

## Supplementary Materials for

### **PD-L2 glycosylation promotes immune evasion and predicts anti-EGFR efficacy**

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## Supplementary Materials and Methods

### Cell culture

Human tongue HNSCC cell lines SCC15, SCC25 were purchased from American Type Culture Collection (ATCC). Murine HNSCC cell line SCC7 cells were purchased from Chinese Center for Type Culture Collection. SCC15 and SCC25 cells were cultured in a mixture of Dulbecco's modified Eagle's medium (DMEM) and Ham's F12 medium with 2.5 mM L-glutamine, 1.2 g/L sodium bicarbonate, 15 mM HEPES and 0.5 mM sodium pyruvate and supplemented with 400 ng/mL hydrocortisone and 10% fetal bovine serum (FBS). SCC7 was cultured in Minimum Essential Medium Eagles with Earle's Balanced Salts (MEM-EBSS) containing 10%FBS. All cell lines were cultured in humidified environment containing 5% CO<sub>2</sub> at 37°C.

### Generation of stable cells using lentiviral transfection

To generate human *PD-L2* knockout cells, the SCC15 or SCC25 cells were transfected with lentiviral vectors harboring clustered regularly interspaced short palindromic repeats (CRISPR)/caspase 9 (Cas9) sequences against human *PD-L2*. The target sequences were as follows: 5'-ACTGTCCTTCGTCCTCACT-3' (sgPD-L2 #1), 5'-CCGTGAAAGAGCCACTTTGC-3' (sgPD-L2 #2), and 5'-TTGCAGCTTCACCAGATAGC-3' (sgPD-L2 #3). To generate mouse *PD-L2* knockout cells, the SCC7 cells were transfected with lentiviral vectors harboring CRISPR/Cas9 sequences against mouse *PD-L2*. The target sequence was 5'-CAGTTTGCAGAAGGTAGAA-3'. The cells were seeded at 50% confluency 24-36 h before lentiviral particle infection. The medium was replaced with a medium containing lentiviral vectors. After transduction for 16 h, the medium was replaced with fresh medium and the transfected cells were selected with 4 µg/mL puromycin (Sigma) for 7 days.

To generate the cells expressing wild-type (WT) or mutant (4NQ or REY) PD-L2 SCC7, SCC15 and SCC25 cells, the lentiviral vectors harboring Flag-tagged WT or mutant PD-L2

sequences, which were purchased from Genechem (China), were transfected into sgPD-L2-infection cells. The HNSCC cells were seeded at 50% confluency 24-36 h before lentiviral particle infection. The medium was replaced with a medium containing lentiviral vectors. After transduction for 16 h, the medium was replaced with fresh medium and the infected cells were selected with 600 µg/mL G418 (Sigma) for 2 weeks.

To establish *FUT8* knockdown stable lines, a lentiviral shRNA system (Genechem) with short hairpin sequences against *FUT8* as follows: 5'-TGGAGTGATCCTGGATATA-3' (shFUT8#1), 5'-ACAGATGACCCTTCTTTAT-3' (shFUT8#2) was used. Two sh*STAT3* clones were selected. The target sequences used for sh*STAT3* were as follows: 5'-GCAAAGAATCACATGCCACTT-3' (sh*STAT3* #1) and 5'-GCACAATCTACGAAGAATCAA-3' (sh*STAT3* #2). The cells were seeded at 50% confluency 24-36 h before lentiviral particle infection. The medium was replaced with a medium containing lentivirus. After transfection for 16 h, the medium was replaced with fresh medium and the transfected cells were selected with 4 µg/mL puromycin for 7 days.

#### **Antibodies and Reagents.**

Cetuximab was purchased from Merck Serono. Cycloheximide and tunicamycin were obtained from Abcam. Stattic (*STAT3* inhibitor, S7024), SB203580 (MAPK inhibitor, S1076), GF109203X (PKC inhibitor, S7208), Rapamycin (mTOR inhibitor, S1039), U0126 (MEK inhibitor, S1102), Nutlin-3 (MDM2 inhibitor, S1061) were purchased from Selleck Chemicals. EGF was purchased from Sino Biological (10605-HNAE).

The antibodies used were as follows: Flag (F1804, Sigma), PD-L2 (MAB1224, R&D Systems), Myc (2276S, Cell Signaling Technology), HA (3724, Cell Signaling Technology), *FUT8* (ab191571, Abcam), EGFR (ab30, Abcam), phospho-EGFR Tyr1068 (3777, Cell Signaling Technology), *STAT3* (ab12640, Abcam), phospho-*STAT3* Tyr705 (9145, Cell Signaling Technology), phospho-MDM2 S166 (ab170880, Abcam), phospho-PKCαS657 (ab180848, Abcam), Phospho-MAPK Thr202/Tyr204 (4370, Cell Signaling Technology), Phospho-mTOR Ser2448 (5536, Cell Signaling Technology), Phospho-MEK1/2 Ser221 (2338, Cell Signaling Technology), PD-1 (ab52587, Abcam), LAMP2 (ab125068,

Abcam, 1:100), Tubulin (66031-1-Ig, Proteintech).

#### **Tissue sample preparation for western blotting**

The tissue sample (30 mg) was lysed with 500  $\mu$ L of ice-cold lysis buffer (40 mM Tris-HCl, 120 mM NaCl, 1% Triton X-100, and protease inhibitor cocktail) for 30 min at 4°C. Next, the samples were centrifuged at 12,000 rpm for 15 min to remove debris. The supernatant was stored at -80°C. The samples were subjected to western blotting with anti-PD-L2 (MAB1224, R&D Systems) and anti-tubulin (66031-1-Ig, Proteintech) antibodies. The sensitive tissue was obtained from the primary lesion that responded to treatment. Informed consent was obtained from all patients whose tumor tissue were used for this study.

#### **Immunohistochemical (IHC) staining**

Paraffin-embedded tissue sections were baked for 3 h at 60°C. The tissue sections were immersed in 10 mM citrate buffer (pH 6.0) and subjected to microwave treatment for antigen retrieval. Next, the samples were incubated with 3% H<sub>2</sub>O<sub>2</sub> for 30 min to block endogenous peroxidase and blocked with 3% BSA for 1 h. The samples were then probed with anti-PD-L2 (MAB1224, R&D Systems) antibody in blocking buffer overnight at 4°C and incubated with the secondary antibodies (ZSGB-Bio, China) at room temperature for 30 min. Immunostaining was performed using a 3,3'-diaminobenzidine kit (ZSGB-Bio, China), following the manufacturer's instructions. The samples were counterstained with hematoxylin. The subcellular localization, intensity, and distribution of the target protein in the immuno-positive cells were quantified using a visual grading system based on the extent of staining. The proportion of cancer cells exhibiting positive staining was graded on a scale from 0 to 4 as follows: 0, < 10%; 1, 10%-25%; 2, 26%-50%; 3, 51%-75%; 4, >75%. The intensity of staining was graded on a scale of 0-3 as follows: 0, none; 1, weak staining; 2, moderate staining; and 3, strong staining. The EI value, which varied from 0 to 12, was determined by multiplying extent (E) score and intensity (I) score.

#### **Glycosidase assay**

Total proteins were incubated with glycoprotein denaturing buffer (ThermoFisher) at

95°C for 10 min. The samples were treated with endoglycosidase H (Endo H), peptide *N*-glycosidase F (PNGase F), or *O*-glycosidase (Sigma) in the presence of GlycoBuffer 2 (10X) and 10% NP-40 at 37°C for 1 h, following the manufacturer's instructions. Next, the samples were boiled in SDS-PAGE sample buffer at 95°C for 5 min. Glycosylated PD-L2 was stained using the glycoprotein staining kit (ThermoFisher).

## Identification of N-glycopeptide

### (1) LC MS/MS analysis

The protein was analyzed using LC–MS/MS (Thermo Easy-nLC 1200). Briefly, the peptide solutions were separated by nano liquid chromatography on a capillary column (150µm×150mm) packed with C18 (3 µm, 100 Å) at a 90 min gradient: 6% buffer B (1 min)-36% buffer B (69 min)-60% buffer B (6 min)-100% buffer B (12.5 min)-1% buffer B (1.5 min), and at a flow-rate of 400 nL/min. The mobile phases came with 0.1% Formic in water (A) and 0.1% FA in acetonitrile (B). The mass spectrometer (Thermo Scientific Orbitrap Fusion Lumos) was run under the positive mode. The MS1 was analyzed with a mass range of 350–1600 *m/z* at a resolution of 120,000 at 200 *m/z*. The automatic gain control (AGC) was set as 4e<sup>5</sup> and the maximum injection time (IT) was set as 50 ms. The top 20 precursor ions were selected from each MS full scan with isolation width of *m/z*<sup>2</sup>. The MS2 was analyzed with 110 *m/z* at a resolution of 30,000 at 200 *m/z*. The MS2 AGC was set as 5e<sup>4</sup> at HCD collisional mode and 2e<sup>5</sup> at ETD collisional mode, respectively. The maximum injection time was 54ms, and the spray voltage was 2.1 kV and the ion transfer tube temperature was 320 °C.

### (2) Data Analysis

All spectra were searched with Byonic (Protein Metrics, San Carlos, CA) against the UniProt human haptoglobin database (P00738). Trypsin and GluC were selected as enzymes with a maximum of two missed cleavages allowed. The search was performed using the following parameters: (1) static modification, carbamidomethyl of C; (2) dynamic modifications, oxidation of M, deamidation of N and Q, and glycan modifications; (3) maximum missed cleavages, 2; (4) precursor ion mass tolerance 10 ppm; (5) fragment ion

mass tolerance 0.01 Da. Results were filtered at 1% FDR and confidence threshold of Byonic score >100, and further validation was performed manually. The abundance of a site-specific glycoform was represented by the sum of all glycopeptides containing the same glycan at the glycosite while with different peptides in the case of miscleavage or deamidation. The relative quantitation of each site-specific glycopeptide was achieved at two levels: the total glycopeptide level and its corresponding glycosite level. Each sample was analyzed with two injections, and the average normalized abundance of a given N-glycopeptide from the two replicates was used to measure its relative levels between disease groups.

#### **PD-1-binding assay**

The cells were fixed with 4% paraformaldehyde at room temperature for 15 min and incubated with recombinant human PD-1 Fc protein (Cohesion, CRP2068) overnight at 4°C. Next, the cells were washed and stained with an anti-human Alexa Fluor 488 dye conjugate (ThermoFisher). Fluorescence intensity was analyzed using a microplate reader (PerkinElmer, Operetta).

#### **T cell-mediated cell killing assay.**

T cells were activated by incubation with anti-CD3 antibody (100 ng/mL) and IL-2 (10 ng/mL) for 24h. To analyze the killing of tumor cells by T cell, tumor cells were co-cultured with activated T cells at 1:5 ratios for 96h in the presence of Caspase 3/7 substrate. Washed the cells by PBS to remove the T cells and nuclei of tumor cells were counterstained with Sytox. Representative green fluorescent (nuclear restricted SYTOX), and red fluorescent (NucView 547 caspase-3/7 substrate) merged images was measured and quantified by a using a microplate reader (PerkinElmer, Operetta). Red fluorescent cells were counted as dead cells.

#### **Chromatin immunoprecipitation assay (ChIP)**

The ChIP assay was performed using the EZ-ChIP kit (Millipore) as described previously. The cells were fixed with 1% formaldehyde, neutralized with 0.125 M glycine, washed with cold PBS, and lysed with SDS lysis buffer (1% SDS, 10 mM EDTA, 50 mM

Tris-HCl (pH 8.0), and protease inhibitor cocktail (Roche, 04693116001). After sonication, 200–1000 bp chromatin fragments were collected and pre-cleared in dilution buffer (0.01% SDS, 1.1% Triton X-100, 1.2 mM EDTA, 167 mM Tris-HCl (pH 8.0), and 16.7 mM NaCl). The fragments were incubated with homologous IgG or primary antibody on a rotating platform overnight at 4°C. After washing the immunocomplexes collected using protein G beads, the DNA-bound antibody fragments were eluted for real-time polymerase chain reaction analysis with the following primers: *FUT8* 5'-TGCTAAGCCTTCTGAGTGCC-3' (forward) and 5'-CACCAGGCCTCATGCAAAAC-3' (reverse).

#### **Promoter activity assay**

Promoter sequence of human *FUT8* gene was obtained from USCS genomic browser. The promoter regions of *FUT8* wild-type (WT) and 5 mutants were cloned into pGL3-basic plasmid and synthesized by Genechem Company (Shanghai, China). The STAT3 binding sequence were predicted by the JASPAR database. Relative threshold was set to 80%. The *FUT8* mutant promoter vector was constructed with STAT3 mutated binding sites at *FUT8* promoter regions. The control or STAT3 vector in conjunction with luciferase *FUT8* WT or mutant promoter vectors were co-transfected with Renilla luciferase reporter into SCC15 and SCC25 cells, respectively. Firefly and Renilla luciferase activity were measured using the Dual-Luciferase Reporter Assay System (Promega).

#### **Immunofluorescence analysis**

Cells were fixed with 4% paraformaldehyde for 15 min at room temperature, permeabilized with 0.25% Triton X-100 for 15 min, and blocked with 3% bovine serum albumin (BSA) for 1 h. Next, the cells were incubated with primary antibodies overnight at 4°C, followed by incubation with anti-mouse Alexa Fluor 488 or 594 dye conjugates and/or anti-rabbit Alexa Fluor 488 dye conjugates (Life Technologies). The nuclei were stained with DAPI (Life Technologies) and the cells were visualized using an FV-1000 laser scanning confocal microscope.

#### **Proximity ligation assays (PLA)**

The cells were washed with cold PBS, fixed with 4% formaldehyde for 15 min, and

permeabilized with 0.25% Triton X-100 for 15 min. Next, the cells were incubated with blocking solution for 1 h and incubated with suitable concentrations of primary antibodies at 4°C overnight. The samples were then incubated with PLA probe solution for 1 h at 37°C, followed by incubation with ligation buffer for 30 min. Further, the samples were incubated with amplification buffer for 100 min at 37°C in the dark. The nuclei were stained with 4',6-diamidino-2-phenylindole (DAPI). The fluorescent signals were detected using an FV-1000 confocal microscope.

### **Silver staining and mass spectrometry analysis**

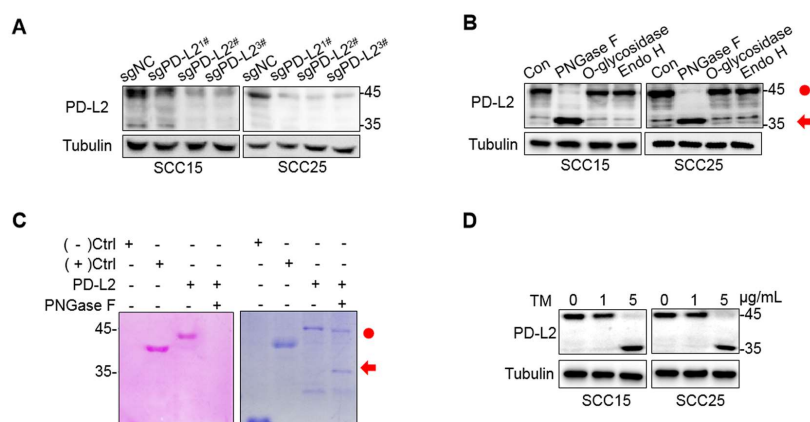
The cells were treated with NETN lysis buffer (50 mM Tris, 150 mM NaCl, 0.2 mM EDTA, 1% Triton X-100, 1% NP-40, and protease inhibitor cocktail (Roche, 04693116001) on ice for 30 min. The lysates were centrifuged for 20 min at 4°C. For immunoprecipitation, the cell lysates were incubated with anti-FLAG M2 affinity gel (Sigma) with gentle rocking at 4°C for 3 h. The cell lysates were then incubated with flag-peptides with gentle rocking at 4°C for 3 h. The proteins were denatured by heating at 70°C for 10 min. The eluents were subjected to NuPAGE with a 4 %-12% Bis-Tris gel (Invitrogen). The bands were visualized using silver staining with a silver staining kit (Pierce, Thermo Fisher). Distinct protein bands were retrieved and subjected to liquid chromatography-tandem mass spectrometry (LC-MS/MS).

### **EGF-EGFR binding assay**

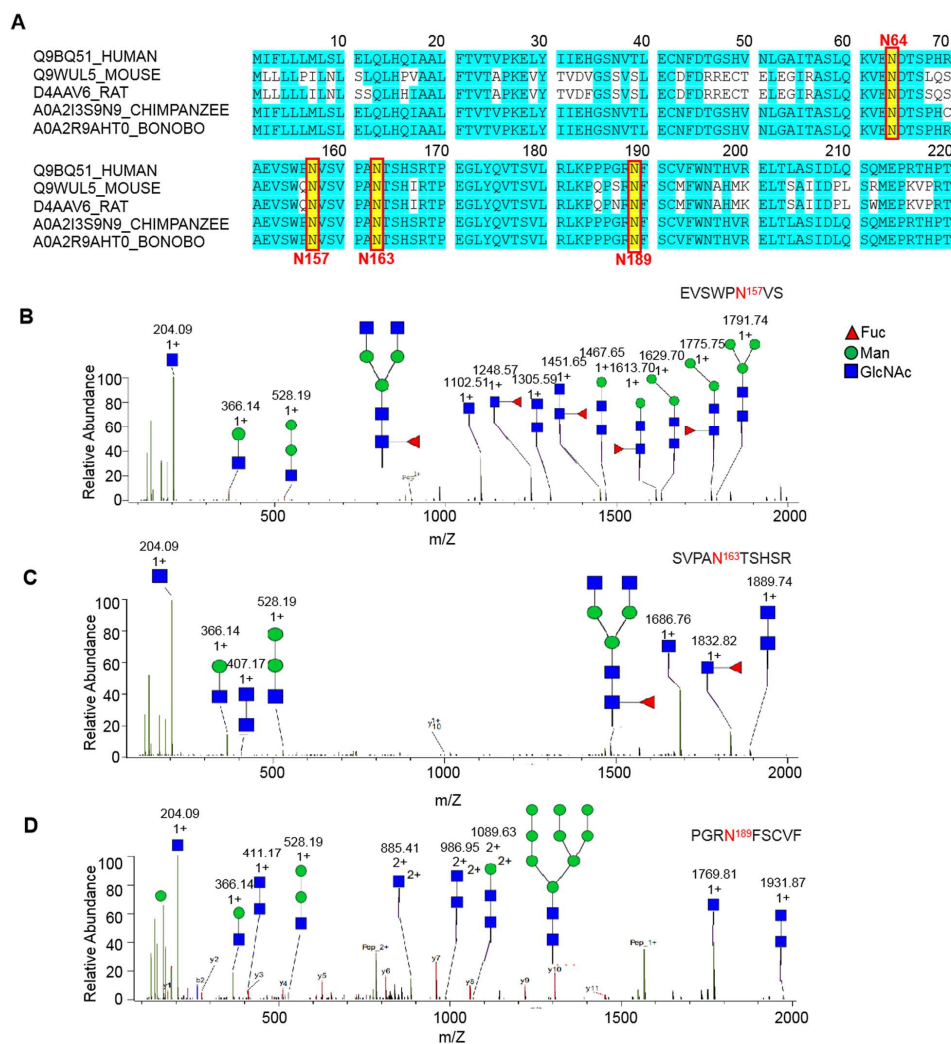
The 96-wells plates were coated with 5 µg/mL anti-EGFR antibody (100 µL/well) in 0.05 M NaCO<sub>3</sub>/NaHCO<sub>3</sub> (pH 9.6) overnight at 4°C. The plates were washed with PBS containing 0.1% Tween-20 (PBST) and blocked with 1% BSA solution for 1.5 h at 37°C. Then incubated with the cell lysate or negative control overnight. Next, the samples were washed with PBST and incubated with recombinant human biotin-conjugated EGF at 37°C for 1.5 h. The samples were washed with PBST and incubated with streptavidin-conjugated HRP (1:10000 in blocking buffer; 100 µL/well) at room temperature for 30 min. Further, the samples were incubated with 200 µL TMB at room temperature for 30 min. The optical density at 370 nm was determined using a BioTek Cytation 5 microplate reader.



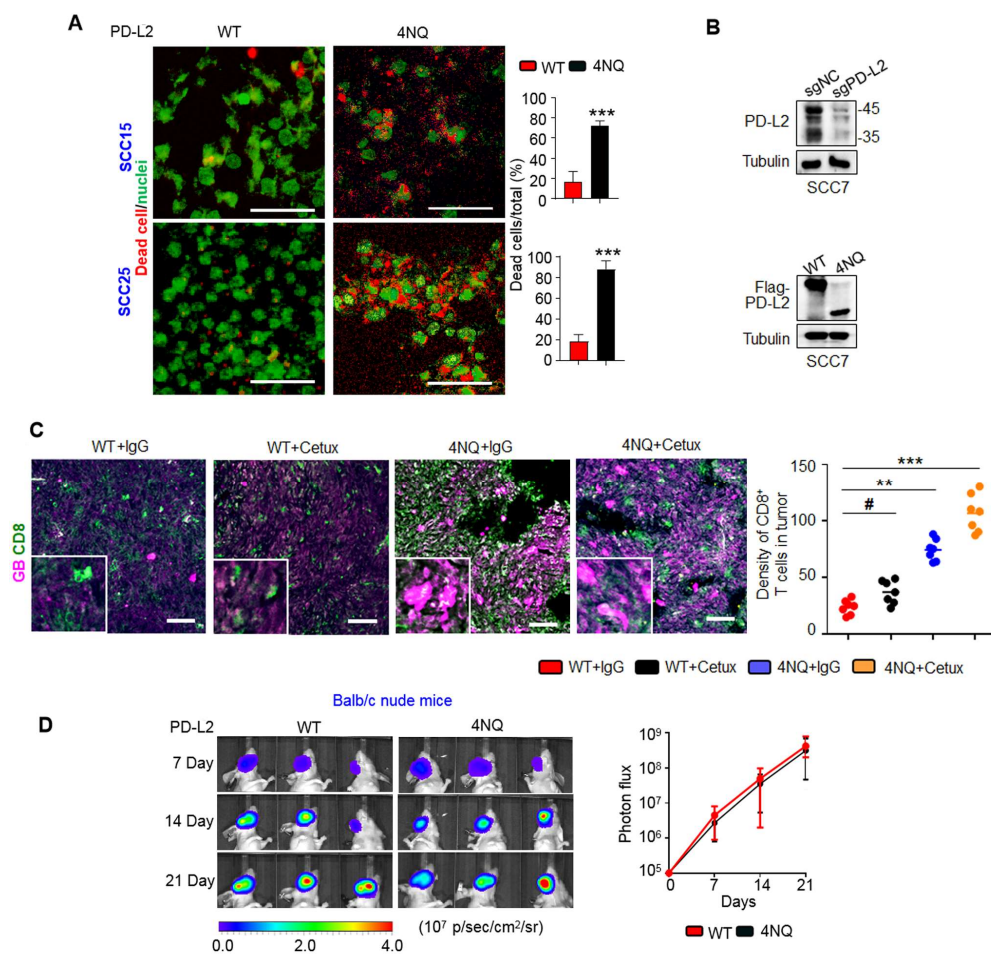
## Supplementary Figures



**Supplementary Figure 1. PD-L2 is N-glycosylated in HNSCC cell lines. (A)** PD-L2 protein levels in sgNC and three independent sgPD-L2 stable clones in SCC15 and SCC25 cells. **(B)** The glycosylation patterns of PD-L2 protein in SCC15 and SCC25 cell lysates were incubated with PNGase F, Endo H or O-glycosidase, and analyzed by Western blotting. **(C)** Glycoprotein staining of purified PD-L2 protein in the presence or absence PNGase F treatment in SCC15 cells. Coomassie blue staining represents total PD-L2 protein. Circle, glycosylated PD-L2; arrowhead, non-glycosylated PD-L2. (-) Ctrl, a control for non-glycoprotein. (+) Ctrl, a positive control for glycoprotein. **(D)** PD-L2 proteins expression in various dose of Tunicamycin (TM) treated cells.



**Supplementary Figure 2. Identification of the glycosylation sites of PD-L2. (A)** The PD-L2 amino acid sequences alignment from distinct species. Four NXT motifs N64, N157, N163, and N189 are highlighted in yellow. **(B-D)** Identification of *N*-glycopeptides based on LC-MS/MS, corresponding to each of the four *N*-glycosylation sites N157, N163 and N189 of PD-L2 (from SCC15 cells).



### Supplementary Figure 3. Glycosylation is required for PD-L2 immunosuppression.

**(A)** T cell-mediated tumor cell-killing effect in PD-L2 WT or 4NQ SCC15 and SCC25 cells.

The quantitative ratio of apoptotic cells was shown in bar graph (right). Scale bar, 50  $\mu$ m.

\*\*\* $P$ <0.001. **(B)** Validations of the transfection efficiency in lentivirus infected SCC7 cells

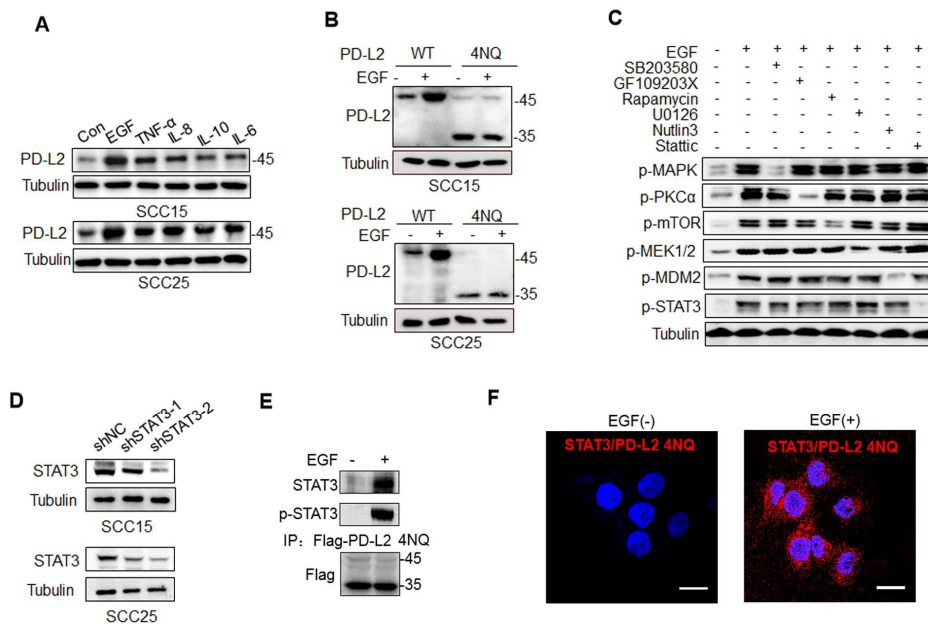
by Western blotting. **(C)** Immunofluorescence staining of the protein expression pattern of

CD8, and granzyme B (GB) in SCC7 tumor masses. Scale bar, 20  $\mu$ m. \*\* $P$ <0.01;

\*\*\* $P$ <0.001; #, not significant. **(D)** Representative BLI of tumors derived from PD-L2 WT

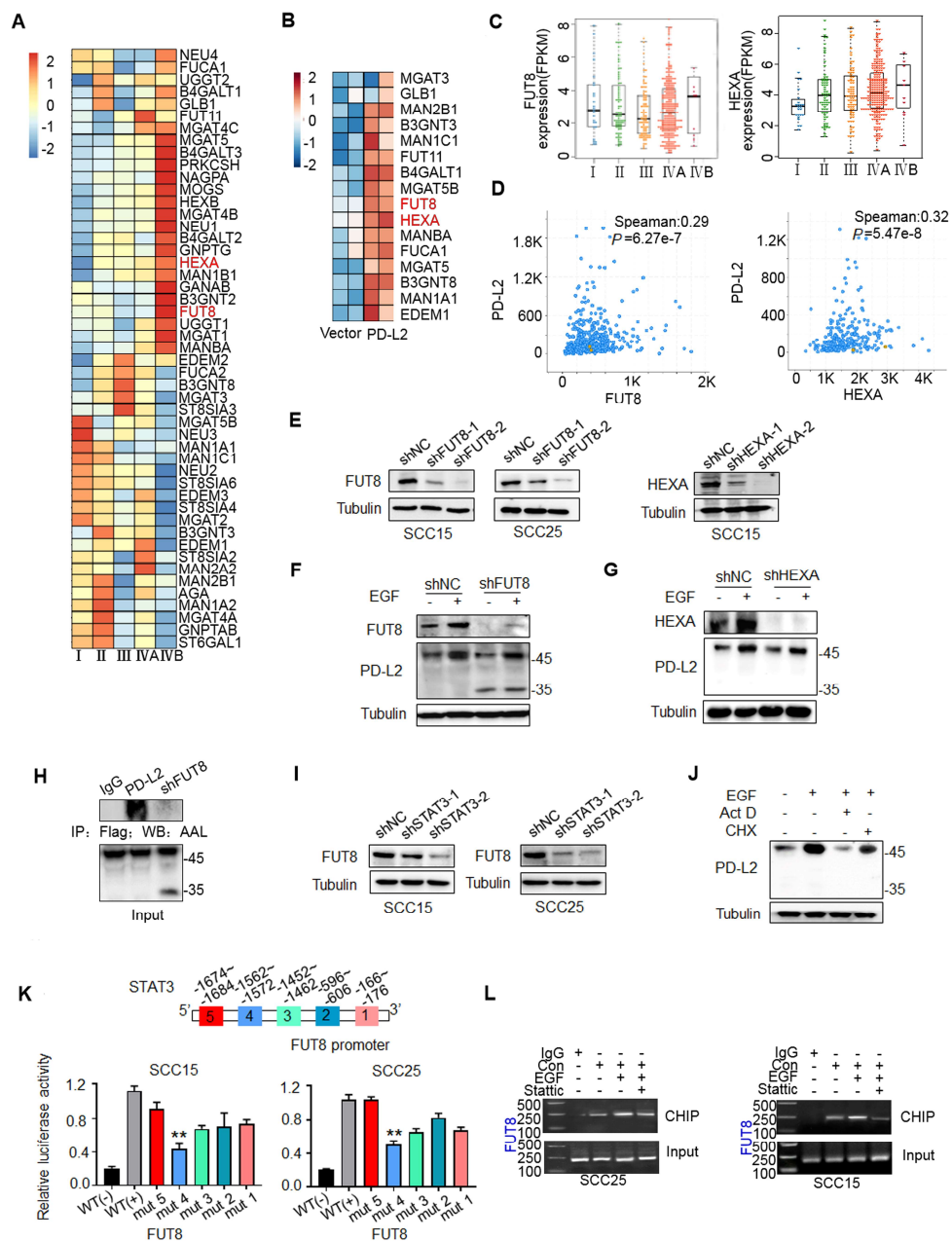
and 4NQ mutant expressing SCC7 cells in BALB/c immune deficient nude mice at 21 days

( $n$  = 5 mice per group).



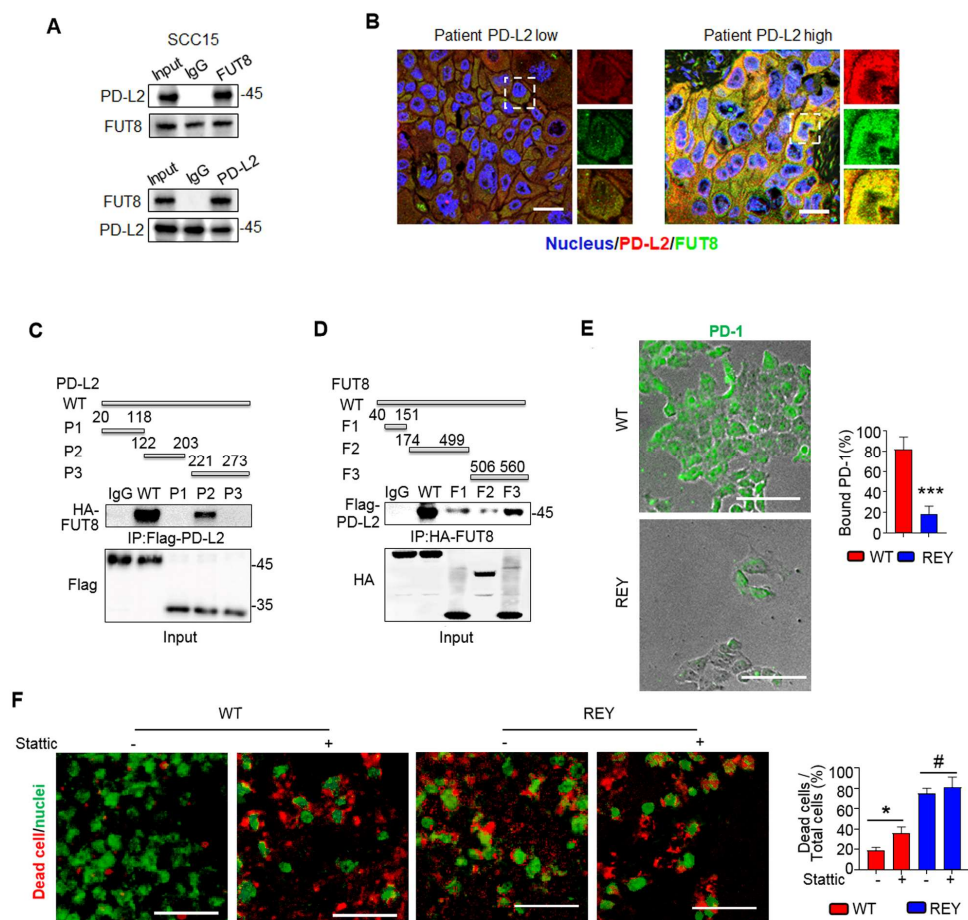
**Supplementary Figure 4. EGF/STAT3 signaling regulates PD-L2 glycosylation. (A)**

PD-L2 protein expression in SCC15 and SCC25 cells treated with multiple cytokines for 15 min. **(B)** WB analysis of exogenous PD-L2 expression in Flag-PD-L2 WT or 4NQ cells with or without exposure to EGF for 15 min. **(C)** SCC15 cells were pretreated with or without 7 $\mu$ M SB203580 (MAPK inhibitor), 7 $\mu$ M GF109203X (PKC $\alpha$  inhibitor), 7 $\mu$ M Rapamycin (mTOR inhibitor), 7 $\mu$ M U0126 (MEK1/2 inhibitor), 7 $\mu$ M Nutlin-3 (MDM2 inhibitor) and 7 $\mu$ M Stattic (STAT3 inhibitor) for 4 h, followed by incubation with EGF for 15 min. Lysates were subjected to immunoblotting analysis. **(D)** Protein levels of STAT3 in shNC or shSTAT3 treated SCC15 and SCC25 cells. **(E)** Co-IP analyzed the (p)STAT3/PD-L2 interaction in SCC15 PD-L2 4NQ cells with or without EGF treatment. **(F)** Immunofluorescence staining of STAT3 and PD-L2 4NQ interaction in SCC15 cells by PLA assay. Scale bar, 20  $\mu$ m.

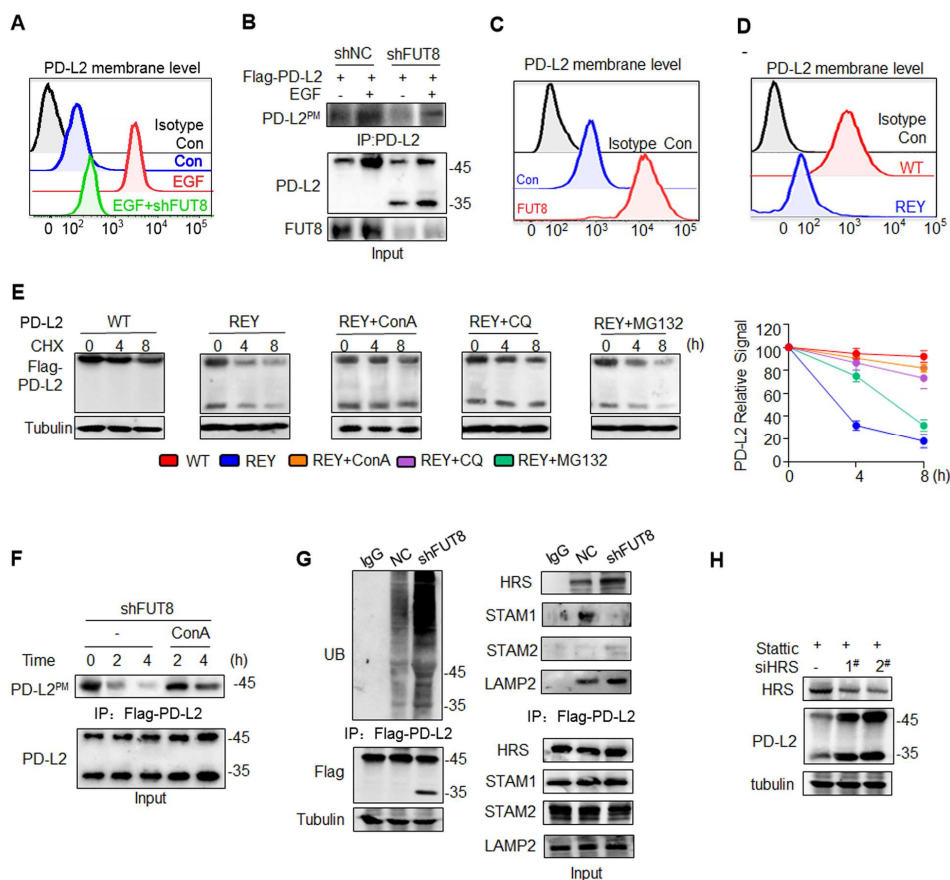


**Supplementary Figure 5. Identification of the candidate *N*-glycosyltransferase responsible for PD-L2 glycosylation. (A)** Heatmap showed *N*-glycosyltransferase gene expression pattern in HNSCC based on The Cancer Genome Atlas (TCGA) database. **(B)** Transcriptome sequencing showed *N*-glycosyltransferase expression in Vector and PD-L2 overexpressing SCC15 cells. **(C)** *N*-linked glycotransferases, FUT8, HEXA expression strongly correlated tumor stage in HNSCC. **(D)** Correlation analysis between FUT8, HEXA

expression and PD-L2 in HNSCC using TCGA data. **(E)** Validations of the knockdown efficiency in shFUT8-1, shFUT8-2, shHEXA-1 and shHEXA-2 lentivirus infected SCC15 and SCC25 cells by Western blotting. **(F)** Protein levels of PD-L2 and FUT8 in EGF treated shNC or shFUT8 SCC25 cells. **(G)** PD-L2 protein levels by shNC or shRNA for HEXA in EGF pretreated SCC15 cells. **(H)** Proteins in the cell lysates were blotted with biotinylated AAL lectin and subjected to the peroxidase (SK-6604, Vector Laboratories). **(I)** Protein levels of FUT8 in shNC or shSTAT3 treated SCC15 and SCC25 cells. **(J)** PD-L2 protein expression was detected in SCC15/PD-L2 cells treated with actinomycin D (Act D) or CHX for 16 h. **(K)** Luciferase reporter assay revealed that FUT8 was the transcriptional target of STAT3. **\*\* $P < 0.01$** . **(L)** CHIP assay revealed that STAT3 knockdown impaired EGF induced STAT3 binding to the promoter of FUT8 in SCC15 and SCC25 cells.



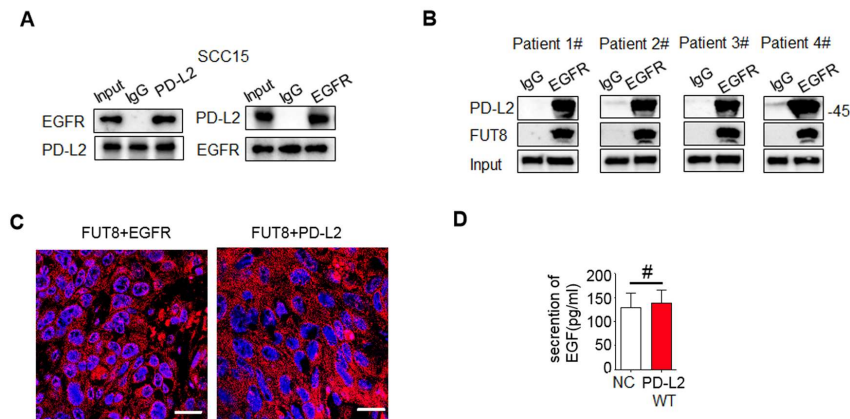
**Supplementary Figure 6. STAT3/FUT8 catalyzes PD-L2 glycosylation contributes to immune surveillance escape in HNSCC. (A)** Co-IP analysis of the interaction between PD-L2 and FUT8 in SCC15 cells. **(B)** Immunofluorescence staining of FUT8 and PD-L2 in HNSCC specimens. Scale bar, 20  $\mu$ m. **(C)** Mapping of the binding site of PD-L2/FUT8 in vitro. Diagrammatic representation of FUT8 and its truncated forms in SCC15 cells. **(D)** Identification of the essential domains required for interactions with FUT8 and PD-L2 in SCC15 cells. **(E)** The bound PD-1/Fc protein in PD-L2 WT, or REY expressing SCC15 cells. Scale bar, 50  $\mu$ m. Significance was detected by one-way ANOVA. \*\*\* $P$ <0.001. **(F)** T-cell-mediated tumor cell-killing assay in PD-L2 WT or REY-expressing SCC15 cells with or without Stattic treatment. Scale bar, 50  $\mu$ m. \* $P$ <0.05; #, not significant.



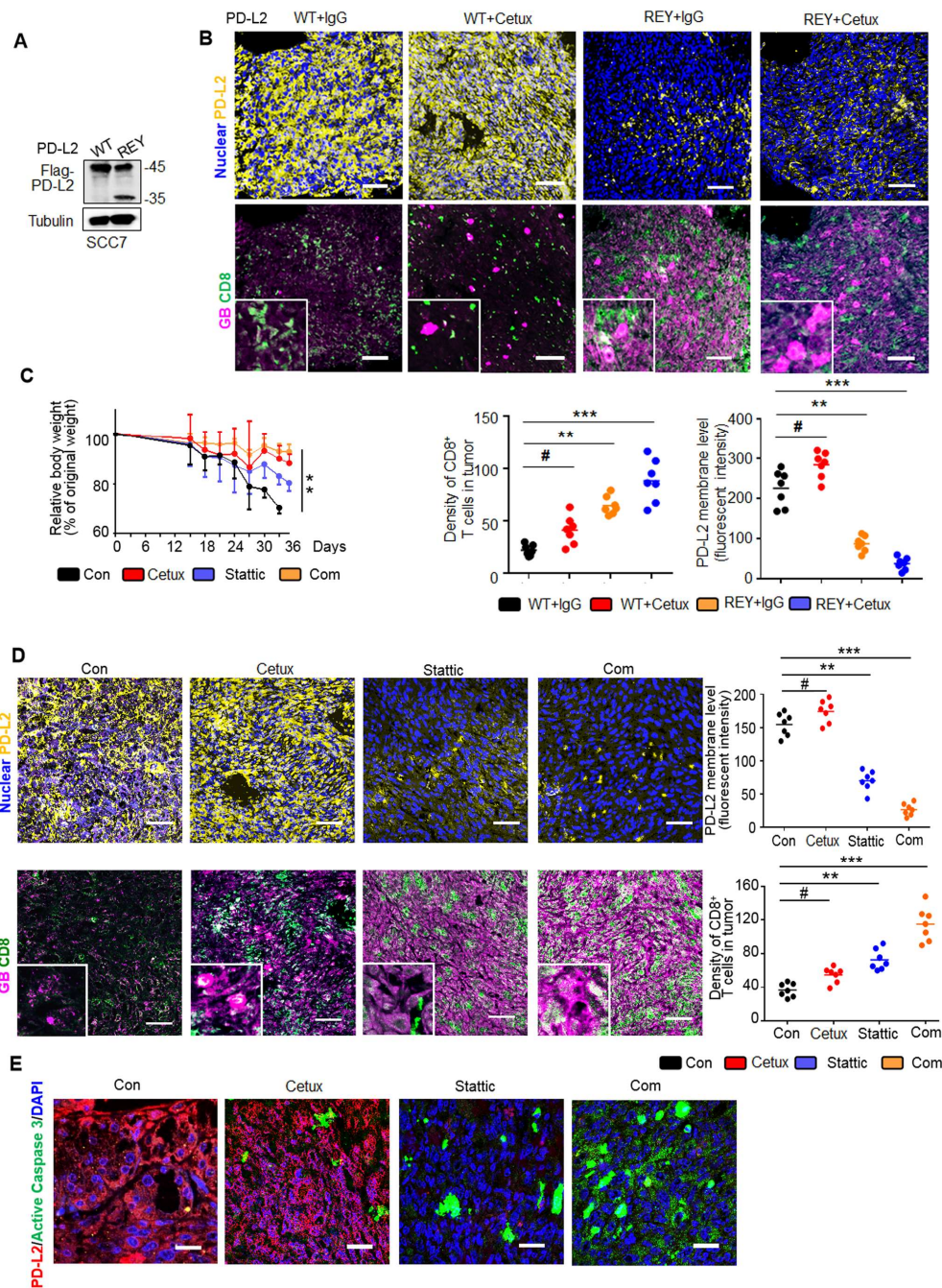
**Supplementary Figure 7. PD-L2 glycosylation blocked ubiquitination mediated lysosome degradation and facilitated PD-L2 membrane abundance. (A)** Cell membrane PD-L2 level in SCC15 cells with or without EGF treatment and/or shFUT8 infection was analyzed by flow cytometry (n=3). **(B)** Cell surface IP (CS-IP) analyzed membrane PD-L2 in EGF treated SCC15 cells expressing FUT8-shRNAs or control shRNAs. **(C)** Flow cytometry analysis measuring the membrane PD-L2 in vector or FUT8 expressing SCC15 cells (n=3). **(D)** The cell membrane PD-L2 level in SCC15 PD-L2 WT and REY cells analyzed by flow cytometry (n = 3). **(E)** Left, the degradation of PD-L2 WT or REY mutant in SCC15 cells was evaluated by CHX-chase assay in the presence of inhibitors for proteasome (MG132) and lysosome (ConA and CQ). Right, quantification of the PD-L2 intensity. **(F)** Cell membrane PD-L2 was measured in FUT8-knockdown cells by CS-IP. Incubation at 37 °C ± 50 nM ConA for 0, 2, 4h. **(G)** Effect of FUT8 knockdown on PD-L2 ubiquitination. The interaction between HRS, LAMP2, STAM1, STAM2 and PD-L2



was determined by Co-IP in SCC15 expressing FUT8 knockdown cells. **(H)** PD-L2 expression levels in Stattic treated with or without HRS-interfering SCC15 cells.



**Supplementary Figure 8. PD-L2 interacts with EGFR in HNSCC specimens. (A)** Co-IP analysis of the interaction between PD-L2 and EGFR in SCC15 cells. **(B)** Association of PD-L2 and EGFR as well as FUT8 was verified in four HNSCC specimens. **(C)** The direct interaction between PD-L2 and EGFR as well as FUT8 in HNSCC specimens by PLA. Scale bar, 20  $\mu$ m. **(D)** EGF secretion from control and PD-L2 expressing SCC15 cell culture supernatant was measured by ELISA (n=3). #, not significant.



**Supplementary Figure 9. Inhibition of PD-L2 glycosylation improves Cetuximab efficacy.** (A) REY mutant PD-L2 transfection efficiency in SCC7 cells was determined by Western blotting. (B) Immunofluorescence staining of PD-L2, CD8 and GB in tumors derived from SCC7 cells transfected with PD-L2 WT or REY mutant and treated with Cetux every week. Scale bar, 20  $\mu$ m. Bottom, Quantification, \*\* $P$ <0.01; \*\*\* $P$ <0.001; #, not

significant. **(C)** Survival of C3H mice bearing SCC7 tumors treated with Cetux, Stattic or the combination therapy.  $**P<0.01$ . **(D)** PD-L2, CD8 and GB protein expression detected by immunofluorescence staining in SCC7 orthotopic tumors. Scale bar, 20  $\mu\text{m}$ . Right, Quantification,  $**P<0.01$ ;  $***P<0.001$ ; #, not significant. **(E)** Immunofluorescence staining of PD-L2 and cleaved-caspase 3 was detected in SCC7 tumor mass. Scale bar, 20  $\mu\text{m}$ .

**Supplementary Tables.****Supplementary Table 1. The clinical characteristics of patients included in single-cell sequencing**

Designation	Age	Sex	Primary Site	TNM Stage	Grade
Patient 1	43	male	Tongue	T3N2M0	IVA
Patient 2	47	male	Tongue	T4N1M0	IVA

**Supplementary Table 2. The differentially expressed genes in Group1 compared to the other groups. (Related to Figure 1C)**

Rank	Gene_ID	Gene_Name	Log2 FC	P value
1	ENSG00000118473	SGIP1	1.985817703	5.57E-34
2	ENSG00000111674	ENO2	1.769523712	4.30E-31
3	ENSG00000134243	SORT1	1.645308732	5.48E-15
4	ENSG00000137809	ITGA11	1.581957425	4.56E-33
5	ENSG00000197646	PDCD1LG2	1.5677836	1.64E-07
6	ENSG00000160886	LY6K	1.510625716	1.22E-13
7	ENSG00000164176	EDIL3	1.508244681	6.40E-42
8	ENSG00000117152	RGS4	1.487518878	4.08E-32
9	ENSG00000108691	CCL2	1.365413954	3.60E-42
10	ENSG00000083857	FAT1	1.326366538	1.00E-26
11	ENSG00000144136	SLC20A1	1.273697799	2.94E-22
12	ENSG00000060718	COL11A1	1.260307192	1.59E-25
13	ENSG00000164930	FZD6	1.24709857	2.88E-08
14	ENSG00000106366	SERPINE1	1.204768913	4.43E-34
15	ENSG00000008517	IL32	1.19628867	1.55E-30
16	ENSG00000074416	MGLL	1.178567364	2.94E-26
17	ENSG00000249992	TMEM158	1.137685961	9.60E-16
18	ENSG00000133816	MICAL2	1.084719236	2.68E-19
19	ENSG00000146674	IGFBP3	1.07633818	1.34E-12
20	ENSG00000112715	VEGFA	1.075761367	7.19E-17
21	ENSG00000134013	LOXL2	1.0696223	1.11E-26
22	ENSG00000134363	FST	1.063960056	1.53E-13
23	ENSG00000251493	FOXD1	1.060066217	6.37E-18
24	ENSG00000182667	NTM	1.053483419	4.16E-20
25	ENSG00000175592	FOSL1	1.043497019	2.20E-17
26	ENSG00000185803	SLC52A2	1.039122601	8.81E-10
27	ENSG00000139318	DUSP6	1.034587543	7.37E-19
28	ENSG00000125148	MT2A	1.012969985	7.29E-27
29	ENSG00000149948	HMGA2	1.005930708	1.36E-15









05017210-10.1371/journal.pone.0248888	en	375124	367881	350261	348861	339271	330277	324281	318075	311727	305262	298742	292163	285522	278919	272244	265597	258977	252381	245811	239271	232751	226251	219771	213311	206871	200451	194051	187671	181311	174971	168651	162351	156071	149811	143571	137351	131151	124971	118811	112671	106551	100451	94351	88271	82211	76171	70151	64151	58171	52211	46271	40351	34451	28571	22711	16871	11051	5251	0
05017210-10.1371/journal.pone.0248888	en	375124	367881	350261	348861	339271	330277	324281	318075	311727	305262	298742	292163	285522	278919	272244	265597	258977	252381	245811	239271	232751	226251	219771	213311	206871	200451	194051	187671	181311	174971	168651	162351	156071	149811	143571	137351	131151	124971	118811	112671	106551	100451	94351	88271	82211	76171	70151	64151	58171	52211	46271	40351	34451	28571	22711	16871	11051	5251	0

**Supplementary Table 4. RNA sequencing revealed the expression of 16 N-linked glycosyltransferase in PD-L2 overexpression cells compared to the control cells (Related to supplemental figure 5B)**

Gene_ID	Gene_name	Log2FC	P value
ENSG00000213614	HEXA	0.719369396	1.73E-08
ENSG00000086062	B4GALT1	0.603475124	0.002689879
ENSG00000104774	MAN2B1	0.586699342	0.178050062
ENSG00000177191	B3GNT8	0.552771466	0.21114345
ENSG00000179163	FUCA1	0.506717284	0.080456431
ENSG00000196968	FUT11	0.319348886	0.045714148
ENSG00000167889	MGAT5B	0.353358629	0.012103315
ENSG00000033170	FUT8	0.394192744	6.37E-07
ENSG00000109323	MANBA	0.413757055	0.040504746
ENSG00000167889	MGAT5	0.394192744	0.012103315
ENSG00000128268	MGAT3	0.2224182	0.068201423
ENSG00000111885	MAN1A1	0.183144943	0.005996254
ENSG00000134109	EDEM1	0.138106781	0.057009002
ENSG00000163521	GLB1	0.130131352	0.001719166
ENSG00000179913	B3GNT3	0.092059765	0.008080418
ENSG00000117643	MAN1C1	0.003980993	0.039809928