

LC-MS/MS Quantitation of Esophagus Disease Blood Serum Glycoproteins by Enrichment with Hydrazide Chemistry and Lectin Affinity Chromatography

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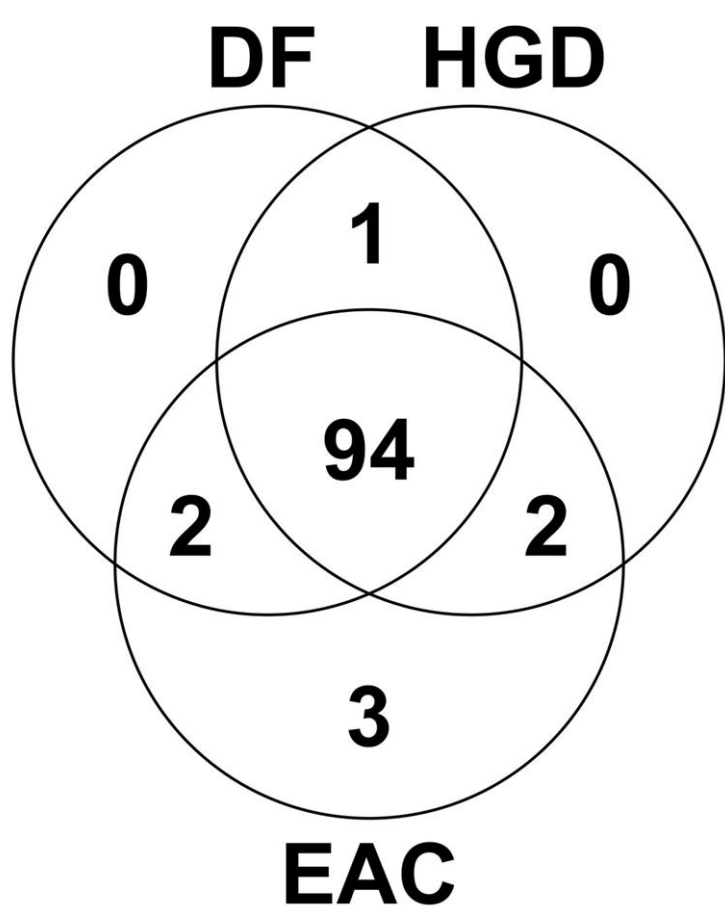
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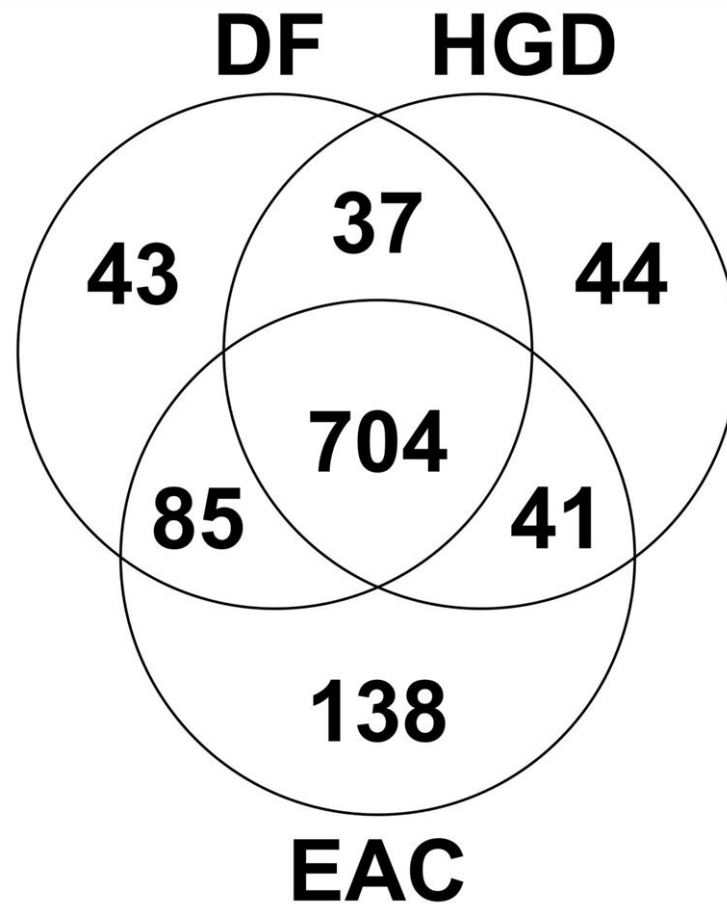
Keywords: Glycoproteins, Lectin Chromatography, Hydrazide-Chemistry Enrichment, LC-MS/MS, Quantitative Glycoproteomics

Supplementary Figure 1. Number of identified glycoproteins (A) and identified unique peptides (B) between DF, HGD, and EAC by lectin affinity chromatographic enrichment.

A. Identified proteins

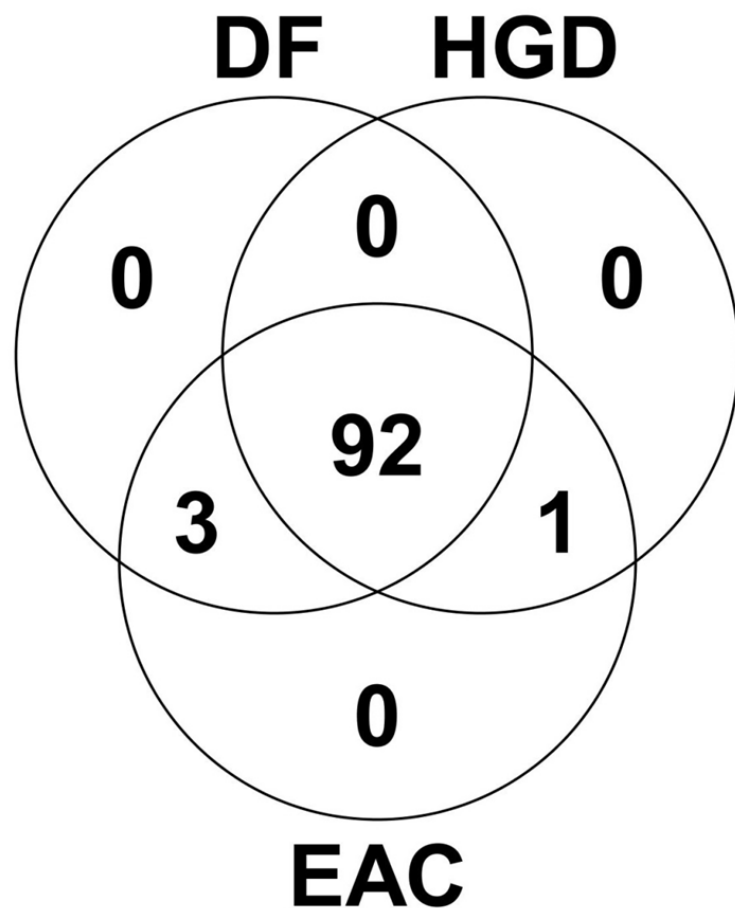


B. Unique peptides

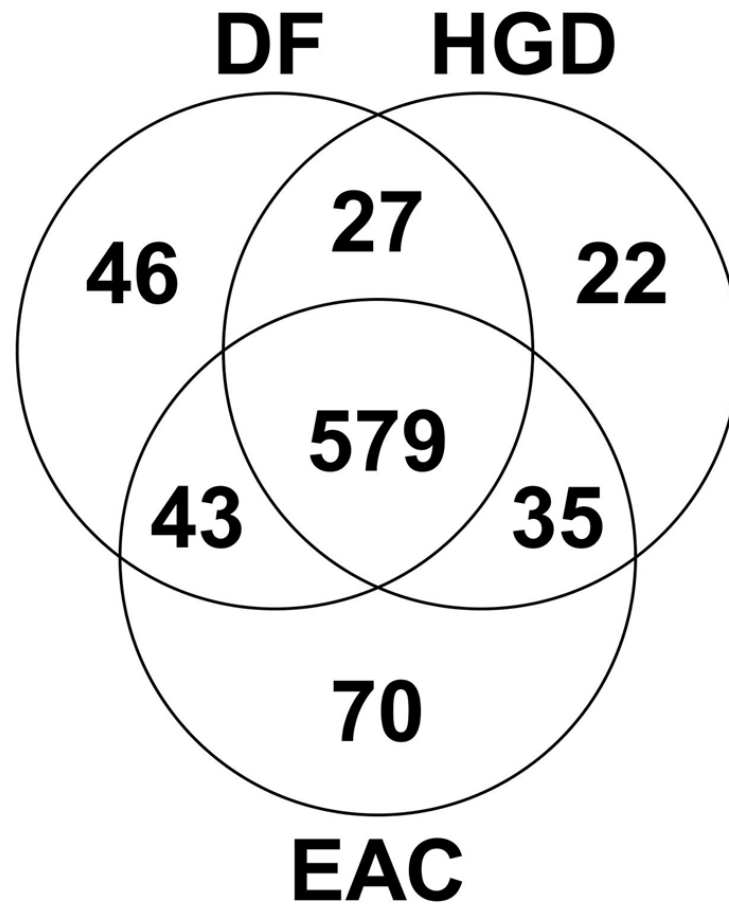


Supplementary Figure 2. Number of identified glycoproteins (A) and identified unique peptides (B) between DF, HGD, and EAC using hydrazide chemistry-based enrichment.

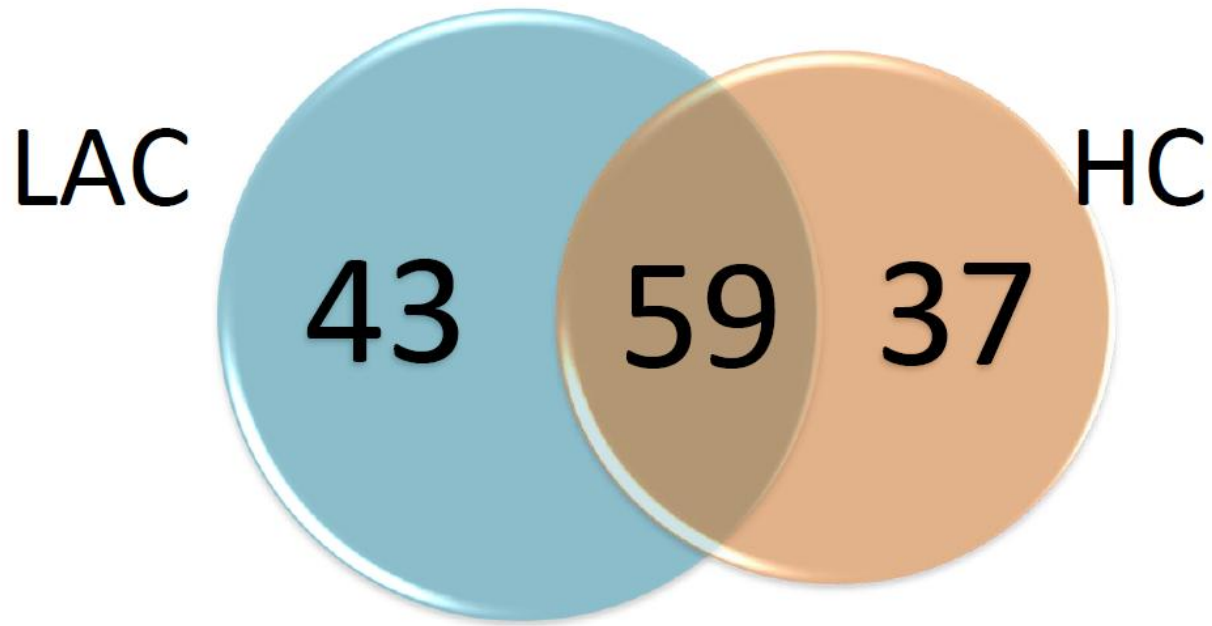
A. Identified proteins



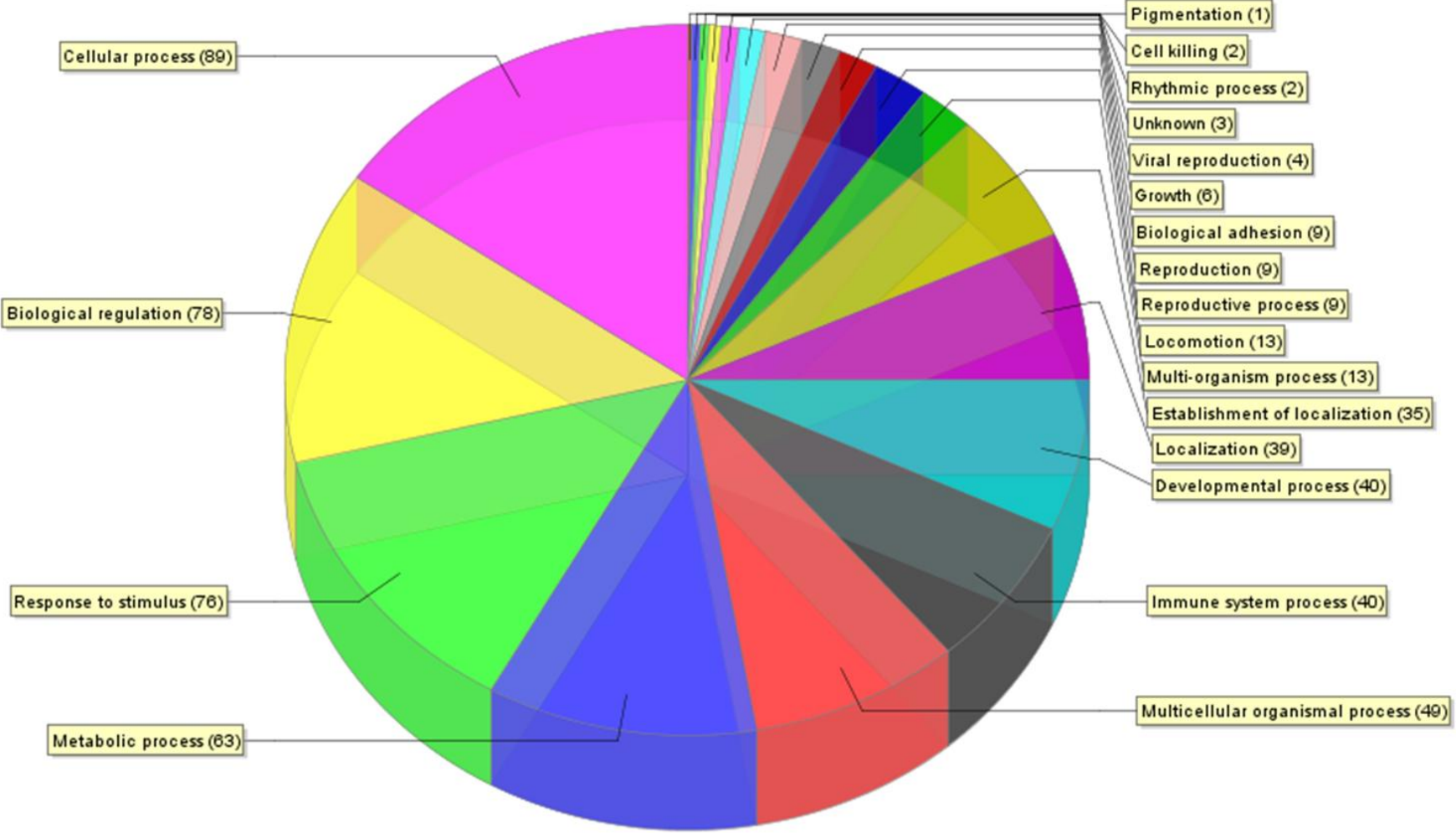
B. Unique peptides



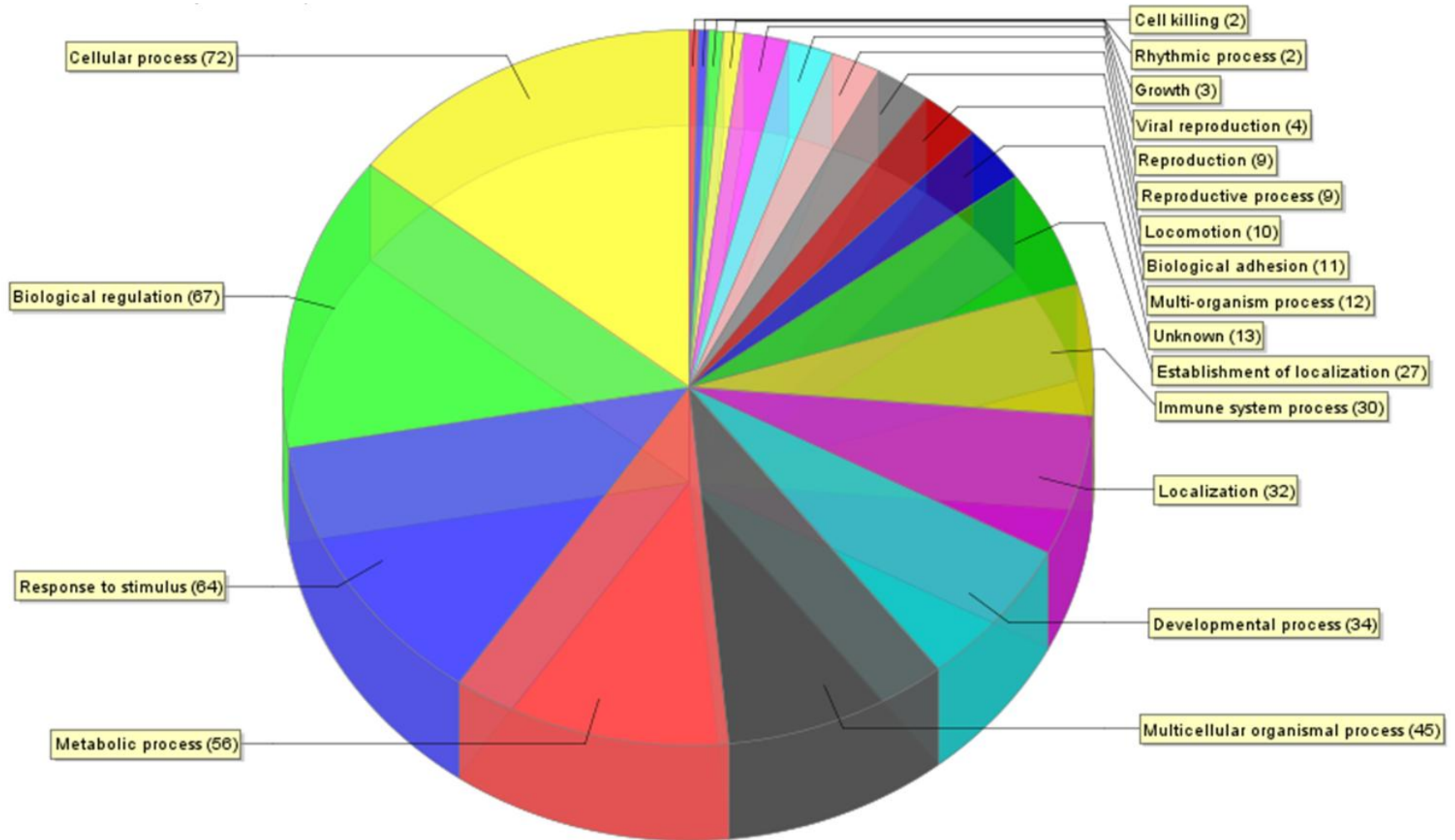
Supplementary Figure 3. Comparisons of number of identified glycoproteins from LC-ESI-MS/MS.



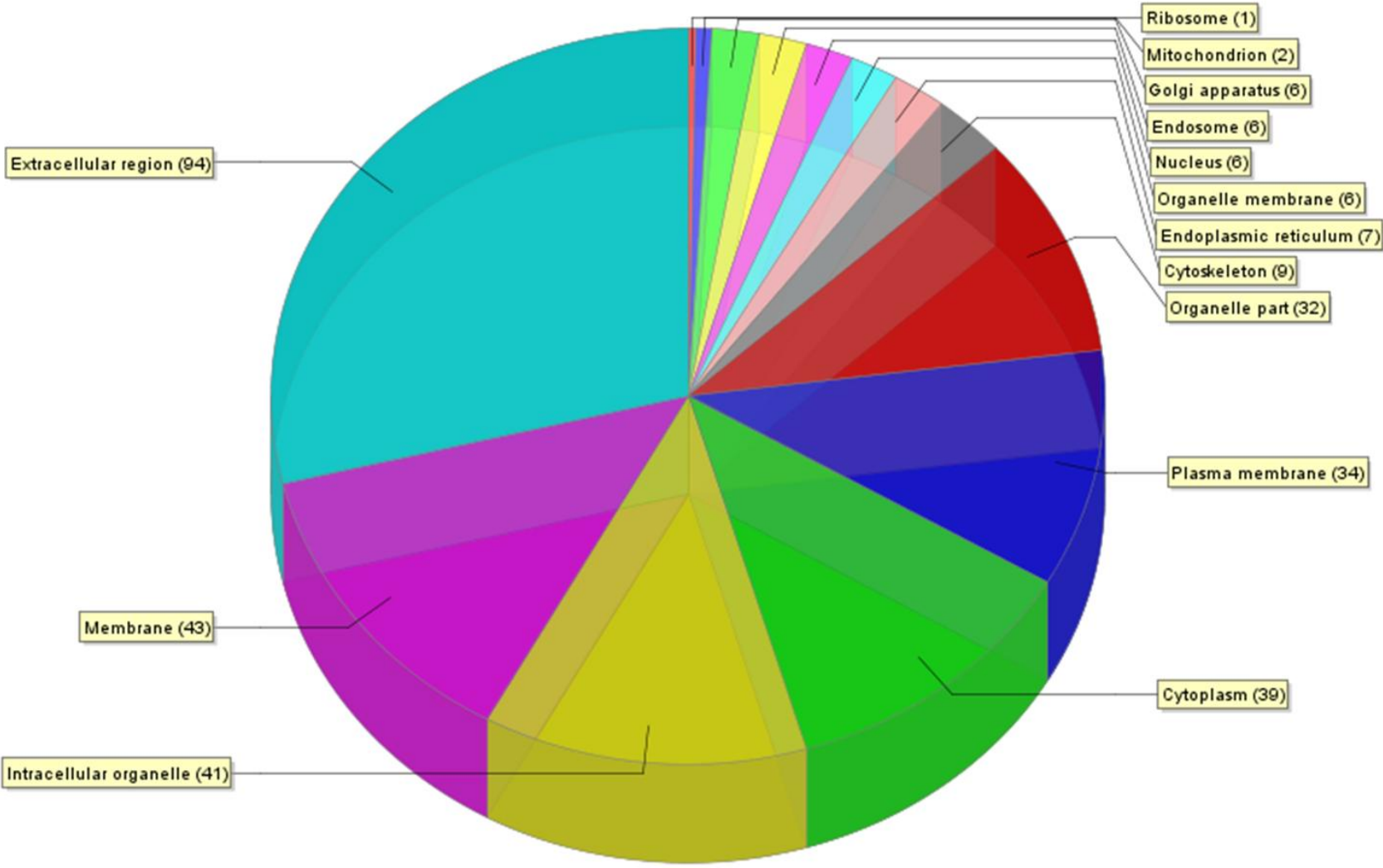
Supplementary Figure 4A. Gene ontology for biological process from identified glycoproteins enriched by lectin affinity chromatographic enrichment.



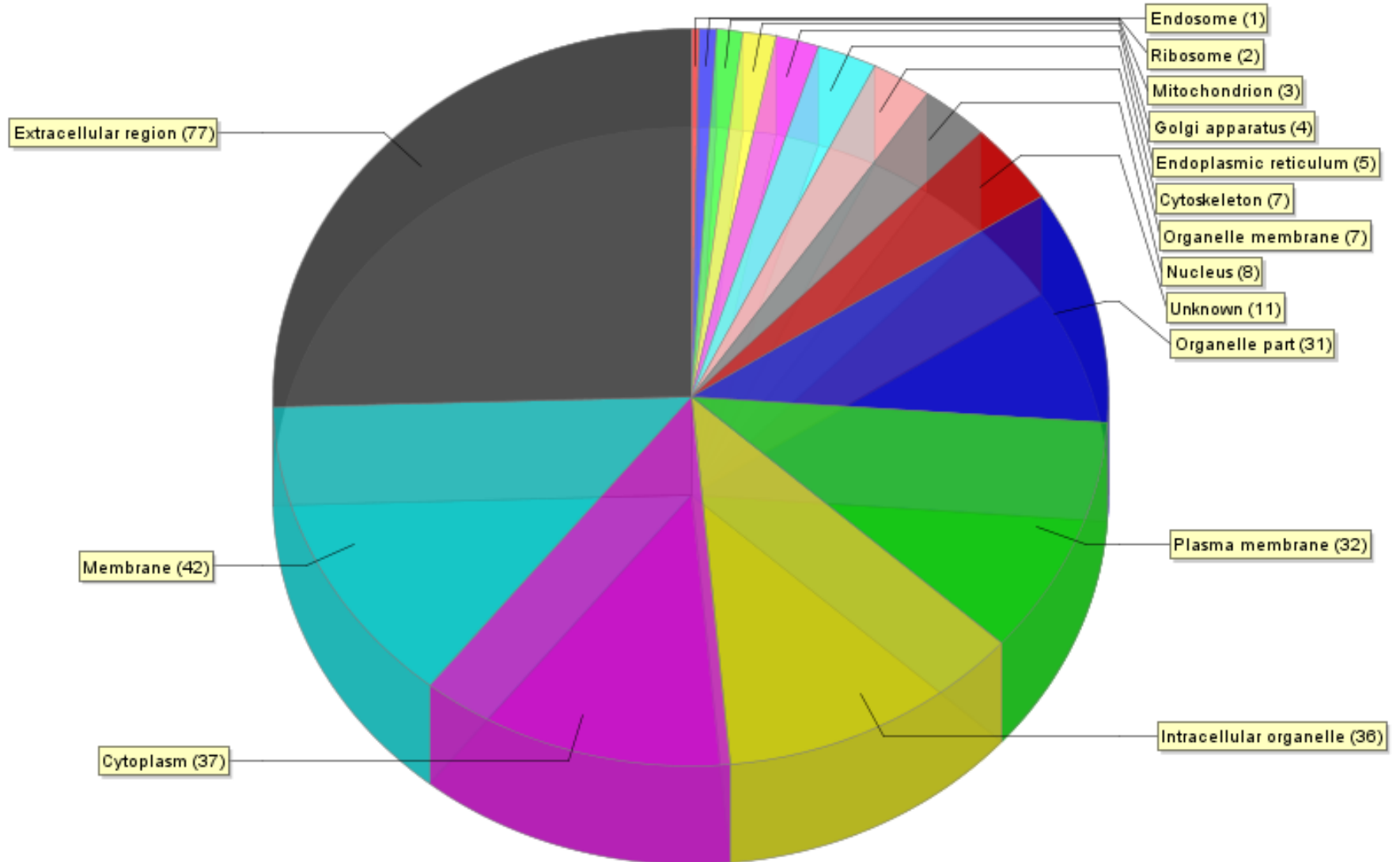
Supplementary Figure 4B. Gene ontology for biological process from identified glycoproteins enriched by hydrazide chemistry.



Supplementary Figure 5A. Gene ontology for cellular component from identified glycoproteins enriched by lectin affinity chromatographic enrichment.

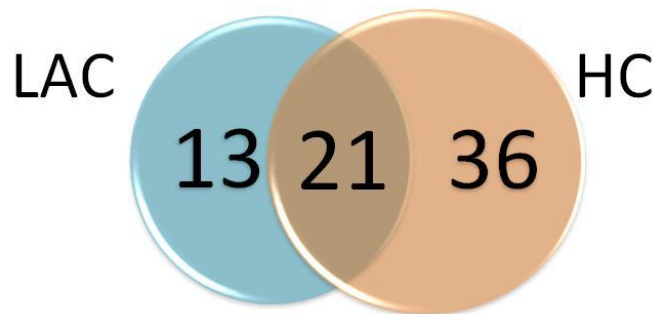


Supplementary Figure 5B. Gene ontology for cellular component from identified glycoproteins enriched by hydrazide chemistry



Supplementary Figure 6. Comparisons of number of targeted glycoproteins (A) and glycosylation sites (B) for MRM experiments and statistical evaluation.

A. Number of glycoproteins
between LAC and HC



B. Number of glycosylation sites
between LAC and HC

