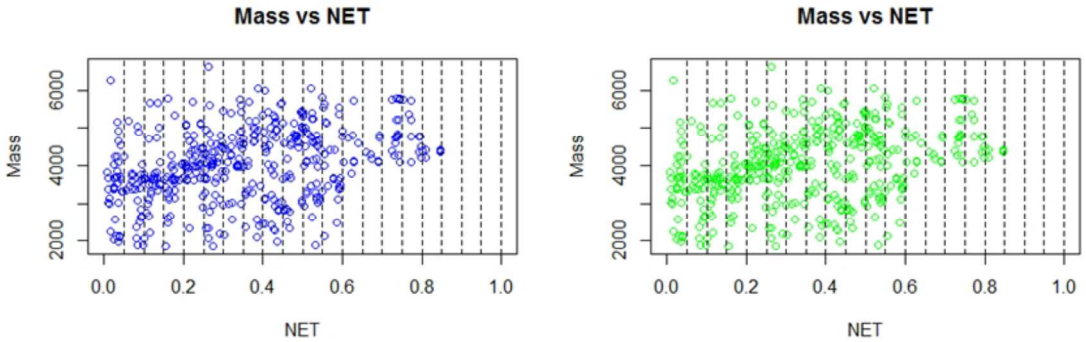
Supplementary Information

Protein	p-value from ANOVA model	p-value from t-test
sp|P00738|HPT_HUMAN	3.72e-04	7.043e-05
sp|P01024|CO3_HUMAN	1.21E-06	0.04646
sp|P02790|HEMO_HUMAN	1.29E-11	0.1803
sp|P04004|VTNC_HUMAN	8.80E-17	0.1386

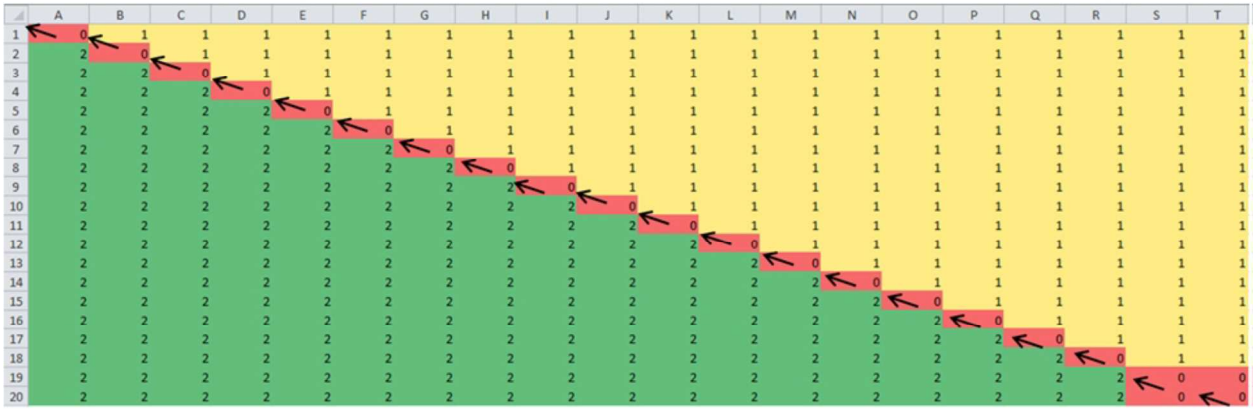
Supplementary Table 1: Comparison of p-values of four significant proteins from the ANOVA model to those acquired from a simple t-test. The t-test fails to capture site-specific variation within a glycoprotein among classes.

Protein	Control Average Spectral Count	Cancer Average Spectral Count
sp|P00738|HPT_HUMAN	6.08	13.39
sp|P01024|CO3_HUMAN	231.11	257.45
sp|P02790|HEMO_HUMAN	48.92	70.71
sp|P04004|VTNC_HUMAN	9.33	8.83

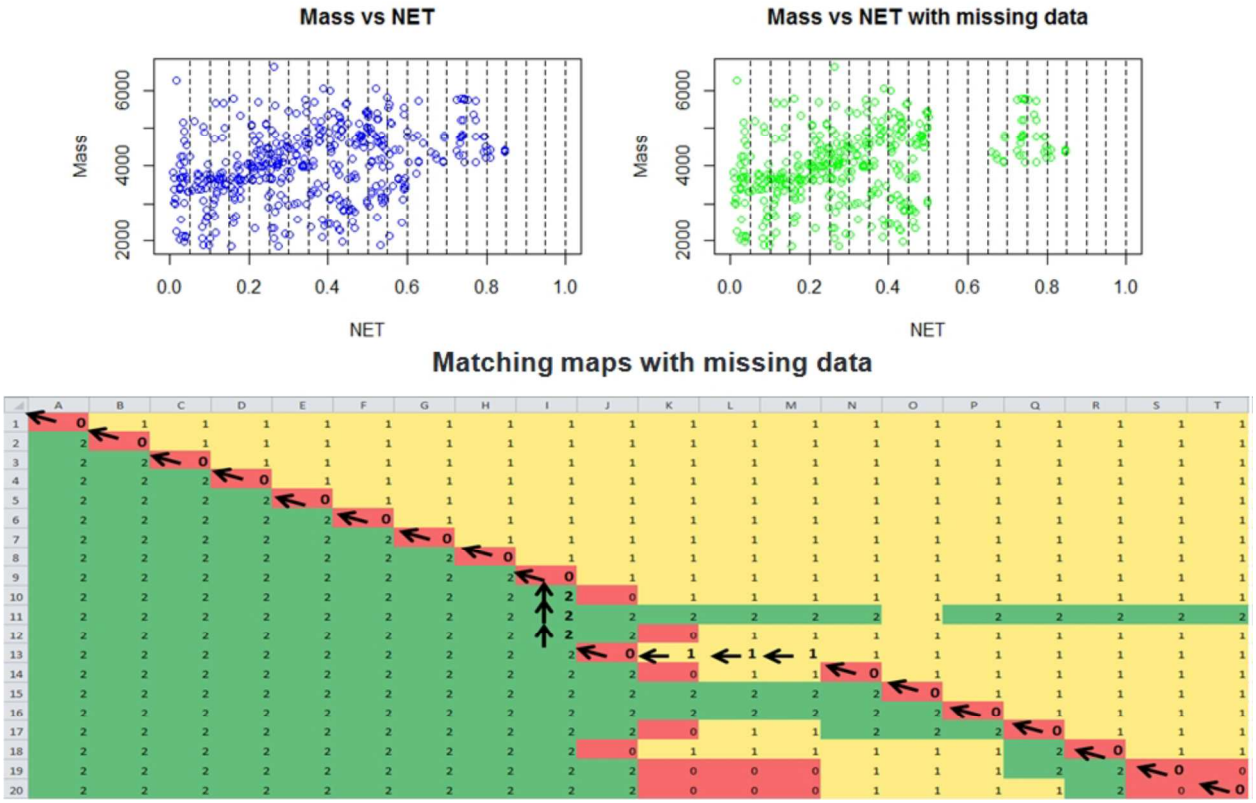
Supplementary Table 2: Average total protein spectral count in pooled cancer and control datasets. The spectral count was derived from doing a MASCOT search on non-glycosylated peptides of the glycoprotein.



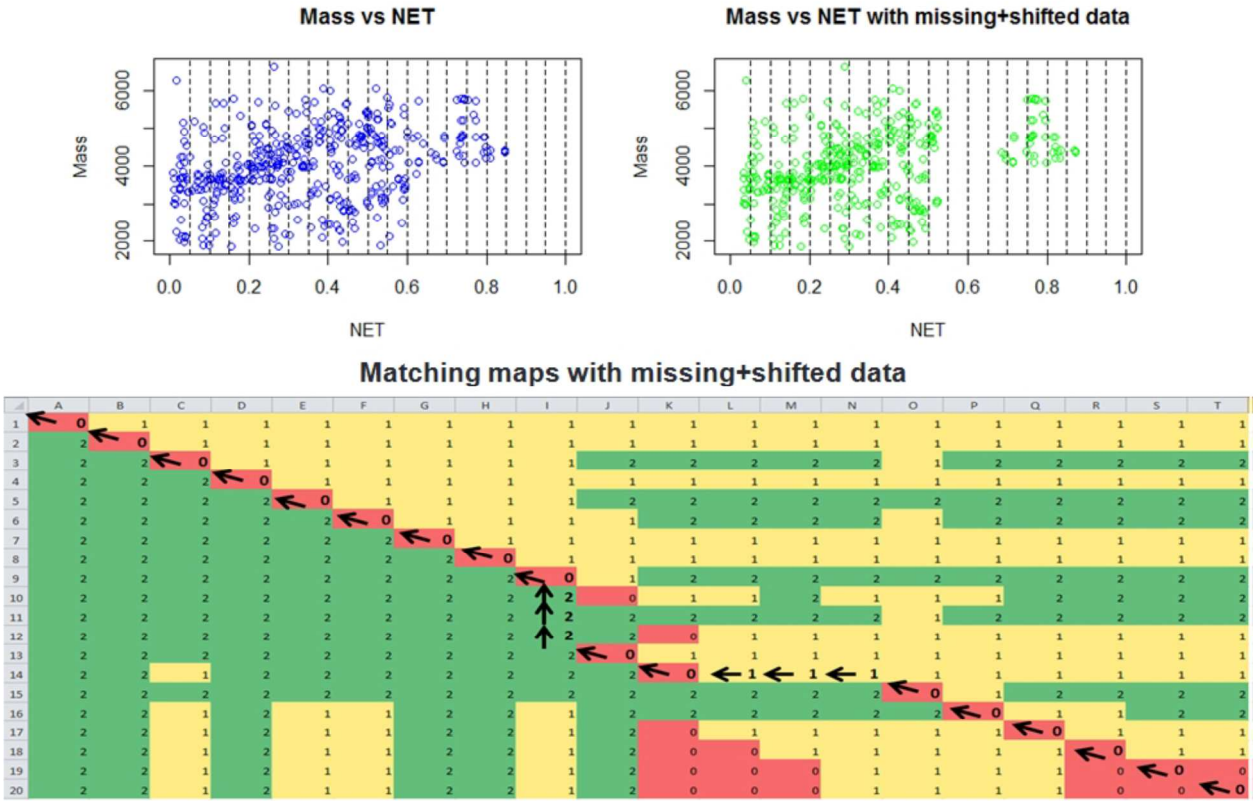
Matching maps that are identical



Supplementary Figure 1: GlycoMap alignment in the scenario when the target and reference are the same



Supplementary Figure 2: GlycoMap alignment in the scenario when the reference is the same as target map but with points missing.



Supplementary Figure 3: GlycoMap alignment in the scenario when the reference is the same as target map but with both missing and shifted points.