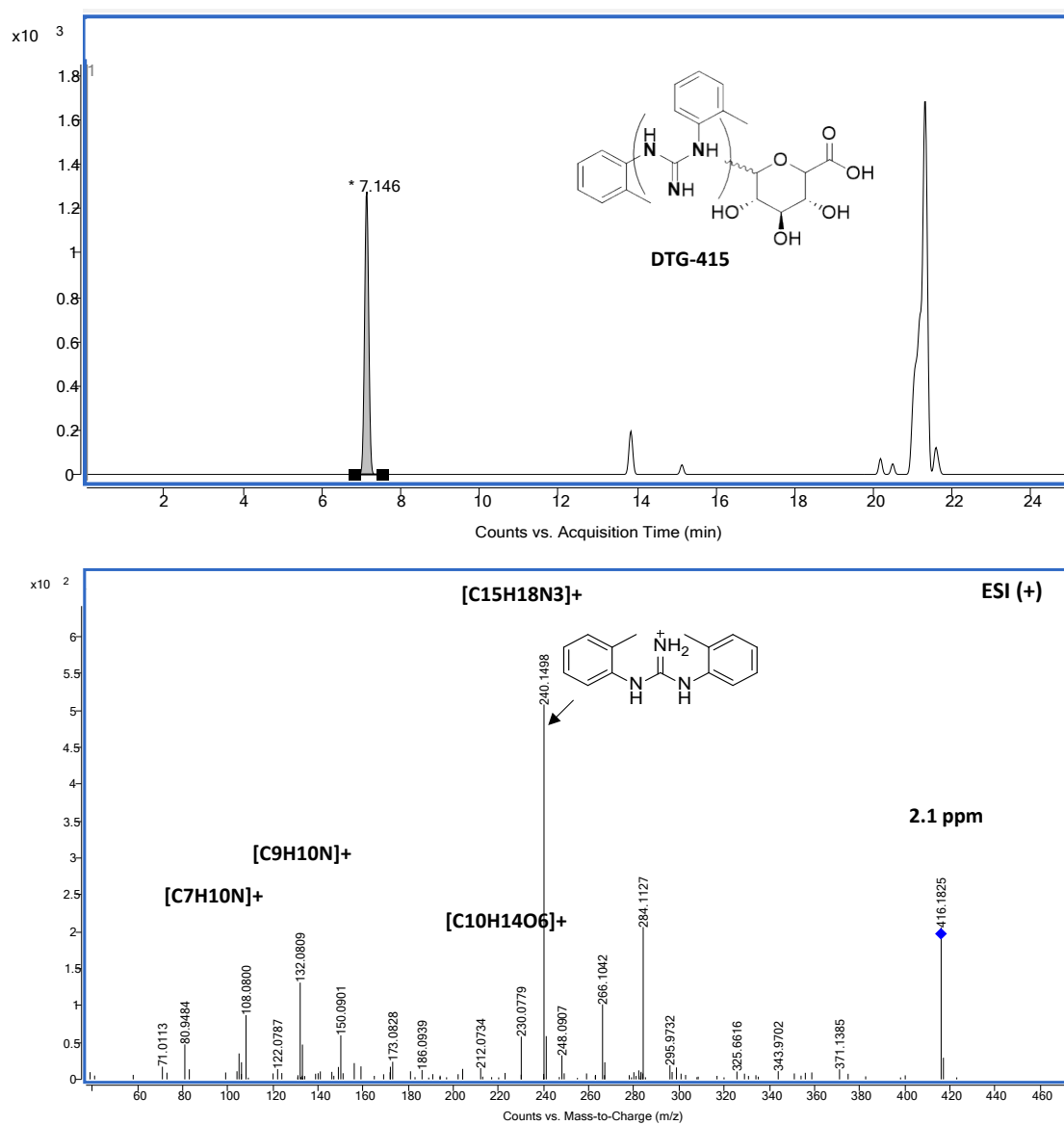


Table S4. Urinary levels of DPG, DPG-227 and DTG and, MS/MS transition ratios of identified target chemicals in pooled samples.

	DPG			DPG-227			DPG-387		DPG-403		DTG		
	Concentration $\mu\text{g L}^{-1}$	Q_2/Q_1	Q_3/Q_1	Concentration ^b $\mu\text{g L}^{-1}$	Q_2/Q_1	Q_3/Q_1	Q_2/Q_1	Q_3/Q_1	Q_2/Q_1	Q_3/Q_1	Concentration $\mu\text{g L}^{-1}$	Q_2/Q_1	Q_3/Q_1
P1	0.119	1.2	0.50	0.092	0.76	0.30	Only Q_1^a	Only Q_1^a	Only Q_1^a	Only Q_1^a	0.063	0.90	0.36
P2	0.083	1.2	0.52	0.035	0.87	0.32	Only Q_1^a	Only Q_1^a	Only Q_1^a	Only Q_1^a	0.058	1.0	0.41
P3	0.043	1.3	0.52	0.043	1.0	0.30	Only Q_1^a	Only Q_1^a	Only Q_1^a	Only Q_1^a	0.056	0.91	0.34
P4	0.040	1.3	0.54	0.025	1.0	0.32	Only Q_1^a	Only Q_1^a	Only Q_1^a	Only Q_1^a	0.024	0.93	0.36
P1d^c	0.227	1.4	0.54	0.101	0.65	0.31	Not detected	Not detected	Not detected	Not detected	0.209	1.0	0.37
P2d^c	0.188	1.3	0.81	0.049	1.0	0.29	Not detected	Not detected	Not detected	Not detected	0.060	1.0	0.40
P3d^c	0.073	1.3	0.78	0.073	0.65	0.19	Not detected	Not detected	Not detected	Not detected	0.115	1.0	0.46
P4d^c	0.090	1.1	0.65	0.045	0.84	0.25	Not detected	Not detected	Not detected	Not detected	0.071	1.1	0.39

^a Only one MS/MS transition was identified.

^b DPG-227 concentration was calculated assuming a response equal to that of DPG, from its standard addition calibration curve.

^c Deconjugated set of urine samples.

Figure S15. Chromatographic peaks of MS/MS transitions for DPG-387 and DPG-403 found in HLM (left) and urine (right) samples.

