Supplementary Information

Variations in *O*-glycosylation Patterns Influence Viral Pathogenicity, Infectivity, and Transmissibility in SARS-CoV-2 Variants

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Supplementary Figure S12. Heatmap showing the relative abundance of individual *O*-glycoforms identified in **lambda.**

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Supplementary Figure S14. Heatmap showing the relative abundance of individual *O*-glycoforms identified in **omicron.**

Supplementary Figure S15. EThcD tandem mass spectra of a tryptic/IMPa digested glycopeptide confirming the occupancy of both T323 and S325 *O*-glycosylation sites. Data extracted from eta variant (H29) with **Scan no., 3354; m/z, 751.6761; z, 3.**

Supplementary Figure S16. EThcD tandem mass spectra of a tryptic/IMPa digested glycopeptide confirming the occupancy of a mutation point (R190S) in Gamma.

Supplementary Tables:

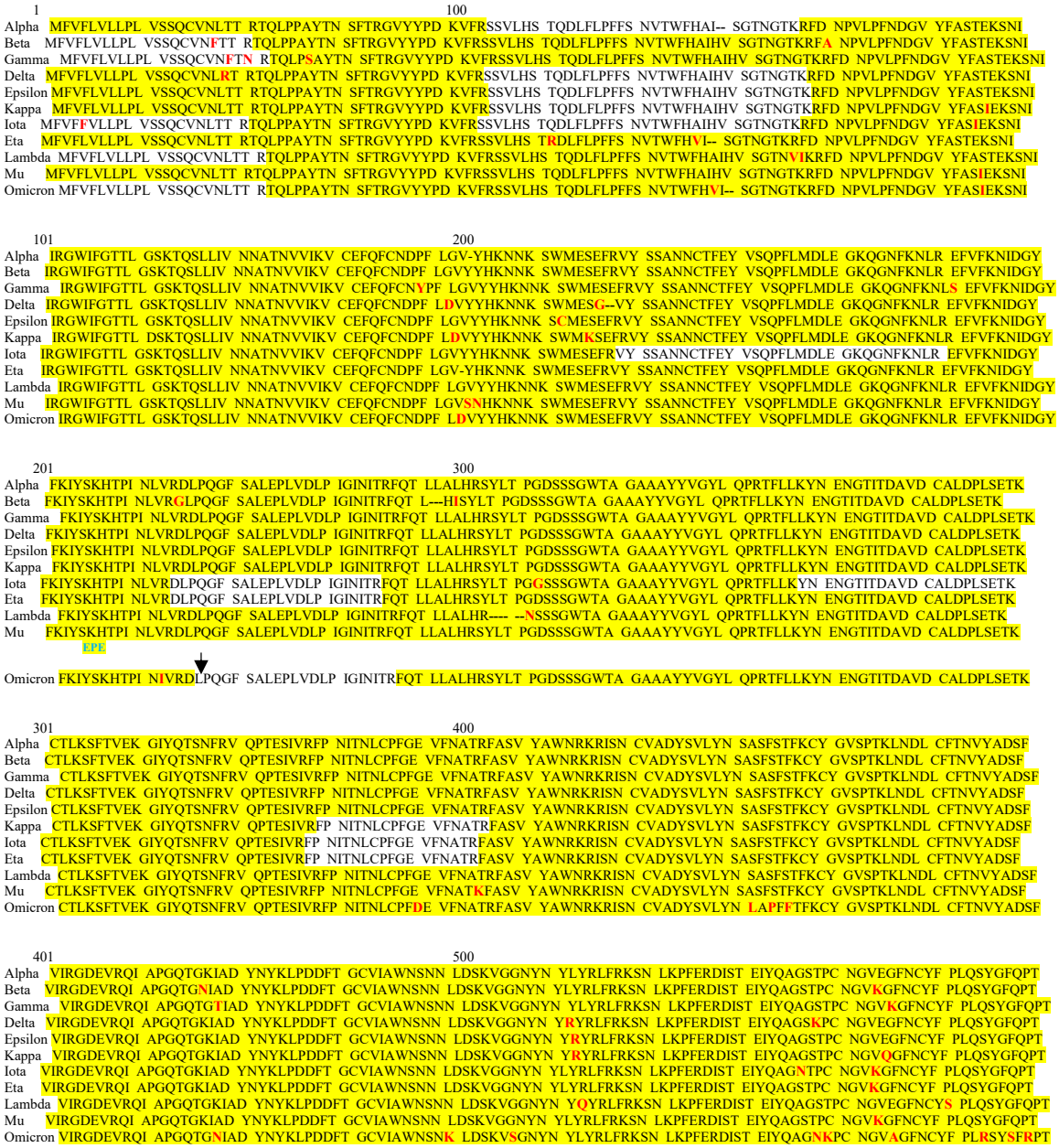
Supplementary Table S1: List of *O*-glycopeptides identified in the different variants by Byonic software.

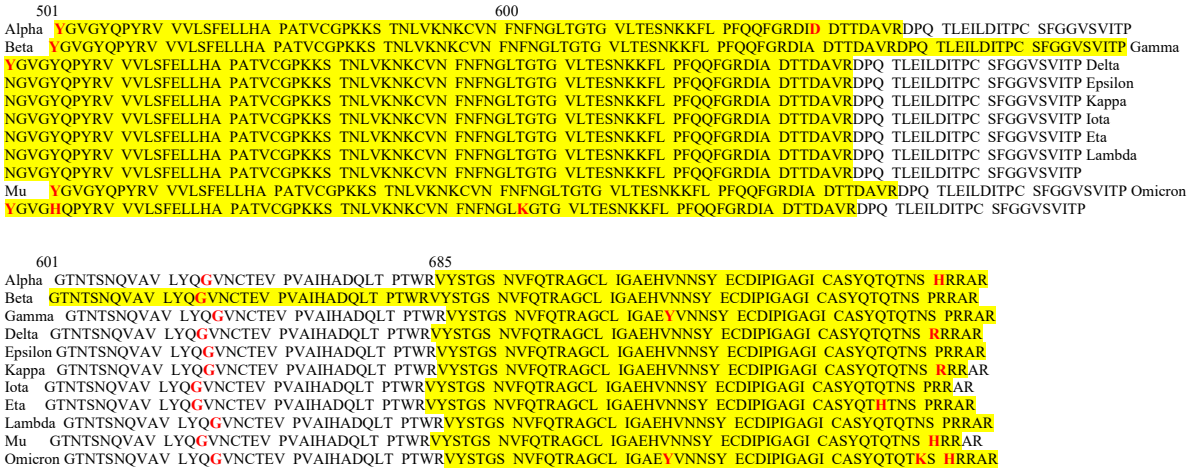
Supplementary Table S2: List of *O*-glycopeptides identified in the different variants by MetaMorpheus software.

Supplementary Table S3: Venn plot results showing the list of *O*-glycopeptides common and unique to Iota, Eta, Lambda, Mu, and Omicron.

Supplementary Table S4: List of O-glycopeptides on G446S mutation in Omicron.

Supplementary Figure S1

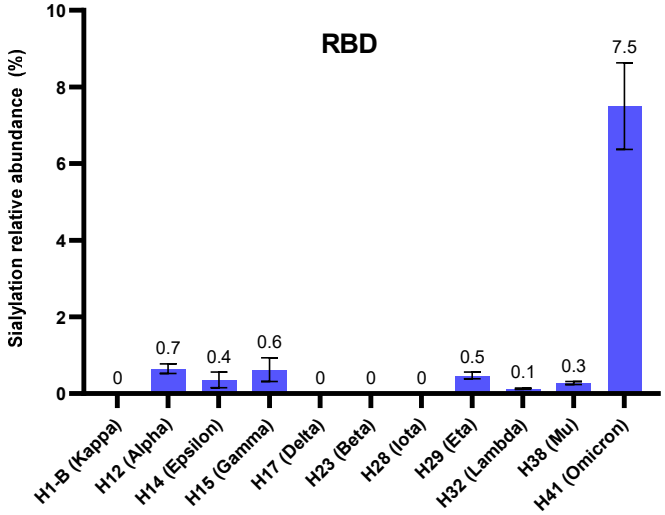




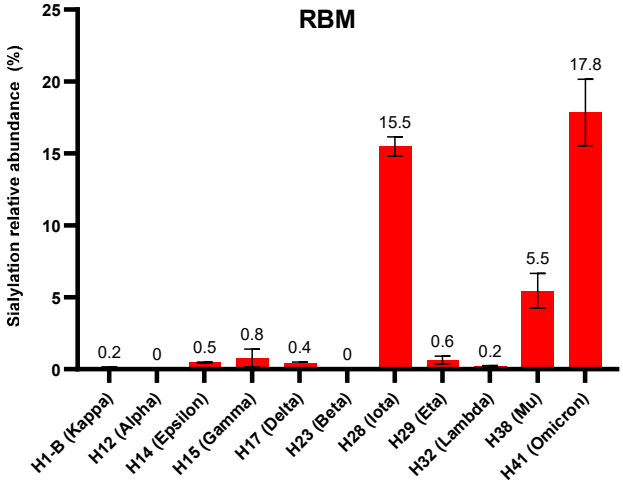
The percentage coverage for each protein determined by Proteome Discoverer is as follows: Alpha 87%; Beta 97%; Gamma 87%; Delta 89%; Epsilon 87%; Kappa 84%; Iota 86%; Eta 70%, Lambda 88%; Mu 85%; and omicron 91%.

*Sections highlighted in yellow show the protein percent coverage
*Amino acid residues in red font are substituted
* “–” Represents deletions
* “↓” Indicates the point of insertion

Supplementary Figure S2



Supplementary Figure S3



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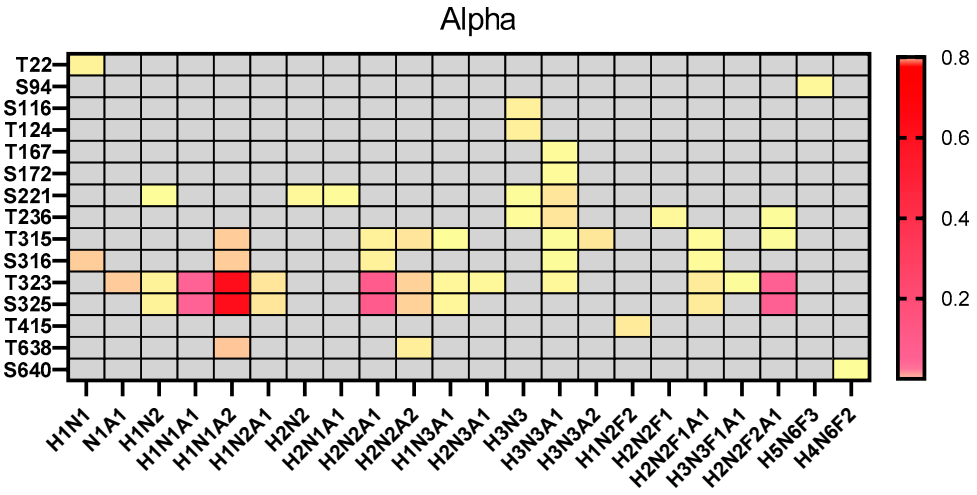

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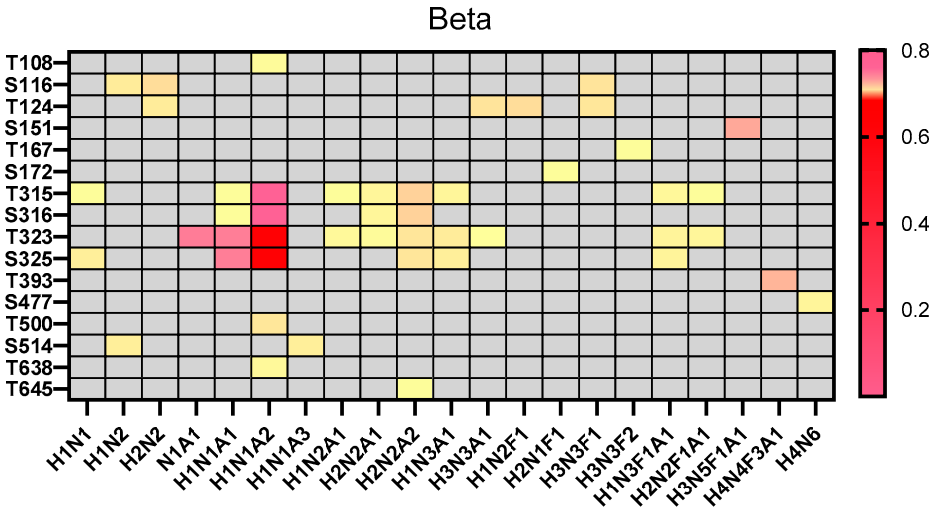

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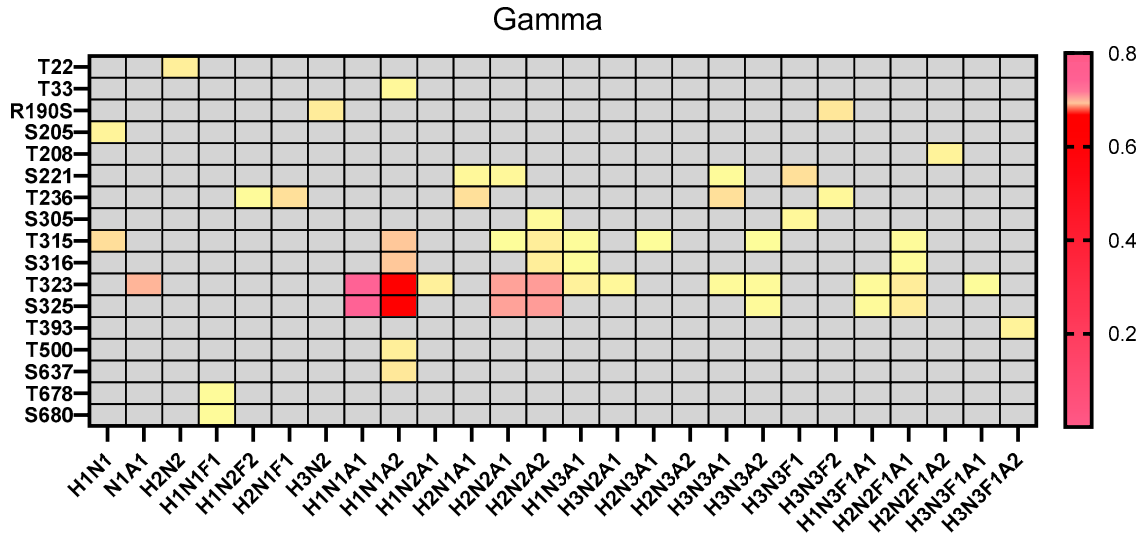

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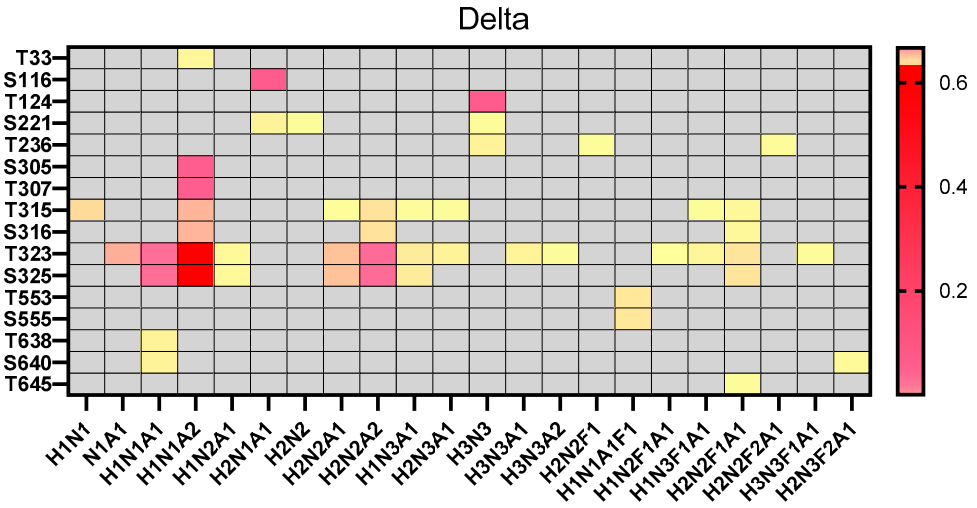

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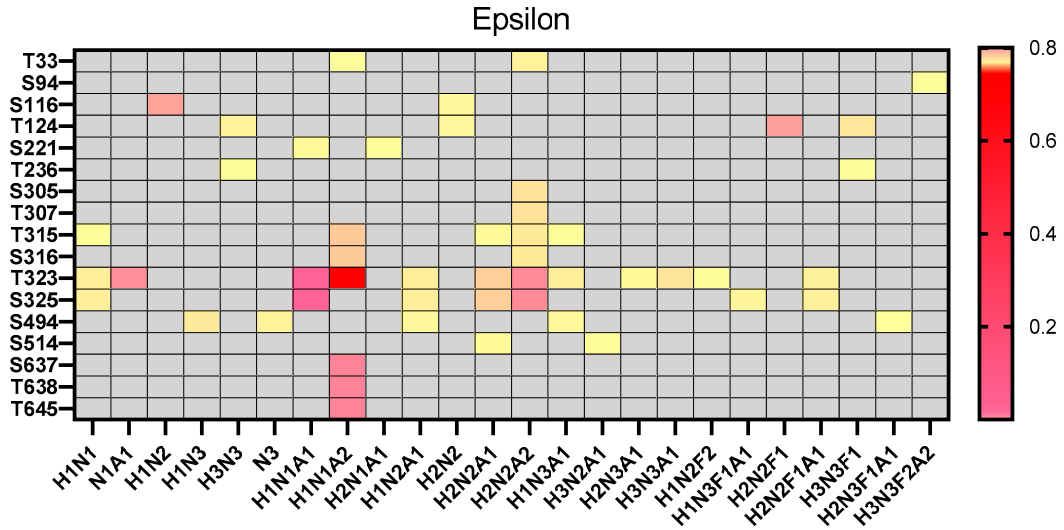

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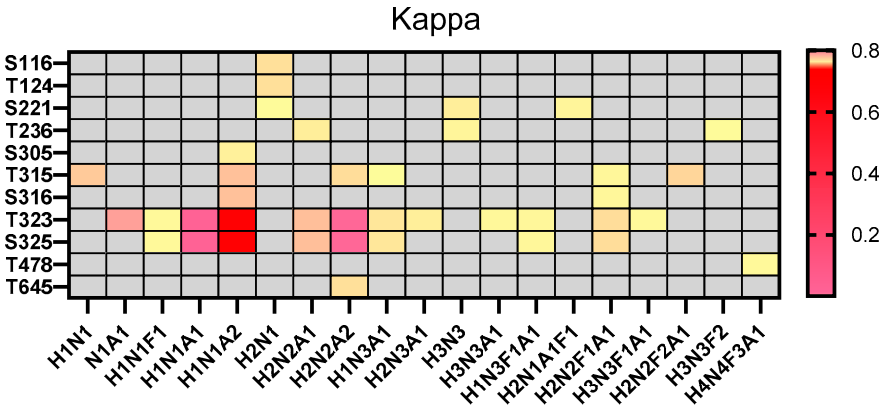

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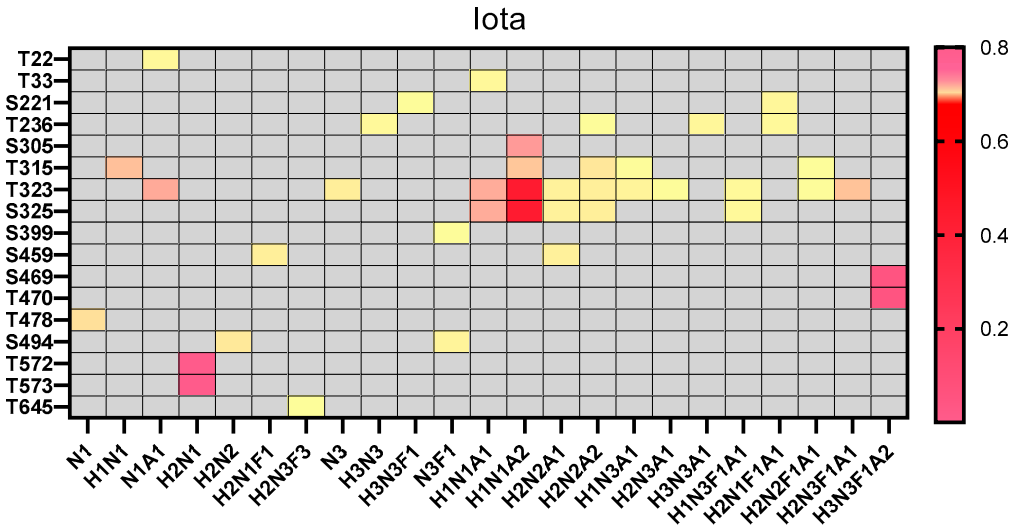
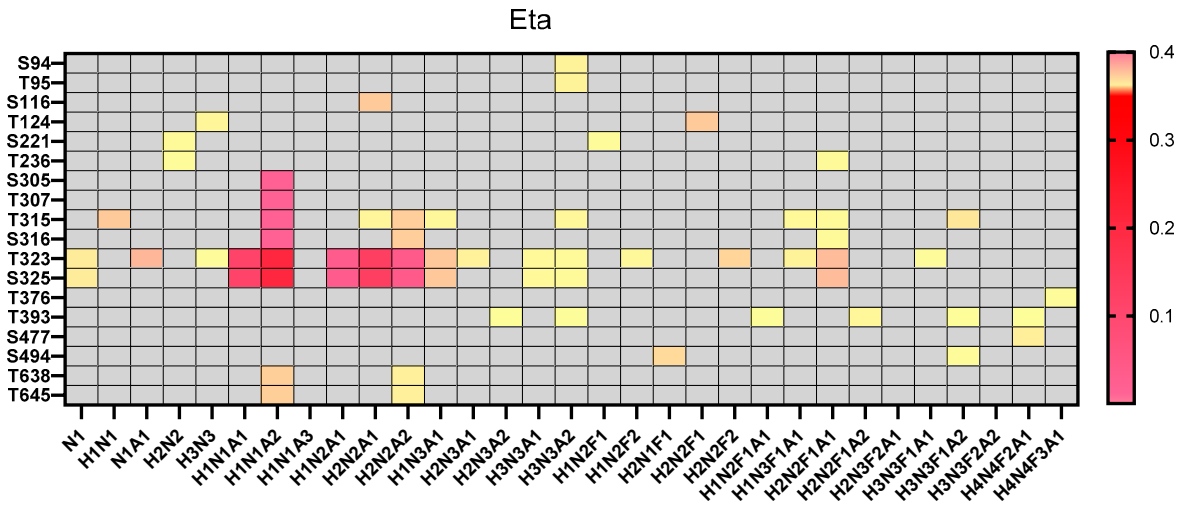


Supplementary Figure S11



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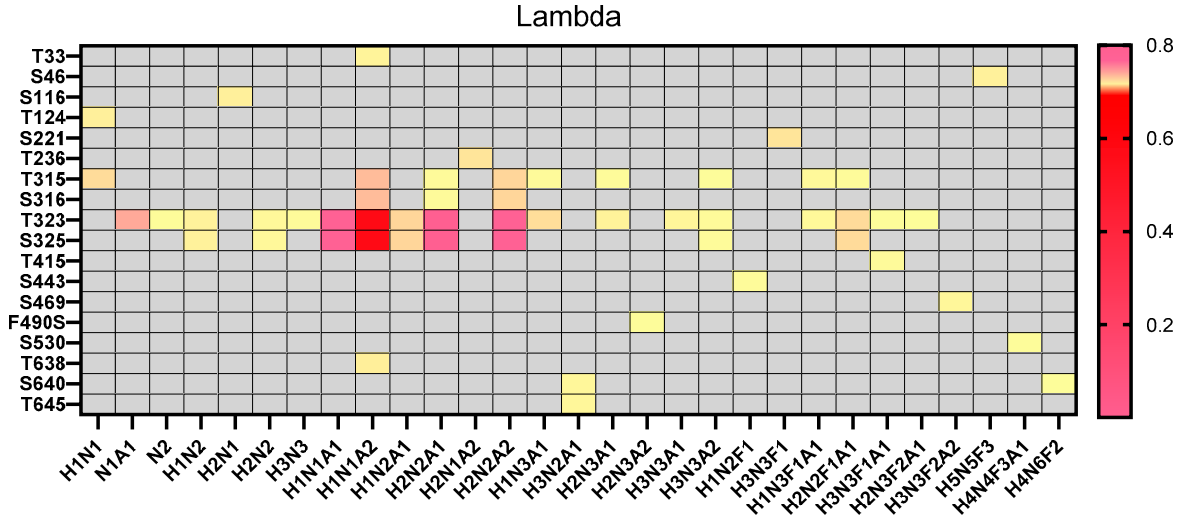

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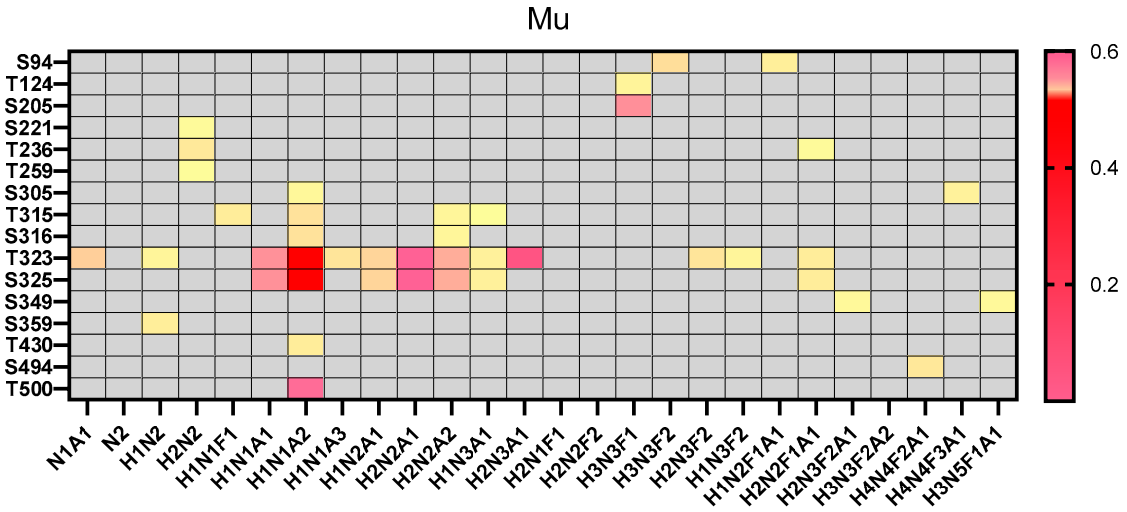

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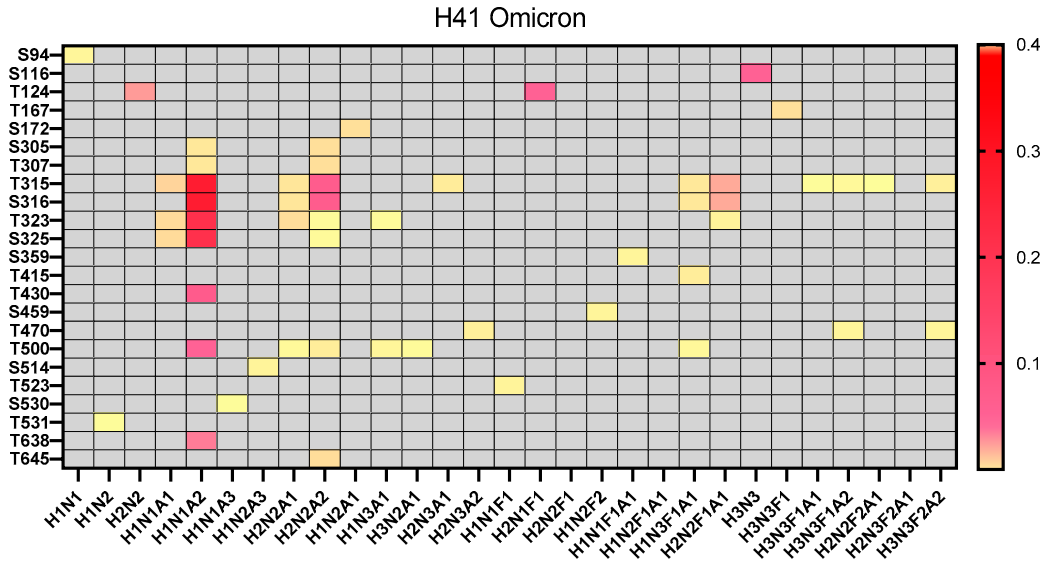

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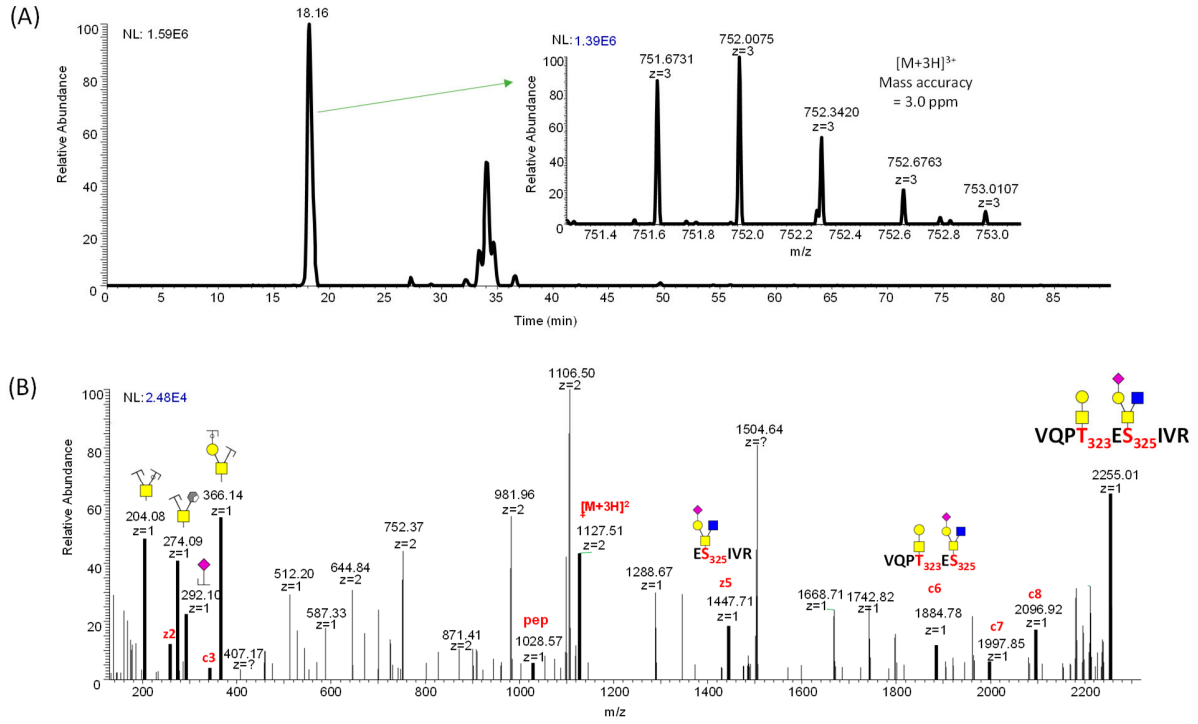

Supplementary Figure S16