

Supplementary Materials

Comparative O-GlcNAc Proteomic Analysis Reveals a Role of O-GlcNAcylated SAM68 in Lung Cancer Aggressiveness

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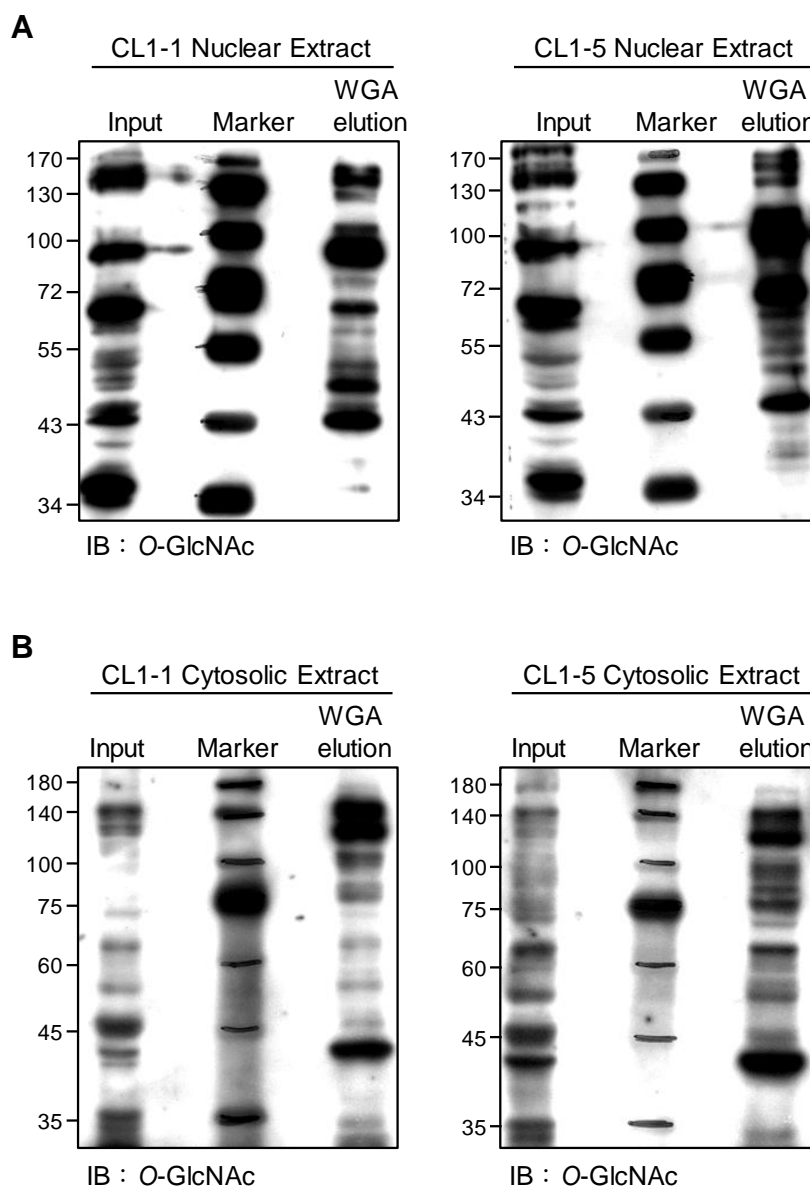


Figure S1. Enrichment of nuclear/cytosolic O-GlcNAcylated proteins. Nuclear (A) and cytosolic (B) extracts from CL1-1 and CL1-5 cells were subjected to GlcNAc-binding lectin-based affinity chromatography using resin-bound wheat germ agglutinin (WGA). Proteins in the extracts (input) and the WGA elution fractions were separated by SDS-PAGE and were immunoblotted (IB) using O-GlcNAc antibodies. Each input sample contained 100 μ g of proteins, and each WGA elution sample contained 5 μ g of proteins. Detailed information about the Western blotting can be found in Figure S14.

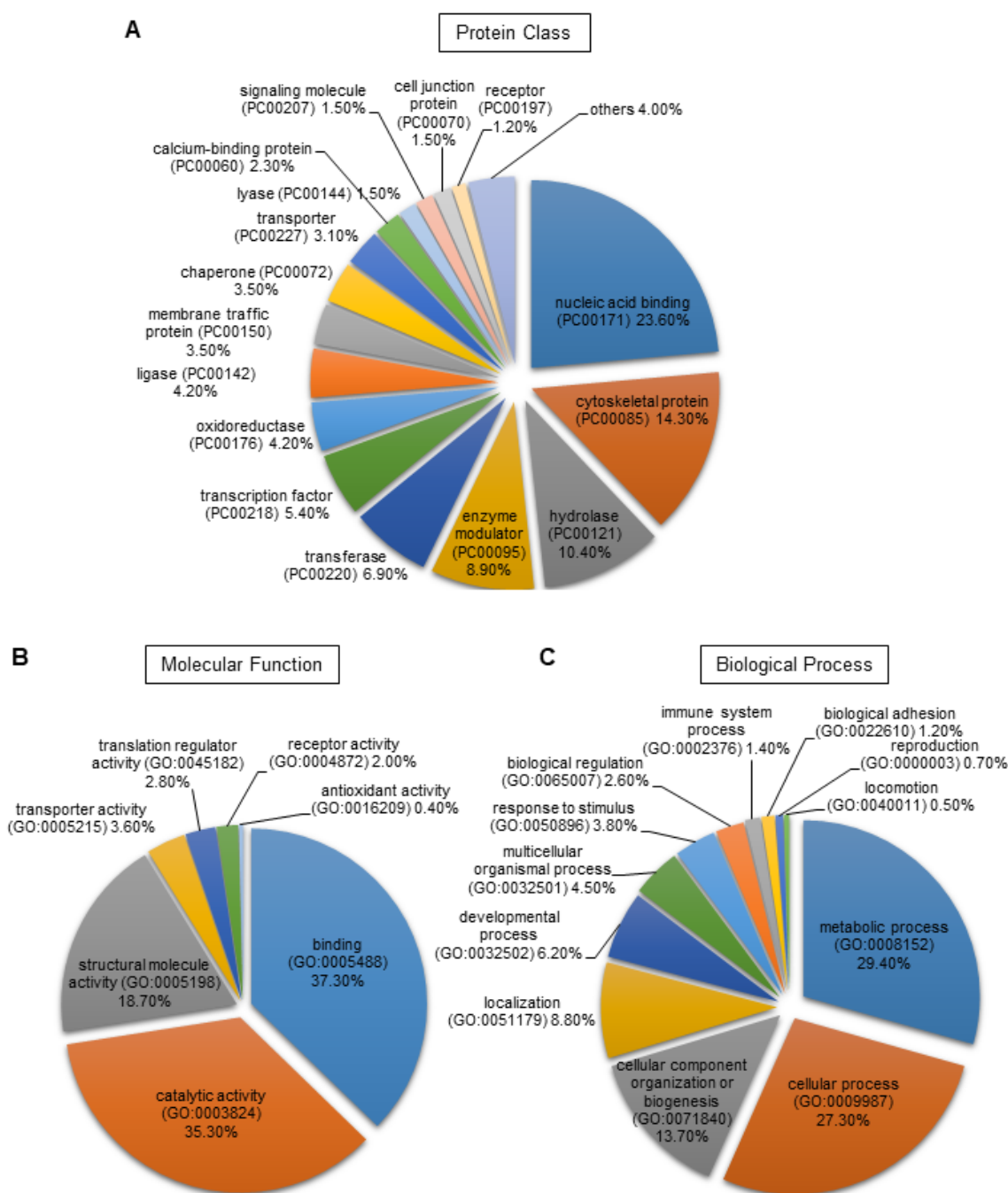


Figure S2. Gene ontology analysis. Differential WGA-bound nuclear/cytosolic glycoproteins between CL1 and CL5 samples were classified according to their protein classes (**A**), molecular functions (**B**), and biological processes (**C**) using the PANTHER classification system (<http://www.pantherdb.org/>, accessed on 13 Feb 2019). WGA, wheat germ agglutinin; PANTHER, Protein ANalysis THrough Evolutionary Relationships.

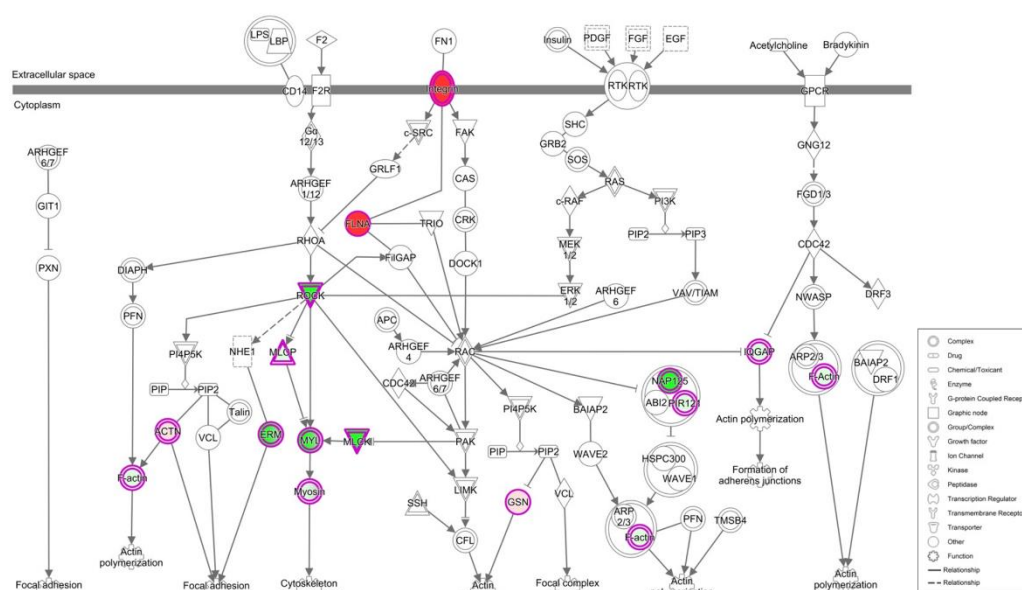


Figure S3. The actin cytoskeleton signaling pathway. Ingenuity Pathway Analysis of the differential wheat germ agglutinin (WGA)-bound nuclear/cytosolic glycoproteins identified this pathway as the top canonical pathway. Proteins with purple outlines are differential WGA-bound glycoproteins identified in this study; those in red and green shades are up- and down-regulated, respectively, in CL1-5 cells relative to CL1-1 cells. Proteins in white-colored symbols are not in our list of differential WGA-bound glycoproteins but were incorporated into the network based on the Ingenuity database.

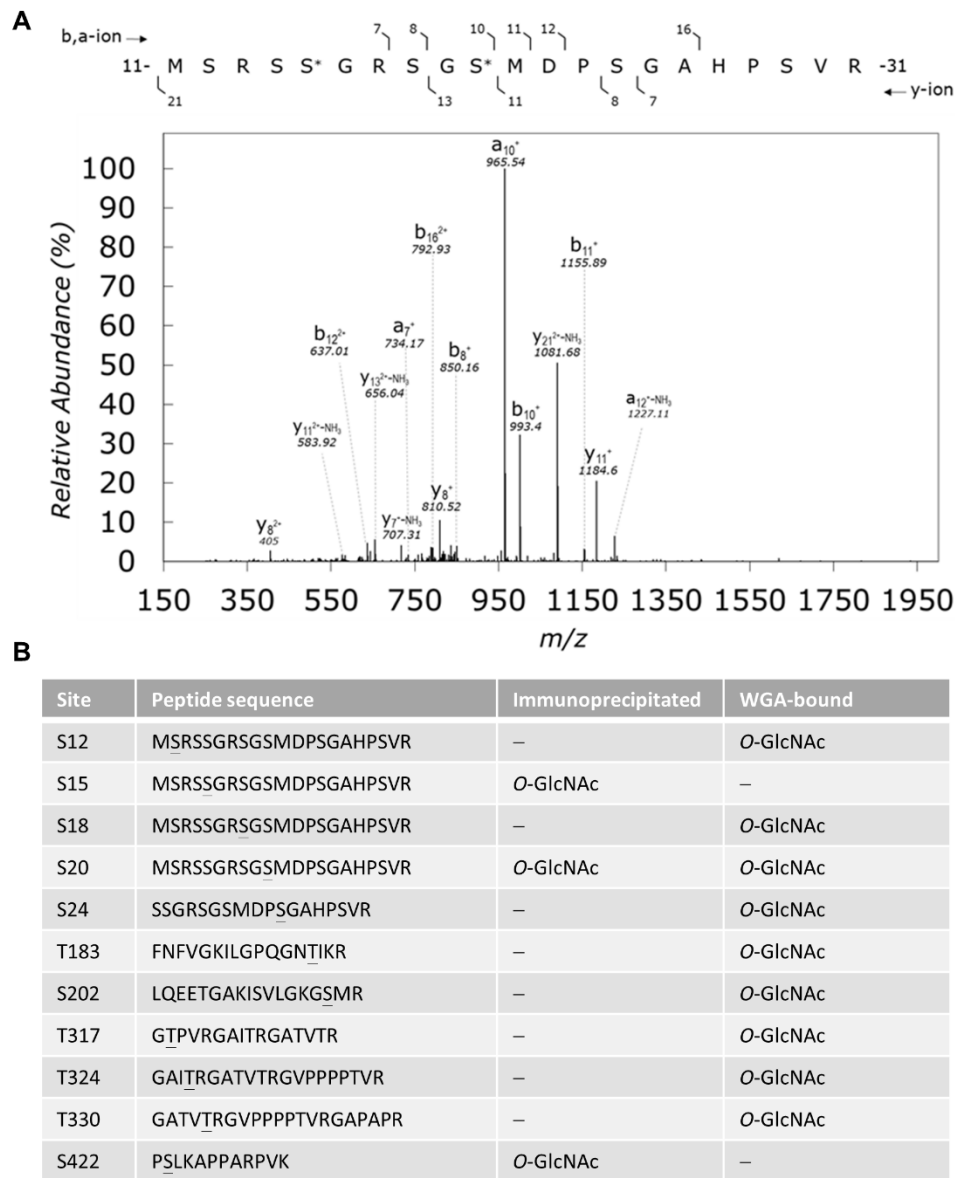


Figure S4. Identification of O-GlcNAcylation sites by MS/MS analysis. **(A)** A representative MS/MS spectrum of the peptide with a sequence of 11-MSRSS*GRSGS*MDPSGAHPSVR-31 is shown as an example for O-GlcNAcylation site identification; *, O-GlcNAcylated Ser residue. **(B)** A summary of O-GlcNAcylation sites revealed by results from multiple experiments of MS/MS analysis on wheat germ agglutinin (WGA)-bound or immunoprecipitated SAM68 samples. Underlined are identified O-GlcNAcylated residues.

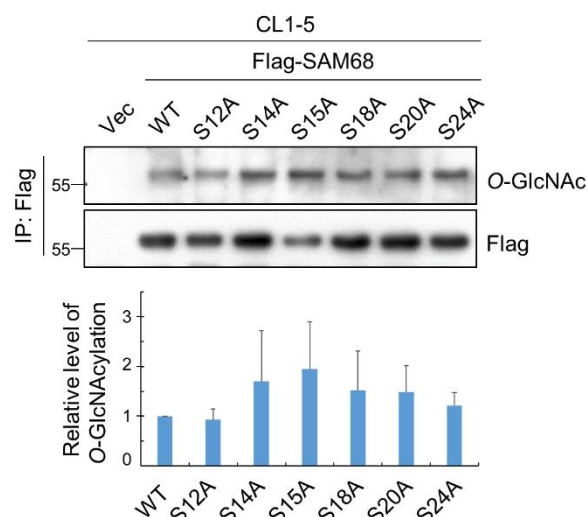


Figure S5. Comparison of O-GlcNAcylation levels of wild-type and mutant SAM68. Whole-cell lysates from CL1-5 cells transfected with the control vector (Vec) or an expression construct of wild-type (WT) or single-site mutant of SAM68 were subjected to immunoprecipitation (IP) and Western analysis. Representative Western results and quantitative data (means \pm SD) from three independent experiments are shown. The relative level of O-GlcNAcylation for each mutant was calculated by normalizing the O-GlcNAc/Flag Western signal ratio to that of the WT samples. Detailed information about the Western blotting can be found in Figure S15.

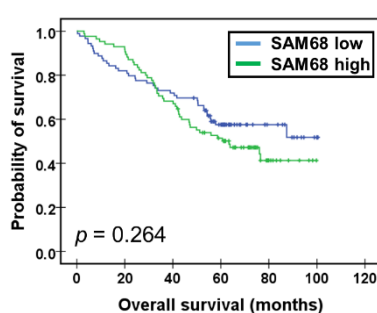


Figure S6. Kaplan-Meier analysis of the overall survival of patients with lung adenocarcinoma. Patients ($n = 174$) were categorized into high and low SAM68 expression groups according to the medium IHC score. p -values were derived from the log-rank test.

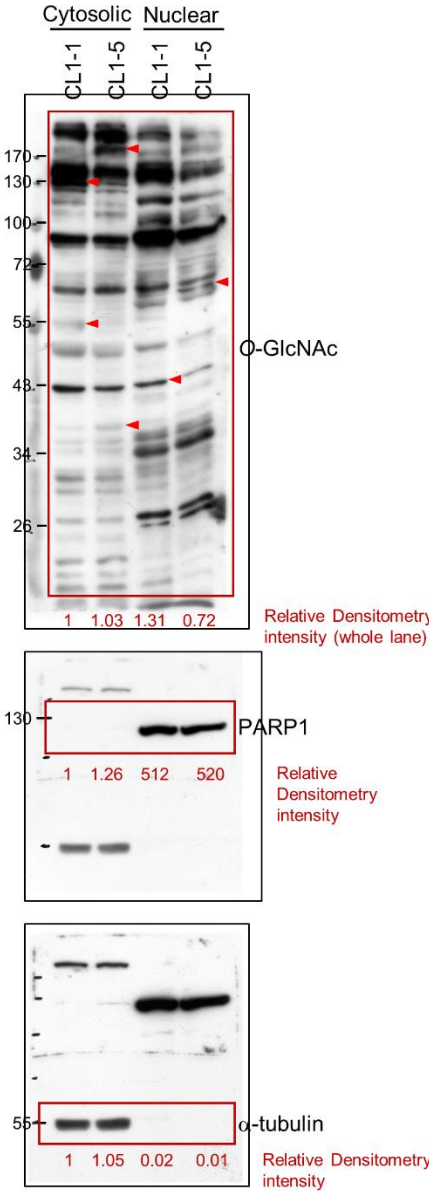


Figure S7. Full Western blot for Figure 1B.

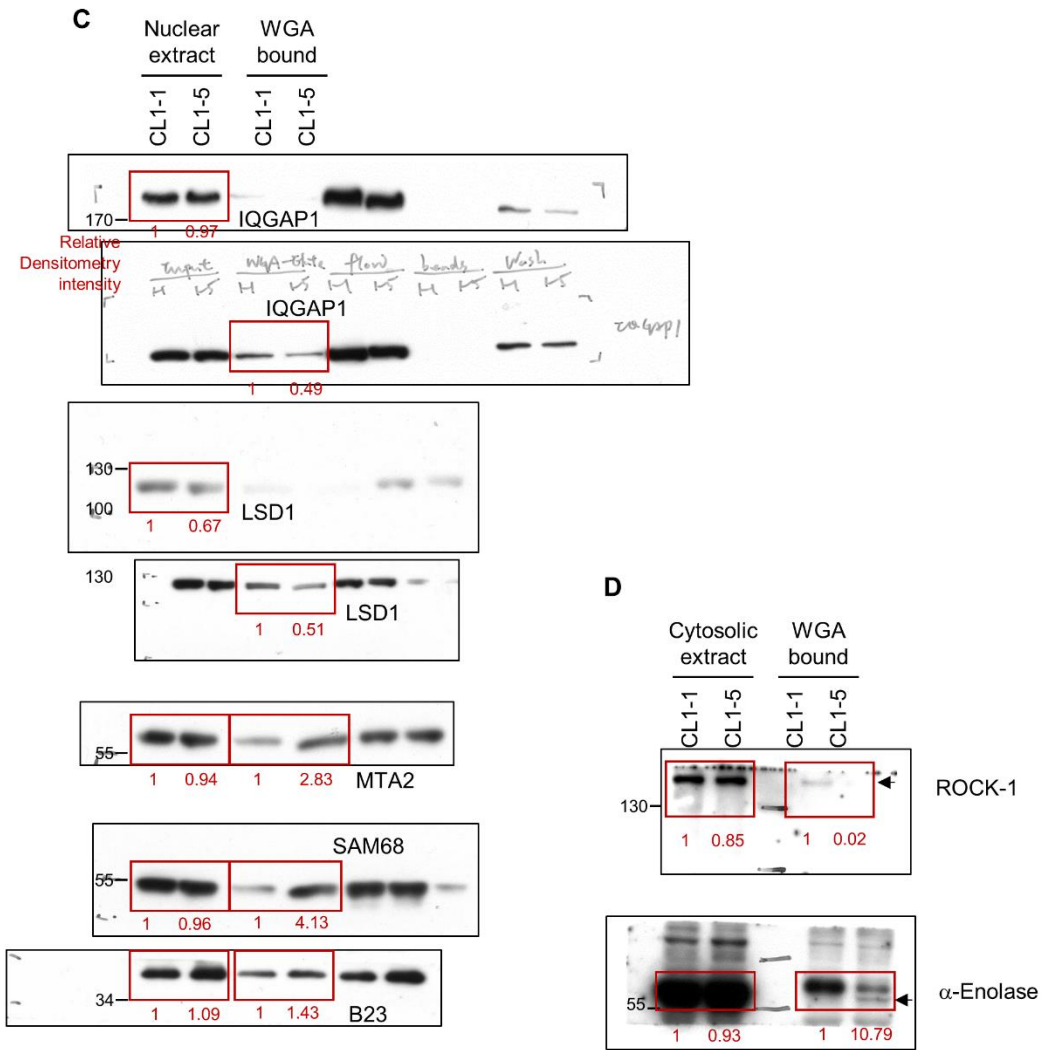


Figure S8. Full Western blot for Figure 2C and 2D. WGA, wheat germ agglutinin.

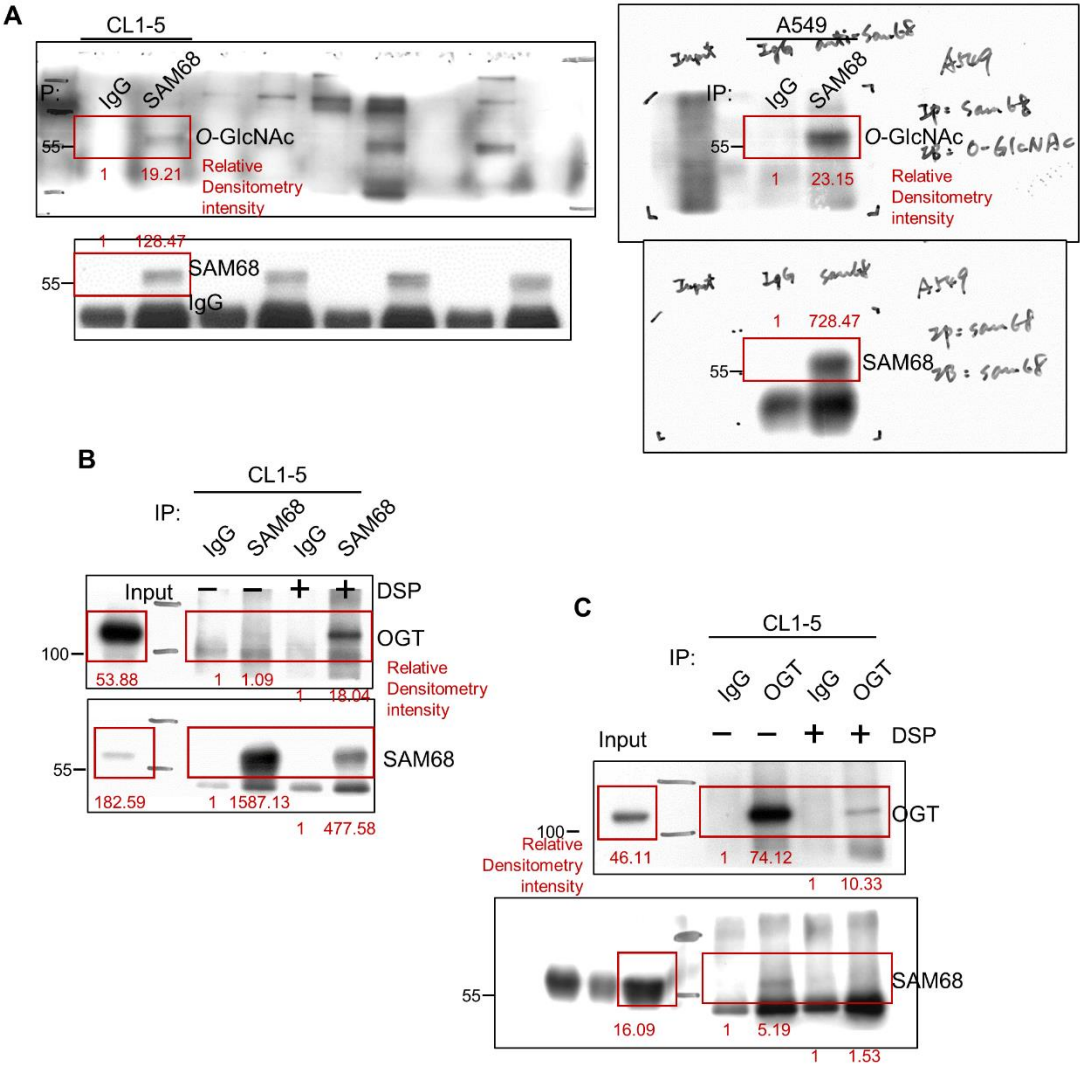


Figure S9. Full Western blot for Figure 3A–C. OGT, O-GlcNAc transferase

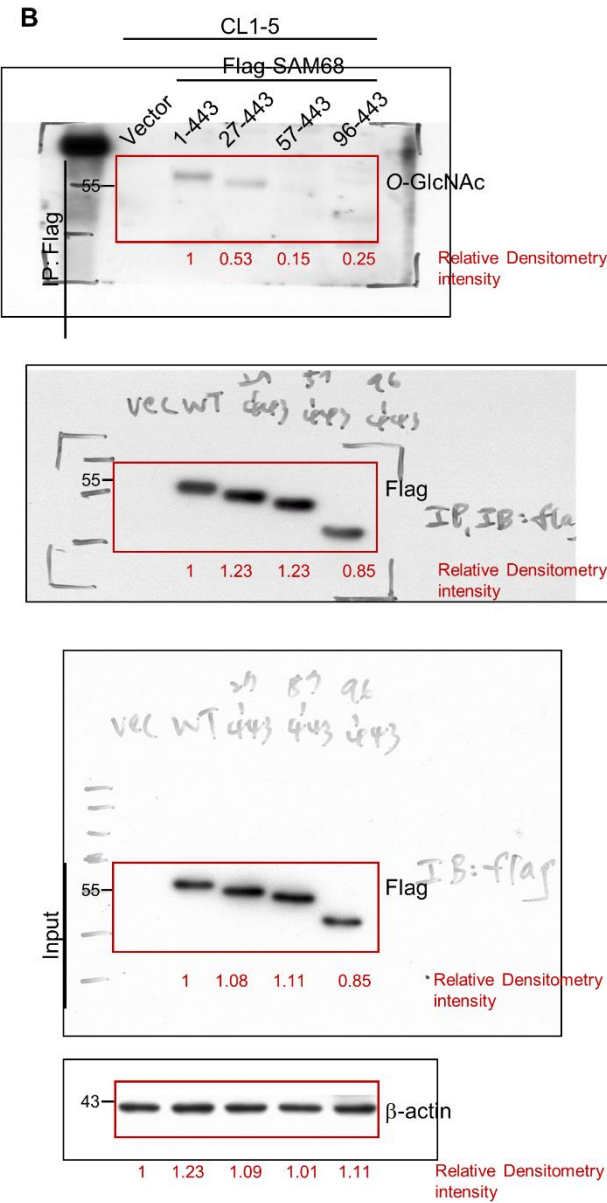


Figure S10. Full Western blot for Figure 4B.

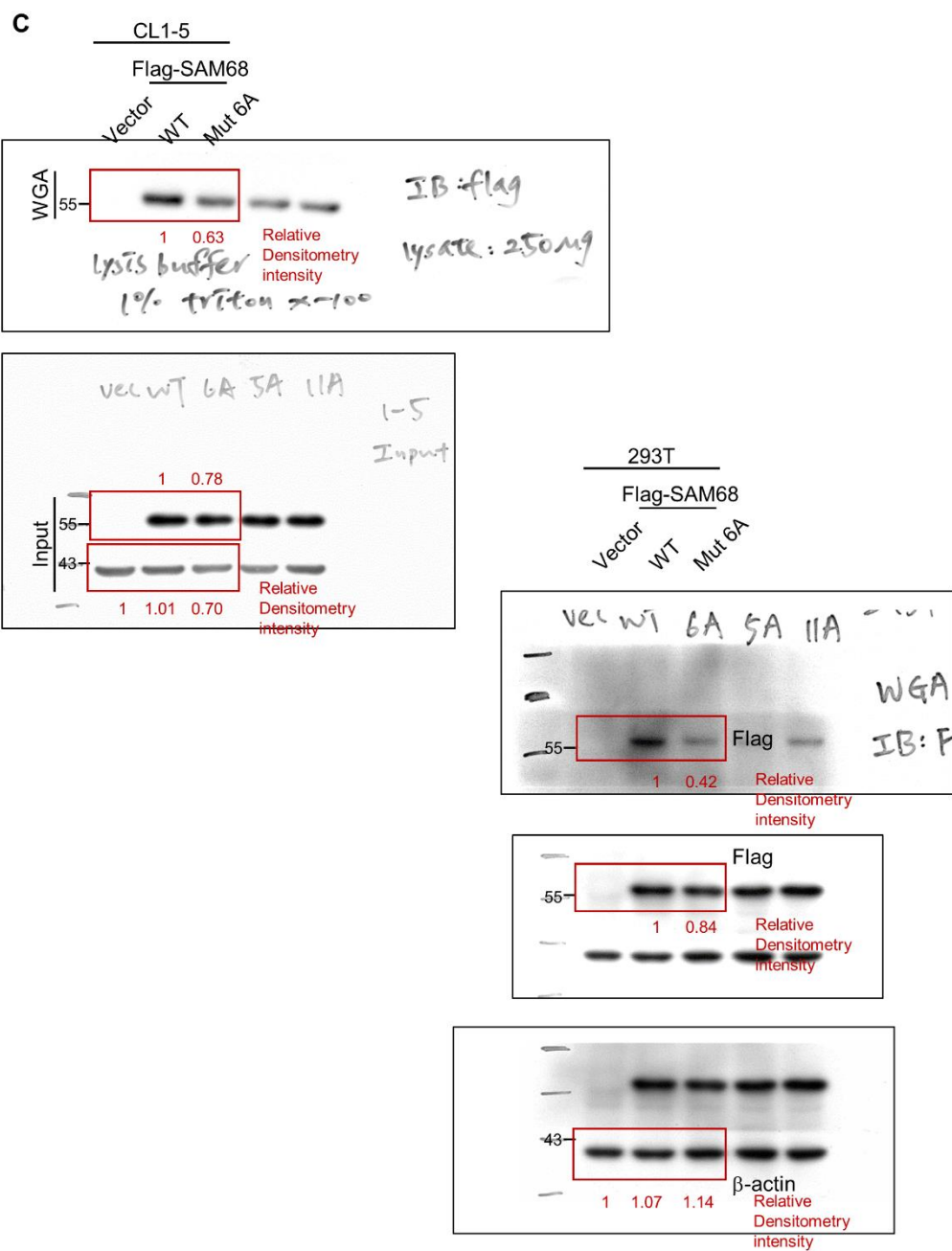


Figure S11. Full Western blot for Figure 4C.

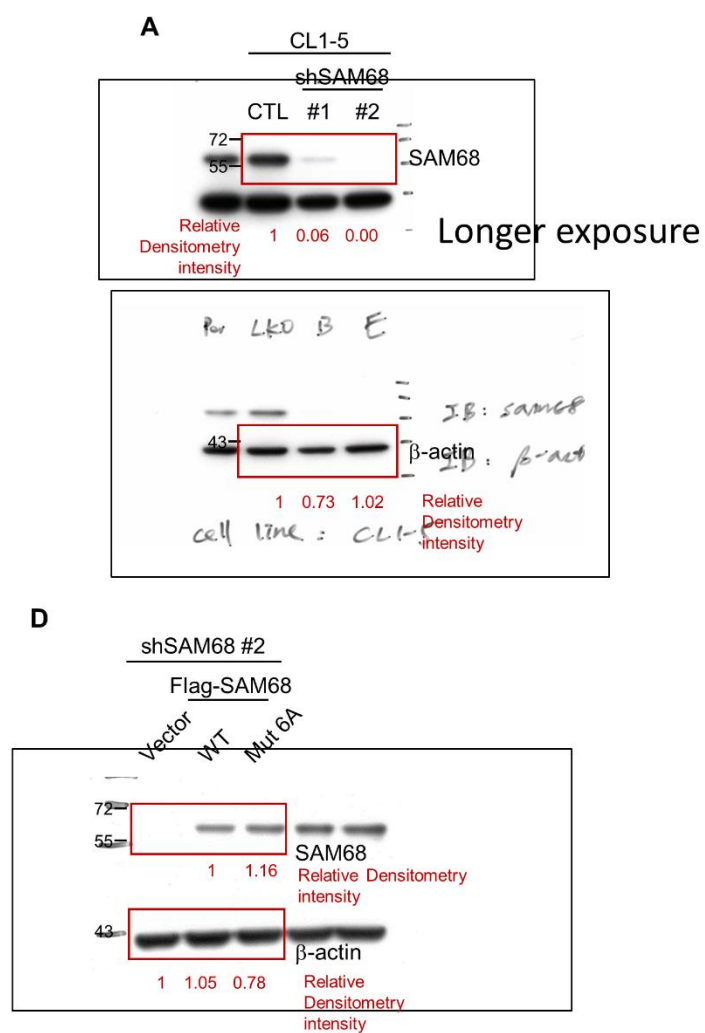


Figure S13. Full Western blot for Figure 5A and 5D.

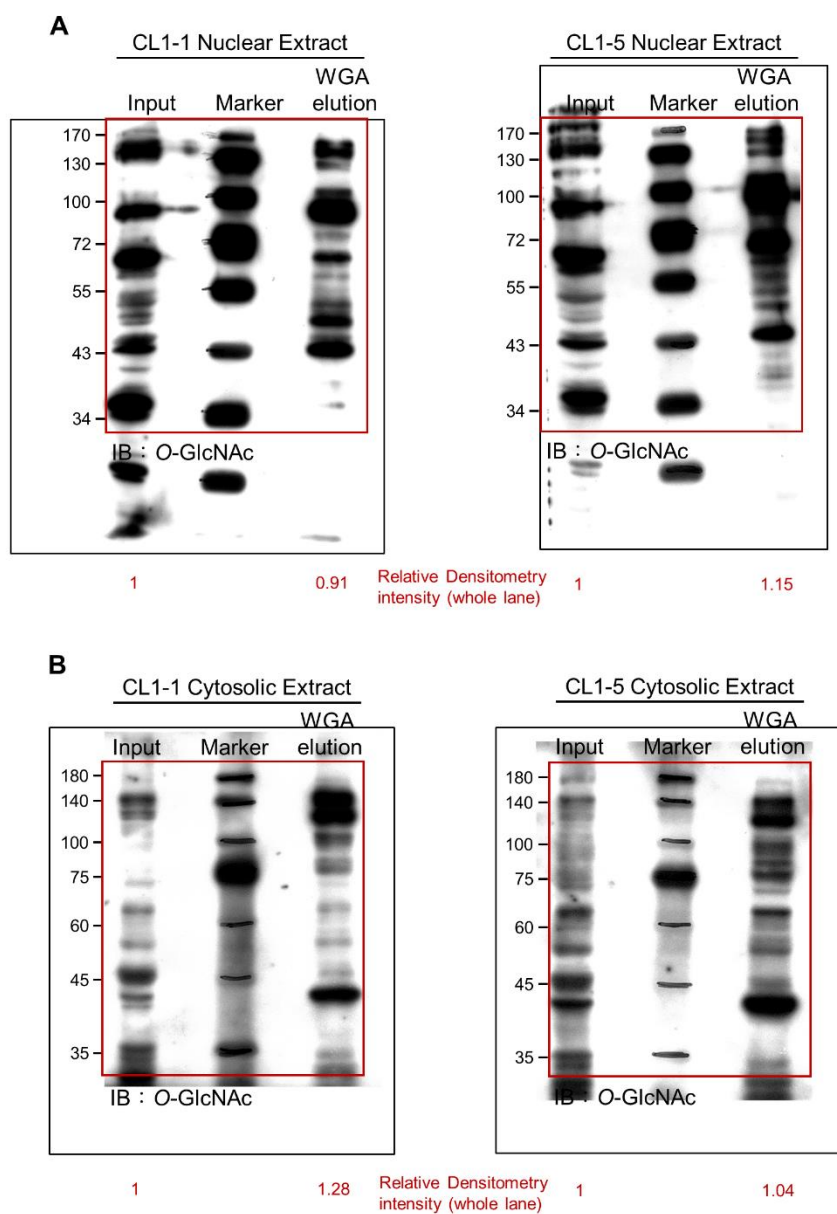


Figure S14. Full Western blot for Figure S1.

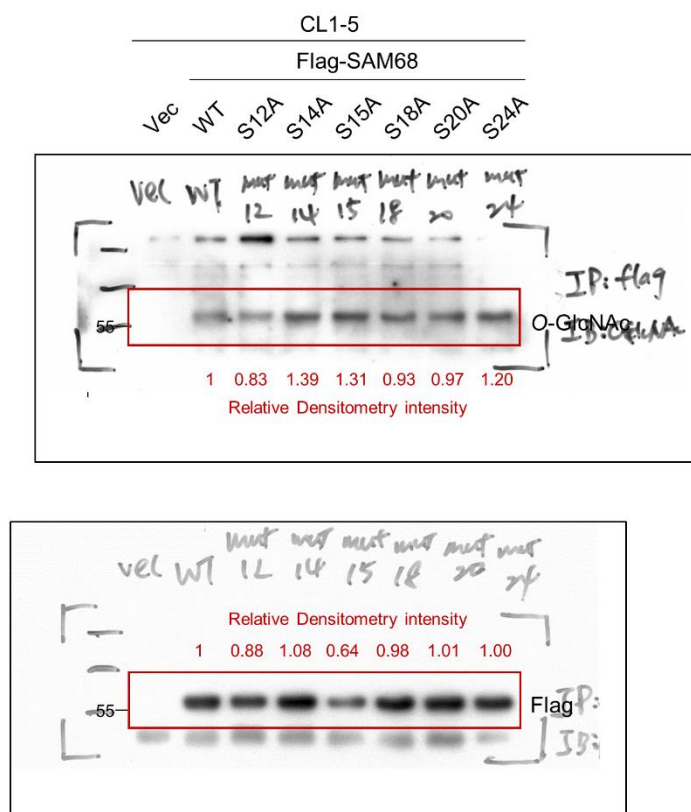


Figure S15. Full Western blot for Figure S5.

Table S1. Differential WGA-bound glycoproteins identified in nuclear extracts from lung adenocarcinoma cell lines CL1-1 and CL1-5.

| Protein ID | Symbol | Protein Name | Normalized Spectral Counts (Mean ± SE) ¹ | | <i>p</i> -Value ² | Fold Change | Listed in the O-GlcNAc Database ³ |
|-------------------------|------------|--|--|----------------|------------------------------|----------------|--|
| | | | In CL1-1 | In CL1-5 | | | |
| Down-regulated in CL1-5 | | | | | | | |
| E7EVA0 | E7EVA0 | Microtubule-associated protein | 23.51 ± 6.02 | 1.03 ± 1.03 | 0.021 | ↓22.90 | no |
| P35580 | MYH10 | Myosin-10 | 155.97 ± 16.06 | 13.93 ± 5.70 | 0.001 | ↓11.20 | yes |
| P12532 | KCRU | Creatine kinase U-type, mitochondrial | 7.74 ± 1.19 | 0.70 ± 0.70 | 0.007 | ↓11.01 | yes |
| P02786 | TFR1 | Transferrin receptor protein 1 | 5.01 ± 0.59 | 0.51 ± 0.51 | 0.005 | ↓9.75 | yes |
| H3BPE1 | H3BPE1 | Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 | 9.46 ± 0.94 | 1.20 ± 1.20 | 0.006 | ↓7.89 | yes |
| Q7L576 | CYFP1 | Cytoplasmic FMR1-interacting protein 1 | 8.96 ± 1.86 | 1.32 ± 1.32 | 0.029 | ↓6.78 | yes |
| P19801 | AOC1 | Amiloride-sensitive amine oxidase [copper-containing] | 4.33 ± 0.28 | 0.69 ± 0.69 | 0.008 | ↓6.32 | no |
| Q06203 | PUR1 | Amidophosphoribosyltransferase | 3.17 ± 0.43 | 0.51 ± 0.51 | 0.016 | ↓6.17 | yes |
| A0A087WWU8 | A0A087WWU8 | Tropomyosin alpha-3 chain | 20.43 ± 2.24 | 3.54 ± 1.78 | 0.004 | ↓5.78 | yes |
| P35749 | MYH11 | Myosin-11 | 37.60 ± 2.06 | 7.07 ± 2.72 | 0.001 | ↓5.32 | yes |
| P78347 | GTF2I | General transcription factor II-I | 4.49 ± 0.43 | 0.99 ± 0.99 | 0.032 | ↓4.53 | yes |
| Q96ST3 | SIN3A | Paired amphipathic helix protein Sin3a | 4.54 ± 0.86 | 1.02 ± 0.51 | 0.025 | ↓4.44 | yes |
| P09874 | PARP1 | Poly [ADP-ribose] polymerase 1 | 5.00 ± 0.44 | 1.19 ± 0.61 | 0.007 | ↓4.21 | yes |
| P12277 | KCRB | Creatine kinase B-type | 25.99 ± 2.47 | 6.22 ± 2.65 | 0.006 | ↓4.18 | yes |
| O60341 | KDM1A | Lysine-specific histone demethylase 1A | 6.24 ± 1.14 | 1.53 ± 0.77 | 0.027 | ↓4.08 | yes |
| Q8NE71 | ABCF1 | ATP-binding cassette sub-family F member 1 | 2.65 ± 0.26 | 0.66 ± 0.66 | 0.049 | ↓4.01 | yes |
| Q16568 | CART | Cocaine- and amphetamine-regulated transcript protein | 2.00 ± 0.06 | 0.51 ± 0.51 | 0.045 | ↓3.90 | no |
| Q7Z406 | MYH14 | Myosin-14 | 24.04 ± 2.58 | 7.91 ± 2.32 | 0.010 | ↓3.04 | yes |
| P55884 | EIF3B | Eukaryotic translation initiation factor 3 subunit B | 6.11 ± 0.94 | 2.04 ± 1.05 | 0.044 | ↓3.00 | yes |
| Q04917 | 1433F | 14-3-3 protein eta | 11.19 ± 1.03 | 3.74 ± 0.59 | 0.003 | ↓2.99 | yes |
| Q15642 | CIP4 | Cdc42-interacting protein 4 | 7.15 ± 0.41 | 2.56 ± 0.28 | 0.001 | ↓2.80 | yes |
| Q9NYU2 | UGGG1 | UDP-glucose:glycoprotein glucosyltransferase 1 | 17.80 ± 1.58 | 6.46 ± 0.89 | 0.003 | ↓2.75 | yes |
| P35579 | MYH9 | Myosin-9 | 285.90 ± 25.16 | 104.71 ± 18.50 | 0.004 | ↓2.73 | yes |
| P67936 | TPM4 | Tropomyosin alpha-4 chain | 17.63 ± 2.69 | 6.66 ± 0.27 | 0.015 | ↓2.65 | yes |
| P46940 | IQGA1 | Ras GTPase-activating-like protein IQGAP1 | 75.84 ± 6.65 | 34.35 ± 5.51 | 0.009 | ↓2.21 | yes |
| Q9Y4L1 | HYOU1 | Hypoxia up-regulated protein 1 | 11.64 ± 1.25 | 5.29 ± 0.44 | 0.009 | ↓2.20 | yes |
| Q6S8J3 | POTEE | POTE ankyrin domain family member E | 41.86 ± 3.77 | 19.18 ± 4.09 | 0.015 | ↓2.18 | yes |
| P22314 | UBA1 | Ubiquitin-like modifier-activating enzyme 1 | 36.53 ± 2.91 | 16.98 ± 2.72 | 0.008 | ↓2.15 | yes |
| P61981 | 1433G | 14-3-3 protein gamma | 21.05 ± 2.90 | 10.01 ± 1.87 | 0.033 | ↓2.10 | yes |
| Q14697 | GANAB | Neutral alpha-glucosidase AB | 40.04 ± 0.65 | 20.45 ± 2.27 | 0.001 | ↓1.96 | yes |
| Q15691 | MARE1 | Microtubule-associated protein RP/EB family member 1 | 23.57 ± 2.35 | 13.29 ± 0.55 | 0.013 | ↓1.77 | yes |
| P34932 | HSP74 | 70-kDa Heat-shock protein 4 | 45.24 ± 1.14 | 26.38 ± 3.04 | 0.004 | ↓1.72 | yes |
| P49321 | NASP | Nuclear autoantigenic sperm protein | 16.74 ± 1.81 | 10.04 ± 1.35 | 0.041 | ↓1.67 | yes |
| V9HVZ7 | V9HVZ7 | Epididymis luminal protein 176 | 73.03 ± 3.75 | 45.49 ± 8.25 | 0.038 | ↓1.61 | no |
| O14776 | TCRG1 | Transcription elongation regulator 1 | 45.05 ± 2.81 | 29.02 ± 4.82 | 0.045 | ↓1.55 | yes |
| Q562R1 | ACTBL | Beta-actin-like protein 2 | 31.54 ± 0.55 | 20.56 ± 3.45 | 0.035 | ↓1.53 | yes |
| Q01970 | PLCB3 | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 | 2.17 ± 0.42 | N.D. | 0.007 | - | yes |

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|-----------------------|--------|--|--------------|---------------|-------|--------|-----|
| P08195 | 4F2 | 4F2 cell-surface antigen heavy chain | 1.84 ± 0.20 | N.D. | 0.001 | - | yes |
| P17050 | NAGAB | Alpha-N-acetylgalactosaminidase | 2.51 ± 0.08 | N.D. | 0.000 | - | yes |
| P04083 | ANXA1 | Annexin A1 | 14.83 ± 3.17 | N.D. | 0.010 | - | yes |
| Q8IZY2 | ABCA7 | ATP-binding cassette sub-family A member 7 | 1.83 ± 0.12 | N.D. | 0.000 | - | yes |
| Q9P2I0 | CPSF2 | Cleavage and polyadenylation specificity factor subunit 2 | 3.33 ± 0.56 | N.D. | 0.004 | - | yes |
| P43246 | MSH2 | DNA mismatch repair protein Msh2 | 4.66 ± 1.42 | N.D. | 0.031 | - | yes |
| P23434 | GCSH | Glycine cleavage system H protein, mitochondrial | 3.54 ± 0.84 | N.D. | 0.014 | - | yes |
| P41250 | SYG | Glycine--tRNA ligase | 4.66 ± 1.15 | N.D. | 0.015 | - | yes |
| Q8WXC9 | GPR98 | G-protein coupled receptor 98 | 3.01 ± 0.09 | N.D. | 0.000 | - | yes |
| P04792 | HSPB1 | Heat-shock protein beta-1 | 3.17 ± 0.71 | N.D. | 0.011 | - | yes |
| A8K9J7 | A8K9J7 | Histone H2B | 2.71 ± 0.77 | N.D. | 0.024 | - | yes |
| D3DS63 | D3DS63 | Importin 4, isoform CRA_f | 4.30 ± 0.56 | N.D. | 0.002 | - | no |
| P05556 | ITB1 | Integrin beta-1 | 2.80 ± 0.60 | N.D. | 0.010 | - | yes |
| P19105 | ML12A | Myosin regulatory light chain 12A | 6.93 ± 1.58 | N.D. | 0.012 | - | yes |
| O14950 | ML12B | Myosin regulatory light chain 12B | 6.93 ± 1.58 | N.D. | 0.012 | - | no |
| Q9Y2A7 | NCKP1 | Nck-associated protein 1 | 2.64 ± 0.67 | N.D. | 0.017 | - | yes |
| H0YN18 | H0YN18 | Proteasome subunit alpha type-4 | 3.15 ± 0.37 | N.D. | 0.001 | - | yes |
| Q04837 | SSBP | Single-stranded DNA-binding protein, mitochondrial | 3.86 ± 0.73 | N.D. | 0.006 | - | yes |
| Q14683 | SMC1A | Structural maintenance of chromosomes protein 1A | 3.64 ± 0.64 | N.D. | 0.005 | - | yes |
| Q6IMI6 | ST1C3 | Sulfotransferase 1C3 | 2.18 ± 0.24 | N.D. | 0.001 | - | no |
| A8K3C3 | A8K3C3 | T-complex protein 1 subunit delta | 2.84 ± 0.22 | N.D. | 0.000 | - | yes |
| Q99598 | TSNAX | Translin-associated protein X | 1.99 ± 0.24 | N.D. | 0.001 | - | yes |
| B7Z596 | B7Z596 | Tropomyosin alpha-1 chain | 10.16 ± 1.86 | N.D. | 0.006 | - | yes |
| Q9Y4Z0 | LSM4 | U6 snRNA-associated Sm-like protein LSM4 | 3.39 ± 0.96 | N.D. | 0.024 | - | yes |
| Q9UMX0 | UBQL1 | Ubiquilin-1 | 5.11 ± 1.38 | N.D. | 0.021 | - | yes |
| P54725 | RD23A | UV excision repair protein RAD23 homolog A | 2.36 ± 0.42 | N.D. | 0.005 | - | yes |
| Up-regulated in CL1-5 | | | | | | | |
| Q6IN85 | P4R3A | Serine/threonine-protein phosphatase 4 regulatory subunit 3A | 0.49 ± 0.48 | 7.65 ± 2.52 | 0.049 | ↑15.78 | yes |
| P07910 | HNRPC | Heterogeneous nuclear ribonucleoproteins C1/C2 | 0.71 ± 0.71 | 11.18 ± 2.67 | 0.019 | ↑15.77 | yes |
| P07355 | ANXA2 | Annexin A2 | 2.89 ± 1.47 | 33.55 ± 3.09 | 0.001 | ↑11.60 | yes |
| P08758 | ANXA5 | Annexin A5 | 2.07 ± 1.23 | 16.18 ± 1.09 | 0.001 | ↑7.83 | yes |
| O43670 | ZN207 | BUB3-interacting and GLEBS motif-containing protein ZNF207 | 0.49 ± 0.48 | 3.07 ± 0.28 | 0.010 | ↑6.33 | yes |
| Q96DI7 | SNR40 | U5 small nuclear ribonucleoprotein 40 kDa protein | 0.97 ± 0.97 | 5.99 ± 1.10 | 0.027 | ↑6.18 | yes |
| O00232 | PSD12 | 26S proteasome non-ATPase regulatory subunit 12 | 0.49 ± 0.49 | 2.72 ± 0.60 | 0.044 | ↑5.58 | yes |
| Q9H0D6 | XRN2 | 5'-3' exoribonuclease 2 | 1.52 ± 0.77 | 7.80 ± 1.36 | 0.016 | ↑5.13 | yes |
| Q9BUT1 | BDH2 | 3-hydroxybutyrate dehydrogenase type 2 | 0.97 ± 0.97 | 4.94 ± 0.90 | 0.040 | ↑5.10 | no |
| O94776 | MTA2 | Metastasis-associated protein MTA2 | 1.34 ± 0.71 | 6.80 ± 0.79 | 0.007 | ↑5.06 | yes |
| Q14997 | PSME4 | Proteasome activator complex subunit 4 | 1.95 ± 1.13 | 9.35 ± 2.03 | 0.033 | ↑4.81 | yes |
| Q9H2G2 | SLK | STE20-like serine/threonine-protein kinase | 0.65 ± 0.65 | 2.74 ± 0.38 | 0.050 | ↑4.23 | yes |
| Q12905 | ILF2 | Interleukin enhancer-binding factor 2 | 5.11 ± 2.08 | 19.82 ± 1.23 | 0.004 | ↑3.88 | yes |
| O14979 | HNRDL | Heterogeneous nuclear ribonucleoprotein D-like | 3.66 ± 1.15 | 12.41 ± 1.50 | 0.010 | ↑3.39 | yes |
| Q99436 | PSB7 | Proteasome subunit beta type-7 | 1.68 ± 0.87 | 5.64 ± 0.65 | 0.022 | ↑3.35 | yes |
| Q15149 | PLEC | Plectin | 26.31 ± 3.07 | 84.28 ± 13.73 | 0.015 | ↑3.20 | yes |

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|------------|------------|--|--------------|--------------|-------|-------|-----|
| P10809 | CH60 | 60-kDa Heat-shock protein, mitochondrial | 13.60 ± 1.96 | 39.35 ± 3.53 | 0.003 | ↑2.89 | yes |
| P35637 | FUS | RNA-binding protein FUS | 2.92 ± 1.85 | 8.37 ± 0.31 | 0.043 | ↑2.87 | yes |
| P08133 | ANXA6 | Annexin A6 | 11.05 ± 5.74 | 31.67 ± 3.18 | 0.035 | ↑2.87 | yes |
| O60568 | PLOD3 | Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 | 3.48 ± 0.70 | 9.79 ± 1.97 | 0.039 | ↑2.81 | yes |
| Q9UMS4 | PRP19 | Pre-mRNA-processing factor 19 | 7.84 ± 0.28 | 18.93 ± 1.39 | 0.001 | ↑2.42 | yes |
| P60900 | PSA6 | Proteasome subunit alpha type-6 | 3.39 ± 1.00 | 8.17 ± 1.38 | 0.049 | ↑2.41 | yes |
| O43684 | BUB3 | Mitotic checkpoint protein BUB3 | 4.81 ± 1.51 | 11.55 ± 1.62 | 0.038 | ↑2.40 | yes |
| O43390 | HNRPR | Heterogeneous nuclear ribonucleoprotein R | 14.48 ± 0.52 | 34.46 ± 5.17 | 0.018 | ↑2.38 | yes |
| A0A087WZV1 | A0A087WZV1 | Heterogeneous nuclear ribonucleoprotein A/B | 9.40 ± 1.87 | 22.25 ± 3.26 | 0.027 | ↑2.37 | yes |
| P17096 | HMGAI | High mobility group protein HMG-I/HMG-Y | 4.89 ± 1.01 | 11.46 ± 1.17 | 0.013 | ↑2.34 | yes |
| O43660 | PLRG1 | Pleiotropic regulator 1 | 5.78 ± 2.07 | 12.80 ± 0.07 | 0.028 | ↑2.22 | yes |
| P55072 | TERA | Transitional endoplasmic reticulum ATPase | 21.21 ± 2.37 | 46.92 ± 5.62 | 0.014 | ↑2.21 | yes |
| P12956 | XRCC6 | X-ray repair cross-complementing protein 6 | 3.02 ± 0.38 | 6.66 ± 1.04 | 0.030 | ↑2.21 | yes |
| P25786 | PSA1 | Proteasome subunit alpha type-1 | 5.25 ± 1.36 | 11.21 ± 1.60 | 0.047 | ↑2.14 | yes |
| P06748 | NPM | Nucleophosmin | 4.00 ± 0.70 | 8.36 ± 1.36 | 0.046 | ↑2.09 | yes |
| Q8N684 | CPSF7 | Cleavage and polyadenylation specificity factor subunit 7 | 3.18 ± 0.39 | 6.62 ± 1.17 | 0.049 | ↑2.08 | yes |
| Q01844 | EWS | RNA-binding protein EWS | 6.60 ± 1.20 | 13.50 ± 0.56 | 0.007 | ↑2.05 | yes |
| P25788 | PSA3 | Proteasome subunit alpha type-3 | 3.39 ± 1.00 | 6.65 ± 0.25 | 0.034 | ↑1.96 | yes |
| P31942 | HNRH3 | Heterogeneous nuclear ribonucleoprotein H3 | 13.49 ± 1.11 | 26.32 ± 3.98 | 0.036 | ↑1.95 | yes |
| P08865 | RSSA | 40S ribosomal protein SA | 10.89 ± 1.56 | 19.95 ± 0.53 | 0.005 | ↑1.83 | yes |
| P61978 | HNRPK | Heterogeneous nuclear ribonucleoprotein K | 41.58 ± 1.70 | 72.76 ± 2.65 | 0.001 | ↑1.75 | yes |
| Q13547 | HDAC1 | Histone deacetylase 1 | 6.35 ± 0.51 | 10.92 ± 0.34 | 0.002 | ↑1.72 | yes |
| Q13409 | DC1I2 | Cytoplasmic dynein 1 intermediate chain 2 | 1.84 ± 0.20 | 3.08 ± 0.35 | 0.037 | ↑1.67 | yes |
| Q07666 | KHDR1 | KH domain-containing, RNA-binding, signal transduction-associated protein 1 | 14.00 ± 2.94 | 23.38 ± 1.68 | 0.047 | ↑1.67 | yes |
| Q13283 | G3BP1 | Ras GTPase-activating protein-binding protein 1 | 6.63 ± 0.71 | 10.93 ± 0.38 | 0.006 | ↑1.65 | yes |
| G3V1C3 | G3V1C3 | Apoptosis inhibitor 5 | 33.06 ± 2.01 | 52.43 ± 1.57 | 0.002 | ↑1.59 | yes |
| Q13765 | NACA | Nascent polypeptide-associated complex subunit alpha | 11.93 ± 1.64 | 18.25 ± 1.23 | 0.037 | ↑1.53 | yes |
| P43686 | PRS6B | 26S protease regulatory subunit 6B | N.D. | 3.57 ± 0.45 | 0.001 | - | yes |
| P62195 | PRS8 | 26S protease regulatory subunit 8 | N.D. | 1.87 ± 0.31 | 0.004 | - | yes |
| O00487 | PSDE | 26S proteasome non-ATPase regulatory subunit 14 | N.D. | 2.55 ± 0.58 | 0.012 | - | yes |
| P55036 | PSMD4 | 26S proteasome non-ATPase regulatory subunit 4 | N.D. | 3.61 ± 0.84 | 0.012 | - | yes |
| P15144 | AMPN | Aminopeptidase N | N.D. | 8.91 ± 0.99 | 0.001 | - | yes |
| E7ETM0 | E7ETM0 | Casein kinase I isoform alpha | N.D. | 3.76 ± 0.35 | 0.000 | - | yes |
| P36957 | ODO2 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial | N.D. | 4.75 ± 1.15 | 0.014 | - | yes |
| O15160 | RPAC1 | DNA-directed RNA polymerases I and III subunit RPAC1 | N.D. | 2.05 ± 0.29 | 0.002 | - | yes |
| P78406 | RAE1L | mRNA export factor | N.D. | 5.33 ± 1.90 | 0.048 | - | yes |
| P49790 | NU153 | Nuclear pore complex protein Nup153 | N.D. | 3.95 ± 0.96 | 0.015 | - | yes |
| Q8NC51 | PAIRB | Plasminogen activator inhibitor 1 RNA-binding protein | N.D. | 7.70 ± 1.11 | 0.002 | - | yes |
| P0CG47 | UBB | Polyubiquitin-B | N.D. | 4.80 ± 0.67 | 0.002 | - | yes |
| P0CG48 | UBC | Polyubiquitin-C | N.D. | 4.80 ± 0.67 | 0.002 | - | yes |
| Q8NBJ5 | GT251 | Procollagen galactosyltransferase 1 | N.D. | 3.92 ± 0.12 | 0.000 | - | yes |

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|--------|--------|---|------|-------------|-------|---|-----|
| O00469 | PLOD2 | Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 | N.D. | 1.54 ± 0.03 | 0.000 | - | yes |
| Q7Z3U7 | MON2 | Protein MON2 homolog | N.D. | 1.87 ± 0.31 | 0.004 | - | yes |
| Q15437 | SC23B | Protein transport protein Sec23B | N.D. | 4.07 ± 0.70 | 0.004 | - | yes |
| Q9BWF3 | RBM4 | RNA-binding protein 4 | N.D. | 1.71 ± 0.20 | 0.001 | - | yes |
| K7ERG4 | K7ERG4 | Small nuclear ribonucleoprotein Sm D2 | N.D. | 4.61 ± 0.26 | 0.000 | - | yes |

¹ From three independent experiments; ² Based on two-tailed unpaired Student's *t* test; ³ The O-GlcNAc Database v1.2 (<https://www.oglcnac.mcw.edu/>, accessed on 14 Dec 2021). ↓ means down-regulated; ↑ means up-regulated.

Table S2. Differential WGA-bound glycoproteins identified in cytosolic extracts from lung adenocarcinoma cell lines CL1-1 and CL1-5.

| Protein ID | Symbol | Protein Name | Normalized Spectral Counts (Mean ± SE) ¹ | | <i>p</i> -Value ² | Fold Change | Listed in the O-GlcNAc Database ³ |
|-------------------------|--------|---|--|--------------|------------------------------|----------------|--|
| | | | In CL1-1 | In CL1-5 | | | |
| Down-regulated in CL1-5 | | | | | | | |
| O14964 | HGS | Hepatocyte growth factor-regulated tyrosine kinase substrate | 10.54 ± 1.27 | 0.93 ± 0.93 | 0.004 | ↓11.32 | yes |
| P46781 | RS9 | 40S ribosomal protein S9 | 5.91 ± 1.33 | 0.74 ± 0.74 | 0.028 | ↓7.95 | yes |
| P22059 | OSBP1 | Oxysterol-binding protein 1 | 3.43 ± 0.69 | 0.60 ± 0.60 | 0.036 | ↓5.71 | yes |
| Q04637 | IF4G1 | Eukaryotic translation initiation factor 4 gamma 1 | 7.47 ± 1.35 | 1.34 ± 0.68 | 0.016 | ↓5.56 | yes |
| Q06203 | PUR1 | Amidophosphoribosyltransferase | 14.36 ± 0.83 | 2.72 ± 0.04 | 0.000 | ↓5.27 | yes |
| P35580 | MYH10 | Myosin-10 | 46.35 ± 5.93 | 9.11 ± 1.59 | 0.004 | ↓5.08 | yes |
| V9HW77 | V9HW77 | Epididymis luminal protein 211 | 27.73 ± 1.42 | 5.92 ± 1.03 | 0.000 | ↓4.68 | no |
| Q9UNF0 | PACN2 | Protein kinase C and casein kinase substrate in neurons protein 2 | 8.50 ± 1.70 | 1.82 ± 1.04 | 0.028 | ↓4.67 | yes |
| P54725 | RD23A | UV excision repair protein RAD23 homolog A | 3.46 ± 0.63 | 0.74 ± 0.74 | 0.050 | ↓4.65 | yes |
| Q15631 | TSN | Translin | 5.27 ± 0.56 | 1.23 ± 0.68 | 0.010 | ↓4.30 | yes |
| P48729 | KC1A | Casein kinase I isoform alpha | 2.50 ± 0.21 | 0.60 ± 0.60 | 0.040 | ↓4.17 | yes |
| Q06830 | PRDX1 | Peroxiredoxin-1 | 5.28 ± 0.98 | 1.37 ± 0.70 | 0.031 | ↓3.85 | yes |
| Q7L576 | CYFP1 | Cytoplasmic FMR1-interacting protein 1 | 14.82 ± 0.84 | 4.23 ± 0.59 | 0.001 | ↓3.50 | yes |
| P49588 | SYAC | Alanine--tRNA ligase, cytoplasmic | 24.93 ± 2.30 | 7.29 ± 1.87 | 0.004 | ↓3.42 | yes |
| P07195 | LDHB | L-lactate dehydrogenase B chain | 25.09 ± 3.18 | 7.72 ± 0.10 | 0.006 | ↓3.25 | yes |
| P53396 | ACLY | ATP-citrate synthase | 16.62 ± 2.49 | 5.14 ± 0.24 | 0.010 | ↓3.24 | yes |
| Q15435 | PP1R7 | Protein phosphatase 1 regulatory subunit 7 | 18.40 ± 1.00 | 5.76 ± 0.47 | 0.000 | ↓3.20 | yes |
| Q9HB07 | MYG1 | UPF0160 protein MYG1, mitochondrial | 4.83 ± 0.04 | 1.52 ± 0.80 | 0.014 | ↓3.17 | yes |
| Q9NQW7 | XPP1 | Xaa-Pro aminopeptidase 1 | 6.98 ± 0.54 | 2.27 ± 1.19 | 0.022 | ↓3.08 | yes |
| Q9UUK9 | NUDT5 | ADP-sugar pyrophosphatase | 7.31 ± 0.13 | 2.42 ± 0.54 | 0.001 | ↓3.02 | yes |
| B7Z2Z8 | B7Z2Z8 | T-complex protein 1 subunit delta | 4.69 ± 0.39 | 1.64 ± 0.91 | 0.036 | ↓2.86 | yes |
| P14868 | SYDC | Aspartate--tRNA ligase, cytoplasmic | 11.51 ± 0.76 | 4.07 ± 0.65 | 0.002 | ↓2.83 | yes |
| P06132 | DCUP | Uroporphyrinogen decarboxylase | 5.60 ± 0.66 | 1.99 ± 1.01 | 0.040 | ↓2.82 | yes |
| P55884 | EIF3B | Eukaryotic translation initiation factor 3 subunit B | 27.73 ± 1.58 | 10.29 ± 0.42 | 0.000 | ↓2.70 | yes |
| Q9UNH7 | SNX6 | Sorting nexin-6 | 7.60 ± 0.67 | 2.89 ± 0.58 | 0.006 | ↓2.63 | yes |
| P06753 | TPM3 | Tropomyosin alpha-3 chain | 43.53 ± 1.70 | 16.91 ± 1.82 | 0.000 | ↓2.58 | yes |
| P41250 | SYG | Glycine--tRNA ligase | 12.86 ± 2.08 | 5.01 ± 0.59 | 0.022 | ↓2.57 | yes |
| E7EVA0 | E7EVA0 | Microtubule-associated protein | 26.98 ± 1.06 | 10.71 ± 1.32 | 0.001 | ↓2.52 | no |

| | | | | | | | |
|------------|------------|---|--------------|--------------|-------|-------|-----|
| P67936 | TPM4 | Tropomyosin alpha-4 chain | 57.10 ± 5.54 | 22.91 ± 3.63 | 0.007 | ↓2.49 | yes |
| P12956 | XRCC6 | X-ray repair cross-complementing protein 6 | 14.12 ± 2.29 | 6.07 ± 0.74 | 0.029 | ↓2.33 | yes |
| P21281 | VATB2 | V-type proton ATPase subunit B, brain isoform | 6.72 ± 0.48 | 3.02 ± 0.36 | 0.004 | ↓2.23 | yes |
| P61247 | RS3A | 40S ribosomal protein S3a | 12.89 ± 1.12 | 5.88 ± 0.88 | 0.008 | ↓2.19 | yes |
| Q7KZF4 | SND1 | Staphylococcal nuclease domain-containing protein 1 | 32.36 ± 2.62 | 14.81 ± 1.82 | 0.005 | ↓2.19 | yes |
| A0MZ66 | SHOT1 | Shootin-1 | 14.06 ± 0.89 | 6.51 ± 0.62 | 0.002 | ↓2.16 | yes |
| P51858 | HDGF | Hepatoma-derived growth factor | 21.46 ± 1.67 | 10.16 ± 1.30 | 0.006 | ↓2.11 | yes |
| O00273 | DFFA | DNA fragmentation factor subunit alpha | 5.74 ± 0.46 | 2.73 ± 0.56 | 0.014 | ↓2.10 | yes |
| P40123 | CAP2 | Adenylyl cyclase-associated protein 2 | 5.60 ± 0.19 | 2.72 ± 0.04 | 0.000 | ↓2.06 | yes |
| Q15436 | SC23A | Protein transport protein Sec23A | 11.61 ± 1.66 | 5.76 ± 0.38 | 0.027 | ↓2.02 | yes |
| P35749 | MYH11 | Myosin-11 | 8.44 ± 0.70 | 4.23 ± 0.59 | 0.010 | ↓2.00 | yes |
| O76003 | GLRX3 | Glutaredoxin-3 | 7.74 ± 1.18 | 3.94 ± 0.18 | 0.033 | ↓1.97 | yes |
| Q15046 | SYK | Lysine: tRNA ligase | 12.15 ± 0.23 | 6.33 ± 1.14 | 0.008 | ↓1.92 | yes |
| Q9Y5X3 | SNX5 | Sorting nexin-5 | 6.06 ± 0.30 | 3.18 ± 0.26 | 0.002 | ↓1.91 | yes |
| A0A024R9E2 | A0A024R9E2 | Poly(A) binding protein, cytoplasmic 1, isoform CRA_c | 6.20 ± 0.69 | 3.31 ± 0.76 | 0.048 | ↓1.87 | no |
| P49327 | FAS | Fatty acid synthase | 73.44 ± 6.17 | 39.26 ± 2.57 | 0.007 | ↓1.87 | yes |
| P68104 | EF1A1 | Elongation factor 1-alpha 1 | 8.09 ± 0.20 | 4.36 ± 1.27 | 0.044 | ↓1.86 | yes |
| P62140 | PP1B | Serine/threonine-protein phosphatase PP1-beta catalytic subunit | 7.77 ± 0.35 | 4.23 ± 0.90 | 0.021 | ↓1.84 | yes |
| P07951 | TPM2 | Tropomyosin beta chain | 64.51 ± 5.63 | 35.72 ± 8.39 | 0.047 | ↓1.81 | yes |
| P07437 | TBB5 | Tubulin beta chain | 14.93 ± 1.53 | 8.46 ± 0.46 | 0.016 | ↓1.76 | yes |
| Q15691 | MARE1 | Microtubule-associated protein RP/EB family member 1 | 18.32 ± 1.41 | 10.43 ± 2.05 | 0.034 | ↓1.76 | yes |
| Q9NYU2 | UGGG1 | UDP-glucose:glycoprotein glucosyltransferase 1 | 28.08 ± 1.47 | 16.24 ± 1.97 | 0.009 | ↓1.73 | yes |
| O94979 | SC31A | Protein transport protein Sec31A | 13.94 ± 1.47 | 8.16 ± 0.61 | 0.022 | ↓1.71 | yes |
| Q96QK1 | VPS35 | Vacuolar protein sorting-associated protein 35 | 9.19 ± 0.62 | 5.43 ± 0.72 | 0.017 | ↓1.69 | yes |
| P26640 | SYVC | Valine--tRNA ligase | 22.07 ± 0.93 | 13.12 ± 1.67 | 0.009 | ↓1.68 | yes |
| Q13347 | EIF3I | Eukaryotic translation initiation factor 3 subunit I | 6.35 ± 0.65 | 3.78 ± 0.14 | 0.018 | ↓1.68 | yes |
| P12004 | PCNA | Proliferating cell nuclear antigen | 6.83 ± 0.52 | 4.08 ± 0.42 | 0.015 | ↓1.68 | yes |
| Q02790 | FKBP4 | Peptidyl-prolyl cis-trans isomerase FKBP4 | 29.12 ± 2.38 | 17.65 ± 2.03 | 0.021 | ↓1.65 | yes |
| P62753 | RS6 | 40S ribosomal protein S6 | 6.70 ± 0.69 | 4.09 ± 0.31 | 0.026 | ↓1.64 | yes |
| P33176 | KINH | Kinesin-1 heavy chain | 16.50 ± 0.59 | 10.10 ± 1.49 | 0.016 | ↓1.63 | yes |
| Q14697 | GANAB | Neutral alpha-glucosidase AB | 46.40 ± 3.53 | 28.95 ± 2.14 | 0.013 | ↓1.60 | yes |
| Q8N1G4 | LRC47 | Leucine-rich repeat-containing protein 47 | 7.17 ± 0.32 | 4.53 ± 0.22 | 0.003 | ↓1.58 | yes |
| Q92526 | TCPW | T-complex protein 1 subunit zeta-2 | 6.70 ± 0.05 | 4.24 ± 0.21 | 0.000 | ↓1.58 | no |
| P09493 | TPM1 | Tropomyosin alpha-1 chain | 29.14 ± 2.76 | 18.46 ± 0.83 | 0.021 | ↓1.58 | yes |
| P38606 | VATA | V-type proton ATPase catalytic subunit A | 10.43 ± 0.49 | 6.80 ± 0.44 | 0.005 | ↓1.54 | yes |
| P13639 | EF2 | Elongation factor 2 | 42.31 ± 2.06 | 27.94 ± 1.89 | 0.007 | ↓1.51 | yes |
| P08195 | 4F2 | 4F2 cell-surface antigen heavy chain | 4.72 ± 0.92 | N.D. | 0.007 | - | yes |
| P62906 | RL10A | 60S ribosomal protein L10a | 2.66 ± 0.22 | N.D. | 0.000 | - | yes |
| P36578 | RL4 | 60S ribosomal protein L4 | 4.97 ± 0.55 | N.D. | 0.001 | - | yes |
| P62424 | RL7A | 60S ribosomal protein L7a | 2.47 ± 0.62 | N.D. | 0.016 | - | yes |
| Q13085 | ACACA | Acetyl-CoA carboxylase 1 | 3.28 ± 0.74 | N.D. | 0.011 | - | yes |
| P04083 | ANXA1 | Annexin A1 | 8.70 ± 0.63 | N.D. | 0.000 | - | yes |
| P13861 | KAP2 | cAMP-dependent protein kinase type II-alpha regulatory subunit | 2.34 ± 0.268 | N.D. | 0.001 | - | yes |

| | | | | | | | |
|-----------------------|------------|---|--------------|----------------|-------|--------|-----|
| P30622 | CLIP1 | CAP-Gly domain-containing linker protein 1 | 2.35 ± 0.57 | N.D. | 0.015 | - | yes |
| Q6P1N0 | C2D1A | Coiled-coil and C2 domain-containing protein 1A | 2.8 ± 0.46 | N.D. | 0.004 | - | yes |
| P12532 | KCRU | Creatine kinase U-type, mitochondrial | 5.15 ± 1.01 | N.D. | 0.007 | - | yes |
| Q13616 | CUL1 | Cullin-1 | 2.49 ± 0.09 | N.D. | 0.000 | - | yes |
| Q86VP6 | CAND1 | Cullin-associated NEDD8-dissociated protein 1 | 2.92 ± 0.78 | N.D. | 0.020 | - | yes |
| P15311 | EZRI | Ezrin | 3.45 ± 0.39 | N.D. | 0.001 | - | yes |
| Q00839 | HNRPU | Heterogeneous nuclear ribonucleoprotein U | 2.98 ± 0.48 | N.D. | 0.004 | - | yes |
| Q9Y2A7 | NCKP1 | Nck-associated protein 1 | 7.80 ± 0.48 | N.D. | 0.000 | - | yes |
| O75694 | NU155 | Nuclear pore complex protein Nup155 | 1.56 ± 0.17 | N.D. | 0.001 | - | yes |
| F8VR77 | F8VR77 | Proliferation-associated protein 2G4 | 4.53 ± 0.36 | N.D. | 0.000 | - | yes |
| Q92734 | TFG | Protein TFG | 3.12 ± 0.16 | N.D. | 0.000 | - | yes |
| Q8N1K5 | THMS1 | Protein THEMIS | 1.88 ± 0.29 | N.D. | 0.003 | - | yes |
| P35241 | RADI | Radixin | 4.98 ± 0.35 | N.D. | 0.000 | - | yes |
| Q13464 | ROCK1 | Rho-associated protein kinase 1 | 3.28 ± 0.31 | N.D. | 0.001 | - | yes |
| Q6IPH7 | Q6IPH7 | RPL14 protein | 2.03 ± 0.20 | N.D. | 0.001 | - | no |
| Q9Y6Y8 | S23IP | SEC23-interacting protein | 2.35 ± 0.33 | N.D. | 0.002 | - | yes |
| P63151 | 2ABA | Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform | 2.83 ± 0.53 | N.D. | 0.006 | - | yes |
| Q92783 | STAM1 | Signal transducing adapter molecule 1 | 4.52 ± 0.45 | N.D. | 0.001 | - | yes |
| A0A0A0MTS7 | A0A0A0MTS7 | Titin | 9.24 ± 1.45 | N.D. | 0.003 | - | yes |
| P02786 | TFR1 | Transferrin receptor protein 1 | 4.73 ± 1.03 | N.D. | 0.010 | - | yes |
| P29144 | TPP2 | Tripeptidyl-peptidase 2 | 6.07 ± 0.92 | N.D. | 0.003 | - | yes |
| Q8TDJ5 | Q8TDJ5 | Tyrosine-protein kinase receptor | 3.12 ± 0.16 | N.D. | 0.000 | - | no |
| P54577 | SYYC | Tyrosine--tRNA ligase, cytoplasmic | 7.55 ± 1.98 | N.D. | 0.019 | - | yes |
| O95155 | UBE4B | Ubiquitin conjugation factor E4 B | 2.77 ± 0.63 | N.D. | 0.012 | - | yes |
| Up-regulated in CL1-5 | | | | | | | |
| Q13813 | SPTN1 | Spectrin alpha chain, non-erythrocytic 1 | 3.54 ± 2.27 | 40.72 ± 6.90 | 0.007 | ↑11.52 | yes |
| Q9H2G2 | SLK | STE20-like serine/threonine-protein kinase | 0.89 ± 0.89 | 8.94 ± 0.51 | 0.001 | ↑10.06 | yes |
| P35609 | ACTN2 | Alpha-actinin-2 | 1.62 ± 1.62 | 12.83 ± 1.03 | 0.004 | ↑7.94 | yes |
| O43707 | ACTN4 | Alpha-actinin-4 | 15.91 ± 0.77 | 95.46 ± 1.67 | 0.000 | ↑6.00 | yes |
| Q5T8M8 | Q5T8M8 | Actin, alpha skeletal muscle | 0.74 ± 0.74 | 3.95 ± 0.82 | 0.044 | ↑5.34 | yes |
| P11310 | ACADM | Medium-chain specific acyl-CoA dehydrogenase, mitochondrial | 0.47 ± 0.47 | 2.42 ± 0.40 | 0.035 | ↑5.11 | yes |
| A0A024R7P5 | A0A024R7P5 | Similar to Laminin receptor 1, isoform CRA_a | 0.95 ± 0.95 | 4.84 ± 0.54 | 0.023 | ↑5.10 | no |
| O75369 | FLNB | Filamin-B | 32.32 ± 1.73 | 148.56 ± 12.81 | 0.001 | ↑4.60 | yes |
| A0A087X111 | A0A087X111 | G antigen 13 | 2.01 ± 0.36 | 7.57 ± 0.21 | 0.000 | ↑3.77 | no |
| P06396 | GELS | Gelsolin | 5.61 ± 0.73 | 19.88 ± 2.64 | 0.007 | ↑3.54 | yes |
| H0YN18 | H0YN18 | Proteasome subunit alpha type-4 | 2.23 ± 1.56 | 7.74 ± 0.80 | 0.035 | ↑3.48 | yes |
| P08758 | ANXA5 | Annexin A5 | 2.60 ± 1.30 | 7.86 ± 0.60 | 0.021 | ↑3.02 | yes |
| Q08043 | ACTN3 | Alpha-actinin-3 | 2.95 ± 1.50 | 7.85 ± 0.45 | 0.035 | ↑2.66 | yes |
| P11413 | G6PD | Glucose-6-phosphate 1-dehydrogenase | 1.55 ± 0.78 | 4.08 ± 0.23 | 0.035 | ↑2.64 | yes |
| P12814 | ACTN1 | Alpha-actinin-1 | 18.09 ± 2.47 | 47.35 ± 1.28 | 0.001 | ↑2.62 | yes |
| O00232 | PSD12 | 26S proteasome non-ATPase regulatory subunit 12 | 2.98 ± 0.38 | 6.36 ± 0.54 | 0.007 | ↑2.13 | yes |
| Q16576 | RBBP7 | Histone-binding protein RBBP7 | 3.75 ± 0.51 | 7.59 ± 0.91 | 0.021 | ↑2.02 | yes |

| | | | | | | | |
|--------|--------|---|--------------|--------------|-------|-------|-----|
| O75131 | CPNE3 | Copine-3 | 5.66 ± 1.17 | 11.36 ± 0.41 | 0.010 | ↑2.01 | yes |
| P45974 | UBP5 | Ubiquitin carboxyl-terminal hydrolase 5 | 8.42 ± 0.47 | 15.88 ± 0.09 | 0.000 | ↑1.89 | yes |
| P56537 | IF6 | Eukaryotic translation initiation factor 6 | 2.80 ± 0.22 | 5.16 ± 0.80 | 0.046 | ↑1.84 | yes |
| P08107 | HSP71 | 70-kDa Heat-shock protein 1A/1B | 33.88 ± 1.91 | 55.01 ± 3.94 | 0.009 | ↑1.62 | no |
| Q16531 | DDB1 | DNA damage-binding protein 1 | 32.49 ± 2.12 | 50.70 ± 0.97 | 0.002 | ↑1.56 | yes |
| P35611 | ADDA | Alpha-adducin | N.D. | 5.58 ± 1.00 | 0.005 | - | yes |
| P06733 | ENOA | Alpha-enolase | N.D. | 3.34 ± 0.57 | 0.004 | - | yes |
| Q8WWH9 | Q8WWH9 | Amphiphysin IIb-1 | N.D. | 2.85 ± 0.77 | 0.021 | - | no |
| P20810 | ICAL | Calpastatin | N.D. | 3.65 ± 0.73 | 0.008 | - | yes |
| Q13185 | CBX3 | Chromobox protein homolog 3 | N.D. | 1.82 ± 0.26 | 0.002 | - | yes |
| P21333 | FLNA | Filamin-A | N.D. | 29.23 ± 1.24 | 0.000 | - | yes |
| P09104 | ENOG | Gamma-enolase | N.D. | 3.79 ± 0.45 | 0.001 | - | yes |
| P05556 | ITB1 | Integrin beta-1 | N.D. | 4.83 ± 0.34 | 0.000 | - | yes |
| P46821 | MAP1B | Microtubule-associated protein 1B | N.D. | 2.57 ± 0.65 | 0.017 | - | yes |
| O00499 | BIN1 | Myc box-dependent-interacting protein 1 | N.D. | 2.85 ± 0.77 | 0.021 | - | yes |
| Q9UJ70 | NAGK | N-acetyl-D-glucosamine kinase | N.D. | 5.17 ± 1.25 | 0.014 | - | yes |
| Q96TA1 | NIBL1 | Niban-like protein 1 | N.D. | 8.33 ± 1.09 | 0.002 | - | yes |
| P0CG47 | UBB | Polyubiquitin-B | N.D. | 3.35 ± 0.66 | 0.007 | - | yes |
| P0CG48 | UBC | Polyubiquitin-C | N.D. | 3.35 ± 0.66 | 0.007 | - | yes |
| O15460 | P4HA2 | Prolyl 4-hydroxylase subunit alpha-2 | N.D. | 3.78 ± 0.14 | 0.000 | - | yes |
| P62714 | PP2AB | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform | N.D. | 2.42 ± 0.31 | 0.002 | - | yes |
| Q08209 | PP2BA | Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform | N.D. | 2.43 ± 0.19 | 0.000 | - | yes |
| Q01082 | SPTB2 | Spectrin beta chain, non-erythrocytic 1 | N.D. | 36.26 ± 4.34 | 0.001 | - | yes |
| Q9H254 | SPTN4 | Spectrin beta chain, non-erythrocytic 4 | N.D. | 3.17 ± 0.23 | 0.000 | - | yes |
| P62979 | RS27A | Ubiquitin-40S ribosomal protein S27a | N.D. | 3.35 ± 0.66 | 0.007 | - | yes |
| P62987 | RL40 | Ubiquitin-60S ribosomal protein L40 | N.D. | 3.35 ± 0.66 | 0.007 | - | yes |
| P08670 | VIME | Vimentin | N.D. | 9.17 ± 2.27 | 0.016 | - | yes |

¹ From three independent experiments; ² Based on two-tailed unpaired Student's *t* test; ³ The O-GlcNAc Database v1.2 (<https://www.oglcnac.mcw.edu/>, accessed on 14 Dec 2021). ↓ means down-regulated; ↑ means up-regulated.

Table S3. Significant network functions for differential WGA-bound glycoproteins identified in lung adenocarcinoma cell lines CL1-1 and CL1-5.

| No. | Associated Network Functions | Score | Molecules in the Network |
|-----|---|-------|--|
| 1 | Neurological Disease, Skeletal and Muscular Disorders, Hereditary Disorder, | 59 | 26S Proteasome, Alpha tubulin, ANXA1, ANXA2, C12orf10, calpain, CCT4, COLGALT1, CPSF2, CUL1, CYFIP1, DARS, EEF1A1, GARS, HSPA4, HSPB1, KARS, MAP1B, MAPK, NPM1, NUP153, PLOD3, PSMA3, PSMD4, RAE1, Rnr, RPS9, RPS3A, RPSA, TSN, UBB, UBQLN1, UGGT1, VARS, VCP |
| 2 | Cellular Assembly, and Organization, Cellular Function | 48 | ACTG1, Actin, ACTN1, ACTN4, ADCY, ADRB, Alpha Actinin, Alpha catenin, ANXA6, API5, ATP6V1A, CaMKII, CAP2, CLIP1, ERK, EZR, FLNA, FLNB, IQGAP1, Lh, MAPRE1, MYH9, NASP, P4HA2, PLCB3, PLEC, PPP1CB, PRKAR2A, Spectrin, SPTAN1, SPTBN1, SPTBN4, THEMIS, TPM1, TUBB |

| | | | |
|---|--|----|--|
| | and Maintenance, Cell-To-Cell Signaling and Interaction | | |
| 3 | Cell Morphology, Protein Trafficking, Cellular Assembly and Organization | 42 | 19S proteasome, 20S proteasome, AOC1, APC/APC2, CPSF7, Dynamin, DYNC1I2, ERK1/2, HGS, Immunoproteasome Pa28/20s, PACSIN2, Proteasome PA700/20s, PSMA, PSMA1, PSMA4, PSMA6, PSMB7, PSMD, PSMD12, PSMD14, PSME4, RAD23A, Sec23, SEC23A, SEC23B, SEC23IP, SEC31A, SNX5, SNX6, STAM, UBA1, UBE4B, Ubiquitin, USP5, VPS35 |
| 4 | RNA Post-Transcriptional Modification, Cellular Assembly and Organization, Cellular Compromise | 38 | 60S ribosomal subunit, ATPase, CAND1, EEF2, ENO1, Erm, FUS, HNRNPH3, HNRNPR, HNRNPU, ILF2, JINK1/2, Jnk, MACF1, MSH2, N-cor, P glycoprotein, PSMC4, PSMC5, Rar, RDX, Rho gdi, RPL4, RPL14, RPL10A, RPL7A, Rxr, SERBP1, SLK, T3-TR-RXR, TCERG1, TFIIH, thyroid hormone receptor, UBA52, XRN2 |
| 5 | RNA Post-Transcriptional Modification, Cell Cycle, DNA Replication, Recombination, and Repair | 33 | ABCF1, Akt, Cdc2, Cyclin A, Cyclin D, Cyclin E, E2f, EIF3, EIF6, EIF3B, EIF3I, Eif4g, EIF4G1, G3BP1, Gcn5l, HNRNPC, LSM4, mediator, Mre11, PA2G4, PABPC1, PLRG1, PPP4R3A, PRPF19, Rb, Ribosomal 40S subunit, RPA, RPS6, RPS27A, SMC1A, SND1, snRNP, SNRNP40, SNRPD2, ZNF207 |

Table S4. IPA-identified significant canonical pathways associated with differential WGA-bound glycoproteins in lung adenocarcinoma cell lines CL1-1 and CL1-5.

| Pathway Name | p-Value | Ratio |
|--|------------------------|---------------|
| All differential WGA-bound glycoproteins identified from CL1-1 and CL1-5 cells | | |
| Actin Cytoskeleton Signaling | 5.91×10^{-15} | 22/228 (9.6%) |
| Protein Ubiquitination Pathway | 4.35×10^{-11} | 19/255 (7.5%) |
| ILK Signaling | 4.10×10^{-10} | 16/196 (8.2%) |
| Remodeling of Epithelial Adherens Junctions | 2.85×10^{-9} | 10/68 (14.7%) |
| EIF2 Signaling | 3.10×10^{-9} | 15/194 (7.7%) |
| WGA-bound glycoproteins Down-regulated in CL1-5 cells | | |
| Actin Cytoskeleton Signaling | 1.49×10^{-12} | 16/228 (7.0%) |
| EIF2 Signaling | 4.44×10^{-9} | 12/194 (6.2%) |
| Cellular Effects of Sildenafil (Viagra) | 1.13×10^{-8} | 10/130 (7.7%) |
| tRNA Charging | 1.68×10^{-7} | 6/39 (15.4%) |
| Regulation of eIF4 and p70S6K Signaling | 7.77×10^{-7} | 9/157 (5.7%) |
| WGA-bound glycoproteins Up-regulated in CL1-5 cells | | |
| Protein Ubiquitination Pathway | 9.75×10^{-12} | 14/255 (5.5%) |
| ILK Signaling | 2.13×10^{-8} | 10/196 (5.1%) |
| Regulation of Cellular Mechanics by Calpain Protease | 2.27×10^{-7} | 6/57 (10.5%) |
| Sertoli Cell-Sertoli Cell Junction Signaling | 1.70×10^{-5} | 7/178 (3.9%) |
| Actin Cytoskeleton Signaling | 8.24×10^{-5} | 7/228 (3.1%) |

Table S5. Statistically significant molecular and cellular functions associated with differential WGA-bound glycoproteins identified in lung adenocarcinoma cell lines CL1-1 and CL1-5.

| Molecular and Cellular Functions | p-Value | Number of Molecules |
|--|--|----------------------------|
| Differentially expressed WGA-bound glycoproteins identified from CL1-1 and CL1-5 cells | | |
| Cell Death and Survival | 4.83×10^{-3} – 6.99×10^{-20} | 121 |
| Cellular Growth and Proliferation | 4.72×10^{-3} – 1.00×10^{-18} | 138 |
| Cellular Assembly and Organization | 4.39×10^{-3} – 5.46×10^{-12} | 94 |
| Cellular Function and Maintenance | 4.44×10^{-3} – 5.46×10^{-12} | 101 |
| Cellular Development | 4.58×10^{-3} – 5.24×10^{-11} | 119 |
| WGA-bound glycoproteins Down-regulated in CL1-5 cells | | |
| Cell Death and Survival | 6.39×10^{-3} – 6.50×10^{-11} | 68 |
| Cellular Growth and Proliferation | 6.39×10^{-3} – 4.94×10^{-10} | 79 |
| Cellular Assembly and Organization | 6.39×10^{-3} – 5.64×10^{-10} | 53 |
| Cellular Function and Maintenance | 6.39×10^{-3} – 5.64×10^{-10} | 66 |
| Protein Synthesis | 1.44×10^{-3} – 1.11×10^{-8} | 31 |
| WGA-bound glycoproteins Up-regulated in CL1-5 cells | | |
| Cell Death and Survival | 6.28×10^{-3} – 1.87×10^{-13} | 57 |
| Cellular Growth and Proliferation | 5.22×10^{-3} – 9.49×10^{-12} | 63 |
| RNA Post-Transcriptional Modification | 2.07×10^{-3} – 2.03×10^{-8} | 12 |
| Cellular Assembly and Organization | 5.73×10^{-3} – 1.29×10^{-7} | 37 |
| Cellular Development | 5.29×10^{-3} – 2.30×10^{-7} | 56 |

Table S6. Association of SAM68 expression with lung adenocarcinoma stage.

| SAM68 Expression | Tumor Stage | | <i>p</i> -Value ¹ |
|------------------|-------------|-----------------|------------------------------|
| | Stage I | Stage II/III/IV | |
| Low SAM68 Count | 58 | 31 | - |
| % within Stage | 59.2% | 40.8% | - |
| High SAM68 Count | 40 | 45 | - |
| % within Stage | 40.8% | 59.2% | <i>p</i> = 0.016 |
| Total Count | 98 | 76 | - |
| % within Stage | 100.0% | 100.0% | - |

¹ Two-sided log-rank test.

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