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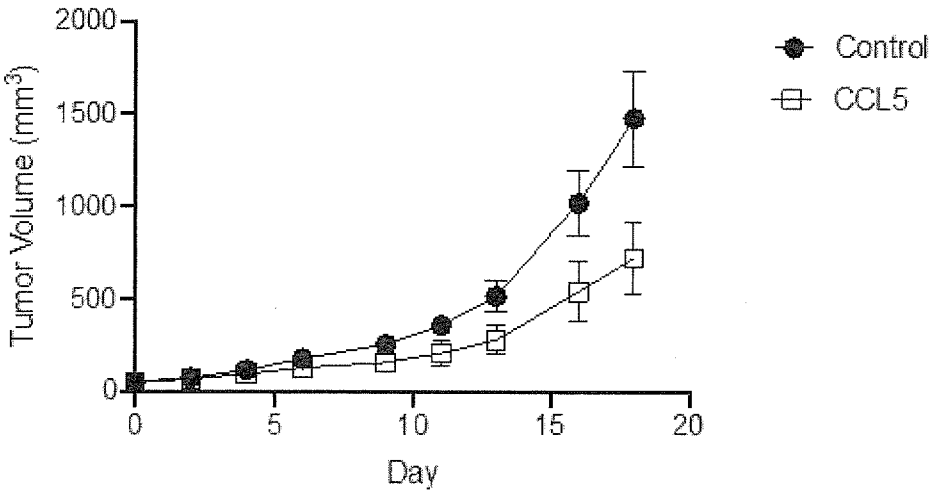
FIG. 4G



(57) Abstract: The present disclosure provides a method of treating cancer using a chemokine, e.g., a CCL5 mimetic. The chemokine can be used individually or in combination with other therapeutics, such as anti-PD-1 antibodies, anti-PD-L1 antibodies, and/or a TGFβ inhibitor (e.g., anti- TGFβ antibody). The present disclosure also provides a method of treating cancer using a a combination therapy with systemic administration of an anti-PD-L1 antibody and intratumoral administration of a TGFβ inhibitor (e.g., anti-TGFβ antibody).

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[Continued on next page]

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Cancer Therapeutics Comprising Chemokine or its Analog

1. CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 63/023,790, filed May 12, 2020, the entire disclosure of which is hereby incorporated by reference in its entirety.

2. BACKGROUND

[0002] Antibodies blocking the PD-1/PD-L1 immune checkpoint pathway have been approved as first-line treatments for a range of cancer types including non-small-cell lung carcinoma (NSCLC), urothelial cancer, head and neck squamous cell carcinoma (HNSCC), microsatellite instability-high cancer and melanoma. However, while effective in some patients, with some patients experiencing dramatic remissions, these immune checkpoints inhibitors are not effective in others. There is a need to improve the response rate to these agents in order to benefit more patients.

3. SEQUENCE LISTINGS

[0003] The instant application contains a Sequence Listing which has been submitted via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on May 12, 2021, is named "48492 WO SEQ LISTING_ST25" and is 2153 kilobytes in size.

4. SUMMARY

[0004] The present disclosure provides a method of treating cancer using a chemokine, e.g., an isolated CCL5 mimetic. The present disclosure also provides a method of treating an infection using a chemokine, e.g., an isolated CCL5 mimetic. The chemokine can be used individually or in combination with other therapeutics, such as anti-PD-1 orPD-L1 antibodies, or TGFβ inhibitors. The combination therapy can be combined with administration of more than one additional therapeutics (e.g., TGFβ inhibitor (e.g., anti-TGFβ antibody) and anti-PD-1 or PD-L1 antibody) to further induce T cell infiltration.

[0005] The combination therapy is based on the discovery by the Applicant that chemokines, such as CCL5 and CXCL9, are highly correlated with immune cell infiltration in various human cancers. Without wishing to be bound by a theory, chemokines are believed to enhance infiltration of immune cells to improve efficacy of anti-PD-1/PD-L1 therapy. This is consistent with earlier studies which demonstrated that anti-tumor activity of anti-PD-1/PD-

L1 therapies correlates with T cell infiltration in tumors and T cell excluded tumors are less likely to respond to immune checkpoint blockade targeting the PD-1/PD-L1 pathway. The present disclosure shows that intratumorally administered CCL5 could enhance the anti-tumor activity of anti-PD-L1 antibody.

[0006] Accordingly, the present disclosure provides a method of increasing immune cell infiltration and migration into a target of interest by administering a chemokine such as CCL5, e.g., an isolated CCL5 mimetic. Specifically, the method can be used for treatment of cancer by recruiting mature NK cells and activated CD8 T cells to the tumor microenvironment. The method can be used for treatment of inflammation or other disorders. The chemokines and their variants can be also used in combination with an ADCC-inducing antibody or in cancer or non-cancer application of adoptive cell therapy.

[0007] In an aspect, the present disclosure provides a pharmaceutical composition, comprising: a CCL5 mimetic, or pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable carrier.

[0008] In some embodiments, the CCL5 mimetic is a human CCL5 peptide, wherein the CCL5 peptide has a sequence of SEQ ID NO: 1. In some embodiments, the CCL5 mimetic is a CCL5 analog. In some embodiments, the CCL5 analog is a polypeptide having the sequence of SEQ ID NO:1. In some embodiments, the CCL5 analog comprises an active fragment of a human CCL5 peptide. In some embodiments, the active fragment of human CCL5 comprises amino acids 12-22 of SEQ ID NO: 1. In some embodiments, the active fragment of human CCL5 comprises one or more of the following amino acid residues selected from the group consisting of: P2, Y3, D6, T7, F12, I15, and R17. In some embodiments, the CCL5 mimetic comprises a polypeptide having at least 70%, 75%, 80%, 85%, 90%, or 95% sequence identity to SEQ ID NO: 1 or SEQ ID NO: 2. In some embodiments, the CCL5 mimetic is a CCL5 analog having a longer half-life in vivo as compared to CCL5.

[0009] In some embodiments, the CCL5 mimetic is a conjugate of CCL5 or a CCL5 analog to a conjugate moiety. In some embodiments, the conjugate moiety is selected from polyethylene glycol (PEG) and hyaluronic acid. In some embodiments, the conjugate moiety is selected from the group consisting of HAS, human IgG, scFv, transferrin, albumin, and an Fc domain of an immunoglobulin. In some embodiments, the conjugate moiety is selected from the group consisting of: XTEN, a proline-alanine-serine polymer (PAS), a

homopolymer of glycine residues (HAP), a gelatin-like protein (GLP), a signal peptide and an elastin-like peptide (ELP). In some embodiments, the CCL5 mimetic comprises one or more modified or non-naturally occurring amino acids, selected from the group consisting of: a steric enantiomer (D isomer), a rare amino acid of plant origin, a non-naturally occurring amino acid or amino acid mimetic, or have been modified by any one or more modifications selected from acetylation, acylation, phosphorylation, dephosphorylation, glycosylation, myristollation, amidation, aspartic acid/asparagine hydroxylation, phosphopantethane attachment, methylation, methylthiolation, prensyl group attachment, intein N-/C-terminal splicing, ADP-ribosylation, bromination, citrullination, deamination, dihydroxylation, formylation, geranyl-geranilation, glycation, palmitoylation, α-methyl-amino acids, Cα-methyl amino acids, and Nα-methyl amino acids.

[0010] In some embodiments, the CCL5 mimetic is chemically-synthesized and comprises one or more non-peptide bonds. In some embodiments, the pharmaceutically acceptable salt of a CCL5 mimetic, wherein the salt is hydrochloride, trihydrochloride, sulfate, mesylate, or tosylate.

[0011] In some embodiments, the CCL5 mimetic activates NK cell or T cell activity. In some embodiments, the CCL5 mimetic recruits activating T cells and/or NK cells to a tumor microenvironment.

[0012] In some embodiments, the pharmaceutical composition is formulated for parenteral administration. In some embodiments, the pharmaceutical composition is formulated for intratumoral injection, intravenous injection or subcutaneous injection.

[0013] In another aspect, the present disclosure provides a kit for treatment of cancer, comprising: the pharmaceutical composition of the present disclosure and an additional therapeutic agent. In some embodiments, the additional therapeutic agent is an anti-PD-L1 antibody, an anti-PD-1 antibody, or a TGFβ inhibitor. In some embodiments, the additional therapeutic agent is a bispecific antibody against PD-L1 and TGFβ or against PD-1 and TGFβ. In some embodiments, the additional therapeutic agent comprises an anti-PD-L1 antibody and an anti-TGFβ antibody. In some embodiments, the additional therapeutic agent comprises an anti-PD-1 antibody and an anti-TGFβ antibody. In some embodiments, the additional therapeutic agent comprises an anti-PD-L1 antibody, wherein the anti-PD-L1 antibody is atezolizumab.

[0014] In some embodiments, the additional therapeutic agent is an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab. In some embodiments, the additional therapeutic agent is an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is GIGA-564. In some embodiments, the additional therapeutic agent is an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is GIGA-2328. Anti-CTLA4 antibodies that can be used in combination with the chemokine mimetics or analogs thereof of the present disclosure can be found in PCT Application Publication No.: WO2020140084A1, which is thereby incorporated by reference in its entirety. In certain embodiments, the anti-CTLA4 antibody has a heavy chain amino acid sequence set forth in SEQ ID NO:5909. In certain embodiments, the anti-CTLA4 antibody has a light chain amino acid sequence set forth in SEQ ID NO:5910. In certain embodiments, the anti-CTLA4 antibody is afucosylated.

[0015] In some embodiments, the additional therapeutic agent comprises a T cell or an NK cell. In some embodiments, the additional therapeutic agent comprises a CAR-NK or CAR-macrophage cell. In some embodiments, the T cell is a CAR-T or TCR-T cell. In some embodiments, the additional therapeutic agent is an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof. In some embodiments, the additional therapeutic agent is an agent activating NK cell or T cell activity. In some embodiments, the additional therapeutic agent is an agent that recruits activating T cells and/or NK cells to a tumor microenvironment. In some embodiments, the additional therapeutic agent is a vaccine, a chemotherapeutic agent, a small molecule inhibitor, or a nucleic acid. In some embodiments, the additional therapeutic agent is a vaccine, chemotherapeutic agent, nucleic acid therapeutic, or small molecule inhibitor.

[0016] In yet another aspect, the present disclosure provides a method of treating cancer, comprising the step of: administering to a subject with the cancer a therapeutically effective amount of an isolated chemokine mimetic, or pharmaceutically acceptable salt thereof. In some embodiments, the isolated chemokine mimetic is selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, and an analog thereof. In some embodiments, the isolated chemokine mimetic is two or more isolated chemokine mimetics selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.

[0017] In some embodiments, the isolated chemokine mimetic is a CCL5 mimetic or pharmaceutically acceptable salt thereof. In some embodiments, the isolated chemokine

mimetic or pharmaceutically acceptable salt thereof is administered in a pharmaceutical composition further comprising a pharmaceutically acceptable carrier or excipient.

[0018] In some embodiments, said administering is via intratumoral injection, intravenous injection, subcutaneous injection, or a combination thereof. In some embodiments, said administering is via intratumoral injection. In some embodiments, the method further comprises the step of administering to the subject an anti-PD-L1 antibody or an anti-PD-1 antibody. In some embodiments, the method further comprises the step of administering to the subject a TGFβ inhibitor. In some embodiments, the method further comprises the steps of administering anti-PD-L1 antibody and an anti-TGFβ antibody. In some embodiments, the method further comprises the step of administering a bi-specific antibody targeting both PD-L1 and TGFβ. In some embodiments, the method further comprises the step of administering a bi-specific antibody targeting both PD-1 and TGFβ.

[0019] In some embodiments, the method further comprises the step of administering to the subject an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab. In some embodiments, the method further comprises the step of administering to the subject a T cell or an NK cell, optionally wherein the T cell is a CAR-T, CAR-NK,TCR-T cell. In some embodiments, the method further comprises the step of administering to the subject an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof. In some embodiments, the method further comprises the step of administering to the subject an agent activating NK cell or T cell activity. In some embodiments, the method further comprises the step of administering to the subject an agent selected from: a vaccine, a chemotherapeutic agent, a small molecule inhibitor, and a nucleic acid.

[0020] In some embodiments, the cancer is selected from the group consisting of: multiple myeloma, adrenocortical carcinoma, acute myeloid leukemia, Bladder Urothelial Carcinoma, glioma, breast invasive carcinoma, glioma, Cervical squamous cell carcinoma, endocervical adenocarcinoma, cholangiocarcinoma, chronic myelogenous leukemia, colon adenocarcinoma, esophageal carcinoma, glioblastoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell lymphoma, mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocyoma, paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma,sarcoma, skin cutaneous melanoma, mucosal melanoma, stomach adenocarcinoma, testicular germ cell tumors, thyomas, thyroid

carcinoma, uterine carcinosarcoma, uterine corps endometrial carcinoma, microsatellite instability-high cancer, basal cell carcinoma, Merkel cell carcinoma, and uveal melanoma.

[0021] In some embodiments, the method further comprises the steps of: intratumorally administering a therapeutically effective amount of an isolated chemokine mimetic, or pharmaceutically acceptable salt thereof, to a subject who has been determined to have expression levels in a biological sample of one or more genes selected from the group consisting of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, CD8, CD3, TCRβ, TCR1, WARS, CD11c, NKp46, NCR1, CD11B, FcRs, collagen genes, CTLA4, CD56, CD16, CD7 CD127, Tbet, Eomes, granzymes, and perforin that are lower than or higher than a predetermined threshold level.

[0022] In some embodiments, the biological sample is a tumor biopsy. In some embodiments, the biological sample is a liquid biopsy. In some embodiments, the biological sample is a blood sample. In some embodiments, the biological sample is a sample containing cells isolated from a subject comprising a disease or condition (e.g., cancer or an infection). In some embodiments, the biological sample is a sample containing cells isolated from a donor. In certain embodiments, the biological sample is a sample containing T cells and/or NK cells isolated from subject comprising a disease or condition (e.g., cancer) or a donor. In some embodiments, the method further comprises the prior step of determining the expression levels of one or more genes selected from the group consisting of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, CD8, CD3, TCRβ, TCR1, CD11c, WARS, NKp46 and NCR1, granzymes, and perforin in the biological sample.

[0023] In some embodiments, the method further comprises the prior step of detecting CD8+ T cells, NK cells, mature NK cells, lymphocytes, fibroblasts, Tregs, or dendritic cells in the biological sample. In some embodiments, the CD8+ T cells, NK cells, mature NK cells, lymphocytes, fibroblasts, Tregs, or dendritic cells are detected by immune histochemistry.

[0024] In some embodiments, the chemokine mimetic is selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof. In some embodiments, the chemokine mimetic is a CCL5 mimetic or pharmaceutically acceptable salt thereof. In some embodiments, the chemokine mimetic is CCL5 or a CCL5 analog.

[0025] In some embodiments, the chemokine mimetic or pharmaceutically acceptable salt thereof is administered in a pharmaceutical composition further comprising a

pharmaceutically acceptable carrier or excipient. In some embodiments, said administering is via intratumoral injection, intravenous injection or subcutaneous injection. In some embodiments, the method further comprises the step of administering to the subject an anti-PD-L1 antibody or an anti-PD-1 antibody. In some embodiments, the method further comprises the step of administering to the subject a TGFβ inhibitor. In some embodiments, the method further comprises the step of administering an anti-PD-L1 antibody and a TGFβ antibody. In some embodiments, the method further comprises the step of administering a bi-specific antibody targeting both PD-L1 and TGFβ. In some embodiments, the method further comprises the step of administering a bi-specific antibody targeting both PD-1 and TGFβ.

[0026] In some embodiments, the method further comprises the step of administering to the subject an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab. In some embodiments, the method further comprises the step of administering to the subject a T cell or an NK cell, optionally wherein the T cell is a CAR-T, CAR-NK,TCR-T cell. In some embodiments, the method further comprises the step of administering to the subject an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof. In some embodiments, the method further comprises the step of administering to the subject an agent activating NK cell or T cell activity. In some embodiments, the method further comprises the step of administering to the subject a vaccine, nucleic acid, small molecule inhibitor, or chemotherapeutic agent.

[0027] In some embodiments, the cancer is selected from the group consisting of: multiple myeloma, adrenocortical carcinoma, acute myeloid leukemia, Bladder Urothelial Carcinoma, glioma, breast invasive carcinoma, glioma, Cervical squamous cell carcinoma, endocervical adenocarcinoma, cholangiocarcinoma, chronic myelogenous leukemia, colon adenocarcinoma, esophageal carcinoma, glioblasoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, liver hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell lymphoma, mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocyoma, paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma,sarcoma, skin cutaneous melanoma, stomach adenocarcinoma, testicular germ cell tumors, thyomas, thyroid carcinoma, uterine carcinosarcoma, uterine corps endometrial carcinoma, microsatellite instability-high cancer, basal cell carcinoma, Merkel cell carcinoma, uveal melanoma, mucosal melanoma.

[0028] The present disclosure also provides a method of treating cancer by administering a combination therapy using an anti-PD-L1 antibody in combination with TGFβ inhibitor (e.g., anti-TGFβ antibody). Specifically, the anti-PD-L1 antibody is administered to a subject systemically, and the anti-TGFβ antibody is administered to a subject intratumorally.

[0029] The combination therapy is based on the discovery by the Applicant that TGFβ inhibitors, when administered intratumorally, can reduce or limit the toxicity levels associated with them. Without wishing to be bound by a theory, the combination therapy including administration of systemic anti-PD-L1 and intratumoral a TGFβ inhibitor are believed to enhance infiltration of immune cells to improve efficacy of anti-PD-1/PD-L1 therapy. The present disclosure shows that intratumorally administered anti-TGFβ in combination with systemic administration of anti-PD-L1 could enhance the anti-tumor activity of anti-PD-L1 antibody.

5. BRIEF DESCRIPTION OF THE DRAWINGS

[0030] FIGs. 1A-1F. Anti-PD-L1 plus anti-TGFβ leads to regression of HuPD-L1-MC38 tumors in Hu-PD-L1 KI mice. HuPD-L1 KI mice bearing HuPD-L1-MC38 tumors (n=6 per a group) were dosed (IP) biweekly for three weeks with PBS, anti-PD-L1 (2mg/kg) or anti-PD-L1 (2mg/kg) plus anti-TGFβ (10mg/kg) combination. (FIG. 1A) Average tumor volume + SEM is shown. P-values were determined using Wilcoxon rank sum test. (FIG. 1B) Spider plots showing tumor volume for individual mice over time. (FIG. 1C) Survival plot for the same study. P-values were determined using log-rank test. (FIG. 1D) Mice from (FIGs. 1A-1C) for which treatment resulted in a complete response (anti-PD-L1, n = 1; anti-PD-L1 plus anti-TGFβ, n = 3) were re-challenged with s.c. HuPD-L1-MC38 tumor cells at the opposite flank. Treatment naïve, wildtype mice (n = 6) were used as a control. Average tumor volume + SEM is shown. P-values shown is for anti-PD-L1 plus anti-TGFβ vs. naïve control (Wilcoxon rank sum test), comparing tumor sizes on day 77 between naïve and aPD-L1 + aTGF-β groups. **(FIG. 1E)** CD3+ cell count in tumors by immunohistochemistry (IHC). Each point represents the number of CD3+ cells counted in the tumor from an individual mouse. Counts were obtained by counting three 200μm^2 fields at 10X magnification. The horizontal black bars of the box plots indicate median cell count, while the lower and upper hinges correspond to the first and third quartiles, respectively. P-values were determined using Wilcoxon rank sum test. **(FIG. 1E Continued)** CD3 IHC score in MC38 tumors. Each point is the IHC score representing the density of CD3+ cells from an individual mouse.

(FIG. 1F) Representative CD3 IHCs images (10X magnification) from each treatment group. The brown cells are CD3 positive cells. The scale bars indicate 250μm.

[0031] FIGs. 2A-2I. scRNA-seq of EMT6 tumors from mice treated with anti-PD-L1 and/or anti-TGFβ. **(FIG. 2A)** Single cell transcriptomes for all cells visualized on a Uniform Manifold Approximation and Projection (UMAP) plot. Cells are labeled based on cell type annotations, as indicated in the legend. **(FIG. 2B)** UMAP plots for cells from individual treatment groups. Cell types are annotated with the same color contrast scheme as **FIG. 2A**. **(FIG. 2C)** Percent composition of cells types within the CD45- cells (top) and the CD45+ (bottom) cells. The different treatment groups are shown in different contrasting colors, as indicated in the legend. **(FIG. 2D)** Functional enrichment analysis of genes down-regulated in CD45- cells, for each of the treatment group when compared to the PBS group. The size and color contrast of the circles indicate the number of down-regulated genes and the -log10 adjusted p-value, respectively, for the enriched terms indicated on the y-axis. **(FIG. 2E)** Gene concept network showing representative enriched terms for the genes down-regulated in CD45- cells in the anti-PD-L1 plus anti-TGFβ group. The down-regulated genes associated with the pathway are shown, with the color contrast of the nodes representing log2 fold change in gene expression relative to the PBS group. **(FIG. 2F)** Heatmap showing relative (z-scored per row) gene expression levels for representative differentially expressed genes in fibroblasts. **(FIG. 2G)** Functional enrichment analysis of genes up-regulated in CD45+ cells, for each of the treatment group when compared to the PBS group. The size and color contrast of the circles indicate the number of up-regulated genes and the -log10 adjusted p-value, respectively, for the enriched terms indicated on the y-axis. **(FIG. 2H)** Gene concept network showing representative enriched terms for the genes up-regulated in CD45+ cells in the anti-PD-L1 plus anti-TGFβ group. The up-regulated genes associated with the pathway are shown, with the color contrast of the nodes representing log2 fold change in gene expression relative to the PBS group. **(FIG. 2I)** Heatmap showing relative (z-scored per row) gene expression levels for differentially expressed chemokine genes in macrophages.

[0032] FIGs. 3A-3C. Association of chemokine gene expression with inferred immune cell infiltration in TCGA cancer types. **(FIG. 3A)** Computational workflow to identify chemokine genes associated with immune cell abundance in TCGA tumor samples. Two parallel methods are used to infer immune cell abundance: image-based estimation from pathology slides and gene signature-based estimation from RNA-seq. Linear regression models are used to find chemokine genes whose expression levels are associated with inferred immune

infiltration. (**FIG. 3B**) Heatmap showing chemokines (rows) significantly associated with the pathology image-based TIL scores across different TCGA cancer types (columns). The color contrast indicates regression coefficients from the linear models (positive regression coefficients indicate positive association between chemokine expression and immune infiltration). (**FIG. 3C**) Heatmap showing chemokines (rows) significantly associated with the gene signature-based immune scores across different TCGA cancer types (columns). The 3 panels represent associations with CD8 T cells, dendritic cells, and NK cells scores, respectively. The chemokines (rows) are ordered descendingly by the sum of the regression coefficients across all cancer types and all 3 immune cell types (i.e. all columns).

[0033] FIGs. 4A-4G. Intratumoral (IT) CCL5 in combination with systemic anti-PD-L1 treatment of mice bearing MC38 tumors led to tumor growth inhibition and increased survival. (**FIG. 4A**) Mice bearing MC38 tumors were administered PBS or CCL5 (1ug/dose) IT three times per a week for 6 doses and on day 12 tumors were harvested and analyzed by flow cytometry Left: percent of CCR5+ cells within the CD8+ T cell population (live cells, CD3+, CD4-, CD8+, CCR5+) in PBS or CCL5 treated tumors. Right: percent of CCR5+ cells within the NK cell (live cells, NK1.1+, CD3-, CCR5+) population. Black cross bars represent median values. P-values were determined using Wilcoxon rank sum test. **FIGs. 4B-4C** show flow cytometry-based expression of key genes in tSNE identified populations. Plots show heat maps of the indicated marker for each parameter used in tSNE analysis in PBS control (FIG. 4B) or recombinant CCL5 (FIG. 4C) treated samples. (**FIGs. 4D-4F**) Mice bearing MC38 tumors were administered PBS (intratumoral, IT, 3 times a week for 3 weeks), CCL5 (IT, 1 ug/animal, 3 times a week for 3 weeks), anti-PD-L1 (1mg/kg, IP, twice a week for 3 weeks) or a combination of CCL5 and anti-PD-L1. n = 12 mice per group. (**FIG. 4D**) Average tumor volume + SEM for each treatment group is shown. P-value was determined using Wilcoxon rank sum test. (**FIG. 4E**) Spider plots showing tumor volume for individual mice over time. (**FIG. 4F**) Survival plot for the same study. P-value was determined using log-rank test. (**FIG. 4G**) Average tumor volume + SEM for CCL5 administered alone compared to PBS (Control).

[0034] FIGs 5A-5D. Intratumorally administered CCL5 enhances intratumoral levels of CCD5+ CD8 T cells and mature CD11b+ NK cells. Mice bearing s.c. MC38 tumors were administered PBS or CCL5 (1 μg/dose) intratumorally three times per a week for 5 doses, and on day 12 tumors were harvested and analyzed by flow cytometry. (**FIG. 5A**) Left: percent of CCR5+ cells within the CD8+ T cell population (live cells, CD4-, CD8+) Right:

percent of CCR5+ cells within the NK cell population (live cells, NK1.1+, CD3-). Black cross bars represent median values. P-values were determined using Wilcoxon rank sum test. (**FIG. 5B**) Density plots (with outlier cells indicated as dots) of populations from a tSNE analysis of flow cytometry of single cell suspensions of tumors treated with intratumoral PBS (control, left) or recombinant CCL5 treated samples. Data is from live, single cells and tSNE was calculated from using data from live, single cells and data from staining with fluorescent antibodies specific for CD4, CD8, CD11b, Ly6C, Ly6G, CD3, NK1.1, CD11c, PD1, CCR5, CD44 and FOXP3 and also data from SSC. Filled black arrows indicate cell populations increased in the CCL5 treated samples. Filled black arrow 1 points to a population of CD11b+ NK cells that are substantially elevated in the CCL5 treated samples. Filled black arrow 2 points to a population of that is Ly6C-hi, SSC-int/hi, Ly6G-lo, CD11c-lo, CCR5-lo, CD11b-lo. Filled black arrow 3 points to a population that is CD11b+, Ly6G-lo, Ly6C-lo. This population is CCR5 - or lo. This indicates that CCL5 can increase the frequency of cell populations in the tumor that are not CCR5+. The open arrows denote populations that decrease upon treatment with CCL5. Open arrow 4 points to a population that has relatively high SSC. This population may not be of hematopoietic origin. Open arrow 5 points to a population that is Ly6C+ CD11b-lo. Of additional note the tSNE analysis suggests that the CCR5+ CD8 T cells are more activated with some of these cells also expressing CD44 and PD1. Density plots (with outlier cells indicated as dots) of populations from the tSNE analysis in control or CCL5 treated samples. Arrows 1 and 6 indicate CD11b+ NK cells (population 23 from **FIG. 5D**). (**FIG. 5C**) Frequency of NK cells (live, single cells, NK1.1+ CD3-) which express CD11b, a marker of mature, more functional NK cells, as determined by flow cytometry. Black cross bars represent median values. P-value was determined using Wilcoxon rank sum test. (**FIG. 5D**) tSNE plots of flow data showing the expression of CCR5 within PBS control (left) or CCL5 treated tumors (right), or where populations are differentiated according to expression of marker genes as indicated in the key (bottom). Heat maps showing expression of each flow marker are in FIG. 7G.

[0035] FIGs. 6A-6B. Anti-PD-L1 plus anti-TGFβ induced tumor growth inhibition of CT26 tumors. Mice bearing CT26 tumors (n = 10 per a group) were dosed IP two times a week for 3 weeks with PBS or anti-PD-L1 (2mg/kg) + anti-TGFβ (10mg/kg). (**FIG. 6A**) Average tumor volume + SEM is shown. P-value was determined using Wilcoxon rank sum test. (FIG. 6B) Spider plots showing tumor volume for individual mice over time.

[0036] FIGs. 7A-7I. Anti-PD-L1 plus anti-TGFβ led to tumor growth inhibition of EMT6 tumors. (**FIGs. 7A-7B**) Mice bearing EMT6 tumors were treated with PBS, anti-PD-L1 (10 mg/kg for the first dose with each subsequent dose at 5 mg/kg), anti-TGFβ (10 mg/kg) or anti-PD-L1 plus anti-TGFβ. For all treatments the first dose was administered i.v. on day 0 and the eight subsequent doses were administered i.p. three times per week. n = 12 mice per group including 3 mice per a group taken down early on day 8 for pre-planned scRNA-seq analysis. (**FIG. 7A**) Average tumor volume + SEM is shown. P-values were determined using Wilcoxon rank sum test. Mice used for scRNA-seq were not included in this average as these mice were euthanized for terminal experiments on day 8. (**FIG. 7B**) Spider plots showing tumor volume for individual mice over time. Mice sacrificed for scRNA-seq (n = 3 per group) are shown in grey. (**FIG. 7C**) Single cell transcriptomes for all CD45- cells visualized on a Uniform Manifold Approximation and Projection (UMAP) plot. Cell clusters are numbered. (**FIG. 7D**) Violin plot showing Fap expression level in the different CD45- cell clusters. (**FIG. 7E**) Inferred copy number for the different CD45- cell types, shown on the y-axis, along the mouse genome, shown on the x-axis. (**FIG. 7F**) Cell-cell communication network involving all TGFβ ligands and receptors, as analyzed using CellPhoneDB. The x-axis displays the cell pairs expressing the ligand and the receptor, respectively, while the y-axis displays the corresponding ligand and receptor pairs expressed by the cell types indicated on the x-axis. The size and color contrast of the points show the significance of the interactions and log2 mean expression values of the ligand-receptor pairs, respectively, as indicated in the key. (**FIG. 7G**) Dot plot showing chemokine gene expression in different cell types under different treatments. The size of the dots indicates percent cells expressing the chemokine gene, while the color contrast of the dots indicates average gene expression level. (**FIG. 7H**) Survival plot for the EMT6 study. P-values were determined using log-rank test. (**FIG. 7I**) CD3 IHC score in EMT6 tumors. Each point is the IHC score representing the density of CD3+ cells from an individual mouse. The horizontal black bars of the box plots indicate median score, while the lower and upper hinges correspond to the first and third quartiles, respectively. P-values were determined using Wilcoxon rank sum test. Non-significant p-values are not shown for all panels.

[0037] FIG. 8A-8B. CCL5 expression correlates with TIL score. The scatter plot shows the correlation between CCL5 expression and pathology image-based tumor infiltrating lymphocyte (TIL) score in breast cancer (BRCA) in TCGA. Each point represents a TCGA tumor sample. Both axes are shown in Z-score space. TIL score is inferred computationally

from H&E-stained pathology images of the tumor samples. Representative images for a high TIL sample and a low TIL sample are shown. **(FIG. 8B)**. Heatmap showing association of chemokines with gene signature-based immune scores for regulatory T cells (Tregs) and M2 macrophages. The order of the chemokines on the y-axis are as shown in FIG. 3C, while the x-axis indicates TCGA cancer types. The color contrast indicates regression coefficients from the linear models (positive regression coefficients indicate positive association between chemokine expression and immune infiltration).

[0038] FIG. 9A-9B Anti-PD-L1 plus anti-TGF-β in the murine tumor model HuPD-L1-MC38. **(FIGs. 9A-9B)** Mice bearing s.c. HuPD-L1-MC38 tumors (n = 6 per group) were dosed I.P. biweekly for three weeks with PBS, aPD-L1 (2 mg/kg; atezolizumab), aTGF-β (10 mg/kg; 1D11), or aPD-L1 plus aTGF-β. **(FIG. 9A)** Average MC38 tumor volume ± SEM is shown. P-values were determined using Wilcoxon rank sum test, comparing tumor sizes on day 17. Non-significant p-values are not shown. **(FIG. 9B)** Spider plots showing tumor volume for individual mice over time.

[0039] FIG. 10A-10F. Anti-PD-L1 plus anti-TGF-β in the murine tumor model CT26. **(FIGs. 10A-10C)** Mice bearing CT26 tumors were dosed intraperitoneally (I.P.) two times a week for 3 weeks with PBS (n = 10), aPD-L1 (2 mg/kg; atezolizumab; n = 12), aTGF-β (10 mg/kg; 1D11; n = 10), or aPD-L1 + aTGF-β (n = 12). **(FIG. 10A)** Average tumor volume ± SEM is shown. P-value was determined using Wilcoxon rank sum test, using tumor sizes on day 28. **(FIG. 10B)** Spider plots showing CT26 tumor volume for individual mice over time. **(FIG. 10C)** Survival plot for the study. P-values were determined using log-rank test. **(FIG. 10D-10F)** Mice bearing CT26 tumors were dosed two times a week for 3 weeks with PBS (I.P.; n = 10; same PBS arm as in **A-C**), aPD-L1 (2 mg/kg; atezolizumab; I.P.) + PBS (intratumorally, I.T.) (n = 12), aTGF-β (10 mg/kg; 1D11; I.T.; n = 6), or aPD-L1 (I.P.) + aTGF-β (I.T.) (n = 12). **(FIG. 10D)** Average tumor volume ± SEM is shown. P-values were determined using Wilcoxon rank sum test, using tumor sizes on day 28. **(FIG. 10E)** Spider plots showing CT26 tumor volume for individual mice over time. **(FIG. 10F)** Survival plot for the study. P-values were determined using log-rank test. Non-significant p-values are not shown for all panels.

[0040] FIG. 11A-11G scRNA-seq of EMT6 tumors from mice treated with anti-PD-L1 ± anti-TGF-β. **(FIG. 11A)** Number of up- (top panel) and down- (bottom panel) regulated genes in various cell types, when comparing each treatment sample to the PBS sample. **(FIG. 11B)** UMAP plot showing the two subclusters of fibroblasts. **(FIG. 11C)** Fraction of

fibroblasts in Fib_0 (solid) and Fib_1 (striped) in each treatment group. **(FIG. 11D)** Representative marker genes in the fibroblast subclusters. The size of the dots indicates percent cells expressing the gene, while the color contrast of the dots indicates average gene expression level. **(FIG. 11E)** Functional enrichment analysis of genes downregulated in the Fib_0 subcluster, for each of the treatment group when compared to the PBS group. The size and color contrast of the circles indicate the number of downregulated genes and the -log10 adjusted p-value, respectively, for the enriched terms indicated on the y-axis. **(FIG. 11F)** Gene concept network showing representative enriched terms for the genes downregulated in Fib_0 in the aPD-L1 plus aTGF-β group. The downregulated genes associated with the pathway are shown, with the color contrast of the nodes representing log2 fold change in gene expression relative to the PBS group. **(FIG. 11G)** Heatmap showing relative (z-scored per row) gene expression levels for representative differentially expressed genes in Fib_0.

[0041] FIG. 12A-12B. Quality control of single cell RNA-seq of anti-PD-L1 ± anti-TGF-β treated EMT6 tumor-bearing mice. **(FIG. 12A)** Violin plots showing the distribution of the number of genes (left) and percent read count that mapped to mitochondrial genes (right) per cell, before removing low quality cells. **(FIG. 12B)** The same plots after removing cells with more than 10% mitochondrial reads and fewer than 200 or more than 5,000 expressed genes, as low and high number of gene counts may indicate low quality cells and cell multiplets, respectively.

[0042] FIG. 13A-13B. scRNA-seq marker gene expression. **(FIG. 13A)** Heatmap showing relative gene expression of top marker genes most differentially expressed in each cell type relative to other cell types. **(FIG. 13B)** Left: Single cell transcriptomes for all cells visualized on a UMAP plot. Right: Relative expression of selected marker genes displayed on the UMAP plot.

[0043] FIG. 14A-14F scRNA-seq analysis of macrophage subclusters. **(FIG. 14A)** UMAP plot showing the four subclusters of macrophages. **(FIG. 14B)** Fraction of macrophages in each subcluster in each treatment group. The subclusters are annotated with the same color scheme as FIG. 14A. **(FIG. 14C)** Representative marker genes in the macrophage subclusters. The size of the dots indicates percent cells expressing the gene, while the color contrast of the dots indicates average gene expression level. **(FIG. 14D)** Functional enrichment analysis of genes upregulated in the Mac_0 subcluster, for each of the treatment group when compared to the PBS group. The size and color contrast of the circles indicate the number of upregulated genes and the -log10 adjusted p-value, respectively, for the

enriched terms indicated on the y-axis. **(FIG. 14E)** Gene concept network showing representative enriched terms for the genes upregulated in Mac_0 in the aPD-L1 plus aTGF-β group. The upregulated genes associated with the pathway are shown, with the color contrast of the nodes representing log2 fold change in gene expression relative to the PBS group. **(FIG. 14F)** Heatmap showing relative (z-scored per row) gene expression levels for differentially expressed chemokine genes in Mac_0.

[0044] FIG. 15A-15C. Tumor volumes (mm^3) from mice with chemokines CXCL9, CCL5, CXCL9 and CCL5, WARS, WARS + WARS at DOI, or control (PBS) alone or in combination with aPD-1. **FIG. 15A** shows a comparison of tumor volumes (mm^3) from mice only treated with chemokines CXCL9, CCL5, CXCL9 and CCL5, WARS, WARS + WARS at DOI, or control (PBS). Mean tumor volume ± SEM is shown. For animals euthanized due to a tumor volume of >2000 mm^3, the last observation was carried forward. Data is shown through day 18, as some animals were euthanized and had their tumors collected at our request on day 19 for potential future analysis. **FIG. 15B** shows comparison of tumor volumes (mm^3) from mice treated with chemokines CXCL9, CCL5, CXCL9 and CCL5, WARS, or WARS + WARS at DOI in combination with aPD-1. Mean tumor volume ± SEM is shown. For animals euthanized due to a tumor volume of >2000 mm^3, the last observation was carried forward. Data is shown through day 18, as some animals were euthanized and had their tumors collected at our request on day 19 for potential future analysis. **FIG. 15C** shows the percent change in body weight after treatment with chemokines only or chemokines in combination with aPDLaPD-L1. Mean body weight change± SEM is shown. For animals euthanized due to a tumor volume of >2000 mm^3, the last observation was carried forward. Data is shown through day 18, as some animals were euthanized and had their tumors collected at our request on day 19 for potential future analysis.

[0045] Table 1. Differentially expressed (DE) genes determined from the EMT6 single cell RNA-seq experiment. Differential expression analysis was performed within each cell type, indicated in the "cell" column. The "comparison" column indicates the treatment group comparison in which a given DE gene was observed. The columns "pct.1" and "pct.2" represent percent cells expressing the gene in the first treatment group and the second treatment group, respectively. The column "avg_logFC" represents log fold-change of the average expression between the two groups. Positive values indicate that the gene is more highly expressed in the antibody treated group. P-values, as shown in the "p_val" column,

were determined using Wilcoxon rank sum test. The column "p_val_adj" shows adjusted p-value, based on bonferroni correction using all genes in the dataset.

[0046] Table 2. Enriched terms as determined by functional enrichment analysis using DE genes from the EMT6 single cell RNA-seq experiment. The functional enrichment analysis was performed using all up- or down-regulated genes (indicated in the "genes_used" column) from the CD45+ or CD45- cells (indicated in the "cells" column), for a given treatment group comparison (indicated in the "comparison" column). The categories tested were biological process (BP), molecular function (MF), and cellular component (CC), as shown in the "ONTOLOGY" column.

[0047] Table 3. Differentially expressed (DE) genes in fibroblasts. Differential expression analysis was performed within each fibroblast subcluster, indicated in the "cluster" column. The "comparison" column indicates the treatment group comparison in which a given DE gene was observed. The columns "pct.1" and "pct.2" represent percent cells expressing the gene in the first treatment group and the second treatment group, respectively. The column "avg_logFC" represents log fold-change of the average expression between the two groups. Positive values indicate that the gene is more highly expressed in the first treatment group. P-values, as shown in the "p_val" column, were determined using Wilcoxon rank sum test. The column "p_val_adj" shows adjusted p-value, based on Bonferroni correction using all genes in the dataset.

[0048] Table 4. Differentially expressed (DE) genes in macrophages. Differential expression analysis was performed within each macrophage subcluster, indicated in the "cluster" column. The "comparison" column indicates the treatment group comparison in which a given DE gene was observed. The columns "pct.1" and "pct.2" represent percent cells expressing the gene in the first treatment group and the second treatment group, respectively. The column "avg_logFC" represents log fold-change of the average expression between the two groups. Positive values indicate that the gene is more highly expressed in the first treatment group. Pvalues, as shown in the "p_val" column, were determined using Wilcoxon rank sum test. The column "p_val_adj" shows adjusted p-value, based on Bonferroni correction using all genes in the dataset.

[0049] The figures depict various embodiments of the present invention for purposes of illustration only. One skilled in the art will readily recognize from the following discussion

that alternative embodiments of the structures and methods illustrated herein may be employed without departing from the principles of the invention described herein.

6. DETAILED DESCRIPTION

6.1. Definitions

[0050] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. As used herein, the following terms have the meanings ascribed to them below.

[0051] The term "**chemokine**" as used herein refers to a family of small cytokines, or signaling proteins secreted by cells. Specifically, the term includes the chemokines listed in Table 1 and Table 2. Chemokines include, not are not limited to, CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and analogs thereof.

[0052] The term "**CCL5**" as used herein refers to Chemokine (C-C motif) ligand 5, also referred to as RANTES. In preferred embodiments, CCL5 is a protein encoded by the human CCL5 gene. CCL5 can be a protein having the sequence of SEQ ID NO: 1 (available from NCBI with accession number P13501 (SEQ ID NO: 1)). However, CCL5 can be a protein encoded by the CCL5 gene of other mammals, such as a non-human primate (*e.g.*, a monkey), a rodent (*e.g.*, a mouse or a rat), a dog, a camel, a cat, a cow, a goat, a horse, or a sheep. CCL5 can be a protein naturally expressed by cells, a recombinant or synthetic protein.

[0053] The term "**chemokine analog**" as used herein refers to a protein including an active fragment of a chemokine or a modification thereof. In some embodiments, a chemokine analog is a polypeptide having one or more amino acid additions, deletions or substitutions compared to the chemokine.

[0054] The term "**chemokine mimetic**" as used herein refers to a chemokine; a chemokine analog; a fusion of the chemokine or its analog to a second peptide or polypeptide; or the chemokine or its analog conjugated to a conjugate moiety. For example, in various embodiments, the chemokine mimetic is a fusion of the chemokine or its analog to a second peptide or polypeptide, optionally with a linker peptide therebetween. In various embodiments, the chemokine mimetic comprises a chemokine or its analog covalently attached to a non-protein conjugate moiety or to a peptide or polypeptide that is not an in-frame fusion. In various embodiments, the chemokine mimetic comprises a chemokine or its

analog covalently attached to a non-protein conjugate moiety or to a peptide or polypeptide that is an in-frame fusion.

[0055] The term "**active fragment**" of a chemokine refers to a fragment of the chemokine (e.g., N-terminal fragments, C-terminal fragments) that is sufficient for activation of or binding to its receptor. Thus, an "active-fragment" of a chemokine can include fragments of the chemokine amino acid sequence that are important for receptor binding and activation.

[0056] The term "**CCL5 analog**" as used herein refers to a protein including an active fragment of CCL5 or a modification thereof. In some embodiments, a CCL5 analog is a polypeptide having the sequence of SEQ ID NO: 2. In some embodiments, a CCL5 analog is a polypeptide having one or more amino acid additions, deletions or substitutions compared to SEQ ID NO: 2.

[0057] The term "**CCL5 mimetic**" as used herein refers to CCL5; a CCL5 analog; a fusion of CCL5 or CCL5 analog to a second peptide or polypeptide; or CCL5 or CCL5 analog conjugated to a conjugate moiety. For example, in various embodiments, the CCL5 mimetic is a fusion of CCL5 or a CCL5 analog to a second peptide or polypeptide, optionally with a linker peptide therebetween. In various embodiments, the CCL5 mimetic comprises CCL5 or a CCL5 analog covalently attached to a non-protein conjugate moiety or to a peptide or polypeptide that is not an in-frame fusion. In various embodiments, the CCL5 mimetic comprises CCL5 or a CCL5 analog covalently attached to a non-protein conjugate moiety or to a peptide or polypeptide that is an in-frame fusion.

[0058] The term "**active fragment**" of CCL5 refers to a fragment of CCL5 (e.g., N-terminal fragments, C-terminal fragments) that is sufficient for activation of or binding to its receptor (e.g., CCR1, CCR3, CCR5). Thus, an "active-fragment" of CCL5 can include fragments of the CCL5 amino acid sequence that are important for receptor binding and activation.

[0059] The term "**antibody**" is used herein in its broadest sense understood in the art and includes, but is not limited to, all polypeptides described as antibodies in Sumit *et al.*, *Antibodies* 2:452-500 (2013), incorporated herein by reference in its entirety, and other types of immunoglobulin molecules comprising one or more antigen-binding domains that specifically bind to an antigen or epitope. "Antibody" specifically includes intact antibodies (*e.g.*, intact immunoglobulins), antibody fragments, and multi-specific antibodies. One example of an antigen-binding domain is an antigen-binding domain formed by a V_H -V_L dimer.

[0060] The term "**bi-specific antibody**" and "**multi-specific antibody**" are used herein in the broadest sense understood in the art and include, but are not limited to, the molecular formats described in Spies *et al.*, *Molecular Immunology* 67:95-106 (2015), incorporated herein by reference in its entirety, and certain types of immunoglobulin molecules comprising one or more antigen-binding domains that specifically bind to two or more different antigens or epitopes. An antigen-binding domain is a portion of antigen binding protein that is capable of binding to an antigen or epitope. For example, bi-specific antibody targeting PD-L1 and TGFβ can be M7824, an anti-PD-L1/TGFβ Trap fusion protein. In some embodiments, bi-specific antibodies disclosed in US9,676,863, incorporated by reference in its entirety herein, are used.

[0061] The term "**PD-L1**," "**PD-L1 protein**," and "**PD-L1 antigen**" are used interchangeably herein to refer to human PD-L1, or any variants (*e.g.*, splice variants and allelic variants), isoforms, and species homologs of human PD-L1 that are naturally expressed by cells, or that are expressed by cells transfected with a polynucleotide encoding PD-L1. In some embodiments, the PD-L1 protein is a PD-L1 protein naturally expressed by a primate (*e.g.*, a monkey or a human), a rodent (*e.g.*, a mouse or a rat), a dog, a camel, a cat, a cow, a goat, a horse, or a sheep. In some embodiments, the PD-L1 protein is human PD-L1 (hPD-L1; SEQ ID NO: 3).

[0062] The term "**PD-L1 antibody**", used interchangeably herein with "**anti-PD-L1 antibody**", as used herein refers to an antibody comprising one or more antigen-binding domains that specifically bind to an antigen or epitope of PD-L1. PD-L1 antibodies which have been developed for therapeutic use can be used in various embodiments of the present disclosure. The PD-L1 antibodies include, but not are limited to, atezolizumab, avelumab, and durvalumab.

[0063] Any of the PD-L1 antibodies or antigen binding domains disclosed in PCT/US19/68826, which is incorporated herein by reference in its entirety herein, can be used. For example, the PD-L1 antibody or antigen binding protein can comprise: a variable light chain (V_L) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 5-29 and a variable heavy chain (V_H) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 30-54; or a variable light chain (V_L) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 207-359 and a variable heavy chain (V_H) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence

selected from SEQ ID NOS: 360-512; or a variable light chain (V_L) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a V_L sequence of any one of the clones in the library deposited under ATCC Accession No. PTA-125513 and a variable heavy chain (V_H) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a V_H sequence of any one of the clones in the library deposited under ATCC Accession No. PTA-125513. In some embodiments, an antibody or antigen-binding protein is selected from A101-A125. In some embodiments, an antibody or antigen-binding protein having one or more CDR sequences of any one of A101-A125 is used. In some embodiments, the V_L and the V_H are a cognate pair.

[0064] The terms "**PD-1**," "**PD-1 protein**," and "**PD-1 antigen**" are used interchangeably herein to refer to human PD-1, or any variants (*e.g.*, splice variants and allelic variants), isoforms, and species homologs of human PD-1 that are naturally expressed by cells, or that are expressed by cells transfected with a *pdcd1* gene. In some embodiments, the PD-1 protein is a PD-1 protein naturally expressed by a primate (*e.g.*, a monkey or a human), a rodent (*e.g.*, a mouse or a rat), a dog, a camel, a cat, a cow, a goat, a horse, or a sheep. In some embodiments, the PD-1 protein is human PD-1 (hPD-1; SEQ ID NO: 4).

[0065] The term "**PD-1 antibody**", used interchangeably herein with "**anti-PD-1 antibody**," as used herein refers to an antibody comprising one or more antigen-binding domains that specifically bind to an antigen or epitope of PD-1. PD-1 antibodies which have been developed for therapeutic use can be used in various embodiments of the present disclosure. The PD-1 antibodies include, but not are limited to, nivolumab, pembrolizumab, and cemiplimab.

[0066] Any of the PD-1 antibodies or antigen binding domains disclosed in PCT/US19/068824, which is incorporated by reference in its entirety herein, can be used. For example, the PD-1 antibody or antigen binding protein can comprise: a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 1462-1489 and a variable heavy chain (V_H) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 1490-1517; or a variable light chain (V_L) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 1687-2209 and a variable heavy chain (V_H) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a sequence selected from SEQ ID NOS: 2210-2732; or a variable light chain (V_L) comprising a sequence at least 97%, 98%, 99%, or 100% identical to a V_L sequence of any one of the clones in the library deposited under ATCC Accession No. PTA-125509 and a variable heavy chain (V_H) comprising a sequence at least

97% identical to a V_H sequence of any one of the clones in the library deposited under ATCC Accession No. PTA-125509. In some embodiments, an antibody or antigen-binding protein is selected from A201-A228. In some embodiments, an antibody or antigen-binding protein having one or more CDR sequences of any one of A201-A228 is used. In some embodiments, the V_L and the V_H are a cognate pair.

[0067] The terms "**TGFβ**," "**TGFβ protein**," and "**TGFβ antigen**" are used interchangeably herein to refer to human TGFβ, or any variants (*e.g.*, splice variants and allelic variants), isoforms (*e.g.*, TGFβ 1-3), and species homologs of human TGFβ that are naturally expressed by cells, or that are expressed by cells transfected with a TGFβ gene. In some embodiments, the TGFβ protein is a TGFβ protein naturally expressed by a primate (*e.g.*, a monkey or a human), a rodent (*e.g.*, a mouse or a rat), a dog, a camel, a cat, a cow, a goat, a horse, or a sheep. In some embodiments, the TGFβ protein is human TGFβ.

[0068] The term "**TGFβ inhibitor**" as used herein refers to an agent that can inhibit TGFβ pathway. TGFβ inhibitor can be an antibody comprising one or more antigen-binding domains that specifically bind to an antigen or epitope of TGFβ or TGFβ receptor. In some cases, TGFβ inhibitor is not an antibody. In some cases, TGFβ inhibitor is a small molecule. Various TGFβ inhibitors which have been developed for therapeutic use can be used in various embodiments of the present disclosure. The TGFβ inhibitors include, but not are limited to, fresolimumab. The TGFβ inhibitors include, but not are limited to, galunisertib, fresolimumab, lucanix, vigil, TGFbRII, TGFBRII-Fc (e.g., TGFBRII trap) and trabedersen.

6.2. Other interpretational conventions

[0069] Ranges recited herein are understood to be shorthand for all of the values within the range, inclusive of the recited endpoints. For example, a range of 1 to 50 is understood to include any number, combination of numbers, or sub-range from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and 50.

[0070] Unless otherwise indicated, reference to a compound that has one or more stereocenters intends each stereoisomer, and all combinations of stereoisomers, thereof.

6.3. Overview of experimental results

[0071] The present disclosure provides therapeutic methods for enhancing T cell and/or NK cell infiltration and response to PD-1/PD-L1 blockade for treatment of cancer.

[0072] Applicant measured transcriptional changes induced by therapeutic regimen using anti-PD-L1 and anti-TGFβ antibodies and identified that anti-TGFβ antibody blocks TGFβ-producing tumor cells from inducing cancer-associated fibroblasts to express collagen and other matrix remodeling genes. Additionally, Applicant found anti-PD-L1 with or without anti-TGFβ induced expression of several chemokines associated with the recruitment of cytotoxic T cells. Additionally, Applicant found a TGFβ inhibitor with or without anti-PD-L1 induced expression of several chemokines associated with the recruitment of cytotoxic T cells. Analysis of TCGA transcriptomes confirmed that a series of chemokines are associated with lymphocyte, T cell, NK cell and dendritic cell infiltration in human tumors, with CCL5 being most highly correlated with immune infiltration across tumor types. This suggested that chemokines, in particular CCL5, will enhance T cell and/or NK cell infiltration and efficacy of PD-1/PD-L1 blockade.

[0073] Intratumoral administration of CCL5, in fact, increased the frequency of CCR5+ CD8 T cells within the tumor and administration of CCL5 alone, or CCL5 plus atezolizumab (anti-PD-L1 antibody) inhibited tumor growth in the otherwise excluded murine tumor model MC38.

[0074] These data demonstrated that (1) CCL5 alone can help immune cell infiltration into tumors, (2) CCL5 can help immune cell infiltration into tumors and enhance response to PD-L1 blockade, by either limiting the physical barrier or providing exogenous immune cell recruitment signals, or both and (3) CCL5 mimetic alone activates NK cell or T cell activity and recruits activating T cells and/or NK cells to a tumor microenvironment.

[0075] Furthermore, Applicant provides surprising evidence that intratumoral administration of an anti-TGFβ in combination with systemic administration of anti-PD-L1 antibody significantly reduces tumor volume. Thus, the combination intratumoral administration of an anti-TGFβ in combination with systemic administration of anti-PD-L1 antibody can be used to treat cancer.

6.4. Chemokine Mimetics

[0076] Aspects of the present disclosure include pharmaceutical compositions, methods of use, and kits comprising one or more chemokine mimetics alone or in combination with an antibody, vaccine, nucleic acid, or small molecule inhibitor; and pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable carrier.

[0077] In some embodiments, the chemokine mimetic is a mimetic of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, or XCL-1. In some embodiments, the chemokine mimetic is selected from one or more of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof. In some embodiments, the isolated chemokine mimetic is two or more isolated chemokine mimetics selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.

[0078] In some embodiments, the chemokine mimetic is a CCL5 mimetic. In some embodiments, the CCL5 analog comprises an active fragment of a human CCL5 peptide.

[0079] In some embodiments, the chemokine mimetic is a CXCL9 mimetic. In some embodiments, the CXCL9 analog comprises an active fragment of a human CXCL9 peptide. In some embodiments, the chemokine mimetic is a combination of CCL5 and CXCL9 mimetic.

[0080] In some embodiments, the chemokine mimetic is a CXCL13 mimetic. In some embodiments, the CXCL13 analog comprises an active fragment of a human CXCL13 peptide.

[0081] In some embodiments, the chemokine mimetic is a CXCL10 mimetic. In some embodiments, the CXCL10 analog comprises an active fragment of a human CXCL10 peptide.

[0082] In some embodiments, the chemokine mimetic is a CXCL11 mimetic. In some embodiments, the CXCL11 analog comprises an active fragment of a human CXCL11 peptide.

[0083] In some embodiments, the chemokine mimetic is a WARS mimetic. In some embodiments, the WARS analog comprises an active fragment of a human WARS peptide.

In some embodiments, the chemokine mimetic is a CL-1 mimetic. In some embodiments, the XCL-1 analog comprises an active fragment of a human XCL-1 peptide.

[0084] In certain embodiments, the CCL5 mimetic is a human CCL5 peptide, wherein the CCL5 peptide has a sequence of SEQ ID NO: 1. In certain embodiments, the CCL5 mimetic is a CCL5 analog. In yet other embodiments, the CCL5 analog is a polypeptide having the sequence of SEQ ID NO: 1. In certain embodiments, the CCL5 analog comprises an active fragment of a human CCL5 peptide. In certain embodiments, the active fragment of human CCL5 comprises amino acids 12-22 of SEQ ID NO: 1.

[0085] In some embodiments, the active fragment of human CCL5 comprises one or more of the following amino acid residues selected from the group consisting of: P2, Y3, D6, T7, F12, I15, and R17.

[0086] In certain embodiments, the CCL5 mimetic comprises a polypeptide having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% sequence identity to SEQ ID NO: 1 or SEQ ID NO: 2.

[0087] In some embodiments, the CCL5 mimetic is a CCL5 analog having a longer half-life *in vivo* as compared to CCL5. In some embodiments, the CXCL9 mimetic is a CXCL9 analog having a longer half-life *in vivo* as compared to CXCL9. In some embodiments, the CXCL13 mimetic is a CXCL13 analog having a longer half-life *in vivo* as compared to CXCL13. In some embodiments, the CXCL10 mimetic is a CXCL10 analog having a longer half-life *in vivo* as compared to CXCL10. In some embodiments, the CXCL11 mimetic is a CXCL11 analog having a longer half-life *in vivo* as compared to CXCL11. In some embodiments, the WARS mimetic is a WARS analog having a longer half-life *in vivo* as compared to WARS. In some embodiments, the XCL-1 mimetic is an XCL-1 analog having a longer half-life *in vivo* as compared to XCL-1.

[0088] In some embodiments, the CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS mimetic is a conjugate of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, XCL-1, or WARS, or a CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS analog to a conjugate moiety.

[0089] In some embodiments, the CCL5 mimetic is a conjugate of CCL5 or a CCL5 analog to a conjugate moiety.

[0090] In some embodiments, the conjugate of CCL5 or CCL5 analog comprises a binding site. In certain embodiments the binding site is an antibody or antigen-binding fragment. In particular embodiments, the binding site is a tumor-targeting antibody or antigen-binding fragment thereof.

[0091] In certain embodiments, the conjugate moiety is selected from polyethylene glycol (PEG) and hyaluronic acid.

[0092] In certain embodiments, the conjugate moiety is an antibody or antigen-binding fragment thereof. In certain embodiments, the conjugate moiety is selected from the group consisting of HAS, human IgG, scFv, F(ab), $(Fab')_2$, transferrin, albumin, and an Fc domain of an immunoglobulin. In some embodiments, the conjugate moiety is an antibody or

antigen-binding fragment specific to a target tissue for treatment. In some embodiments, the conjugate moiety is an antibody or antigen-binding fragment specific to a tumor antigen.

[0093] In some embodiments, the conjugate moiety is selected from the group consisting of: XTEN, a proline-alanine-serine polymer (PAS), a homopolymer of glycine residues (HAP), a gelatin-like protein (GLP), a signal peptide and an elastin-like peptide (ELP).

[0094] In some embodiments, the CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS mimetic comprises one or more modified or non-naturally occurring amino acids, selected from the group consisting of: a steric enantiomer (D isomer), a rare amino acid of plant origin, a non-naturally occurring amino acid or amino acid mimetic, or have been modified by any one or more modifications selected from acetylation, acylation, phosphorylation, dephosphorylation, glycosylation, myristollation, amidation, aspartic acid/asparagine hydroxylation, phosphopantethane attachment, methylation, methylthiolation, prensyl group attachment, intein N-/C-terminal splicing, ADP-ribosylation, bromination, citrullination, deamination, dihydroxylation, formylation, geranyl-geranilation, glycation, palmitoylation, α-methyl-amino acids, Cα-methyl amino acids, and Nα-methyl amino acids.

[0095] In some embodiments, the CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS mimetic is chemically-synthesized and comprises one or more non-peptide bonds.

6.5. Polynucleotides encoding a chemokine mimetic and cells comprising the polynucleotides

[0096] In another aspect, the present disclosure provides a polynucleotide encoding the chemokine mimetic. In some embodiments, the polynucleotide is DNA (e.g., such as dsDNA, ssDNA, cDNA), RNA (e.g., such as dsRNA, ssRNA, mRNA), combinations thereof, or derivatives (e.g., as PNA) thereof. In some embodiments, mRNA or DNA encodes the chemokine mimetic (e.g., a CCL5 chemokine mimetic). In some embodiments, the polynucleotide further comprises a sequence homologous to a target genomic region for site-specific integration.

[0097] In some embodiments, the pharmaceutical composition comprises a polynucleotide comprising a nucleotide sequence encoding the chemokine mimetic selected from CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS.

[0098] In certain embodiments, the polynucleotide comprises a nucleotide sequence encoding a CCL5 mimetic. In certain embodiments, the polynucleotide comprises a nucleotide sequence encoding a CXCL9 mimetic. In certain embodiments, the polynucleotide comprises

a nucleotide sequence encoding a CXCL13 mimetic. In certain embodiments, the polynucleotide comprises a nucleotide sequence encoding a CXCL10 mimetic. In certain embodiments, the polynucleotide comprises a nucleotide sequence encoding a CXCL11 mimetic. In certain embodiments, the polynucleotide comprises a nucleotide sequence encoding a WARS mimetic.

[0099] In some embodiments, the polynucleotide encoding a chemokine mimetic is codon optimized for expression in mammalian cells, preferably for expression in human cells.

[00100] Codon-optimization refers to the exchange in a sequence of interest of codons that are generally rare in highly expressed genes of a given species by codons that are generally frequent in highly expressed genes of such species, such codons encoding the same amino acids as the codons that are being exchanged. The skilled artisan will be able to design and utilize suitable codon optimizations of the polynucleotide disclosed herein.

[00101] Within the scope of the present disclosure are also the polynucleotide having a sequence obtained due to the degeneration of the genetic code of the nucleotide sequences of the chemokine mimetics described herein.

[00102] In some embodiments, the polynucleotide is in a viral or a non-viral vector. The vector can be used to deliver the polynucleotide to a target cell in vitro or in vivo. In some embodiments, the polynucleotide is in a viral construct. In some embodiments, the polynucleotide is in a plasmid.

[00103] In certain embodiments, the viral or non-viral vector comprises a nucleotide sequence encoding CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS mimetic, e.g., a coding sequence of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, or WARS.

[00104] In another aspect, the present disclosure provides a cell comprising a chemokine mimetic disclosed herein. In some embodiments, the cell comprises a polynucleotide encoding a chemokine mimetic. In some embodiments, the cell is generated by transformation of the cell with a viral or non-viral vector containing the polynucleotide encoding a chemokine mimetic.

6.6. Pharmaceutical Compositions

[00105] In one aspect, the present disclosure provides a pharmaceutical composition comprising a chemokine mimetic described herein. In some cases, a pharmaceutical composition comprises a polynucleotide encoding a chemokine mimetic, or a cell comprising a chemokine mimetic, instead of a chemokine mimetic protein.The chemokine mimetic,

polynucleotide or cellin the pharmaceutical composition can be formulated in any appropriate pharmaceutical composition for administration by any suitable route of administration. Suitable routes of administration include, but are not limited to, oral, intravenous, and intratumoral routes of administration. The most suitable route may depend upon the condition and disorder of the recipient. The formulations may conveniently be presented in unit dosage form and may be prepared by any of the methods known in the art of pharmacy.

[00106] A composition can be administered alone or in combination with other treatments, for administration either simultaneously or sequentially dependent upon the condition to be treated. For example, the pharmaceutical composition can be administered in combination with one or more drugs targeting a different check point receptor, such as CTLA-4 inhibitor (*e.g.*, anti-CTLA-4 antibody) or TIGIT inhibitor (*e.g.,* anti-TIGIT antibody). In some embodiments, a composition can be administered alone or in combination with an antibody, such as an anti-TGFb antibody, an anti-PD-L1 antibody, or an anti-PD-1 antibody. In some embodiments, a pharmaceutical composition comprising a chemokine mimetic further comprises one or more additional therapeutic agents.

[00107] In another aspect, the present disclosure provides a pharmaceutical composition comprising a TGFβ inhibitor. In some embodiments, the pharmaceutical composition is formulated for intratumoral administration.

[00108] In another aspect, the present disclosure provides a pharmaceutical composition comprising a PD-L1 antibody. In some embodiments, the pharmaceutical composition is formulated for systemic administration.

[00109] Formulations of the present methods suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets each containing a predetermined amount of the active ingredient; as a powder or granules; as a solution or a suspension in an aqueous liquid or a non-aqueous liquid; or as an oil-in-water liquid emulsion or a water-in-oil liquid emulsion. The active ingredient may also be presented as a bolus, electuary, pump, or paste.

[00110] Formulations for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain antioxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient. Formulations for parenteral administration also include aqueous and non-aqueous sterile suspensions,

which may include suspending agents and thickening agents. The formulations may be presented in unit-dose of multi-dose containers, for example sealed ampoules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of a sterile liquid carrier, for example saline, phosphate-buffered saline (PBS) or the like, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described.

[00111] The pharmaceutical composition may comprise one or more pharmaceutical excipients. Any suitable pharmaceutical excipient may be used, and one of ordinary skill in the art is capable of selecting suitable pharmaceutical excipients. Accordingly, the pharmaceutical excipients provided below are intended to be illustrative, and not limiting. Additional pharmaceutical excipients include, for example, those described in the Handbook of Pharmaceutical Excipients, 8th Revised Ed. (2017), incorporated by reference in its entirety.

[00112] The pharmaceutical composition described herein can be used for treatment of cancer or infection.

[00113] The pharmaceutical composition can be in any form appropriate for human or veterinary medicine, including a liquid, an oil, an emulsion, a gel, a colloid, an aerosol, nanoparticle (e.g., lipid nanoparticle), lipid bilayer, or a solid.

[00114] The pharmaceutical composition can be formulated for administration by any route of administration appropriate for human or veterinary medicine, including enteral and parenteral routes of administration.

[00115] In various embodiments, the pharmaceutical composition is formulated for oral administration, for buccal administration, or for sublingual administration.

[00116] In some embodiments, the pharmaceutical composition is formulated for intravenous, intramuscular, intratumoral, subcutaneous administration, or a combination thereof. In certain embodiments, the pharmaceutical composition is formulated for intravenous infusion.

[00117] In some embodiments, the pharmaceutical composition is formulated for intrathecal or intracerebroventricular administration.

[00118] For intravenous, cutaneous or subcutaneous injection, or injection at the site of affliction, the active ingredient will be in the form of a parenterally acceptable aqueous

solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of relevant skill in the art are well able to prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's Injection, Lactated Ringer's Injection. Preservatives, stabilisers, buffers, antioxidants and/or other additives can be included, as required.

[00119] In some embodiments, the pharmaceutical composition is in a unit dosage form. In some embodiments, the unit dosage form is in a vial, ampule, bottle, or pre-filled syringe. In some embodiments, the unit dosage form contains 0.01 mg, 0.1 mg, 0.5 mg, 1 mg, 2.5 mg, 5 mg, 10 mg, 12.5 mg, 25 mg, 50 mg, 75 mg, or 100 mg of a chemokine mimetic. In some embodiments, the unit dosage form contains 125 mg, 150 mg, 175 mg, or 200 mg of the chemokine mimetic. In some embodiments, the unit dosage form contains 250 mg of the chemokine mimetic.

[00120] In typical embodiments, the pharmaceutical unit dosage form contains 0.1 to 10 μg of thechemokine mimetic per 50 mm^3 to 1000 mm^3 tumor area.

[00121] In typical embodiments, the pharmaceutical composition in the unit dosage form is in liquid form. In various embodiments, the unit dosage form contains between 0.1 mL and 50 ml of the pharmaceutical composition. In some embodiments, the unit dosage form contains 1 ml, 2.5 ml, 5 ml, 7.5 ml, 10 ml, 25 ml, or 50 ml of pharmaceutical composition.

[00122] In particular embodiments, the unit dosage form is a vial containing 1 ml of the pharmaceutical composition at a concentration of 0.01 mg/ml, 0.1 mg/ml, 0.5 mg/ml, or 1mg/ml of a chemokine mimetic. In some embodiments, the unit dosage form is a vial containing 2 ml of the pharmaceutical composition at a concentration of 0.01 mg/ml, 0.1 mg/ml, 0.5 mg/ml, or 1mg/ml.

[00123] In some embodiments, the pharmaceutical composition in the unit dosage form is in solid form, such as a lyophilate, suitable for solubilization.

[00124] Unit dosage form embodiments suitable for subcutaneous, intradermal, intratumoral, or intramuscular administration include preloaded syringes, auto-injectors, and autoinject pens, each containing a predetermined amount of the pharmaceutical composition described hereinabove.

[00125] In various embodiments, the unit dosage form is a preloaded syringe, comprising a syringe and a predetermined amount of the pharmaceutical composition. In

certain preloaded syringe embodiments, the syringe is adapted for subcutaneous administration. In certain embodiments, the syringe is suitable for self-administration. In particular embodiments, the preloaded syringe is a single use syringe.

[00126] In various embodiments, the preloaded syringe contains about 0.1 mL to about 0.5 mL of the pharmaceutical composition. In certain embodiments, the syringe contains about 0.5 mL of the pharmaceutical composition. In specific embodiments, the syringe contains about 1.0 mL of the pharmaceutical composition. In particular embodiments, the syringe contains about 2.0 mL of the pharmaceutical composition. In some embodiments, the syringe contains from 2.0 mL to 5.0 mL of the pharmaceutical composition.

[00127] In some embodiments, the pharmaceutical composition is administered in an amount sufficient to increase filtration of immune cells and enhance the anti-tumor activity of an anti-PD-L1 antibody, TGF-β inhibitor, or both.

6.7. Dosage Regimens

[00128] In various embodiments, the pharmaceutical compositions described in the present disclosure is administered at a dose sufficient to treat a disease or condition, such as cancer, by itself or in combination with an additional therapeutic agent.

[00129] In various embodiments, the chemokine mimetic is administered at a dose sufficient to treat a disease or condition, such as cancer, by itself or in combination with an additional therapeutic agent.

[00130] In some embodiments, the chemokine mimetic is present in the pharmaceutical composition at a concentration of at least 0.01 mg/ml, at least 0.05 mg/ml, at least 0.1mg/ml, at least 0.5mg/ml, or at least 1mg/ml. In certain embodiments, the chemokine mimetic is present in the pharmaceutical composition at a concentration of at least 0.5 mg/ml, 1 mg/ml, 2 mg/ml, 3 mg/ml, 4 mg/ml, 5 mg/ml, 10 mg/ml, 15 mg/ml, 20 mg/ml, or 25 mg/ml. In certain embodiments, the chemokine mimetic is present in the pharmaceutical composition at a concentration of at least 30 mg/ml, 35 mg/ml, 40 mg/ml, 45 mg/ml or 50 mg/ml.

[00131] In some embodiments, the chemokine mimetic is administered in an amount of at least 0.001 mg/kg. In certain embodiments, the chemokine mimetic is administered in an amount of at least 0.01 mg/kg. In certain embodiments, the chemokine mimetic is administered in an amount of at least 0.05 mg/kg. In certain embodiments, the chemokine mimetic is administered in an amount of at least 0.5 mg/kg. In certain embodiments, the

chemokine mimetic is administered orally in an amount of at least 1 mg/kg. In certain embodiments, the dose is at least 2 mg/kg, at least 3 mg/kg, at least 4 mg/kg, at least 5 mg/kg, at least 6 mg/kg, at least 7 mg/kg, at least 8 mg/kg, at least 9 mg/kg, or at least 10 mg/kg.

[00132] In various embodiments, the dose of the chemokine mimetic is at least 0.01 mg/kg. In various embodiments, the dose of the chemokine mimetic is at least 0.1 mg/kg. In various embodiments, the dose of the chemokine mimetic is at least 0.05 mg/kg. In various embodiments, the dose of the chemokine mimetic is at least 0.5 mg/kg. In various embodiments, the dose of the chemokine mimetic is at least 1 mg/kg. In various embodiments, the dose of chemokine mimetic is at least 1.5 mg/kg, at least 2 mg/kg, at least 2.5 mg/kg, at least 3 mg/kg, at least 3.5 mg/kg, at least 4 mg/kg, at least 4.5 mg/kg, at least 5 mg/kg, at least 5.5 mg/kg, at least 6 mg/kg, at least 6.5 mg/kg, at least 7 mg/kg, at least 7.5 mg/kg, at least 8 mg/kg, at least 8.5 mg/kg, at least 9 mg/kg, at least 9.5 mg/kg, or at least 10 mg/kg. In certain embodiments, the dose is at least 5 mg/kg, at least 10 mg/kg at least 15 mg/kg, at least 20 mg/kg, at least 25 mg/kg, 30 mg/kg, at least 35 mg/kg, at least 40 mg/kg, at least 45 mg/kg, at least 50 mg/kg, at least 55 mg/kg, at least 60 mg/kg, at least 65 mg/kg, at least 70 mg/kg, at least 75 mg/kg, at least 80 mg/kg, at least 85 mg/kg, at least 90 mg/kg, at least 95 mg/kg, at least 100 mg/kg, at least 125 mg/kg, at least 150 mg/kg, at least 160 mg/kg, at least 175 mg/kg, or at least 200 mg/kg. In certain embodiments, the dose is 250 mg/kg, 300 mg/kg, 350 mg/kg, 400 mg/kg, 450 mg/kg, 500 mg/kg, 600 mg/kg, 650 mg/kg, 700 mg/kg, 750 mg/kg, 800 mg/kg, 850 mg/kg, 900 mg/kg, 950 mg/kg, or 1000 mg/kg. In certain embodiments, the dose is 0.001 mg/kg to 100 mg/kg per day. In certain embodiments, the dose is 2 mg/kg to 100 mg/kg per day. In certain embodiments, the dose is 25 mg/kg to 1000 mg/kg per day.

[00133] In various embodiments, the dose of the chemokine mimetic is at least 0.5 mg/kg. In certain embodiments, the dose is at least 1 mg/kg. In certain embodiments, the dose is at least 40 mg/kg, at least 40 mg/kg, at least 50 mg/kg, at least 100 mg/kg, at least 150 mg/kg, at least 175 mg/kg, or at least 200 mg/kg. In certain embodiments, the dose is 250 mg/kg, 500 mg/kg, 750 mg/kg, or 1000 mg/kg. In certain embodiments, the dose is 25 mg/kg to 1,000 mg/kg per day.

[00134] In some embodiments, the chemokine mimetic is administered at a dose of 0.001 mg/kg, 0.01 mg/kg, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg or 0.1 mg/kg. In some embodiments, the chemokine mimetic or analog thereof is administered at a dose of 0.1 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3

mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, or 1.0 mg/kg. In some embodiments, the chemokine mimetic or analog thereof is administered at a dose of 1.5 mg/kg, 2 mg/kg, 2.5 mg/kg, 3 mg/kg, 3.5 mg/kg, 4 mg/kg, 4.5 mg/kg, or 5 mg/kg. In some embodiments, the chemokine mimetic or analog thereof is administered at a dose of 6 mg/kg, 7 mg/kg, 8 mg/kg, 9 mg/kg, 10 mg/kg, 12 mg/kg, 15 mg/kg, 20 mg/kg, 30 mg/kg, 40 mg/kg, or 50 mg/kg. In some embodiments, the chemokine mimetic or analog thereof is administered at a dose of 10 mg/kg, 50 mg/kg, 8 mg/kg, 100 mg/kg, 150 mg/kg, 200 mg/kg, 250 mg/kg, 300 mg/kg, 350 mg/kg, 400 mg/kg, or 450 mg/kg, 500 mg/kg, 550 mg/kg, 600 mg/kg, 650 mg/kg, 700 mg/kg, 750 mg/kg, 800 mg/kg, 850 mg/kg, 900 mg/kg, 950 mg/kg, or 1000 mg/kg.

[00135] In some embodiments, the chemokine mimetic or analog thereof is administered in a dose that is independent of patient weight or surface area (flat dose).

[00136] In some embodiments, the flat dose is 0.001 mg, 0.01 mg, 0.1 mg, 0.2 mg, 0.3 mg, 0.4 mg, 0.5 mg, 0.6 mg, 0.7 mg, 0.8 mg, 0.9 mg, or 1 mg. In some embodiments, the flat dose is 1 mg, 2 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, or 10 mg. In some embodiments, the flat dose is 11 mg, 12 mg, 13 mg, 14 mg, 15 mg, 16 mg, 17 mg, 18 mg, 19 mg, or 20 mg. In some embodiments, the flat dose is 25 mg, 30 mg, 35 mg, 40 mg, 45 mg, 46 mg, 47 mg, 48 mg, 49 mg, or 50 mg. In some embodiments, the flat dose is 40 mg, 42 mg, 44 mg, 46 mg, 48 mg, 50 mg, 60 mg, 70 mg, 80 mg, 90 mg, or 100 mg. In some embodiments, the flat dose is 200 mg, 300 mg, 400 mg, 500 mg, 600 mg, 700 mg, 800 mg, 900 mg, or 1000 mg. In some embodiments, the flat dose ranges from 0.1 to 40 mg. In some embodiments, the flat dose ranges from 12 to 30 mg. In some embodiments, the flat dose is 0.1 – 1 mg, 1 – 10 mg, 10 – 15 mg, 15 – 20 mg, 20 – 30 mg, 30 – 40 mg, or 40 – 50 mg. In some embodiments, the flat dose is 1 – 50 mg, 50 – 100 mg, 100 mg – 200 mg, 200 mg – 300 mg, 300 mg – 400 mg, 400 mg – 500 mg, 500 mg – 600 mg, 600 mg – 700 mg, 700 mg – 800 mg, 800 mg – 900 mg, or 900 mg – 1000 mg.

[00137] In various embodiments, the dose is 1-5000 mg. In various embodiments, the flat dose is 12-30 mg. In various embodiments, the flat dose is 1-11 mg. In various embodiments, the flat dose is 12-40 mg. In certain embodiments, the dose is 1 mg, 2 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg, 15 mg, 20 mg, 25 mg, 30 mg, 35 mg, 40 mg, 45 mg, 50 mg, 75 mg, 100 mg, 125 mg, 150 mg, 175 mg, 200 mg, 225 mg, 250 mg, 275 mg, 300 mg, 325 mg, 350 mg, 375 mg, 400 mg, 450 mg, 500 mg, 550 mg, 600 mg, 650 mg,

700 mg, 750 mg, 800 mg, 850 mg, 900 mg, 950 mg, or 1000 mg. In certain embodiments, the dose is 1500 mg, 2000 mg, 2500 mg, 3000 mg, 3500 mg, 4000 mg, 4500 mg, or 5000 mg.

[00138] In various embodiments, the dose is 25-2000 mg. In certain embodiments, the dose is 25 mg, 50 mg, 75 mg, 100 mg, 125 mg, 150 mg, 175 mg, 200 mg, 225 mg, 250 mg, 275 mg, 300 mg, 350 mg, 375 mg, 400 mg, 425 mg, 450 mg, 475 mg, 500 mg, 525 mg, 550 mg, 575 mg, 600 mg, 625 mg, 650 mg, 675 mg, 700 mg, 725 mg, 750 mg, 775 mg, 800 mg, 825 mg, 900 mg, 925 mg, 950 mg, 975 mg, or 1000 mg.

[00139] In some embodiments, the dose is determined based on the tumor volume. In some embodiments, the dose is 0.01 to 100 μg for 50 – 1000mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 50 – 1000mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 50 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 100 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 500 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 1000 mm^3 tumor volume.

[00140] The chemokine mimetic can be administered in a single dose or in multiple doses. In certain embodiments, the chemokine mimetic can be administered in multiple doses, e.g., to different tumor sites or throughout a tumor. In various embodiments, the chemokine mimetic is administered once a day, once every 2 days, once every 3 days, once every 4 days, once every 5 days, once every 6 days, once every 7 days, once every 14 days, once every 21 days, once every 28 days, or once a month. In various embodiments, chemokine mimetic is administered twice a day, twice every 2 days, twice every 3 days, twice every 4 days, twice every 5 days, twice every 6 days, twice every 7 days, twice every 14 days, twice every 21 days, twice every 28 days, or twice a month. In various embodiments, the chemokine mimetic is administered 1 time a week, 2 times a week, 3 times a week, four times a week, or five times a week.

[00141] In another aspect, the present disclosure provides a pharmaceutical composition comprising the combination of an anti-PD-L1 antibody and TGFβ inhibitor (e.g.,anti-TGFβ antibody). The anti-PD-L1 antibody and TGFβ inhibitor is administered at individual doses sufficient to treat a disease or condition, such as cancer, in when administered together in combination. The pharmaceutical composition can be admininistered for a combination therapy. For example, aspects of the present disclosure also include a method of treating cancer by: administering systemically to a subject with cancer, an

effective amount of an anti-PD-L1 antibody; and administering intratumorally to the subject, an TGFβ inhibitor (e.g., anti-TGFβ antibody). The pharmaceutical composition includes the combination of an anti-PD-L1 antibody (e.g., for administering systemically) and an TGFβ inhibitor (e.g., anti-TGFβ antibody) (e.g., for administering intratumorally).

[00142] In some embodiments, the anti-PD-L1 antibody is present in the pharmaceutical composition at a concentration of at least 0.01 mg/ml, at least 0.05 mg/ml, at least 0.1mg/ml, at least 0.5mg/ml, or at least 1mg/ml. In certain embodiments, the anti-PD-L1 antibody is present in the pharmaceutical composition at a concentration of at least 0.5 mg/ml, 1 mg/ml, 2 mg/ml, 3 mg/ml, 4 mg/ml, 5 mg/ml, 10 mg/ml, 15 mg/ml, 20 mg/ml, or 25 mg/ml. In certain embodiments, the anti-PD-L1 antibody is present in the pharmaceutical composition at a concentration of at least 30 mg/ml, 35 mg/ml, 40 mg/ml, 45 mg/ml or 50 mg/ml.

[00143] In some embodiments, the anti-PD-L1 antibody is administered in an amount of at least 0.001 mg/kg. In certain embodiments, the anti-PD-L1 antibody is administered in an amount of at least 0.01 mg/kg. In certain embodiments, the anti-PD-L1 antibody is administered in an amount of at least 0.05 mg/kg. In certain embodiments, the anti-PD-L1 antibody is administered in an amount of at least 0.5 mg/kg. In certain embodiments, the anti-PD-L1 antibody is administered orally in an amount of at least 1 mg/kg. In certain embodiments, the dose is at least 2 mg/kg, at least 3 mg/kg, at least 4 mg/kg, at least 5 mg/kg, at least 6 mg/kg, at least 7 mg/kg, at least 8 mg/kg, at least 9 mg/kg, or at least 10 mg/kg.

[00144] In various embodiments, the dose of the anti-PD-L1 antibody is at least 0.01 mg/kg. In various embodiments, the dose of the anti-PD-L1 antibody is at least 0.1 mg/kg. In various embodiments, the dose of the anti-PD-L1 antibody is at least 0.05 mg/kg. In various embodiments, the dose of the anti-PD-L1 antibody is at least 0.5 mg/kg. In various embodiments, the dose of the anti-PD-L1 antibody is at least 1 mg/kg. In various embodiments, the dose of anti-PD-L1 antibody is at least 1.5 mg/kg, at least 2 mg/kg, at least 2.5 mg/kg, at least 3 mg/kg, at least 3.5 mg/kg, at least 4 mg/kg, at least 4.5 mg/kg, at least 5 mg/kg, at least 5.5 mg/kg, at least 6 mg/kg, at least 6.5 mg/kg, at least 7 mg/kg, at least 7.5 mg/kg, at least 8 mg/kg, at least 8.5 mg/kg, at least 9 mg/kg, at least 9.5 mg/kg, or at least 10 mg/kg. In certain embodiments, the dose is at least 5 mg/kg, at least 10 mg/kg at least 15 mg/kg, at least 20 mg/kg, at least 25 mg/kg, 30 mg/kg, at least 35 mg/kg, at least 40 mg/kg, at least 45 mg/kg, at least 50 mg/kg, at least 55 mg/kg, at least 60 mg/kg, at least 65 mg/kg, at least 70 mg/kg, at least 75 mg/kg, at least 80 mg/kg, at least 85 mg/kg, at least 90 mg/kg, at

least 95 mg/kg, at least 100 mg/kg, at least 125 mg/kg, at least 150 mg/kg, at least 160 mg/kg, at least 175 mg/kg, or at least 200 mg/kg. In certain embodiments, the dose is 250 mg/kg, 300 mg/kg, 350 mg/kg, 400 mg/kg, 450 mg/kg, 500 mg/kg, 600 mg/kg, 650 mg/kg, 700 mg/kg, 750 mg/kg, 800 mg/kg, 850 mg/kg, 900 mg/kg, 950 mg/kg, or 1000 mg/kg. In certain embodiments, the dose is 0.001 mg/kg to 100 mg/kg per day. In certain embodiments, the dose is 2 mg/kg to 100 mg/kg per day. In certain embodiments, the dose is 25 mg/kg to 1000 mg/kg per day.

[00145] In various embodiments, the dose of the anti-PD-L1 antibody is at least 0.5 mg/kg. In certain embodiments, the dose is at least 1 mg/kg. In certain embodiments, the dose is at least 40 mg/kg, at least 40 mg/kg, at least 50 mg/kg, at least 100 mg/kg, at least 150 mg/kg, at least 175 mg/kg, or at least 200 mg/kg. In certain embodiments, the dose is 250 mg/kg, 500 mg/kg, 750 mg/kg, or 1000 mg/kg. In certain embodiments, the dose is 25 mg/kg to 1,000 mg/kg per day.

[00146] In some embodiments, the anti-PD-L1 antibody is administered at a dose of 0.001 mg/kg, 0.01 mg/kg, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg or 0.1 mg/kg. In some embodiments, the anti-PD-L1 antibody or analog thereof is administered at a dose of 0.1 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, or 1.0 mg/kg. In some embodiments, the anti-PD-L1 antibody or analog thereof is administered at a dose of 1.5 mg/kg, 2 mg/kg, 2.5 mg/kg, 3 mg/kg, 3.5 mg/kg, 4 mg/kg, 4.5 mg/kg, or 5 mg/kg. In some embodiments, the anti-PD-L1 antibody or analog thereof is administered at a dose of 6 mg/kg, 7 mg/kg, 8 mg/kg, 9 mg/kg, 10 mg/kg, 12 mg/kg, 15 mg/kg, 20 mg/kg, 30 mg/kg, 40 mg/kg, or 50 mg/kg. In some embodiments, the anti-PD-L1 antibody or analog thereof is administered at a dose of 10 mg/kg, 50 mg/kg, 8 mg/kg, 100 mg/kg, 150 mg/kg, 200 mg/kg, 250 mg/kg, 300 mg/kg, 350 mg/kg, 400 mg/kg, or 450 mg/kg, 500 mg/kg, 550 mg/kg, 600 mg/kg, 650 mg/kg, 700 mg/kg, 750 mg/kg, 800 mg/kg, 850 mg/kg, 900 mg/kg, 950 mg/kg, or 1000 mg/kg.

[00147] In some embodiments, the anti-PD-L1 antibody is administered in a dose that is independent of patient weight or surface area (flat dose).

[00148] In some embodiments, the flat dose is 0.001 mg, 0.01 mg, 0.1 mg, 0.2 mg, 0.3 mg, 0.4 mg, 0.5 mg, 0.6 mg, 0.7 mg, 0.8 mg, 0.9 mg, or 1 mg. In some embodiments, the flat dose is 1 mg, 2 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, or 10 mg. In some

embodiments, the flat dose is 11 mg, 12 mg, 13 mg, 14 mg, 15 mg, 16 mg, 17 mg, 18 mg, 19 mg, or 20 mg. In some embodiments, the flat dose is 25 mg, 30 mg, 35 mg, 40 mg, 45 mg, 46 mg, 47 mg, 48 mg, 49 mg, or 50 mg. In some embodiments, the flat dose is 40 mg, 42 mg, 44 mg, 46 mg, 48 mg, 50 mg, 60 mg, 70 mg, 80 mg, 90 mg, or 100 mg. In some embodiments, the flat dose is 200 mg, 300 mg, 400 mg, 500 mg, 600 mg, 700 mg, 800 mg, 900 mg, or 1000 mg. In some embodiments, the flat dose ranges from 0.1 to 40 mg. In some embodiments, the flat dose ranges from 12 to 30 mg. In some embodiments, the flat dose is 0.1 – 1 mg, 1 – 10 mg, 10 – 15 mg, 15 – 20 mg, 20 – 30 mg, 30 – 40 mg, or 40 – 50 mg. In some embodiments, the flat dose is 1 – 50 mg, 50 – 100 mg, 100 mg – 200 mg, 200 mg – 300 mg, 300 mg – 400 mg, 400 mg – 500 mg, 500 mg – 600 mg, 600 mg – 700 mg, 700 mg – 800 mg, 800 mg – 900 mg, or 900 mg – 1000 mg.

[00149] In various embodiments, the dose is 1-5000 mg. In various embodiments, the flat dose is 12-30 mg. In various embodiments, the flat dose is 1-11 mg. In various embodiments, the flat dose is 12-40 mg. In certain embodiments, the dose is 1 mg, 2 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg, 15 mg, 20 mg, 25 mg, 30 mg, 35 mg, 40 mg, 45 mg, 50 mg, 75 mg, 100 mg, 125 mg, 150 mg, 175 mg, 200 mg, 225 mg, 250 mg, 275 mg, 300 mg, 325 mg, 350 mg, 375 mg, 400 mg, 450 mg, 500 mg, 550 mg, 600 mg, 650 mg, 700 mg, 750 mg, 800 mg, 850 mg, 900 mg, 950 mg, or 1000 mg. In certain embodiments, the dose is 1500 mg, 2000 mg, 2500 mg, 3000 mg, 3500 mg, 4000 mg, 4500 mg, or 5000 mg.

[00150] In various embodiments, the dose is 25-2000 mg. In certain embodiments, the dose is 25 mg, 50 mg, 75 mg, 100 mg, 125 mg, 150 mg, 175 mg, 200 mg, 225 mg, 250 mg, 275 mg, 300 mg, 350 mg, 375 mg, 400 mg, 425 mg, 450 mg, 475 mg, 500 mg, 525 mg, 550 mg, 575 mg, 600 mg, 625 mg, 650 mg, 675 mg, 700 mg, 725 mg, 750 mg, 775 mg, 800 mg, 825 mg, 900 mg, 925 mg, 950 mg, 975 mg, or 1000 mg.

[00151] In some embodiments, the dose is determined based on the tumor volume. In some embodiments, the dose is 0.01 to 100 μg for 50 – 1000mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 50 – 1000mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 50 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 100 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 500 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 1000 mm^3 tumor volume.

[00152] The anti-PD-L1 antibody can be administered in a single dose or in multiple doses. In certain embodiments, the anti-PD-L1 antibody can be administered in multiple doses, e.g., to different tumor sites or throughout a tumor. In various embodiments, the anti-PD-L1 antibody is administered once a day, once every 2 days, once every 3 days, once every 4 days, once every 5 days, once every 6 days, once every 7 days, once every 14 days, once every 21 days, once every 28 days, or once a month. In various embodiments, anti-PD-L1 antibody is administered twice a day, twice every 2 days, twice every 3 days, twice every 4 days, twice every 5 days, twice every 6 days, twice every 7 days, twice every 14 days, twice every 21 days, twice every 28 days, or twice a month. In various embodiments, the anti-PD-L1 antibody is administered 1 time a week, 2 times a week, 3 times a week, four times a week, or five times a week.

[00153] In some embodiments, the TGFβ inhibitor is present in the pharmaceutical composition at a concentration of at least 0.01 mg/ml, at least 0.05 mg/ml, at least 0.1mg/ml, at least 0.5mg/ml, or at least 1mg/ml. In certain embodiments, the TGFβ inhibitor is present in the pharmaceutical composition at a concentration of at least 0.5 mg/ml, 1 mg/ml, 2 mg/ml, 3 mg/ml, 4 mg/ml, 5 mg/ml, 10 mg/ml, 15 mg/ml, 20 mg/ml, or 25 mg/ml. In certain embodiments, the TGFβ inhibitor is present in the pharmaceutical composition at a concentration of at least 30 mg/ml, 35 mg/ml, 40 mg/ml, 45 mg/ml or 50 mg/ml.

[00154] In some embodiments, the TGFβ inhibitor is administered in an amount of at least 0.001 mg/kg. In certain embodiments, the TGFβ inhibitor is administered in an amount of at least 0.01 mg/kg. In certain embodiments, the TGFβ inhibitor is administered in an amount of at least 0.05 mg/kg. In certain embodiments, the TGFβ inhibitor is administered in an amount of at least 0.5 mg/kg. In certain embodiments, the TGFβ inhibitor is administered orally in an amount of at least 1 mg/kg. In certain embodiments, the dose is at least 2 mg/kg, at least 3 mg/kg, at least 4 mg/kg, at least 5 mg/kg, at least 6 mg/kg, at least 7 mg/kg, at least 8 mg/kg, at least 9 mg/kg, or at least 10 mg/kg.

[00155] In various embodiments, the dose of the TGFβ inhibitor is at least 0.01 mg/kg. In various embodiments, the dose of the TGFβ inhibitor is at least 0.1 mg/kg. In various embodiments, the dose of the TGFβ inhibitor is at least 0.05 mg/kg. In various embodiments, the dose of the TGFβ inhibitor is at least 0.5 mg/kg. In various embodiments, the dose of the TGFβ inhibitor is at least 1 mg/kg. In various embodiments, the dose of TGFβ inhibitor is at least 1.5 mg/kg, at least 2 mg/kg, at least 2.5 mg/kg, at least 3 mg/kg, at least 3.5 mg/kg, at least 4 mg/kg, at least 4.5 mg/kg, at least 5 mg/kg, at least 5.5 mg/kg, at least 6 mg/kg, at

least 6.5 mg/kg, at least 7 mg/kg, at least 7.5 mg/kg, at least 8 mg/kg, at least 8.5 mg/kg, at least 9 mg/kg, at least 9.5 mg/kg, or at least 10 mg/kg. In certain embodiments, the dose is at least 5 mg/kg, at least 10 mg/kg at least 15 mg/kg, at least 20 mg/kg, at least 25 mg/kg, 30 mg/kg, at least 35 mg/kg, at least 40 mg/kg, at least 45 mg/kg, at least 50 mg/kg, at least 55 mg/kg, at least 60 mg/kg, at least 65 mg/kg, at least 70 mg/kg, at least 75 mg/kg, at least 80 mg/kg, at least 85 mg/kg, at least 90 mg/kg, at least 95 mg/kg, at least 100 mg/kg, at least 125 mg/kg, at least 150 mg/kg, at least 160 mg/kg, at least 175 mg/kg, or at least 200 mg/kg. In certain embodiments, the dose is 250 mg/kg, 300 mg/kg, 350 mg/kg, 400 mg/kg, 450 mg/kg, 500 mg/kg, 600 mg/kg, 650 mg/kg, 700 mg/kg, 750 mg/kg, 800 mg/kg, 850 mg/kg, 900 mg/kg, 950 mg/kg, or 1000 mg/kg. In certain embodiments, the dose is 0.001 mg/kg to 100 mg/kg per day. In certain embodiments, the dose is 2 mg/kg to 100 mg/kg per day. In certain embodiments, the dose is 25 mg/kg to 1000 mg/kg per day.

[00156] In various embodiments, the dose of the TGFβ inhibitor is at least 0.5 mg/kg. In certain embodiments, the dose is at least 1 mg/kg. In certain embodiments, the dose is at least 40 mg/kg, at least 40 mg/kg, at least 50 mg/kg, at least 100 mg/kg, at least 150 mg/kg, at least 175 mg/kg, or at least 200 mg/kg. In certain embodiments, the dose is 250 mg/kg, 500 mg/kg, 750 mg/kg, or 1000 mg/kg. In certain embodiments, the dose is 25 mg/kg to 1,000 mg/kg per day.

[00157] In some embodiments, the TGFβ inhibitor is administered at a dose of 0.001 mg/kg, 0.01 mg/kg, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg, 0.08 mg/kg, 0.09 mg/kg or 0.1 mg/kg. In some embodiments, the TGFβ inhibitor or analog thereof is administered at a dose of 0.1 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, or 1.0 mg/kg. In some embodiments, the TGFβ inhibitor or analog thereof is administered at a dose of 1.5 mg/kg, 2 mg/kg, 2.5 mg/kg, 3 mg/kg, 3.5 mg/kg, 4 mg/kg, 4.5 mg/kg, or 5 mg/kg. In some embodiments, the TGFβ inhibitor or analog thereof is administered at a dose of 6 mg/kg, 7 mg/kg, 8 mg/kg, 9 mg/kg, 10 mg/kg, 12 mg/kg, 15 mg/kg, 20 mg/kg, 30 mg/kg, 40 mg/kg, or 50 mg/kg. In some embodiments, the TGFβ inhibitor or analog thereof is administered at a dose of 10 mg/kg, 50 mg/kg, 8 mg/kg, 100 mg/kg, 150 mg/kg, 200 mg/kg, 250 mg/kg, 300 mg/kg, 350 mg/kg, 400 mg/kg, or 450 mg/kg, 500 mg/kg, 550 mg/kg, 600 mg/kg, 650 mg/kg, 700 mg/kg, 750 mg/kg, 800 mg/kg, 850 mg/kg, 900 mg/kg, 950 mg/kg, or 1000 mg/kg.

[00158] In some embodiments, the TGFβ inhibitor is administered in a dose that is independent of patient weight or surface area (flat dose).

[00159] In some embodiments, the flat dose is 0.001 mg, 0.01 mg, 0.1 mg, 0.2 mg, 0.3 mg, 0.4 mg, 0.5 mg, 0.6 mg, 0.7 mg, 0.8 mg, 0.9 mg, or 1 mg. In some embodiments, the flat dose is 1 mg, 2 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, or 10 mg. In some embodiments, the flat dose is 11 mg, 12 mg, 13 mg, 14 mg, 15 mg, 16 mg, 17 mg, 18 mg, 19 mg, or 20 mg. In some embodiments, the flat dose is 25 mg, 30 mg, 35 mg, 40 mg, 45 mg, 46 mg, 47 mg, 48 mg, 49 mg, or 50 mg. In some embodiments, the flat dose is 40 mg, 42 mg, 44 mg, 46 mg, 48 mg, 50 mg, 60 mg, 70 mg, 80 mg, 90 mg, or 100 mg. In some embodiments, the flat dose is 200 mg, 300 mg, 400 mg, 500 mg, 600 mg, 700 mg, 800 mg, 900 mg, or 1000 mg. In some embodiments, the flat dose ranges from 0.1 to 40 mg. In some embodiments, the flat dose ranges from 12 to 30 mg. In some embodiments, the flat dose is 0.1 – 1 mg, 1 – 10 mg, 10 – 15 mg, 15 – 20 mg, 20 – 30 mg, 30 – 40 mg, or 40 – 50 mg. In some embodiments, the flat dose is 1 – 50 mg, 50 – 100 mg, 100 mg – 200 mg, 200 mg – 300 mg, 300 mg – 400 mg, 400 mg – 500 mg, 500 mg – 600 mg, 600 mg – 700 mg, 700 mg – 800 mg, 800 mg – 900 mg, or 900 mg – 1000 mg.

[00160] In various embodiments, the dose is 1-5000 mg. In various embodiments, the flat dose is 12-30 mg. In various embodiments, the flat dose is 1-11 mg. In various embodiments, the flat dose is 12-40 mg. In certain embodiments, the dose is 1 mg, 2 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg, 15 mg, 20 mg, 25 mg, 30 mg, 35 mg, 40 mg, 45 mg, 50 mg, 75 mg, 100 mg, 125 mg, 150 mg, 175 mg, 200 mg, 225 mg, 250 mg, 275 mg, 300 mg, 325 mg, 350 mg, 375 mg, 400 mg, 450 mg, 500 mg, 550 mg, 600 mg, 650 mg, 700 mg, 750 mg, 800 mg, 850 mg, 900 mg, 950 mg, or 1000 mg. In certain embodiments, the dose is 1500 mg, 2000 mg, 2500 mg, 3000 mg, 3500 mg, 4000 mg, 4500 mg, or 5000 mg.

[00161] In various embodiments, the dose is 25-2000 mg. In certain embodiments, the dose is 25 mg, 50 mg, 75 mg, 100 mg, 125 mg, 150 mg, 175 mg, 200 mg, 225 mg, 250 mg, 275 mg, 300 mg, 350 mg, 375 mg, 400 mg, 425 mg, 450 mg, 475 mg, 500 mg, 525 mg, 550 mg, 575 mg, 600 mg, 625 mg, 650 mg, 675 mg, 700 mg, 725 mg, 750 mg, 775 mg, 800 mg, 825 mg, 900 mg, 925 mg, 950 mg, 975 mg, or 1000 mg.

[00162] In some embodiments, the dose is determined based on the tumor volume. In some embodiments, the dose is 0.01 to 100 μg for 50 – 1000mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 50 – 1000mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 50 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 100 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10

μg for 500 mm^3 tumor volume. In some embodiments, the dose is 0.1 to 10 μg for 1000 mm^3 tumor volume.

[00163] The TGFβ inhibitor can be administered in a single dose or in multiple doses. In certain embodiments, the TGFβ inhibitor can be administered in multiple doses, e.g., to different tumor sites or throughout a tumor. In various embodiments, the TGFβ inhibitor is administered once a day, once every 2 days, once every 3 days, once every 4 days, once every 5 days, once every 6 days, once every 7 days, once every 14 days, once every 21 days, once every 28 days, or once a month. In various embodiments, TGFβ inhibitor is administered twice a day, twice every 2 days, twice every 3 days, twice every 4 days, twice every 5 days, twice every 6 days, twice every 7 days, twice every 14 days, twice every 21 days, twice every 28 days, or twice a month. In various embodiments, the TGFβ inhibitor is administered 1 time a week, 2 times a week, 3 times a week, four times a week, or five times a week.

6.8. Methods of Treating Cancer

[00164] Aspects of the present disclosure include a method of treating cancer by administering a chemokine mimetic, e.g., an isolated CCL5 mimetic.

[00165] The method can be used for treatment of cancer by recruiting mature NK cells and activated CD8 T cells to the tumor microenvironment. The method can be used for treatment of inflammation, or other disorders, such as treating infections. The method can also be used for recruiting, activating, and/or maturing NK cells.

[00166] In some cases, the method of treating cancer comprises the step of administering a subject with the cancer a therapeutically effective amount of a polynucleotide encoding a chemokine mimetic or a cell expressing a chemokine mimetic, instead of administering a chemokine mimetic as a protein.

[00167] In some embodiments, the method further comprises the step of administering an additional therapeutic agent before or after administration of a chemokine mimetic or a chemokine polynucleotide or cell. In some embodiments, a chemokine mimetic (protein, polynucleotide or cell) and an additional therapeutic agent are administered concurrently.

[00168] In some embodiments, the combination therapy of a chemokine mimetic (protein, polynucleotide, or cell) and an additional therapeutic agent enables reduction of the therapeutic dose of the additional therapeutic agent. For example, when a CCL5 mimetic and

an anti-PD-L1 antibody are used together, a therapeutic dose of the anti-PD-L1 antibody can be reduced compared to anti-PD-L1 mono-therapy.

[00169] The chemokines and their variants can be also used in combination with an ADCC-inducing antibody, ADCP-inducing antibody, or in cancer or non-cancer application of adoptive cell therapy.

[00170] In one aspect, the present disclosure includes a method of treating cancer, comprising the step of: administering to a subject with the cancer a therapeutically effective amount of an isolated chemokine mimetic, or pharmaceutically acceptable salt thereof.

[00171] In typical embodiments, the isolated chemokine mimetic is selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof. In certain embodiments, the isolated chemokine mimetic is two or more isolated chemokine mimetics selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.

[00172] In some embodiments, isolated chemokine mimetic is a CCL5 mimetic. In certain embodiments, the isolated chemokine mimetic is administered in a pharmaceutical composition further comprising a pharmaceutically acceptable carrier or excipient.

[00173] In some embodiments, the isolated chemokine is administered via intratumoral injection, intravenous injection or subcutaneous injection.

[00174] In some embodiments, the isolated is administered is via intratumoral injection.

[00175] In some embodiments, the method further comprises the step of administering to the subject an anti-PD-L1 antibody or an anti-PD-1 antibody. In certain embodiments, the anti-PD-L1 antibody or anti-PD-1 antibody is administered systemically. In certain embodiments, the anti-PD-L1 antibody or anti-PD-1 antibody is administered intratumorally.

[00176] In some embodiments, the method further comprises the step of administering to the subject a TGFβ inhibitor. In certain embodiments, the TGFβ inhibitor is administered systemically. In certain embodiments, the TGFβ inhibitor is administered intratumorally.

[00177] In some embodiments, the method further comprises the steps of administering anti-PD-L1 antibody and an anti-TGFβ inhibitor.

[00178] In some embodiments, the method further comprises the step of administering a bi-specific antibody targeting both PD-1 and TGFβ.

[00179] In some embodiments, the method further comprises step of administering to the subject an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab. In some embodiments, the antibody is an anti-CTLA4 antibody disclosed in PCT/US2019/068820, incorporated by reference in its entirety herein. In certain embodiments, the anti-CTLA4 antibody has a heavy chain amino acid sequence set forth in SEQ ID NO:5909. In certain embodiments, the anti-CTLA4 antibody has a light chain amino acid sequence set forth in SEQ ID NO:5910. In certain embodiments, the anti-CTLA4 antibody is afucosylated.

[00180] In some embodiments, the method further comprises the step of administering to the subject a T cell, an NK cell, macrophage, B cell, or dendritic cell, optionally wherein the T cell is a CAR-T, CAR-NK, CAR-macrophage, or CAR-T cell.

[00181] In some embodiments, the method further comprises the step of administering to the subject an IL-15, IL-15 complex, IL-7, IL-2, or a variant thereof.

[00182] In some embodiments, the method further comprises the step of administering to the subject an agent activating NK cell, T cell activity, or dendritic cell activity. In some embodiments, the method further comprises the step of administering to the subject a vaccine, nucleic acid therapeutic, small molecule inhibitor, or chemotherapeutic agent.

[00183] In some aspects, the present disclosure provides a method of treating cancer, comprising the steps of: intratumorally administering a therapeutically effective amount of an isolated chemokine mimetic, or pharmaceutically acceptable salt thereof, to a subject who has been determined to have expression levels in a biological sample of one or more genes selected from the group consisting of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, CD8, CD3, TCRβ, TCR1, CD11c, XCL-1, WARS, NKp46 and NCR1, granzymes, and perforin that are lower than or higher than a predetermined threshold level.

[00184] In some embodiments, the biological sample is a tumor biopsy. In certain embodiments, the biological sample is a blood sample. In yet other embodiments, the biological sample is a liquid biopsy. In some embodiments, the biological sample is a sample containing cells isolated from a subject comprising a disease or condition (e.g., cancer). In some embodiments, the biological sample is a sample containing cells isolated from a donor. In certain embodiments, the biological sample is a sample containing T cells and/or NK cells isolated from subject comprising a disease or condition (e.g., cancer) or a donor.

[00185] In some embodiments, the method comprises the prior step of determining the expression levels of one or more genes selected from the group consisting of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, CD8, CD3, TCRβ, TCR1, CD11c, XCL-1, WARS, NKp46, NCR1, CD11B, FcRs, collagen genes, CTLA4, CD56, CD16, CD7 CD127, Tbet, Eomes, granzymes, and perforin in the biological sample.

[00186] In some embodiments, the method comprises the prior step of detecting CD8+ T cells, NK cells, mature NK cells, lymphocytes, fibroblasts, Tregs, or dendritic cells in the biological sample. In certain embodiments, the CD8+ T cells, NK cells, lymphocytes, or dendritic cells are detected by immune histochemistry.

[00187] In some embodiments, the chemokine mimetic is selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof. In certain embodiments, the chemokine mimetic is two or more chemokine mimetics selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.

[00188] In certain embodiments, the method further comprises the step of administering to the subject a vaccine, nucleic acid therapeutic, chemotherapeutic agent, or a small molecule inhibitor.

[00189] In some embodiments, the cancer is selected from the group consisting of: multiple myeloma, adrenocortical carcinoma, acute myeloid leukemia, Bladder Urothelial Carcinoma, glioma, breast invasive carcinoma, glioma, Cervical squamous cell carcinoma, endocervical adenocarcinoma, cholangiocarcinoma, chronic myelogenous leukemia, colon adenocarcinoma, esophageal carcinoma, glioblastoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell lymphoma, mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocyoma, paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma,sarcoma, skin cutaneous melanoma, stomach adenocarcinoma, testicular germ cell tumors, thyomas, thyroid carcinoma, uterine carcinosarcoma, uterine corps endometrial carcinoma, microsatellite instability-high cancer, basal cell carcinoma, Merkel cell carcinoma, mucosal melanoma, and uveal melanoma.

[00190] Aspects of the present disclosure also include a method of treating cancer by: administering systemically to a subject with cancer, an effective amount of an anti-PD-L1

antibody; and administering intratumorally to the subject, an TGFβ inhibitor (e.g., anti-TGFβ antibody). The method includes a combination therapy which comprises systemic administration of an anti-PD-L1 antibody and intratumoral administration of an TGFβ inhibitor (e.g., anti-TGFβ antibody).

[00191] The method can be used for treatment of cancer by recruiting mature NK cells and activated CD8 T cells to the tumor microenvironment. The method can be used for treatment of inflammation, or other disorders, such as treating infections. The method can also be used for recruiting, activating, and/or maturing NK cells.

6.9. Antibodies

[00192] In some embodiments, a pharmaceutical composition comprises an additional therapeutic agent. In some embodiments, the pharmaceutical composition comprises one or more additional active ingredients in addition to or separate from the chemokine mimetic of the present invention. The one or more additional active ingredients can be a drug targeting a different check point receptor, such as CTLA-4 inhibitor (*e.g.*, anti-CTLA-4 antibody), PD-L1 inhibitor (*e.g.*, anti-PD-L1 antibody), PD-1 inhibitor (*e.g.*, anti-PD-1 antibody), a TGFβ inhibitor (*e.g.*, anti-TGFβ antibody), or a bispecific antibody (e.g., against PD-L1 and TGFβ or against PD-1 and TGFβ).

[00193] In some embodiments, the therapeutic agent comprises a T cell or an NK cell. In certain embodiments, the T cell is a CAR-T, CAR-NK, or TCR-T cell.

[00194] In some embodiments, the therapeutic agent comprises a dendritic cell or macrophage.

[00195] In certain embodiment, the therapeutic agent is an agent activating NK cell, T cell activity, dendritic cell activity, or a combination thereof.

[00196] In certain embodiments, the additional therapeutic agent is an IL-15, IL-15 complex, IL-2, IL-7 or a variant thereof.

[00197] In certain embodiments, the additional therapeutic agent is selected from a vaccine, chemotherapeutic agent, nucleic acid therapeutic, or a small molecule inhibitor. In certain embodiments, the small molecule inhibitor is an inhibitor of TGF-β.

[00198] In certain embodiments, the additional therapeutic agent is one or more ADCC-inducing antibodies and/or ADCP-inducing antibodies.

6.10. Kits

[00199] In another aspect, the present disclosure provides a kit for treatment of cancer, comprising a pharmaceutical composition comprising a chemokine mimetic or analog thereof.

[00200] In another aspect, the present disclosure provides a kit for treatment of an infection, comprising a pharmaceutical composition comprising a chemokine mimetic or analog thereof

[00201] In certain embodiments, the kit further comprises a second pharmaceutical composition comprising an additional therapeutic agent. In typical embodiments, the additional therapeutic agent is an anti-PD-L1 antibody, an anti-PD-1 antibody, or a TGFβ inhibitor. In certain embodiments, the therapeutic agent is a bispecific antibody against PD-L1 and TGFβ or against PD-1 and TGFβ. In certain embodiments, the additional therapeutic agent comprises an anti-PD-L1 antibody and an anti-TGFβ antibody. In certain embodiments, the additional therapeutic agent comprises an anti-PD-1 antibody and an anti-TGFβ antibody. In certain embodiments, the additional therapeutic agent comprises an anti-PD-L1 antibody, wherein the anti-PD-L1 antibody is atezolizumab.

[00202] In another aspect, the present disclosure provides a kit comprising a first pharmaceutical composition comprising a TGFβ inhibitor and a second pharmaceutical composition comprising an anti-PD-L1 antibody. In some embodiments, the first pharmaceutical composition comprising a TGFβ inhibitor is formulated for intratumoral administration and a second pharmaceutical composition comprising an anti-PD-L1 antibody is formulated for systemic administration.

[00203] In some embodiments, the kit comprises a second and a third pharmaceutical composition. For example, the kit can comprise a second pharmaceutical composition comprising an anti-PD-L1 antibody or an anti-PD-1 antibody, and a third pharmaceutical composition comprising a TGFβ inhibitor.

[00204] In certain embodiments, the additional therapeutic agent is an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab. In certain embodiment, the additional therapeutic agent is an ADCC/ADCP inducing antibody.

[00205] In certain embodiments, the additional therapeutic agent comprises a T cell or an NK cell. In certain embodiments, the T cell is a CAR-T, CAR-NK, CAR-macrophage, or TCR-T cell.

[00206] In certain embodiments, the additional therapeutic agent is an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof.

[00207] In certain embodiments, the additional therapeutic agent is an agent activating NK cell, T cell activity, dendritic cell activity, or a combination thereof.

[00208] In some embodiments, the first pharmaceutical composition and the second pharmaceutical composition are in a single container. In some embodiments, the first pharmaceutical composition and the second pharmaceutical composition are separate pharmaceutical compositions in two or more separate containers.

[0100] The kit can comprise one or more unit doses of the first pharmaceutical composition. The kit can further comprise one or more unit doses of the second pharmaceutical composition. In some embodiments, the kit comprises one or more vials containing the first pharmaceutical composition, and one or more vials containing the second pharmaceutical composition. The kit can further comprise one or more unit doses of the third pharmaceutical composition.

[0101] The kit can further comprise an instruction explaining the method of administering the first pharmaceutical composition, the second pharmaceutical composition, the second pharmaceutical composition, or all of the three. The method can be any of the administration methods provided herein.

[0102] The kit described herein can be used for treatment of cancer or infection.

6.11. Examples

[00209] The following examples are provided by way of illustration not limitation.

Materials and Methods

[00210] **Murine models:** Murine experiments were approved by the Institutional Animal Care and Use Committees of Explora BioLabs, Crown Bioscience or Champions Oncology.

[00211] Experiments using Hu-PD-L1 KI mice were done at Crown Biosciences (Taicang Jiangsu Province, China) and mice were obtained from Shanghai Model Organisms Center, Inc., Shanghai Lingchang Biotechnology Co., Ltd. 1 x 10^6 MC38 cell expressing

human PD-L1 (Hu-PD-L1 MC38) were implanted subcutaneously into the flank of HuPD-L1 knock-in C57/BL6 mice (female, 9-11 weeks old). The mice were randomized into 3 treatment groups (n = 6 per group) when average tumor volume reached 90.48mm^3. Dosing was initiated on the same day (day 0). The mice were dosed (intraperitoneal, IP) biweekly for 3 weeks with PBS, anti-PD-L1 (Atezolizumab, Roche, 2mg/kg) or a combination of anti-PD-L1 (2mg/kg) and anti-TGFβ (mouse IgG1 clone 1D11 from BioXCell, 10mg/kg). Individual animals were removed from the study as their tumor volumes measured greater than 3000 mm^3. All mice that did not have a complete response within the initial 28 day observation period were euthanized and tumors were collected to generate formalin-fixed paraffin-embedded (FFPE) blocks. Mice with full tumor regression (tumor volume of 0.00 mm^3) after 4 weeks were re-challenged on study day 49. Six wildtype C57BL/6 mice (16-18 weeks of age) from Shanghai Lingchang Biotechnology Co., Ltd were used as a naïve control for the re-challenge experiment. Mice for the re-challenge experiment were inoculated subcutaneously at the opposite flank (left lower flank) with 1 x 106 HuPD-L1-MC38 cells. Following tumor implantation, tumor volume and body weight were measured twice a week for an additional 4 weeks. Two-sided Wilcoxon rank sum test was used to determine if the differences in average tumor volume are statistical significance. Survival analysis was performed using the R package survminer (version 0.4.5) and p-values were determined using log-rank test.

[00212] The EMT6 tumor study was performed at Champions Oncology, Inc. 250,000 EMT6 cells suspended in 0.1mL 1x PBS were implanted orthotopically in the 4th right mammary fat pad of female BALB/C mice (Taconic). When tumors reached an average tumor volume of 176.56 mm^3 with a range of 15 – 400 mm^3, animals were matched by tumor volume into blinded groups (n = 12 mice per group) used for dosing. The four treatment groups were PBS, anti-PD-L1 (10 mg/kg for the first dose with each subsequent dose at 5 mg/kg, Atezolizumab, Roche), anti-TGFβ (10 mg/kg, mouse IgG1 clone 1D11, BioXCell), or a combination of anti-PD-L1 plus anti-TGFβ. For all treatments the first dose was administered i.v. on day 0 and the eight subsequent doses were administered i.p. using a dose volume of 5 ml/kg three times per a week. Tumor volumes were measured three times weekly. Mice were observed for 28 days post initiation of dosing, with individual animals being removed from the study as their tumor volumes measured >2000 mm^3. On day 8, three mice per group (chosen based on day-6 tumor volumes that were representative of the entire group) were sacrificed. Whole tumors from the selected mice were sterilely harvested,

removing adjacent skin but leaving the exterior surface of the tumor intact. If there was a large amount of mammary fat attached to the tumor or if the tumor had invaded the adjacent tissue, the tumor was cut away from the tissue and approximately 1-2mm of the tissues was kept attached to the tumor, so that the boundary between the tumor and non-tumor tissues was not disturbed. Tumors were placed into MACS tissue storage solution buffer (Miltenyi 130-100-008) on ice packs and shipped overnight for scRNA-seq processing.

[00213] The CT26 tumor study was performed at Explora BioLabs by GigaGen staff. 500,000 CT26 cells suspended in 0.1mL 1x PBS were implanted s.c into the right hind flank of female BALB/c mice (Taconic). On day 11 post implantation, when tumors were an average tumor volume of 70.6 mm^3, animals randomized into blinded groups (n = 10 per a group) based on tumor volume into blinded groups. Mice received PBS or a combination of Atezolizumab (anti-PD-L1, 2mg/kg) and anti-TGFβ (10mg/kg, clone 1D11, BioXcell). Starting on day 11, mice were treated i.p. two times a week for three weeks. Tumor were measured three times weekly. Mice were observed for 33 days post implantation, with individual animals being removed from the study as their tumor volumes measured greater than 2000mm^3.

[00214] The MC38 tumors study was performed at Champions Oncology, Inc. 5 x 10^5 MC38 cells suspended in 100 ul of PBS were injected s.c. into the left flank of female C57BL/6 mice (Taconic). When tumors reached an average tumor volume of 71.1mm^3 with a range of 32 – 113mm^3, animals were randomized into blinded groups (n = 12 mice per group) on day 0. The four treatment groups were given PBS, recombinant human CCL5 (R&D systems, 278-RN-050/CF), PBS plus anti-PD-L1 (Atezolizumab, Roche), and CCL5 plus anti-PD-L1, respectively. PBS and CCL5 (1 μg/animal) were administered intratumorally (IT), three times a week for three weeks. The recombinant human CCL5 has the sequence of SEQ ID NO: 2. Anti-PD-L1 (1mg/kg) was administered IP, twice a week for three weeks. Dosing started on day 1. Tumor volumes were measured three times weekly. Mice were observed for 28 days, with individual animals being removed from the study as their tumor volumes measured >2000 mm^3. Two-sided Wilcoxon rank sum test was used to determine statistical significance in difference in average tumor volume.

[00215] **Immunohistochemistry:** Formalin-fixed tumors from studies at Crown Biosciences or Champions Oncology were trimmed and paraffin embedded by those organizations, respectively. Tumors from the CT26 study were formalin fixed for 24h before being transferred to ethanol and transferred to Allele Biotechnology (San Diego) where they

were trimmed and paraffin embedded. All immunohistochemistry (IHC) was performed by Allele Biotechnology. 4 μm sections were cut and placed on glass slides for Haemotoxylin and Eosin (H&E) or antibody staining as indicated. A board-certified veterinary pathologist with experience in laboratory animals and toxicologic pathology and who was blinded from the study evaluated the slides from the huPD-L1 KI mouse study. Briefly, IHC findings were reviewed for intensity of staining (0 to 5, where 0 = no staining and 5 = most intense staining) and for number of positive cells per 200 μm^2 field at 10X magnification counting 3 fields for each slide. Statistical significance in the difference in CD3+ cell count was determined using Wilcoxon rank sum test.

[00216] **Single cell RNA sequencing:** EMT6 mammary fat pad tumors and the neighboring tissue were collected from mice such that the entire tumor and the interface between tumor and normal tissue was preserved and tissue was stored overnight in MACS Tissue Storage Solution (Miltenyi Biotec Cat #: 130-100-008) at 4°C. The following day tumor tissue was minced and dissociated using the mouse Tumor Dissociation Kit (Miltenyi Biotec) and gentleMACS Octo Dissociator with Heaters (Miltenyi Biotec). The "37C_m_TDK_2" and "m_imptumor_01" programs were used for the primary and secondary gentle MACS dissociation programs. Tumor suspensions were filtered through a 70μm MACS Smart Strainers (Miltenyi Biotec) and washed with PBS containing 0.5% BSA and 2mM EDTA. Cells were pelleted by centrifugation at 500 g for 7 min. A red blood cell lysis step was performed by incubating cells for 2 minutes with 1X Red Blood Cell Lysis Solution (Miltenyi Biotech). Cells were washed again and then cell viability was measured using the Nexcelom Cellometer K2 Fluorescent Viability Cell Counter and the ViaStain AOPI Staining Solution (Nexcelom). Single cell suspensions were then cryopreserved using CryoStor CS10 solution (STEMCELL technologies) and stored in liquid nitrogen.

[00217] The day samples were to be run on the 10X Genomics Chromium instrument, cells were thawed and FACS sorted for DAPI- CD45+ (live, hematopoietic cells) and DAPI-CD45- (live, non-hematopoietic cells) populations. Briefly, cells were thawed in a 37°C water bath, resuspended in 10 ml of RPMI (Gibco cat # 22400-089) with 10% FBS (Gibco # 26140-095), centrifuged at 500g for 5 minutes, washed in PBS containing 0.5% BSA and 2mM EDTA, and counted using the Nexcelom Cellometer. Approximately 1 x 10^6 cells were transferred to a new tube, washed in PBS with 0.5% BSA and 2mM EDTA, and centrifuged at 500g for 5 minutes. The liquid was poured off from the cells (leaving approximately 100ul in each tube) and 5 μl of mouse Fc Blocking Reagent (rat anti-Mouse CD16/CD32 BD) was

added to samples and incubated for 5 minutes at 4C. 162.5 µl of Brilliant Stain Buffer (BD) containing 12.5 µl of mouse CD45-PE clone 30-F11 (BioLegend) was added to cells and incubated on ice for 30 minutes protected from light. Cells were washed, resuspended in 1X DAPI solution (in PBS plus 0.5% BSA and 2mM EDTA) (BioLegend) at a concentration of 5 x 10^6 cells/ml, and filtered into 5mL FACS tubes with cell-strainer caps (Falcon). Cells were sorted using the BD FACSMelody using the 100µm nozzle. Mouse splenocytes were used as a positive control to determine the voltage needed to identify CD45+ immune cells in the initial side scatter area and forward scatter area gate that would be used for tumor cell suspensions. Singlet and DAPI- (live cell) gates were then applied. Stained single cell suspensions from EMT6 tumors were then sorted and approximately 1 x 10^5 Live CD45+ and 1 x 10^5 Live CD45- cells were collected at 4°C. Cells were washed in RPMI with 10% FBS, centrifuged at 500g for 5 minutes, and counted as described above. Cells were resuspended in RPMI with 10% FBS at 7 x 10^5 cells/ml and were placed on ice. CD45+ and CD45- sorted cells from each of the four groups were run on the 10X Genomics Chromium device using the Single Cell 3′ Reagent Kit v3 (work performed at SeqMatic). Libraries were sequenced at SeqMatic with an Illumina NovaSeq SP 100 cycle kit (read 1 28 bp, read 2 91 bp).

[00218] **Single cell RNA-seq data analysis:** Raw sequencing FASTQ files were processed using the Cell Ranger (version 3.1.0) analysis pipeline. Briefly, alignment and filtering of sequencing reads, barcode counting, and UMI counting were performed using the *cellranger count* command. The reads were aligned to the Mus musculus reference genome assembly GRCm38 (mm10). The outputs of *cellranger count* for all samples were aggregated using the command *cellranger aggr*, normalizing the runs to the same sequencing depth. Secondary analyses were performed using the Seurat package (version 3.1.2) in R (version 3.6.0) {Stuart:2019id}. First, quality control was performed by removing cells with fewer than 200 or more than 5,000 expressed genes, as low and high number of gene counts may indicate low quality cells and cell multiplets, respectively. Cells with more than 10% mitochondrial gene expression were removed. This resulted in 27,797 cells, including 18,002 CD45+ and 9,795 CD45- cells. *sctransform* was used to normalize the expression data and to regress out mitochondrial mapping percentage as a confounding source of variation {Hafemeister:2019ba}. Principal component analysis was performed using the *RunPCA* function in Seurat. Principal components 1 to 30 were provided as an input for non-linear dimensionality reduction via Uniform Manifold Approximation and Projection (UMAP) using the *RunUMAP* function.

[00219] For cell type annotation, the R package SingleR was used, which leveraged reference transcriptomic datasets of pure cell types to infer the cell of origin of each of the single cells independently {Aran:2019ei}. The ImmGen (immgen.org) reference dataset was used. The cells were first annotated using the main cell type labels generated by SingleR. Since the ImmGen reference did not include tumor cell as a cell type, it was required to manually discern tumor cells from host non-immune cells within the CD45- cells. Therefore the CD45- cells was reanalyzed using *RunUMAP*, followed by clustering using the *FindNeighbors* and *FindClusters* functions in Seurat. These functions applied shared nearest neighbor (SNN) based clustering on the scRNA-seq data, identifying 15 clusters of cells. Cells in cluster 7 were annotated as fibroblasts based on expression of fibroblast marker gene, *Fap*. Cells previously annotated by SingleR as endothelial cells or epithelial cells were assigned their original SingleR labels. All other CD45- cells were annotated as tumor cells. To validate the annotations, copy number alterations were analyzed for the CD45- cells using InferCNV {Anonymous:wa}, using epithelial and endothelial cells as reference cells. This revealed copy number aberrations in the tumor cells but not in the fibroblast cells.

[00220] **Differential gene expression and functional enrichment analysis:** Differential gene expression analysis was performed within each cell type using the *FindMarkers* function in Seurat. Each treatment group was compared to the PBS control, using Wilcoxon rank sum test to identify differentially expressed (DE) genes (log fold change > 0.25, adjusted p value < 0.05) between the two groups of cells. The aPD-L1 plus aTGFβ treatment group was also compared to the single treatment groups.

[00221] ClusterProfiler (version 3.12.0) {Yu:2012ec} was used to perform functional enrichment analysis. For each treatment group, foreground gene lists containing genes up- or down-regulated in any CD45+ and CD45- cell types were generated, respectively. These gene lists were tested against background gene lists containing all expressed genes (expressed in at least 5 cells) in CD45+ and CD45- cells, respectively. The enrichment analysis was performed using the *enrichGO* function in ClusterProfiler using the org.Mm.eg.db database and the gene ontology (GO) categories biological process (BP), molecular function (MF), and cellular component (CC). Multiple testing correction was performed using the Benjamini and Hochberg method. The enriched pathways were visualized as gene concept networks using the *cnetplot* function of the enrichplot package (version 1.4.0) {enrichplotVisualiz:2019ty}.

[00222] **Cell-cell communication using CellphoneDB:** Cell-cell communication analysis was performed using CellphoneDB {Efremova:2020cb}, a repository of curated

receptors, ligands and their interactions. First, all mouse genes from this study were mapped to their human orthologs using biomaRt {Durinck:2009ki}. scRNA-seq count tables and cell type annotations for each treatment group were used as inputs for running CellphoneDB, using the method "statistical analysis" and default parameters. Receptor-ligand interactions were visualized as dot plots using ggplot2 (version 3.2.1) {Wickham:2016bq}.

[00223] **Association of chemokine expression and immune cell abundance in TCGA:** Intratumoral immune cell abundance was inferred using either an image-based approach or a gene signature-based approach. For the image-based approach, 4,612 published TIL scores estimated from TCGA H&E images were downloaded {Saltz:2018ig, Thorsson:2018ji}. Briefly, Saltz et al. developed deep learning-based image recognition to classify and quantify lymphocytes on H&E diagnostic images from 13 TCGA cancer types (LUAD, BRCA, PAAD, COAD, LUSC, PRAD, UCEC, READ, BLCA, STAD, CESC, SKCM and UVM). The deep learning model training process was repeated until pathologists judged that the lymphocyte classification was adequate. The TIL scores were reported as "TIL Regional Fraction" in Table 1 by Thorsson et al. {Thorsson:2018ji}. For the gene signature-based approach, pre-calculated xCell immune cell scores were downloaded for 9,358 TCGA samples (www(dot)xcell(dot)ucsf(dot)edu/) {Aran:2017do} and filtered for immune cell types of interest: CD8+ T cells, dendritic cells (aDC), NK cells, Tregs, and M2 macrophages.

[00224] For TCGA tumor gene expression data, RNA-seq quantifications (in Fragments Per Kilobase of transcript per Million mapped reads, FPKM) were downloaded from the TCGA portal (www(dot)portal(dot)gdc(dot)cancer(dot)gov/) for 32 cancer types (ACC, BLCA, BRCA, CESC, CHOL, COAD, DLBC, ESCA, GBM, HNSC, KICH, KIRC, KIRP, LGG, LIHC, LUAD, LUSC, MESO, OV, PAAD, PCPG, PRAD, READ, SARC, SKCM, STAD, TGCT, THCA, THYM, UCEC, UCS, UVM). Chemokine genes were filtered by retaining only expression data for genes whose names started with CXC, CCL, CX3C or XC. Within each cancer type, genes that were not or lowly expressed (median expression across all samples < 0.01 FPKM) were excluded from further analysis.

[00225] For each TCGA cancer type, the chemokine gene expression data frame was combined with either the image-based or the gene signature-based immune score data frame. Only samples with data present in both data frames were analyzed. A pseudo count of 0.01 was added to the expression and immune scores, followed by log2 and z-score transformation, in preparation for linear regression analysis. Linear regression analysis was

performed for each chemokine gene using immune score as the dependent variable and chemokine gene expression as the independent variable. P-values were adjusted for multiple testing using the Benjamini and Hochberg method. Chemokines significantly associated with immune scores were further ranked by the sum of their regression coefficients across different cancer types. The results were visualized as heatmaps using ggplot2 (version 3.2.1) {Wickham:2016bq}. All data manipulations and analyses were performed in R 3.6.0.

[00226] ***Flow cytometry:*** For flow cytometry MC38 tumors were harvested, cut into small pieces approximately of 2-4 mm and dissociated using the MACS Miltenyi Biotec Tumor Dissociation Kit according to manufacturer instructions. Dissociated cell suspensions were filtered through a 70um strainer with 10mL of RPMI 1640 media and centrifuged at 300xg for 7 minutes. Cells were resuspended in MACs buffer and Red Blood Cell Lysis Solution was added to remove erythrocytes and dead cells. Cells were pelleted, washed, and resuspended with MACS buffer. Cells were then plated into 96 well plates and stained with fluorescently labelled antibodies: CD11b (BUV395, clone M1/70, BD), CD4 (BUV496, clone RM4-5, BD), CD8 (9BUV661, clone 53-6.7, BD), CD3 (BUV805, clone 17A2, BD), CD11c (BV421, clone N418, BD), CD45 (BV480, 30F11, BD), Ly6G (BV605, clone 1A8, BD), CD44 (BV786, clone IM7, BD), Ly6C (AF488, clone HK1.4, BL), PD1 (BB700, clone j43, BD), FOXP3 (PE, clone FJK-16S, Fisher), NK1.1 (PECy7, clone PK136, BL), CCR5 (CD195) (APC, Clone 2D7, BD), and FVS780. Populations were named based on expression of the indicated marker(s).

[00227] **Data availability:** Single cell RNA-seq fastq sequence files are deposited at the Sequence Read Archive (www(dot)ncbi(dot)nlm(dot)nih(dot)gov/sra/), under BioProject ID PRJNA615238.

[00228] ***Supplemental materials:*** Table 1 lists the differentially expressed (DE) genes identified in the single cell RNA-seq of tumor samples from mice treated with anti-PD-L1 and/or anti-TGFβ. Table 2 contains the list of enriched terms as determined by functional enrichment analysis using the DE genes from Table 1.

Example 1: PD-L1 plus TGFβ blockade reduces tumor growth and enhances immune cell infiltration

[00229] Human PD-L1 knock-in mice bearing MC38 tumors expressing Hu-PD-L1 (Hu-PD-L1 MC38) were treated with vehicle, anti-PD-L1 or a combination of anti-PD-L1 plus anti-TGFβ. Anti-PD-L1 significantly limited tumor growth ($p = 0.0087$; FIGs. 1A-1B),

while anti-TGF-β alone was not efficacious (FIGs. 9A-9B). Additionally, combination treatment with anti-PD-L1 plus anti-TGFβ was significantly more efficacious than anti-PD-L1 alone ($p = 0.038$) and led to tumor regression in 66.67% of animals by day 28 (FIGs. 1A, 1B). Both anti-PD-L1 and anti-PD-L1 plus anti-TGFβ also improved survival relative to control (FIG. 1C). 1 of 6 (16.67%) mice from the anti-PD-L1 group and 3 of 6 (50%) mice from the anti-PD-L1 plus anti-TGFβ group had a complete response and were re-challenged with Hu-PD-L1 MC38 cells, implanted subcutaneously on the opposite flank from the original tumor. Tumor-naïve, wild-type C57BL/6 mice were used as controls. All previously cured mice, but not the naïve mice, were protected from tumor re-challenge, indicating the presence of anti-tumor immune memory (FIG. 1D).

[00230] To investigate if PD-L1 plus TGFβ blockade had an effect on T cell infiltration, CD3 immunohistochemistry (IHC) was performed on tumors from the treated mice. Anti-PD-L1 plus anti-TGFβ significantly increased T cell infiltration while anti-PD-L1 alone did not (FIG. 1E, 1F). Tumor growth inhibition was also observed upon anti-PD-L1 plus anti-TGFβ treatment in a different mouse colon carcinoma tumor model, CT26 (FIG. 6A, 6B). Overall, these results established that dual blockade of PD-L1 and TGFβ effectively controlled tumor growth and improved T cell infiltration into the tumor. It was thus reasoned that *in vivo* inhibition of PD-L1 plus TGFβ could be used as an experimental model to identify genes important for immune cell infiltration and anti-tumor response, and this information could be used to uncover strategies to enhance immunotherapy.

[00231] In a different mouse colon carcinoma tumor model, CT26, significant tumor growth inhibition was also observed upon anti-PD-L1 (atezolizumab, which cross reacts with murine PD-L1) plus anti-TGF-β treatment, whether anti-TGF-β was given intraperitoneally (I.P.) or intratumorally (I.T.) (FIG. 10).

[00232] To study this therapeutic regimen in an orthotopic tumor type, mice harboring EMT6 breast tumors orthotopically grown in the mammary fat pad were treated with PBS, anti-PD-L1 (atezolizumab), anti-TGF-β, or anti-PD-L1 (atezolizumab) plus anti-TGF-β. While efficacy from either single agent was not observed, anti-PD-L1 plus anti-TGF-β significantly reduced tumor size relative to PBS or anti-TGF-β alone ($p<0.03$; FIGs. 7A, 7B). Further, the combination treatment improved the survival relative to all individual arms ($p<0.01$; FIG. 7H). Anti-PD-L1 plus anti-TGF-β in combination, but neither monotherapy alone, enhanced CD3 immune cell infiltration relative to all individual arms ($p<0.03$; FIG. 7I).

Example 2: Single cell RNA-seq of tumors from anti-PD-L1 and anti-TGFβ treated mice

[00233] To identify potential novel therapeutic strategies, the present inventors aimed to characterize the molecular responses upon anti-PD-L1 and/or anti-TGFβ treatment at the single cell level, using the syngeneic breast tumor model, EMT6. Mice harboring EMT6 tumors were treated with either PBS, anti-PD-L1, anti-TGFβ or anti-PD-L1 plus anti-TGFβ. While efficacy was not observed from the single agents, anti-PD-L1 plus anti-TGFβ significantly reduced tumor size relative to PBS ($p = 0.024$) (FIG. 7A, 7B). The EMT6 orthotopic tumor model provided with an opportunity to characterize the single cell molecular responses to anti-PD-L1 ± anti-TGF-β treatment in a setting where anti-TGF-β addition overcomes resistance to anti-PD-L1 therapy. Eight days after the first dose, three mice per a group with representative tumors were euthanized and their tumors were harvested, dissociated, and flow sorted for CD45+ immune cells and CD45- non-immune cells, which were subjected to single cell RNA sequencing (scRNA-seq) using the 10x Genomics platform. After quality control (FIG. 12), single cell transcriptomic profiles were generated for 27,797 high-quality cells, including including 17,665 CD45+ and 9,795 CD45- cells. Uniform Manifold Approximation and Projection (UMAP) dimensionality reduction of the transcriptomes revealed distinct clusters of cells present in all treatment groups (FIG. 2A, 2B). Cell type labels were assigned using SingleR, which annotated cell type based on reference transcriptomes of pure cell types in the ImmGen database {Heng:2008jj}. To discern tumor cells from host stromal cells, fine UMAP clustering was performed on the CD45- cells, generating 15 distinct clusters (FIG. 7C). Cells in cluster 7 had high expression of the fibroblast marker, *Fap,* and were annotated as fibroblasts (FIG. 7D). The remaining cells were annotated as tumor cells or assigned their original SingleR labels as endothelial or epithelial cells. Copy number analysis confirmed that the annotated tumor cells exhibited aberrant copy number while the fibroblasts did not (FIG. 7E). In total, 12 cells types that had both unique and overlapping marker gene expression patterns were identified (FIG. 13). When comparing the different treatment groups, differences in cell type composition was observed. For example, the anti-PD-L1, anti-TGFβ and anti-PD-L1 plus anti-TGFβ samples had lower numbers of macrophages (9.2 – 20.3% of CD45+ cells) compared to the PBS control (33.3% of CD45+ cells). On the contrary, relative to the PBS sample where B cells represented 9.5%% of the CD45+ cells, the three treatment groups had higher number of B cells (23.8%-32.1%, respectively, of the CD45+ cells) (FIG. 2C).

[00234] Next, differential gene expression analysis was performed between each drug treatment group and the control sample, within each annotated cell type. Anti-PD-L1, anti-TGFβ and anti-PD-L1 plus anti-TGFβ treatments resulted in 568, 123 and 358 differentially expressed genes, respectively, across different cell types, respectively (Table 1). To assess the overall impact of the drug treatments on the non-immune and immune compartments, functional enrichment analysis of the differentially expressed genes within the CD45- and CD45+ cells were performed, respectively. While single agent inhibition of PD-L1 did not result in down-regulation of specific functional categories for the CD45- cells, TGFβ blockade led to down-regulation of WNT-signaling related pathways including Wnt-protein binding and frizzled binding (FIG. 2D, Table 2). Interestingly, WNT/beta-catenin pathway was previously shown to contribute to T cell exclusion {Spranger:2015ge}. More strikingly, dual blockade of PD-L1 plus TGFβ led to significant down-regulation of matrix remodeling associated functional categories including extracellular matrix, contractile fiber and collagen-containing extracellular matrix (FIG. 2D). For example, collagen and metalloproteinase genes such as *Col1a1*, *Col1a2*, *Cthrc1*, *P3h4* and *Mmp23* were down-regulated in fibroblasts following dual antibody blockade (FIG. 2E, 2F). This is consistent with previous observation that TGFβ blockade synergizes with anti-PD-L1 to reprogram the peritumoral stromal fibroblasts {Mariathasan:2018dx}. To elucidate the interactions between various cell types involved in TGFβ signaling, a cell-cell communication network was generated involving all TGFβ ligands and receptors using CellPhoneDB {Efremova:2020cb}. CellPhoneDB analysis implicated multiple cell types as the source of TGFβ ligands, including B cells, dendritic cells, macrophages, NK cells and intriguingly, tumor cells. Tumor cell-expressed TGFβ molecules were predicted to interact with TGFβ receptors on fibroblast cells, macrophages and tumor cells themselves. Interestingly, these interactions were largely abolished following anti-TGFβ treatment, alone or in combination with anti-PD-L1 (FIG. 7F). This suggests that tumor cell produced TGFβ can induce fibroblasts to express collagen and other extracellular matrix genes resulting in a physical barrier to T cell exclusion and that TGFβ blockade counteracts this immune suppression.

[00235] Functional enrichment analysis of the up-regulated genes within the CD45+ cells showed clear enhanced immune responses following anti-PD-L1 and anti-TGFβ treatments, whether administered alone or in combination. For example, anti-PD-L1 plus anti-TGFβ induced upregulation of genes involved in response to bacterium (eg. *H2-K1*, *B2m*, *Cd274*, *Il1b*), response to interferon-gamma (eg. *H2-Aa*, *Stat1*, *Irf1*) and positive

regulation of cytokine production (eg. *Cd74*, *Cd83*, *Ccl4*) (FIG. 2G, 2H, Table 2). Notably, multiple chemokines were upregulated in the macrophages of the anti-PD-L1 sample (*Cxcl9*, *Ccl5*, *Ccl4*, *Cxcl14*), the anti-TGFβ sample (*Ccl12*, *Ccl4*) and the anti-PD-L1 plus anti-TGFβ sample (*Cxcl10*, *Cxcl9*, *Ccl4*, *Ccl5*, *Ccl3*, *Ccl2*, *Ccl7*) (FIG. 2I). This is consistent with previous *in vivo* studies showing anti-PD-1/L1 treatment favors polarization of macrophages towards a more immunostimulatory state {Gubin:2018iw, Xiong:2019fx}. Further analysis revealed that chemokines were upregulated in fibroblasts, neutrophils and T cells in tumors from anti-PD-L1 and anti-PD-L1 plus anti-TGFβ treated mice (FIG. 7G). Additionally, anti-PDL-L1 plus anti-TGFβ combination treatment led to upregulation of additional chemokines such as *Cxcl1* and *Cxcl2* above and beyond those induced by either single treatment alone (Table 1). Chemokines lay a critical role in recruiting various immune cells to create an inflamed TME {Vilgelm:2019jw, Nagarsheth:2017dp}. The increase in chemokine expression in anti-PD-L1 and anti-PD-L1 plus anti-TGFβ treated samples suggests that chemokines may facilitate the success of checkpoint blockade treatments. Indeed, both pre-treatment and post-treatment *CXCL9* and *CXCL10* expression levels have been shown to be correlated with response to anti-PD-1 and anti-PD-L1 treatment, in melanoma and urothelial cancer patients, respectively {Rosenberg:2016hh, Lim:2018jy, Chow:2019gj}.

[00236] Because multiple tumors were pooled for each treatment group for the scRNA-seq analysis, it is possible that some of the gene expression differences observed could be skewed by a single tumor sample, leading to a higher number of false positives from this analysis. Among CD45- cells, the combo treatment resulted in the highest number of down-regulated genes in fibroblasts (FIG. 11A). To further investigate the changes in fibroblasts, unsupervised re-clustering of fibroblasts was performed, revealing two subclusters. Cluster Fib_0 was associated with higher expression of genes including Clec3b, Tnxb, Col14a1, Pi16, and Lbp, while cluster Fib_1 was associated with higher expression of Tnc, Gapdh, Spp1, Cxcl14, and Timp1 (FIGs. 11B-11D). Differential gene expression and functional enrichment analysis was performed within the fibroblast subclusters. Interestingly, within Fib_0, dual blockade of PD-L1 plus TGF-β led to significant downregulation of matrix remodeling associated functional categories including collagen fibril organization, extracellular matrix organization, and fibrillar collagen trimer (FIG. 11E). For example, collagen and metalloproteinase genes such as Col1a2, Col5a2, Col1a1, P3h4, Cthrc1, and Mmp2 were downregulated in Fib_0 following combination blockade (FIGs. 11F-11G; Table 3).

[00237] Among CD45+ cell types, macrophages had the highest number of up-regulated genes following anti-PD-L1 plus anti-TGF-β treatment (FIG. 11A). Fine clustering of macrophages revealed four subclusters, with subclusters Mac_0 and Mac_1 representing more than 90% of the cells (FIGs. 14A-14B). Cells in Mac_0 were characterized by expression of complement-related genes (C1qa, C1qb, C1qc) and cytokines (Spp1, Ccl12), while cells in Mac_1 expressed higher levels of several tumor-associated macrophages-related genes such as Arg1, Cebpb, and Ier3 (FIG. 14C). Differential expression and functional enrichment analysis showed that anti-PD-L1, administered alone or in combination with anti-TGF-β, resulted in enhanced immune responses in Mac_0. For example, both anti-PD-L1 and anti-PD-L1 plus anti-TGF-β induced upregulation of genes involved in antigen processing and presentation, adaptive immune response, response to bacterium, and response to interferon-gamma (FIGs. 14D-14E). Anti-TGF-β, administered alone or in combination with anti-PD-L1, induced upregulation of genes involved in monocyte chemotaxis, response to chemokine, and eosinophil migration (FIG. 14D). Notably, many chemokines were upregulated in the Mac_0 population of the anti-PD-L1 sample (Ccl5, Cxcl9, Ccl4) and the anti-TGF-β sample (Ccl2, Ccl12, Ccl4), while multiple chemokines showed further upregulation after anti-PD-L1 plus anti-TGF-β combination treatment (Ccl5, Ccl2, Ccl7, Ccl3, Cxcl10) (FIG. 14F; Table 4).

[00238] Further analysis revealed that chemokines were upregulated in fibroblasts, neutrophils, and T cells in anti-PD-L1 and anti-PD-L1 plus anti-TGF-β treated tumors (FIG. 7G). Additionally, anti-PD-L1 plus anti-TGF-β combination treatment led to upregulation of additional chemokines such as Cxcl1 and Cxcl2 in tumor cells above and beyond those induced by either single treatment alone (Table 1). Chemokines lay a critical role in recruiting various immune cells to create an inflamed tumor microenvironment. The enhanced chemokine expression in samples after anti-PD-L1 plus anti-TGF-β combination treatment suggests that chemokines may facilitate the success of checkpoint blockade treatments.

[00239] A major goal in immunotherapy is to find strategies to enhance immune cell infiltration. While anti-TGFβ monoclonal antibodies in combination with anti-PD-L1s have been shown to enhance immune infiltration and efficacy in preclinical models, these molecules have been plagued by toxicity leading to the halting of several clinical trials with these agents. However, these data suggest the possibility that a chemokine administered therapeutically may improve immune cell infiltration and efficacy of anti-PD-L1 antibodies.

Example 3: CCL5 expression and CXCL9 expression are associated with immune cell infiltration across human cancer types

[00240] To prioritize chemokines most likely to enhance efficacy of anti-PD-L1 antibodies, an unbiased computational approach was taken to identify chemokines associated with immune cell infiltration in different human cancer types in The Cancer Genome Atlas (TCGA). For this tumor-infiltrating lymphocyte (TIL) scores for TCGA tumor samples were utilized, which have been previously quantified using two distinct methods. For one method Saltz et al. used a deep learning image recognition algorithm to quantify tumor infiltrating lymphocytes from H&E-stained pathology images for 13 TCGA cancer types {Saltz:2018ig, Thorsson:2018ji}. Independently, Aran et al. developed a gene signature-based method termed xCell to infer immune cell abundance based on tumor gene expression profiles {Aran:2017do}. Specifically, the immune cell abundance scores was of focus for three cytotoxicity relevant cell types: CD8+ T cells, dendritic cells and NK cells. Using linear regression models, association between gene expression levels for a panel of chemokine genes (i.e. genes starting with CXC, CCL, CX3C or XC) was tested for with the immune infiltration scores, based on both the image-based scoring method and the gene signature-based scoring method (FIG. 3A). Chemokines significantly (multiple testing adjusted p-values < 0.05) associated with immune infiltration scores were further ranked based on their association strengths (i.e. regression coefficients) across cancer types (FIG. 3A).

[00241] The expression levels of six chemokine genes were significantly associated with the image-based immune scores, across all 13 tested cancer types (FIG. 3B). Of these *CCL5*, *CXCL9*, *CXCL13*, *CXCL10 CXCL11, and CCL19)* were, also, among the top chemokine genes associated with the gene expression-based immune scores across multiple cancer types (FIG. 3C). For example, correlation of CCL5 expression in breast cancer (BRCA) with the image-based infiltration scores is shown in FIG. 8A. In contrast, these chemokines were weakly associated with the gene expression-based immune scores for immunosuppressive Tregs and M2 macrophages (FIG. 8B). Notably, *CCL5* and *CXCL9* were consistently the top chemokines associated with immune infiltration scores, as determined by the image-based and the gene signature-based methods (FIG. 3B, 3C). *CCL5* and *CXCL9* expression levels were significantly associated with inferred CD8+ T cells, dendritic cells and NK cells abundance across multiple cancer types (FIG. 3C).

Example 4: CCL5 enhances immune cell infiltration and synergizes with anti-PD-L1 in vivo

[00242] Given its chemotactic roles, it was hypothesized that intratumoral delivery of recombinant CCL5 or CXCL9 proteins may enhance immune cell recruitment and control tumor growth. While multiple intratumoral cell subsets express CCR5 (FIG. 5D; Additional file 1, FIGs. 4B-4C), intratumorally administering recombinant CCL5 to s.c. MC38 tumors resulted in an increased frequency of CD8+ T cells in the tumor that were CCR5 positive twelve days after starting dosing ($p = 0.03$; FIG. 5D, 4A; FIGs. 4B-4C), though no significant difference was seen for total CD8+ T cells (FIG. 5D). There was also a trend towards an increase in the frequency of NK cells expressing CCR5 ($p = 0.09$; FIG. 5D, 4A; FIGs. 4B-4C) but not for total NK cells (FIG. 5D). Furthermore, it was found that intratumoral CCL5 resulted in an increased frequency of NK cells expressing CD11b+ ($p = 0.04$; FIG. 5B, 5C; FIGs. 4B-4C). Though after multiple hypothesis correction (Bonferroni), none of the p-values in Figure 4A or 5C remain significant ($p>0.05$). Together these data suggest that intratumorally administered CCL5 altered the tumor microenvironment, including by recruiting cytotoxic lymphocytes. However, several intratumoral immune cell subsets have higher expression of CCR5 than CD8 T cells or NK cells (FIG. 5A).

[00243] To determine if the totality of cells recruited by intratumorally administered CCL5 was able to enhance the efficacy of anti-PD-L1 therapy, the ability of CCL5, alone or in combination with anti-PD-L1 was tested, to limit tumor growth using the same tumor model. While neither CCL5 or 1 mg/kg of anti-PD-L1 alone limited tumor growth, CCL5 in combination with anti-PD-L1 significantly reduced tumor growth relative to all individual arms ($p<0.05$;FIG. 4D, 4E). Mice that received intratumoral CCL5 plus anti-PD-L1 combination therapy also had significantly prolonged survival compared to compared to all individual arms ($p<0.02$;(FIG. 4F). Thus, intratumorally administered CCL5 is able to overcome resistance to anti-PD-L1 therapy.

Example 5: In vivo efficacy of intratumoral CCL5, CXCL9, or WARS in a MC38 tumor model

[00244] The chemokines CXCL9 and CCL5 correlate to immune infiltration in human tumors and were found to recruit immune cells important for anti-tumor immune responses. For example, CXCL9 is able to recruit cytotoxic T cells, T helper-type 1 (Th1) CD4 T cells, and NK cells, which express the CXCL9 receptor CXCR3. CCL5 was shown to recruit dendritic cells in murine tumor models. Thus, the study herein evaluates i.t. administration of recombinant CXCL9 or CCL5 on tumor growth inhibition (TGI).

[00245] An MC38 syngeneic tumor model was used in order to evaluate anti-tumor activity of intratumorally (i.t.) administered recombinant CCL5, CXCL9, or WARS.

[00246] Further, the present inventors hypothesized whether combination therapy with CCL5 and CXCL9 would synergize since recruitment of activated T cells to the tumor microenvironment and result in a productive anti-tumor immune response if anti-tumor T cells are properly primed (i.e. recruiting T cells to the tumor will not induce productive anti-tumor response if no anti-tumor T cells are activated). Productive priming of tumor-specific T cells likely requires that activated dendritic cells pick up antigen in the tumor and traffic back to the lymph node where they can prime these T cells. Thus, combination therapy that both recruits dendritic cells and activated T cells to the tumor may be a powerful combination if it enabled both effective priming of anti-tumor T cells and recruitment of these T cells to the tumor microenvironment.

[00247] Thus, the study provided herein evaluates i.t. administration of one or both of these chemokines in improving the anti-tumor response induced by anti-PD-L1 treatment.

Study Design

[00248] A MC38 syngeneic colorectal tumor model was used in this study. The model included C57BL/6 female mice (Taconic) that implanted between 7.5 and 12 weeks of age. Weight criteria at the initial dosing was at least 18 grams.

Pre-dosing:

[00249] *Pre-study Animals:*

[00250] Groups 1-10: 120 C57BL/6 mice were injected with 0.1 mL volume containing $5x10^5$ MC38 cells in 1x PBS into the left flank; these animals were used for randomization into groups 1-10 based on tumor volumes.

[00251] Group 11: 12 C57BL/6 mice were injected in the left flank with a 100uL mixture containing $5x10^5$ MC38 cells in 1x PBS mixed with 1 ug of recombinant WARS. These 12 animals were placed onto study at the time that groups 1-10 were randomized.

[00252] Study Animals: Once sufficient pre-study animals reached an average tumor volume of 50.3 mm^3, with a tumor volume range of 37 to 85 mm^3, 80 animals were randomized into groups 1 - 10. The tumor volume range for group 11 was 16-68 mm^3 at that time point.

Treatment

[00253] Table 5 outlines the parameters used for each sample group (sample size, test agent, dosage and volume, route of administration, and frequency of administration).

Table 5: Study Design

Group	Sample Size	Test Agent	Dose	Volume	ROA/Schedule
1	8	PBS	1 ug/mouse	20ul	IT (intratumoral)/TIW (3 times a week)
2	8	CXCL9	1 ug/mouse	20ul	IT/TIW
3	8	CCL5	1 ug/mouse	20ul	IT/TIW
4*	8	CXCL9	1 ug/mouse	20ul	IT/TIW
		CCL5	1 ug/mouse		
5	8	WARS	1 ug/mouse	20ul	IT/TIW
6	8	PBS	1 ug/mouse	20ul	IT/TIW
		aPD-L1 (10F.9G2)	200 ug/mouse	200ul	IP/BIWx2
7	8	CXCL9	1 ug/mouse	20ul	IT/TIW
		aPD-L1 (10F.9G2)	200 ug/mouse	200ul	IP/BIWx2
8	8	CCL5	1 ug/mouse	20ul	IT/TIW
		aPD-L1 (10F.9G2)	200 ug/mouse	200ul	IP/BIWx2
9**	8	CXCL9	1 ug/mouse	20ul	IT/TIW
		CCL5	1 ug/mouse		
		aPD-L1 (10F.9G2)	200 ug/mouse	200ul	IP/BIWx2
10	8	WARS	1 ug/mouse	20ul	IT/TIW
		aPD-L1 (10F.9G2)	200 ug/mouse	200ul	IP/BIWx2
11***	12	WARS	1 ug/mouse	100ul (with cells)	Mixed with cell /DOI
		WARS	1 ug/mouse	200ul	IT/TIW

* Group 4 test agents were mixed together and dosed as a cocktail
** Group 9 test agents CXCL9 and CCL5 were mixed together and dosed IT as a cocktail, while aPD-L1 (10F.9G2) was dosed separately IP
*** Group 11 test agent was mixed with tumor cells on day of tumor implantation (DOI). TIW dosing initiated on Study Day 0.

In-Life:

[00254] *Tumor volumes:* Tumor volumes were measured three times weekly and a final tumor volume was measured on the day study reached endpoint.

[00255] *Animal weights:* Animals were weighed three times weekly and a final weight was taken on the day the study reached end point. If any animal exhibited >15% weight loss

when compared to day 0, all mice in that specific group were provided DietGel ad libitum equally for the remainder of the study. Fresh DietGel was supplied once daily.

[00256] *Clinical observations:* Animals were observed daily.

[00257] *Tumor ulceration:* Tumor ulceration was defined as a break in the skin through the basement membrane exposing the dermis and associated vasculature and nerves. Mice with ulceration greater than 50% of the tumor total surface area or impacting the overall health and well-being were euthanized. As antibiotic use is known to affect immuno-oncology drug efficacy, no antibiotic ointment was added to tumors.

Study Termination:

[00258] Individuals animals were removed from the study as their tumor volumes measured >2000 mm^3. Some animals were euthanized and had their tumors collected at our request on day 19 for potential future analysis.

Results

[00259] *Tumor Measurements:*

[00260] Comparison of tumor volumes (mm^3) from mice only treated with chemokines is shown in FIG. 15A. Monotherapy treatment with recombinant CCL5 (1 ug/dose) induced TGI when administered intratumorally for MC38 tumors that started at ~50 mm^3.

[00261] Additionally, it was also found that expression of the gene WARS correlated to immune infiltration in tumors, suggesting that WARS is also able to recruit immune to the tumor leading to an anti-tumor response.

[00262] Comparison of tumor volumes (mm^3) from mice treated with chemokines and aPD-L1 is shown in FIG. 15B.

[00263] *Body weights (% change).* The percent change in body weight for each treatment group is shown in FIG. 15C. CCL5 alone and CCL5 in combination with aPDL-1 had the greatest increase in body weight over time.

7. SEQUENCE

SEQ ID NO	SEQUENCE	
1	MKVSAAALAV ILIATALCAP ASASPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP AVVFVTRKNR QVCANPEKKW VREYINSLEM S	(CCL5)

SEQ ID NO	SEQUENCE	
2	SPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP AVVFVTRKNR QVCANPEKKW VREYINSLEM S	(CCL5 from R&D systems – 278RN)
3	MRIFAVFIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIEC KFPVEKQLDLAALIVYWEMEDKNIIQFVHGEEDLKVQHSS YRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYG GADYKRITVKVNAPYNKINQRILVVDPVTSEHELTCQAEG YPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTLRIN TTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPPNERTHLVI LGAILLCLGVALTFIFRLRKGRMMDVKKCGIQDTNSKKQS DTHLEET	(human PD-L1)
4	MQIPQAPWPVVWAVLQLGWRPGWFLDSPDRPWNPPTFSP ALLVVTEGDNATFTCSFSNTS ESFVLNWYRMSPSNQTDKLAAFPEDRSQPGQDCRFRVTQL PNGRDFHMSVVRARRNDSGT YLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPSPRP AGQFQTLVVGVVGGLLGS LVLLVWVLAVICSRAARGTIGARRTGQPLKEDPSAVPVFSV DYGELDFQWREKTPEPPVP CVPEQTEYATIVFPSGMGTSSPARRGSADGPRSAQPLRPED GHCSWPL	(human PD-1)
5	EIVMTQSPATLSLSPGERATLSCWASQSVSSSYLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLPYTFGQGTKLEIK	L101 (A101)
6	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPG KAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFA TYYCQQYNSYPYTFGQGTKLEIK	L102 (A102)
7	AIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQQPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQDYNYPPTFGQGTKVEIK	L103 (A103)
8	AIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQQPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQDYNYPPTFGQGTKVEIK	L104 (A104)
9	EIVMTQSPATLSLSPGERATLSCRASQSVSSTYLSWYQQKP GQAPRLLIFGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLPPTFGPGTKVDIK	L105 (A105)
10	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLFTFGPGTKVDIK	L106 (A106)
11	EIVMTQSPTTLSLSPGERATLSCRASQSVSSSYLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLRTFGQGTKVEIK	L107 (A107)
12	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPYTFGQGTKLEIK	L108 (A108)
13	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKP GQAPRLLMYGASTRATGIPARFSGSGSGTDFTLTISSLQPED FAVYYCQQDYNLPYTFGQGTKLEIK	L109 (A109)
14	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLPHTFGQGTKLEIK	L110 (A110)

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16	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPRTFGQGTKVEIK	L112 (A112)
17	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLITFGQGTRLEIK	L113 (A113)
18	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLPHTFGQGTKLEIK	L114 (A114)
19	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHDSYPLTFGGGTKVEIK	L115 (A115)
20	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPRTFGQGTKVEIK	L116 (A116)
21	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNTYPWTFGQGTKVEIK	L117 (A117)
22	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYNNWPYTFGQGTKLEIK	L118 (A118)
23	DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPG KAPKLLIYDASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA IYYCQQLNTYPLTFGGGTKVEIK	L119 (A119)
24	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPYTFGQGTKLEIK	L120 (A120)
25	DIQLTQSPPFLSASVGDRVTITCRASQGISSYLAWYQQKPG KAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQLNSYPFTFGQGTKLEIK	L121 (A121)
26	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE KAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQYNSYPPTVGGGTKVEIK	L122 (A122)
27	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPMFTFGQGTKLEIK	L123 (A123)
28	EIVMTQSPATLSLSPGERATLSCRASQSVSSSHLSWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQPEDF AVYYCQQDYNLLTFGGGTKVEIK	L124 (A124)
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30	QVQLVQSGAEVKKPGASVKVSCKASGFTFTSYDINWVRQA TGQGLEWMGWMHPNSGITGYAQKFQGRVTMTRNTSISTA YMELSSLSSEDTAVYFCARYYYVSGSYDYWGQGTLVTVSS A	H101 (A101)
31	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYDMSWVRQA PGKGLEWVSTISGSGGSTYYADSVKGRFTISRDNSKTTLYL QMISLRAEDTAVYYCAKAGFTMIVVAFDYWGQGTLVTVS SA	H102 (A102)

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32	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIWFDGNTKYYTDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDTTMVPMDVWGQGTTATVSSA	H103 (A103)
33	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIWFDGNTKYYTDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDITMVPMDVWGQGTTVTVSSA	H104 (A104)
34	QVQLVESGGGVVQPGRSLRLSCAASGFAFSSYGMHWVRQAPGKGLEWVALIWFDGNNKFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDTTAASFDYWGQGTLVTVSSA	H105 (A105)
35	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWFDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDKTVSPFDIWGQGTMVTVSSA	H106 (A106)
36	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYFCARDNWHDGGVDYWGQGTLVTVSSA	H107 (A107)
37	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGSTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVFYCARDDRIAVADYYYYFGMDVWGQGTTVTVSSA	H108 (A108)
38	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWFDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDVTTVPFDYWGQGTLVTVSSA	H109 (A109)
39	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGINKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDSTASPFDYWGQGTLVTVSSA	H110 (A110)
40	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWSDGSNKFYADSVKGRFTISRDNSKNTLFLQMSSLRAEDTAVYYCARDIAAAIDYWGQGTLVTVSSA	H111 (A111)
41	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKSYADSVKGRFTFSRDNSKNTLYLQMNSLRAEDTAVYYCARDMDYFGLDVWGQGTTVTVSSA	H112 (A112)
42	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIHYSGSTKYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARDRGIGAFDIWGQGTMVTVSSA	H113 (A113)
43	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSVKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTGVPFDYWGQGTLVTVSSA	H114 (A114)
44	QLQLQESGPGLVKPSETLSLTCTVSGGSFNRSNYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLKSRLTISADTSKTQFSLKRNSVTAADTAVYYCAREDIVVVPAAQPPHFYFGMDVWGQGTTVTVSSA	H115 (A115)
45	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSNDTLFLQMNSLRAEDTAVYYCARDFDWFGMDVWGQGTTVTVSSA	H116 (A116)

SEQ ID NO	SEQUENCE	
46	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYSWSWIRQPP GKGLEWIGYIYYSGSTNNNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYFCARDDGIAVAGYYFYYGLDVWGQGTTVT VSSA	H117 (A117)
47	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFALHWVRQA PGKGLEWVAVLWYDGISKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDVVGVHDAFDIWGQGTMVTV SSA	H118 (A118)
48	QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQ APGKGLEWVAVIWYDGSNKFYIDSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARGGAVAGTSWYYYYGMDVW GQGTTVTVSSA	H119 (A119)
49	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPP GKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARDDRIAVGPYYYYYGMDVWGQGTTV TVSSA	H120 (A120)
50	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVAVIWYDGSNKFYEDSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARGGVNWNDVGYYYYGMDVW GQGTTVTVSSA	H121 (A121)
51	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQA PGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTA YMELRSLRSDDTAVYYCARGFYYGSWYFDYWGQGTLVT VSSA	H122 (A122)
52	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQ APGQGLEWMGWISAYNGNTNYEQKVQGRVTMTTDTSTST AYMELRSLRSDDTAVYYCARSLTGLFDYWGQGTLVTVSS A	H123 (A123)
53	QLQLQESGPGLVKPSETLSLTCTVSGGSISNSSSFWGWIRQP PGKGLEWIGSIYYSGSTYYNPSLKSRVTMSVDTPKTQSSRK RSSVPAADTAVYYCARLGFGGFDYWGQGTLVTVSSA	H124 (A124)
54	QVQLVQSGAEVKKPGASVKVSCKASGFTFTSYDINWVRQA TGQGLEWMGWMHPKSGITGYAQKFQGRVTMTRNTSISTA YMELSNLSSEDTAVYFCARYNYVSGSYDYWGQGTLVTVS SA	H125 (A125)
55	QSVSSSY	CDR1-L1 (A101)
56	QGISNY	CDR1-L2 (A102)
57	QDIRND	CDR1-L3 (A103)
58	QDIRND	CDR1-L4 (A104)
59	QSVSSTY	CDR1-L5 (A105)
60	QSVSSSY	CDR1-L6 (A106)
61	QSVSSSY	CDR1-L7 (A107)
62	QGIRND	CDR1-L8 (A108)
63	QSVSSSY	CDR1-L9 (A109)

SEQ ID NO	SEQUENCE	
64	QSVSSSY	CDR1-L10 (A110)
65	QGIRND	CDR1-L11 (A111)
66	QGIRND	CDR1-L12 (A112)
67	QSVSSSY	CDR1-L13 (A113)
68	QSVSSSY	CDR1-L14 (A114)
69	QGIRND	CDR1-L15 (A115)
70	QGIRND	CDR1-L16 (A116)
71	QGIRND	CDR1-L17 (A117)
72	QSVSSN	CDR1-L18 (A118)
73	QGISSY	CDR1-L19 (A119)
74	QGIRND	CDR1-L20 (A120)
75	QGISSY	CDR1-L21 (A121)
76	QGISSW	CDR1-L22 (A122)
77	QGIRND	CDR1-L23 (A123)
78	QSVSSSH	CDR1-L24 (A124)
79	QSVSSSY	CDR1-L25 (A125)
80	GAS	CDR2-L1 (A101)
81	AAS	CDR2-L2 (A102)
82	AAS	CDR2-L3 (A103)
83	AAS	CDR2-L4 (A104)
84	GAS	CDR2-L5 (A105)
85	GAS	CDR2-L6 (A106)
86	GAS	CDR2-L7 (A107)
87	AAS	CDR2-L8 (A108)
88	GAS	CDR2-L9 (A109)
89	GAS	CDR2-L10 (A110)
90	AAS	CDR2-L11

SEQ ID NO	SEQUENCE	
		(A111)
91	AAS	CDR2-L12 (A112)
92	GAS	CDR2-L13 (A113)
93	GAS	CDR2-L14 (A114)
94	AAS	CDR2-L15 (A115)
95	AAS	CDR2-L16 (A116)
96	AAS	CDR2-L17 (A117)
97	GAS	CDR2-L18 (A118)
98	DAS	CDR2-L19 (A119)
99	AAS	CDR2-L20 (A120)
100	AAS	CDR2-L21 (A121)
101	AAS	CDR2-L22 (A122)
102	AAS	CDR2-L23 (A123)
103	GAS	CDR2-L24 (A124)
104	GAS	CDR2-L25 (A125)
105	QQDYNLPYT	CDR3-L1 (A101)
106	QQYNSYPYT	CDR3-L2 (A102)
107	LQDYNYPPT	CDR3-L3 (A103)
108	LQDYNYPPT	CDR3-L4 (A104)
109	QQDYNLPPT	CDR3-L5 (A105)
110	QQDYNLFT	CDR3-L6 (A106)
111	QQDYNLRT	CDR3-L7 (A107)
112	LQHNSYPYT	CDR3-L8 (A108)
113	QQDYNLPYT	CDR3-L9 (A109)
114	QQDYNLPHT	CDR3-L10 (A110)
115	LQDYNYPYT	CDR3-L11 (A111)
116	LQHNSYPRT	CDR3-L12 (A112)

SEQ ID NO	SEQUENCE	
117	QQDYNLIT	CDR3-L13 (A113)
118	QQDYNLPHT	CDR3-L14 (A114)
119	LQHDSYPLT	CDR3-L15 (A115)
120	LQHNSYPRT	CDR3-L16 (A116)
121	LQHNTYPWT	CDR3-L17 (A117)
122	QQYNNWPYT	CDR3-L18 (A118)
123	QQLNTYPLT	CDR3-L19 (A119)
124	LQHNSYPYT	CDR3-L20 (A120)
125	QQLNSYPFT	CDR3-L21 (A121)
126	QQYNSYPPT	CDR3-L22 (A122)
127	LQHNSYPMFT	CDR3-L23 (A123)
128	QQDYNLLT	CDR3-L24 (A124)
129	QQDYYLPYT	CDR3-L25 (A125)
130	GFTFTSYD	CDR1-H1 (A101)
131	GFTFSRYD	CDR1-H2 (A102)
132	GFTFSNYG	CDR1-H3 (A103)
133	GFTFSNYG	CDR1-H4 (A104)
134	GFAFSSYG	CDR1-H5 (A105)
135	GFTFSSYG	CDR1-H6 (A106)
136	GGSISSYY	CDR1-H7 (A107)
137	GYTFTSYG	CDR1-H8 (A108)
138	GFTFSSYG	CDR1-H9 (A109)
139	GFTFSSYG	CDR1-H10 (A110)
140	GFTFSSYG	CDR1-H11 (A111)
141	GFTFSSYG	CDR1-H12 (A112)
142	GGSISSYY	CDR1-H13 (A113)
143	GFTFSSYG	CDR1-H14

SEQ ID NO	SEQUENCE	
		(A114)
144	GGSFNRSNYY	CDR1-H15 (A115)
145	GFTFSSYG	CDR1-H16 (A116)
146	GGSISGYS	CDR1-H17 (A117)
147	GFTFSSFA	CDR1-H18 (A118)
148	GFTFSSYG	CDR1-H19 (A119)
149	GGSISSYY	CDR1-H20 (A120)
150	GFTFSSYG	CDR1-H21 (A121)
151	GYTFTSYG	CDR1-H22 (A122)
152	GYTFTNYG	CDR1-H23 (A123)
153	GGSISNSSSF	CDR1-H24 (A124)
154	GFTFTSYD	CDR1-H25 (A125)
155	MHPNSGIT	CDR2-H1 (A101)
156	ISGSGGST	CDR2-H2 (A102)
157	IWFDGNTK	CDR2-H3 (A103)
158	IWFDGNTK	CDR2-H4 (A104)
159	IWFDGNNK	CDR2-H5 (A105)
160	IWFDGSNK	CDR2-H6 (A106)
161	IFYSGST	CDR2-H7 (A107)
162	ISAYNGST	CDR2-H8 (A108)
163	IWFDGNNK	CDR2-H9 (A109)
164	IWYDGINK	CDR2-H10 (A110)
165	IWSDGSNK	CDR2-H11 (A111)
166	IWYDGSNK	CDR2-H12 (A112)
167	IHYSGST	CDR2-H13 (A113)
168	IWYDGSVK	CDR2-H14 (A114)
169	IYYSGST	CDR2-H15 (A115)

SEQ ID NO	SEQUENCE	
170	IWYDGSNK	CDR2-H16 (A116)
171	IYYSGST	CDR2-H17 (A117)
172	LWYDGISK	CDR2-H18 (A118)
173	IWYDGSNK	CDR2-H19 (A119)
174	IYYSGST	CDR2-H20 (A120)
175	IWYDGSNK	CDR2-H21 (A121)
176	ISAYNGNT	CDR2-H22 (A122)
177	ISAYNGNT	CDR2-H23 (A123)
178	IYYSGST	CDR2-H24 (A124)
179	MHPKSGIT	CDR2-H25 (A125)
180	ARYYYVSGSYDY	CDR3-H1 (A101)
181	AKAGFTMIVVAFDY	CDR3-H2 (A102)
182	ARDTTMVPMDV	CDR3-H3 (A103)
183	ARDITMVPMDV	CDR3-H4 (A104)
184	ARDTTAASFDY	CDR3-H5 (A105)
185	ARDKTVSPFDI	CDR3-H6 (A106)
186	ARDNWHDGGVDY	CDR3-H7 (A107)
187	ARDDRIAVADYYYYFGMDV	CDR3-H8 (A108)
188	ARDVTTVPFDY	CDR3-H9 (A109)
189	ARDSTASPFDY	CDR3-H10 (A110)
190	ARDIAAAIDY	CDR3-H11 (A111)
191	ARDMDYFGLDV	CDR3-H12 (A112)
192	ARDRGIGAFDI	CDR3-H13 (A113)
193	ARDRTGVPFDY	CDR3-H14 (A114)
194	AREDIVVVPAAQPPHFYFGMDV	CDR3-H15 (A115)
195	ARDFDWFGMDV	CDR3-H16 (A116)
196	ARDDGIAVAGYYFYYGLDV	CDR3-H17

SEQ ID NO	SEQUENCE	
		(A117)
197	ARDVVGVHDAFDI	CDR3-H18 (A118)
198	ARGGAVAGTSWYYYYGMDV	CDR3-H19 (A119)
199	ARDDRIAVGPYYYYYGMDV	CDR3-H20 (A120)
200	ARGGVNWNDVGYYYYGMDV	CDR3-H21 (A121)
201	ARGFYYGSWYFDY	CDR3-H22 (A122)
202	ARSLTGLFDY	CDR3-H23 (A123)
203	ARLGFGGFDY	CDR3-H24 (A124)
204	ARYNYVSGSYDY	CDR3-H25 (A125)
1462	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYVASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPLTFGGGTKVEIKR	L1 (A201)
1463	DIQMTQSPSSLSASVGDRVTITCRASQAIRNDLGWFQQKPG KAPKRLIYAASSLQSGVPLRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSFPWTFGQGTKVEIKR	L2 (A202)
1464	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHYIYPWTFGQGTKVEIKR	L3 (A203)
1465	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE KAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQYNSYPYTFGQGTKLEIKR	L4 (A204)
1466	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPG KAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQFNNYPWTFGQGTKVEIKR	L5 (A205)
1467	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLLYAASNLQLGVPSRFSGSGSETEFTLTISSLQPEDF ATYYCLQHNSYPWTFGQGTKVEIKR	L6 (A206)
1468	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGSSTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYNNWPYTFGQGTKLEIKR	L7 (A207)
1469	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPG QAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQRNTWPYTFGQGTKLEIKR	L8 (A208)
1470	AIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPG KAPKLLIYAASLLRSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQDNNYPRTFGQGTKVEIK	L9 (A209)
1471	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE KAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQYNSYPYTFGQGTKLEIK	L10 (A210)
1472	DIQMTQSPSSLSASVGDSITITCRASQGISSWLAWYQQKPEK APKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQFNSYPYTFGQGTKLEIK	L11 (A211)
1473	DIQMTQSPSSLSASVGDRVTVTCRSSQGIAHYLAWYQQKP GKVPKVLLYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPED	L12 (A212)

SEQ ID NO	SEQUENCE	
	VATYYCQKYNSAPYTFGQGTKLEIK	
1474	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYNNWPFTFGPGTKVDIK	L13 (A213)
1475	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYVASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPLTFGGGTKVEIK	L14 (A214)
1476	DIQMTQSPSTLSASVGDRVTITCRASQTISSWLAWYQQKPG TAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFA TYYCQQYNSYSYTFGQGTKLEIK	L15 (A215)
1477	DIQMTQSPSSLSASVGDRVTITCRTSQDIRNDLGWYQQKPG KAPKRLIYAVSSLQSGVPSRFSGSGSGTEFTFTISSLQPEDFA TYYCLQYNTYPFTFGPGTTVDIK	L16 (A216)
1478	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQYISYPWTFGQGTKVEIK	L17 (A217)
1479	AIRMTQSPSSFSASTGDRVTITCRASQGISSYLAWYQQKPG KAPTLLIYAASTLQSGVPSRFSGSGSGTDFTLTISCLQSEDFA TYYCQQYYSDPPTFGQGTKVEIK	L18 (A218)
1480	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQYKSYLYTFGQGTKLEIK	L19 (A219)
1481	DIQLTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPG KAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCHQLNSFPLTFGGGTKVEIK	L20 (A220)
1482	AIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPG KAPKLLICAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQDYIYPYTFGQGTKLEIK	L21 (A221)
1483	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPG KAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCLQHNSYPFTFGPGTKVEIK	L22 (A222)
1484	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFA VYYCQQYHNWPLTFGGGTKVEIK	L23 (A223)
1485	EIVMTQSPATLSVFPGERATLSCRASQSVSSNLGWYQQKPG QAPRLLMYGASTRVTGIPARFSGSGSGTEFTLTISSLQSEDF AVYYCQQYNTWPRTFGQGTKVEIK	L24 (A224)
1486	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPG QAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQRNNWPYTFGQGTKLEIK	L25 (A225)
1487	DIQMTQSPSSLSASVGDRVTISCRASQGISNYLAWYQQKPG KVPKVLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDV ATYYCQKYNSAPYTFGQGTKLEIK	L26 (A226)
1488	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPG KAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQFNDYALTFGGGTKVEIK	L27 (A227)
1489	AIQMTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPG KAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQDYNYPWTFGQGTKVEIK	L28 (A228)
1490	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQ APGKGLEWVAVIWYDGSNKYYTDSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAGGGNYYGDYWGQGTLVTVSS AKTT	H1 (A201)

SEQ ID NO	SEQUENCE	
1491	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVALISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGYFDPYGDYYYGMDVWGQGTTVTVSSAKTT	H2 (A202)
1492	QVQLVESGGGEVQPGRSLRLSCAASGFTFSDYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGGGSYWGDYWGQGTLVTVSSAKTT	H3 (A203)
1493	QVQLVQSGAEVKKPGASVKVSCKASGYTFATYGVSWVRQAPGQGLEWMGWISAYSDNINYAQNLQGRVTITTDTSTSTAYMELRSLRSDDTAVYYCARDGSHGDYYYGMDVWGQGTTVTVSSAKTT	H4 (A204)
1494	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGTHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRIYCSSTRCIGFGYYYYGMDVWGQGTTVTVSSAKTT	H5 (A205)
1495	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGGGNYWGDFWGQGTLVTVSSAKTT	H6 (A206)
1496	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGINWVRQAPGQGLEWMGWISAYNGNRNYAQNLQGRVTMTSDTSTNTAYMELRSLRSYDTAVYYCARDHYDILTGYYKGGFDYWGQGTLVTVSSAKTT	H7 (A207)
1497	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSIKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCANDILTGSFDYWGQGTLVTVSSAKTT	H8 (A208)
14984	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIWYDGTNKFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATNSDDYWGQGTLVTVSSA	H9 (A209)
1499	QVQLVQSGAEVKKPGASVKVSCKASGYTFAIYGISWVRQAPGQGLEWMGWISAYSDNSNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCVRDGSHGDYYYGMDVWGQGTTVTVSSA	H10 (A210)
1500	QVQLVQSGAEVKKPGASVKVSCRASGYTFTNYGISWVRQAPGQGLEWMGWISVYSDNTHYPQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDGSHGDYYYVMDLWGQGTTVTVSSA	H11 (A211)
1501	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCVCNPFDYWGQGTLVTVSSA	H12 (A212)
1502	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWISAHNGNTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCVRDGAVADYYYGMDVWGQGTTVTVSSA	H13 (A213)
1503	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDQWYYFVYWGQGTLVTVSSA	H14 (A214)
1504	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISEDTSKNQFSLKLSSVTAADTAVYYCARDEGATFFDYWGQGTLVTVSSA	H15 (A215)
1505	QVQLVESGGGVVQPGRSLTLSCAASGFTFSNYGMYWVRQ	H16

SEQ ID NO	SEQUENCE	
	APGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCAGGGSYSGDYWGQGTLVTVSS A	(A216)
1506	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVAVIWYDGSNQYYADSVKGRFTISRDNSKNT LFLQMNSLRAEDTAVYFCAGGGNYYGDFWGQGTLVTVSS A	H17 (A217)
1507	QVQLVQSGTEVKKPGASVKVSCQASGYTFTSYDISWVRRA PGQGLEWMGWISAYNGNTNYAQKLQGRVTLTTDTSTSTA YMELRSLRSDDTAVYYCARRYYDILTEGGYYYVLDVWGQ GTTVTVSSA	H18 (A218)
1508	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMYWVRQ APGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCAGGGDILTGDYWGQGTLVTVS SA	H19 (A219)
1509	EVQLVESGGGLVQPGGSLRLSCAASGFTFSFYDMHWVRQ AKGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLY LQMNSLRAGDTAVYYCARGYCSTTNCFADYFDYWGQGTL VTVSSA	H20 (A220)
1510	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQ APGQGLEWMGIINPSGSSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARYGVWGSYRSLDYWGQGTLVT VSSA	H21 (A221)
1511	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQ APGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARLYYYDSSGYYPDAFDIWGQ GTMVTVSSA	H22 (A222)
1512	QVQLVESGGGVVQPGRSLRLSCVASGFTFSNYGMHWVRQ APGKGLEWVAIIWYDGSIKYYADSVKGRFTISRDNSKNTLH LQMNSLRAEDTAVYYCARWGIYFDYWGQGTLVTVSSA	H23 (A223)
1513	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDSGMHWVRQ APGKGLEWVAVIWYDGSKKYYVDSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCATEGDYWGQGTLVTVSSA	H24 (A224)
1514	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVGVIWYDGSIKYYADSVKGRFTISRDNSMNTL NLQMNSLRAEDTAVYYCAGDILTGSFDYWGQGTLVTVSS A	H25 (A225)
1515	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDYGMHWVRQ APGKGLEWVAVIWYDGSNKYYTDSVKGRFTISRDNSKNTL YLQMSSLRAEDAAVYYCAVNPFDYWGQGTLVTVSSA	H26 (A226)
1516	QVQLVQSGAELVRPGTSVKLSCRASGYTFTTYWMHWVKQ RPGQGLEWIGVIDPSDSYTYYNQKFKGKATLTVDTSSSTAY MQLSSLTSEDSAVYFCARNWDYWGQGTTLTVSSA	H27 (A227)
1517	QVQLVESGGGLVKPGGSLKLSCAASGFTFSDYGMHWVRQ APEKGLEWVAYISSGSFAIYYADTVRGRFTISRDSAKNTLFL QMTSLRSEDTAMYYCARRGPYPYYYSMDYWGQGTSVTV SSA	H28 (A228)
1518	QGIRND	CDR1-L1 (A201)
1519	QAIRND	CDR1-L2 (A202)
1520	QGIRNE	CDR1-L3 (A203)

SEQ ID NO	SEQUENCE	
1521	QGISSW	CDR1-L4 (A204)
1522	QGISSA	CDR1-L5 (A205)
1523	QGIRND	CDR1-L6 (A206)
1524	QSVSSN	CDR1-L7 (A207)
1525	QSVSSY	CDR1-L8 (A208)
1526	QDIRND	CDR1-L9 (A209)
1527	QGISSW	CDR1-L10 (A210)
1528	QGISSW	CDR1-L11 (A211)
1529	QGIAHY	CDR1-L12 (A212)
1530	QSVSSN	CDR1-L13 (A213)
1531	QGIRND	CDR1-L14 (A214)
1532	QTISSW	CDR1-L15 (A215)
1533	QDIRND	CDR1-L16 (A216)
1534	QGIRND	CDR1-L17 (A217)
1535	QGISSY	CDR1-L18 (A218)
1536	QGIRND	CDR1-L19 (A219)
1537	QGISNY	CDR1-L20 (A220)
1538	QGIRNE	CDR1-L21 (A221)
1539	QGIRND	CDR1-L22 (A222)
1540	QSVSSN	CDR1-L23 (A223)
1541	QSVSSN	CDR1-L24 (A224)
1542	QSVSSY	CDR1-L25 (A225)
1543	QGISNY	CDR1-L26 (A226)
1544	QGISSA	CDR1-L27 (A227)
1545	QGISSA	CDR1-L28 (A228)
1546	VAS	CDR2-L1 (A201)
1547	AAS	CDR2-L2

SEQ ID NO	SEQUENCE	
		(A202)
1548	AAS	CDR2-L3 (A203)
1549	AAS	CDR2-L4 (A204)
1550	DAS	CDR2-L5 (A205)
1551	AAS	CDR2-L6 (A206)
1552	GSS	CDR2-L7 (A207)
1553	DAS	CDR2-L8 (A208)
1554	AAS	CDR2-L9 (A209)
1555	AAS	CDR2-L10 (A210)
1556	AAS	CDR2-L11 (A211)
1557	AAS	CDR2-L12 (A212)
1558	GAS	CDR2-L13 (A213)
1558	VAS	CDR2-L14 (A214)
1559	KAS	CDR2-L15 (A215)
1560	AVS	CDR2-L16 (A216)
1562	AAS	CDR2-L17 (A217)
1563	AAS	CDR2-L18 (A218)
1564	AAS	CDR2-L19 (A219)
1565	AAS	CDR2-L20 (A220)
1566	AAS	CDR2-L21 (A221)
1567	AAS	CDR2-L22 (A222)
1568	GAS	CDR2-L23 (A223)
1569	GAS	CDR2-L24 (A224)
1570	DAS	CDR2-L25 (A225)
1571	GAS	CDR2-L26 (A226)
1572	DAS	CDR2-L27 (A227)
1573	AAS	CDR2-L28 (A228)

SEQ ID NO	SEQUENCE	
1574	LQHNSYPLT	CDR3-L1 (A201)
1575	LQHNSFPWT	CDR3-L2 (A202)
1576	LQHYIYPWT	CDR3-L3 (A203)
1577	QQYNSYPYT	CDR3-L4 (A204)
1578	QQFNNYPWT	CDR3-L5 (A205)
1579	LQHNSYPWT	CDR3-L6 (A206)
1580	QQYNNWPYT	CDR3-L7 (A207)
1581	QQRNTWPYT	CDR3-L8 (A208)
1582	LQDNNYPRT	CDR3-L9 (A209)
1583	QQYNSYPYT	CDR3-L10 (A210)
1584	QQFNSYPYT	CDR3-L11 (A211)
1585	QKYNSAPYT	CDR3-L12 (A212)
1586	QQYNNWPFT	CDR3-L13 (A213)
1587	LQHNSYPLT	CDR3-L14 (A214)
1588	QQYNSYSYT	CDR3-L15 (A215)
1589	LQYNTYPFT	CDR3-L16 (A216)
1590	LQYISYPWT	CDR3-L17 (A217)
1591	QQYYSDPPT	CDR3-L18 (A218)
1592	LQYKSYLYT	CDR3-L19 (A219)
1593	HQLNSFPLT	CDR3-L20 (A220)
1594	LQDYIYPYT	CDR3-L21 (A221)
1595	LQHNSYPFT	CDR3-L22 (A222)
1596	QQYHNWPLT	CDR3-L23 (A223)
1597	QQYNTWPRT	CDR3-L24 (A224)
1598	QQRNNWPYT	CDR3-L25 (A225)
1599	QKYNSAPYT	CDR3-L26 (A226)
1600	QQFNDYALT	CDR3-L27

SEQ ID NO	SEQUENCE	
		(A227)
1601	LQDYNYPWT	CDR3-L28 (A228)
1602	GFTFSNYG	CDR1-H1 (A201)
1603	GFTFSSYG	CDR1-H2 (A202)
1604	GFTFSDYG	CDR1-H3 (A203)
1605	GYTFATYG	CDR1-H4 (A204)
1606	GFTFSNYG	CDR1-H5 (A205)
1607	GFTFSSYG	CDR1-H6 (A206)
1608	GYTFTSYG	CDR1-H7 (A207)
1609	GFTFSSYG	CDR1-H8 (A208)
1610	GFTFSNYG	CDR1-H9 (A209)
1611	GYTFAIYG	CDR1-H10 (A210)
1612	GYTFTNYG	CDR1-H11 (A211)
1613	GFTFSSYG	CDR1-H12 (A212)
1614	GYTFTTYG	CDR1-H13 (A213)
1615	GFTFSSYA	CDR1-H14 (A214)
1616	GGSISSYY	CDR1-H15 (A215)
1617	GFTFSNYG	CDR1-H16 (A216)
1618	GFTFSSYG	CDR1-H17 (A217)
1619	GYTFTSYD	CDR1-H18 (A218)
1620	GFTFSNYG	CDR1-2H19 (A219)
1621	GFTFSFYD	CDR1-H20 (A220)
1622	GYTFTSYY	CDR1-H21 (A221)
1623	GFTFSNYG	CDR1-H22 (A222)
1624	GFTFSNYG	CDR1-H23 (A223)
1625	GFTFSDSG	CDR1-H24 (A224)
1626	GFTFSSYG	CDR1-H25

SEQ ID NO	SEQUENCE	
		(A225)
1627	GFTFSDYG	CDR1-H26 (A226)
1628	GYTFTTYW	CDR1-H27 (A227)
1629	GFTFSDYG	CDR1-H28 (A228)
1630	IWYDGSNK	CDR2-H1 (A201)
1631	ISYDGSNK	CDR2-H2 (A202)
1632	IWYDGSNK	CDR2-H3 (A203)
1633	ISAYSDNI	CDR2-H4 (A204)
1634	IWYDGSNK	CDR2-H5 (A205)
1635	IWYDGSNK	CDR2-H6 (A206)
1636	ISAYNGNR	CDR2-H7 (A207)
1637	IWYDGSIK	CDR2-H8 (A208)
1638	IWYDGTNK	CDR2-H9 (A209)
1639	ISAYSDNS	CDR2-H10 (A210)
1640	ISVYSDNT	CDR2-H11 (A211)
1641	IWYDGSNK	CDR2-H12 (A212)
1642	ISAHNGNT	CDR2-H13 (A213)
1643	ISGSGGST	CDR2-H14 (A214)
1644	IYYSGST	CDR2-H15 (A215)
1645	IWYDGSNK	CDR2-H16 (A216)
1646	IWYDGSNQ	CDR2-H17 (A217)
1647	ISAYNGNT	CDR2-H18 (A218)
1648	IWYDGSNK	CDR2-H19 (A219)
1649	IGTAGDT	CDR2-H20 (A220)
1650	INPSGSST	CDR2-H21 (A221)
1651	IWYDGSNK	CDR2-H22 (A222)
1652	IWYDGSIK	CDR2-H23 (A223)

SEQ ID NO	SEQUENCE	
1653	IWYDGSKK	CDR2-H24 (A224)
1654	IWYDGSIK	CDR2-H25 (A225)
1655	IWYDGSNK	CDR2-H26 (A226)
1656	IDPSDSYT	CDR2-H27 (A227)
1657	ISSGSFAI	CDR2-H28 (A228)
1658	AGGGNYYGDY	CDR3-H1 (A201)
1659	ARGGYFDPYGDYYYGMDV	CDR3-H2 (A202)
1660	AGGGSYWGDY	CDR3-H3 (A203)
1661	ARDGSHGDYYYGMDV	CDR3-H4 (A204)
1662	ARDRIYCSSTRCIGFGYYYYGMDV	CDR3-H5 (A205)
1663	AGGGNYWGDF	CDR3-H6 (A206)
1664	ARDHYDILTGYYKGGFDY	CDR3-H7 (A207)
1665	ANDILTGSFDY	CDR3-H8 (A208)
1666	ATNSDDY	CDR3-H9 (A209)
1667	VRDGSHGDYYYGMDV	CDR3-H10 (A210)
1668	ARDGSHGDYYYVMDL	CDR3-H11 (A211)
1669	VCNPFDY	CDR3-H12 (A212)
1670	VRDGAVADYYYGMDV	CDR3-H13 (A213)
1671	AKDQWYYFVY	CDR3-H14 (A214)
1672	ARDEGATFFDY	CDR3-H15 (A215)
1673	AGGGSYSGDY	CDR3-H16 (A216)
1674	AGGGNYYGDF	CDR3-H17 (A217)
1675	ARRYYDILTEGGYYYVLDV	CDR3-H18 (A218)
1676	AGGGDILTGDY	CDR3-H19 (A219)
1677	ARGYCSTTNCFADYFDY	CDR3-H20 (A220)
1678	ARYGVWGSYRSLDY	CDR3-H21 (A221)
1679	ARLYYYDSSGYYPDAFDI	CDR3-H22

SEQ ID NO	SEQUENCE	
		(A222)
1680	ARWGIYFDY	CDR3-H23 (A223)
1681	ATEGDY	CDR3-H24 (A224)
1682	AGDILTGSFDY	CDR3-H25 (A225)
1683	AVNPFDY	CDR3-H26 (A226)
1684	ARNWDY	CDR3-H27 (A227)
1685	ARRGPYPYYYSMDY	CDR3-H28 (A228)

8. INCORPORATION BY REFERENCE

[00264] All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entireties for all purposes to the same extent as if each individual publication, patent, patent application or other document were individually indicated to be incorporated by reference for all purposes.

9. EQUIVALENTS

[00265] While various specific embodiments have been illustrated and described, the above specification is not restrictive. It will be appreciated that various changes can be made without departing from the spirit and scope of the invention(s). Many variations will become apparent to those skilled in the art upon review of this specification.

Table 1

gene	p_val	p_val_adj	avg_logFC	pct.1	pct.2	cell	comparison
AY036118	5.95E-300	1.06E-295	-1.32	0.63	0.998	B cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	3.08E-255	5.49E-251	-1.48	0.65	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	4.87E-178	8.67E-174	-1.16	0.87	0.988	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Gm42418	1.05E-176	1.87E-172	-1.11	1.00	1	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rps29	1.69E-174	3.01E-170	-0.35	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	7.58E-174	1.35E-169	-0.70	0.59	0.876	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps27	3.49E-166	6.22E-162	-0.38	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rps27	3.12E-160	5.56E-156	0.34	1.00	1	B cells	aPD-L1 + aTGF-β vs aTGF-β
AY036118	2.08E-147	3.7E-143	1.17	1.00	0.789	T cells	aPD-L1 vs PBS
Gm42418	2.19E-145	3.91E-141	-0.53	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	1.41E-139	2.52E-135	1.01	0.99	0.904	Neutrophils	aPD-L1 vs PBS
Rpl41	1.31E-138	2.33E-134	0.37	1.00	1	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rps27	2.69E-123	4.79E-119	0.76	1.00	1	B cells	aPD-L1 vs PBS
Gm42418	2.47E-121	4.41E-117	-0.68	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl39	2.01E-117	3.59E-113	0.77	1.00	1	B cells	aPD-L1 vs PBS
Rpl30	1.07E-115	1.9E-111	0.33	1.00	0.999	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	3.12E-115	5.56E-111	1.22	1.00	0.707	B cells	aPD-L1 vs PBS
Rps21	1.62E-113	2.89E-109	0.70	1.00	1	B cells	aPD-L1 vs PBS
Rpl39	8.09E-113	1.44E-108	-0.34	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl37a	2.32E-112	4.13E-108	0.67	1.00	0.998	T cells	aPD-L1 vs PBS
Rpl37a	4.14E-112	7.38E-108	0.70	1.00	1	B cells	aPD-L1 vs PBS
Rps29	1.58E-109	2.82E-105	0.57	1.00	1	B cells	aPD-L1 vs PBS
Rpl39	2.50E-106	4.45E-102	0.73	1.00	0.998	T cells	aPD-L1 vs PBS
Gm42418	9.98E-105	1.78E-100	-0.44	1.00	1	Tumor_cells	aTGF-β vs PBS
Gm42418	9.69E-103	1.727E-98	0.85	1.00	1	Tumor_cells	aPD-L1 vs PBS
Rps27	1.39E-102	2.47E-98	0.74	1.00	1	T cells	aPD-L1 vs PBS
Rps21	3.58E-102	6.375E-98	0.30	1.00	1	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl39	1.34E-100	2.397E-96	0.47	1.00	0.998	T cells	aPD-L1 + aTGF-β vs PBS
Rpl35a	1.67E-100	2.974E-96	0.60	1.00	0.997	B cells	aPD-L1 vs PBS
Rpl37a	3.16E-100	5.629E-96	0.31	1.00	0.998	B cells	aPD-L1 + aTGF-β vs aTGF-β
Irf1	8.74E-100	1.557E-95	0.41	0.64	0.334	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps21	5.13E-99	9.151E-95	-0.29	1.00	0.999	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl39	3.98E-98	7.103E-94	0.31	1.00	0.999	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl37a	5.62E-98	1.001E-93	-0.30	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rps28	8.97E-98	1.599E-93	-0.40	0.96	0.997	B cells	aPD-L1 + aTGF-β vs aPD-L1
Cxcl1	2.38E-96	4.235E-92	0.56	0.80	0.537	Tumor_cells	aPD-L1 + aTGF-β vs PBS
AY036118	5.50E-96	9.798E-92	-0.50	0.70	0.876	Tumor_cells	aTGF-β vs PBS
Rpl36	6.17E-96	1.099E-91	0.58	1.00	0.995	T cells	aPD-L1 vs PBS
Rpl37	2.03E-95	3.611E-91	0.60	1.00	0.995	T cells	aPD-L1 vs PBS
Rpl37	3.20E-94	5.713E-90	0.64	1.00	1	B cells	aPD-L1 vs PBS
Gm10076	8.07E-94	1.439E-89	0.50	0.87	0.558	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps21	9.19E-94	1.638E-89	0.63	1.00	1	T cells	aPD-L1 vs PBS
S100a6	2.56E-93	4.558E-89	0.36	1.00	1	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl38	2.61E-93	4.661E-89	-0.33	1.00	0.999	B cells	aPD-L1 + aTGF-β vs aPD-L1
Nfkbia	3.53E-93	6.285E-89	0.42	0.92	0.747	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Zfand5	1.64E-92	2.926E-88	0.42	0.71	0.473	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Gm42418	2.75E-91	4.908E-87	-0.60	1.00	1	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rpl36	1.18E-90	2.098E-86	0.31	1.00	0.998	B cells	aPD-L1 + aTGF-β vs aTGF-β
Irf1	4.38E-87	7.81E-83	0.34	0.64	0.398	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
AY036118	9.76E-87	1.739E-82	-1.34	0.65	0.989	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Rpl36	4.58E-86	8.16E-82	0.57	1.00	0.997	B cells	aPD-L1 vs PBS
Rpl37a	3.28E-85	5.838E-81	0.42	1.00	0.998	T cells	aPD-L1 + aTGF-β vs PBS
Rps29	3.29E-84	5.865E-80	0.59	1.00	0.998	T cells	aPD-L1 vs PBS
Rpl41	4.18E-84	7.446E-80	0.58	1.00	0.997	B cells	aPD-L1 vs PBS
Nfkbia	4.45E-84	7.937E-80	0.35	0.92	0.847	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Actb	6.98E-84	1.244E-79	-0.37	1.00	1	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rps15a	4.18E-83	7.456E-79	0.29	1.00	0.994	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl34	2.85E-82	5.076E-78	0.49	1.00	1	B cells	aPD-L1 vs PBS
Rpl38	5.49E-82	9.785E-78	0.56	1.00	0.991	B cells	aPD-L1 vs PBS
Cxcl1	9.25E-82	1.648E-77	0.48	0.80	0.639	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl37	3.51E-81	6.252E-77	0.28	1.00	1	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rps29	2.00E-80	3.562E-76	-0.41	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl38	1.72E-79	3.058E-75	0.53	1.00	0.99	T cells	aPD-L1 vs PBS
Zfand5	1.96E-79	3.493E-75	0.34	0.71	0.523	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Gm10076	3.72E-79	6.623E-75	0.58	0.87	0.586	T cells	aPD-L1 + aTGF-β vs PBS
Rpl41	5.38E-78	9.599E-74	0.50	1.00	0.998	T cells	aPD-L1 vs PBS
Rps27	3.61E-77	6.441E-73	0.39	1.00	1	B cells	aPD-L1 + aTGF-β vs PBS
Rpl35a	1.05E-76	1.88E-72	0.29	1.00	0.989	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rps27	1.37E-76	2.449E-72	-0.39	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl37	2.63E-76	4.697E-72	0.41	1.00	0.995	T cells	aPD-L1 + aTGF-β vs PBS
Gm42418	5.66E-76	1.008E-71	0.54	1.00	1	Neutrophils	aPD-L1 vs PBS
Rpl36	2.35E-75	4.191E-71	0.39	1.00	0.995	T cells	aPD-L1 + aTGF-β vs PBS
Rpl35a	3.57E-74	6.369E-70	-0.26	1.00	0.999	B cells	aPD-L1 + aTGF-β vs aPD-L1
Actg1	4.91E-74	8.756E-70	-0.34	0.98	0.992	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Sgk1	5.10E-74	9.084E-70	0.40	0.75	0.501	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl35a	1.49E-73	2.647E-69	0.53	1.00	0.995	T cells	aPD-L1 vs PBS

Rpl35	2.84E-73	5.057E-69	0.57	1.00	0.986	B cells	aPD-L1 vs PBS
Rpl35	3.91E-73	6.977E-69	0.60	1.00	0.955	T cells	aPD-L1 vs PBS
Rpl37a	1.88E-72	3.348E-68	0.32	1.00	1	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps28	4.85E-71	8.648E-67	0.60	1.00	0.966	T cells	aPD-L1 vs PBS
Ifrd1	2.91E-69	5.186E-65	0.37	0.80	0.614	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Mt2	4.55E-69	8.106E-65	0.34	0.76	0.568	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl37	1.14E-68	2.024E-64	-0.26	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rps21	2.92E-68	5.211E-64	0.41	1.00	1	B cells	aPD-L1 + aTGF-β vs PBS
Rpl39	1.11E-67	1.987E-63	0.33	1.00	1	T cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl22l1	2.16E-67	3.857E-63	0.32	0.99	0.952	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	4.52E-67	8.061E-63	-1.56	0.84	1	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Rpl39	1.81E-65	3.22E-61	0.43	1.00	1	B cells	aPD-L1 + aTGF-β vs PBS
Rpl34	2.51E-65	4.477E-61	0.42	1.00	1	T cells	aPD-L1 vs PBS
Hspa1b	7.83E-65	1.395E-60	0.39	0.82	0.616	Tumor_cells	aTGF-β vs PBS
Rps27	1.80E-63	3.211E-59	0.59	0.99	0.983	Neutrophils	aPD-L1 vs PBS
Irf1	4.81E-63	8.57E-59	0.72	0.69	0.375	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rplp2	4.95E-62	8.824E-58	-0.25	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl39	1.31E-61	2.341E-57	0.38	0.99	0.98	Macrophages	aPD-L1 + aTGF-β vs PBS
Smad7	1.79E-61	3.198E-57	-0.59	0.65	0.857	T cells	aPD-L1 + aTGF-β vs aPD-L1
Tmsb10	2.93E-61	5.227E-57	0.61	0.97	0.917	Macrophages	aPD-L1 + aTGF-β vs PBS
Sqstm1	4.10E-61	7.309E-57	0.30	0.69	0.465	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl37a	3.09E-60	5.512E-56	0.40	1.00	1	B cells	aPD-L1 + aTGF-β vs PBS
Rps15a	4.35E-60	7.751E-56	0.37	1.00	1	B cells	aPD-L1 vs PBS
Gm10076	7.72E-60	1.376E-55	0.55	0.90	0.586	T cells	aPD-L1 vs PBS
Gm42418	1.12E-59	1.99E-55	-0.26	1.00	1	Tumor_cells	aPD-L1 + aTGF-β vs PBS
B2m	1.15E-59	2.053E-55	-0.35	1.00	0.999	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl35	1.94E-59	3.464E-55	-0.28	0.99	0.998	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rps28	4.38E-59	7.813E-55	-0.41	0.98	0.999	T cells	aPD-L1 + aTGF-β vs aPD-L1
Dennd4a	5.38E-59	9.592E-55	0.44	0.78	0.528	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rps29	1.06E-58	1.883E-54	-0.50	0.98	0.995	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Actb	1.21E-58	2.162E-54	-0.27	1.00	1	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl36a	1.22E-58	2.178E-54	0.54	0.99	0.954	B cells	aPD-L1 vs PBS
H2-K1	2.47E-58	4.4E-54	0.45	1.00	0.989	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl38	1.00E-57	1.789E-53	0.26	1.00	0.986	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rps28	1.31E-57	2.338E-53	0.52	1.00	0.949	B cells	aPD-L1 vs PBS
Irf1	2.74E-57	4.892E-53	0.56	0.55	0.22	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl37a	4.39E-57	7.828E-53	0.31	1.00	1	T cells	aPD-L1 + aTGF-β vs aTGF-β
Rplp2	5.22E-57	9.311E-53	0.42	1.00	1	B cells	aPD-L1 vs PBS
Cxcl2	5.44E-57	9.696E-53	0.58	0.48	0.267	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Nfkbiz	5.88E-57	1.048E-52	0.29	0.53	0.305	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl37a	9.28E-57	1.655E-52	0.49	1.00	1	Macrophages	aPD-L1 vs PBS
Igkc	1.15E-56	2.05E-52	0.44	0.28	0.015	Neutrophils	aPD-L1 vs PBS
Gm10076	1.24E-56	2.205E-52	0.36	0.83	0.644	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rps29	2.01E-56	3.575E-52	0.55	1.00	0.977	Neutrophils	aPD-L1 vs PBS
Rpl37	2.28E-56	4.069E-52	0.31	1.00	0.99	T cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl41	3.81E-56	6.794E-52	-0.25	1.00	1	B cells	aPD-L1 + aTGF-β vs aPD-L1
Ccnl1	4.48E-56	7.992E-52	0.27	0.51	0.285	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps21	1.20E-55	2.144E-51	0.32	1.00	0.999	T cells	aPD-L1 + aTGF-β vs aTGF-β
Uba52	1.78E-55	3.169E-51	0.53	0.74	0.362	T cells	aPD-L1 vs PBS
Mt2	4.90E-55	8.737E-51	0.35	0.76	0.561	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl34	4.99E-55	8.894E-51	0.30	1.00	1	T cells	aPD-L1 + aTGF-β vs PBS
Gm10076	1.18E-54	2.098E-50	0.62	0.91	0.49	B cells	aPD-L1 vs PBS
Dnajb1	1.36E-54	2.429E-50	0.48	0.80	0.647	Tumor_cells	aTGF-β vs PBS
Hspa1b	2.56E-54	4.571E-50	-0.30	0.67	0.818	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl30	4.57E-54	8.153E-50	0.37	1.00	1	B cells	aPD-L1 vs PBS
Rplp2	1.70E-53	3.024E-49	0.40	1.00	0.994	T cells	aPD-L1 vs PBS
S100a4	2.05E-53	3.652E-49	0.38	0.97	0.912	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Cthrc1	3.20E-53	5.696E-49	-0.40	0.45	0.635	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps21	3.54E-53	6.311E-49	0.33	1.00	1	T cells	aPD-L1 + aTGF-β vs PBS
Rpl41	7.65E-53	1.364E-48	0.34	1.00	0.998	T cells	aPD-L1 + aTGF-β vs PBS
Rps27	7.91E-53	1.41E-48	0.35	1.00	1	T cells	aPD-L1 + aTGF-β vs PBS
Hspb1	1.00E-52	1.782E-48	-0.35	0.88	0.924	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl36	1.19E-52	2.123E-48	0.29	1.00	0.999	T cells	aPD-L1 + aTGF-β vs aTGF-β
Irf1	1.29E-52	2.297E-48	0.42	0.48	0.212	B cells	aPD-L1 + aTGF-β vs aTGF-β
Eno1	2.10E-52	3.752E-48	-0.26	0.70	0.84	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Tmsb10	2.41E-52	4.29E-48	0.36	1.00	0.998	T cells	aPD-L1 + aTGF-β vs PBS
Fos	2.70E-52	4.817E-48	0.34	0.88	0.694	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Gm47283	2.91E-52	5.193E-48	-0.49	0.60	0.833	T cells	aPD-L1 + aTGF-β vs aPD-L1
Gm10076	3.69E-52	6.582E-48	0.60	0.83	0.49	B cells	aPD-L1 + aTGF-β vs PBS
Rpl37	7.52E-52	1.34E-47	0.29	0.99	0.996	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl38	1.39E-51	2.485E-47	-0.30	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Ltb	1.95E-51	3.483E-47	-0.38	0.60	0.792	B cells	aPD-L1 + aTGF-β vs aTGF-β
Ubc	2.54E-51	4.528E-47	0.29	0.87	0.718	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps27	3.72E-51	6.629E-47	0.32	1.00	1	T cells	aPD-L1 + aTGF-β vs aTGF-β
Rel	4.88E-51	8.696E-47	0.39	0.85	0.675	B cells	aPD-L1 + aTGF-β vs aTGF-β
Spp1	5.50E-51	9.801E-47	0.46	0.99	0.968	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Lars2	6.56E-51	1.169E-46	-0.35	0.31	0.612	B cells	aPD-L1 + aTGF-β vs aPD-L1
Mt1	8.76E-51	1.561E-46	0.28	0.94	0.836	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps27	9.18E-51	1.637E-46	0.64	0.99	0.974	Macrophages	aPD-L1 vs PBS
Pfn1	1.65E-50	2.95E-46	0.44	0.98	0.976	T cells	aPD-L1 + aTGF-β vs aPD-L1
B2m	4.74E-50	8.455E-46	0.42	1.00	0.998	Neutrophils	aPD-L1 vs PBS
Rpl35a	4.80E-50	8.555E-46	0.35	1.00	0.997	B cells	aPD-L1 + aTGF-β vs PBS
Rps21	5.12E-50	9.125E-46	-0.29	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Nupr1	7.55E-50	1.346E-45	0.31	0.78	0.606	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Fos	9.99E-50	1.78E-45	0.35	0.86	0.694	Tumor_cells	aTGF-β vs PBS
Tmsb10	1.29E-49	2.304E-45	0.42	1.00	0.998	T cells	aPD-L1 vs PBS

mt-Atp8	3.55E-49	6.323E-45	0.46	0.65	0.262	T cells	aPD-L1 vs PBS
Hspa1b	6.26E-49	1.116E-44	-0.59	0.41	0.653	B cells	aPD-L1 + aTGF-β vs aTGF-β
Hspb1	6.61E-49	1.178E-44	0.38	0.92	0.87	Tumor_cells	aTGF-β vs PBS
Dusp1	6.81E-49	1.214E-44	0.36	0.82	0.664	Tumor_cells	aTGF-β vs PBS
Rpl36a	7.50E-49	1.338E-44	0.49	0.99	0.954	T cells	aPD-L1 vs PBS
Gm42418	4.24E-48	7.55E-44	0.44	1.00	1	B cells	aPD-L1 vs PBS
Rpl37	1.09E-47	1.936E-43	0.37	1.00	1	B cells	aPD-L1 + aTGF-β vs PBS
Tpi1	2.00E-47	3.572E-43	-0.26	0.92	0.961	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Gm10076	2.60E-47	4.637E-43	0.40	0.87	0.682	T cells	aPD-L1 + aTGF-β vs aTGF-β
Gm10076	4.41E-47	7.863E-43	0.34	0.87	0.678	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Tmsb10	1.25E-46	2.226E-42	0.74	0.97	0.917	Macrophages	aPD-L1 vs PBS
Kdm6b	1.25E-46	2.232E-42	0.37	0.60	0.342	B cells	aPD-L1 + aTGF-β vs aTGF-β
Igkc	1.46E-46	2.606E-42	0.41	0.30	0.008	T cells	aPD-L1 vs PBS
Pgk1	2.04E-46	3.629E-42	-0.28	0.91	0.959	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps23	3.12E-46	5.555E-42	0.32	1.00	1	B cells	aPD-L1 vs PBS
Pnrc1	4.68E-46	8.347E-42	0.27	0.68	0.502	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Egr1	6.26E-46	1.117E-41	0.28	0.81	0.649	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Vps37b	6.62E-46	1.179E-41	0.47	0.59	0.35	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl37a	7.03E-46	1.253E-41	0.56	0.95	0.914	Neutrophils	aPD-L1 vs PBS
Cd79b	8.62E-46	1.536E-41	-0.36	0.76	0.861	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl36	1.66E-45	2.959E-41	0.35	1.00	0.997	B cells	aPD-L1 + aTGF-β vs PBS
Lars2	1.91E-45	3.4E-41	-0.54	0.40	0.668	T cells	aPD-L1 + aTGF-β vs aPD-L1
H2-D1	3.39E-45	6.036E-41	0.38	1.00	0.999	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rps27	3.58E-45	6.378E-41	0.35	0.99	0.974	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps21	5.13E-45	9.151E-41	0.30	0.99	0.982	Macrophages	aPD-L1 + aTGF-β vs PBS
AY036118	7.27E-45	1.295E-40	-1.37	0.64	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Rps15a	1.74E-44	3.107E-40	0.35	1.00	1	T cells	aPD-L1 vs PBS
Gbp2	1.78E-44	3.171E-40	0.50	0.55	0.266	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rps24	5.45E-44	9.708E-40	0.55	0.97	0.923	Neutrophils	aPD-L1 vs PBS
Gbp2b	6.25E-44	1.114E-39	0.51	0.60	0.312	Neutrophils	aPD-L1 + aTGF-β vs PBS
Irf1	6.57E-44	1.171E-39	0.70	0.69	0.375	Neutrophils	aPD-L1 vs PBS
Phlda1	1.22E-43	2.166E-39	0.32	0.92	0.772	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Gm47283	1.39E-43	2.486E-39	0.53	0.83	0.55	T cells	aPD-L1 vs PBS
Neat1	1.52E-43	2.708E-39	0.31	0.79	0.639	Tumor_cells	aPD-L1 + aTGF-β vs PBS
B2m	2.23E-43	3.973E-39	0.34	1.00	0.998	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rps29	2.96E-43	5.277E-39	0.40	1.00	1	Macrophages	aPD-L1 vs PBS
Fosb	3.70E-43	6.587E-39	0.34	0.64	0.465	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Ubc	4.29E-43	7.644E-39	0.49	0.86	0.718	Tumor_cells	aPD-L1 vs PBS
Ifitm3	5.05E-43	8.998E-39	-0.32	0.15	0.533	B cells	aPD-L1 vs PBS
Gm47283	6.30E-43	1.122E-38	-0.36	0.63	0.842	B cells	aPD-L1 + aTGF-β vs aPD-L1
Lgals1	2.00E-42	3.567E-38	-0.35	0.19	0.615	B cells	aPD-L1 vs PBS
Rps27	3.74E-42	6.672E-38	-0.42	0.98	0.992	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Pfn1	3.93E-42	7.014E-38	-0.28	0.94	0.98	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl36al	4.37E-42	7.789E-38	0.27	0.54	0.254	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Cxcl2	4.64E-42	8.263E-38	0.44	0.48	0.329	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Ier3	1.06E-41	1.894E-37	0.28	0.93	0.799	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl35a	1.23E-41	2.193E-37	-0.28	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
mt-Atp8	1.59E-41	2.828E-37	-0.31	0.39	0.632	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl34	2.45E-41	4.376E-37	0.30	1.00	1	B cells	aPD-L1 + aTGF-β vs PBS
Lgals1	2.51E-41	4.481E-37	0.26	1.00	0.996	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Cthrc1	2.55E-41	4.542E-37	-0.38	0.48	0.635	Tumor_cells	aTGF-β vs PBS
AY036118	3.01E-41	5.368E-37	-0.71	0.65	0.836	Macrophages	aPD-L1 + aTGF-β vs PBS
Lars2	3.74E-41	6.672E-37	-0.54	0.27	0.571	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rps24	4.71E-41	8.4E-37	-0.42	0.90	0.965	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Satb1	4.98E-41	8.881E-37	0.34	0.76	0.546	B cells	aPD-L1 + aTGF-β vs aTGF-β
Lgals1	5.18E-41	9.231E-37	-0.27	1.00	0.999	Tumor_cells	aPD-L1 vs PBS
Gbp2	6.19E-41	1.104E-36	0.48	0.53	0.266	Neutrophils	aTGF-β vs PBS
H2-Eb1	7.19E-41	1.282E-36	0.96	0.84	0.502	Macrophages	aPD-L1 vs PBS
Gm10260	8.68E-41	1.548E-36	-0.29	0.87	0.936	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
S100a6	9.61E-41	1.713E-36	-0.29	0.18	0.59	B cells	aPD-L1 vs PBS
Fosb	1.02E-40	1.824E-36	0.32	0.65	0.465	Tumor_cells	aTGF-β vs PBS
Rpl39	1.10E-40	1.961E-36	0.50	0.94	0.914	Neutrophils	aPD-L1 vs PBS
Dnajb1	1.67E-40	2.97E-36	-0.29	0.69	0.803	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Crem	1.84E-40	3.284E-36	0.29	0.32	0.115	B cells	aPD-L1 + aTGF-β vs aTGF-β
Irf1	1.95E-40	3.48E-36	0.88	0.81	0.396	Monocytes	aPD-L1 + aTGF-β vs PBS
Sgk1	2.14E-40	3.814E-36	0.30	0.68	0.501	Tumor_cells	aTGF-β vs PBS
Samhd1	2.69E-40	4.802E-36	0.55	0.69	0.476	Neutrophils	aPD-L1 + aTGF-β vs PBS
AY036118	4.22E-40	7.518E-36	0.63	0.99	0.836	Macrophages	aPD-L1 vs PBS
Rpl35	5.71E-40	1.017E-35	0.27	0.98	0.968	Macrophages	aPD-L1 + aTGF-β vs PBS
Gm10260	6.17E-40	1.1E-35	0.35	0.97	0.907	T cells	aPD-L1 + aTGF-β vs PBS
Malat1	6.79E-40	1.21E-35	-0.35	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Gm11361	7.85E-40	1.399E-35	0.27	0.58	0.315	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl41	9.21E-40	1.642E-35	0.33	1.00	0.997	B cells	aPD-L1 + aTGF-β vs PBS
Rpl39	1.05E-39	1.864E-35	-0.25	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Cxcl10	1.16E-39	2.059E-35	0.53	0.23	0.051	Tumor_cells	aPD-L1 vs PBS
Fdps	1.29E-39	2.301E-35	-0.32	0.41	0.556	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Uba52	1.54E-39	2.745E-35	0.49	0.72	0.279	B cells	aPD-L1 vs PBS
H2-Aa	1.73E-39	3.079E-35	0.87	0.87	0.537	Macrophages	aPD-L1 vs PBS
Irf1	1.82E-39	3.237E-35	0.42	0.58	0.334	Tumor_cells	aPD-L1 vs PBS
Uqcrb	6.71E-39	1.197E-34	0.27	0.86	0.702	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Cxcl10	8.62E-39	1.536E-34	1.12	0.28	0.07	Neutrophils	aTGF-β vs PBS
Rpl35	9.40E-39	1.675E-34	0.34	0.99	0.955	T cells	aPD-L1 + aTGF-β vs PBS
Rps21	1.06E-38	1.887E-34	0.47	1.00	0.982	Macrophages	aPD-L1 vs PBS
Rsad2	1.07E-38	1.9E-34	0.75	0.72	0.502	Neutrophils	aTGF-β vs PBS
Irf1	1.23E-38	2.195E-34	0.46	0.55	0.257	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
H2-K1	1.36E-38	2.422E-34	0.40	1.00	0.989	Neutrophils	aPD-L1 vs PBS

Rpl30	2.23E-38	3.98E-34	0.31	1.00	0.998	T cells	aPD-L1 vs PBS
Rpl39	3.41E-38	6.082E-34	0.29	0.99	0.991	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Gm42418	3.74E-38	6.674E-34	0.26	1.00	1	T cells	aPD-L1 vs PBS
Ier3	6.61E-38	1.178E-33	0.45	0.93	0.829	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Serpina3g	1.13E-37	2.015E-33	0.39	0.31	0.083	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl35a	1.87E-37	3.339E-33	0.26	0.99	0.981	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl38	2.54E-37	4.521E-33	0.42	1.00	0.987	Macrophages	aPD-L1 vs PBS
Fosb	3.34E-37	5.954E-33	0.49	0.70	0.465	Tumor_cells	aPD-L1 vs PBS
Gbp2b	3.78E-37	6.74E-33	0.52	0.56	0.312	Neutrophils	aTGF-β vs PBS
Rpl27	3.94E-37	7.029E-33	0.43	0.82	0.558	T cells	aPD-L1 vs PBS
Irgm1	4.47E-37	7.963E-33	0.46	0.48	0.226	Neutrophils	aPD-L1 + aTGF-β vs PBS
Gm10076	5.41E-37	9.644E-33	0.47	0.82	0.558	Macrophages	aPD-L1 vs PBS
H2-D1	6.39E-37	1.139E-32	0.41	1.00	0.999	Neutrophils	aPD-L1 vs PBS
Iigp1	6.94E-37	1.237E-32	0.43	0.33	0.12	Tumor_cells	aPD-L1 vs PBS
Rps15a	1.41E-36	2.519E-32	0.25	1.00	1	T cells	aPD-L1 + aTGF-β vs PBS
Rps20	2.18E-36	3.886E-32	0.49	0.95	0.918	Neutrophils	aPD-L1 vs PBS
Gm10260	2.47E-36	4.397E-32	0.38	0.99	0.907	T cells	aPD-L1 vs PBS
Rpl37a	2.80E-36	4.993E-32	0.68	1.00	0.962	Monocytes	aPD-L1 vs PBS
Parp14	4.05E-36	7.216E-32	0.49	0.56	0.324	Neutrophils	aTGF-β vs PBS
AY036118	6.97E-36	1.243E-31	-0.52	0.59	0.76	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Snrpe	8.52E-36	1.519E-31	0.25	0.72	0.5	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Hnrnpa0	1.23E-35	2.187E-31	0.28	0.84	0.692	Tumor_cells	aPD-L1 vs PBS
Rpl37	2.54E-35	4.527E-31	0.40	1.00	0.996	Macrophages	aPD-L1 vs PBS
Nr4a1	2.94E-35	5.24E-31	0.30	0.70	0.451	B cells	aPD-L1 + aTGF-β vs aTGF-β
Cd74	3.03E-35	5.407E-31	0.81	0.95	0.805	Macrophages	aPD-L1 vs PBS
Gm42418	4.56E-35	8.137E-31	-0.97	0.99	1	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Irgm1	4.97E-35	8.866E-31	0.54	0.51	0.226	Neutrophils	aPD-L1 vs PBS
Rps8	5.15E-35	9.177E-31	0.25	1.00	1	B cells	aPD-L1 vs PBS
Ifit1	6.22E-35	1.109E-30	0.75	0.53	0.301	Neutrophils	aTGF-β vs PBS
Cd274	6.92E-35	1.234E-30	0.52	0.70	0.475	Neutrophils	aPD-L1 + aTGF-β vs PBS
Dusp1	7.32E-35	1.304E-30	0.29	0.82	0.664	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Cxcl10	8.54E-35	1.522E-30	0.37	0.18	0.051	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rps15a	8.92E-35	1.59E-30	0.44	0.94	0.905	Neutrophils	aPD-L1 vs PBS
Gbp5	1.02E-34	1.816E-30	0.45	0.34	0.118	Neutrophils	aTGF-β vs PBS
H2-Eb1	1.04E-34	1.86E-30	0.78	0.71	0.502	Macrophages	aPD-L1 + aTGF-β vs PBS
H2-D1	1.11E-34	1.986E-30	0.32	1.00	0.999	Neutrophils	aTGF-β vs PBS
Trib1	2.03E-34	3.616E-30	0.32	0.47	0.237	Tumor_cells	aPD-L1 vs PBS
Acta2	2.80E-34	4.987E-30	-0.43	0.59	0.722	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Sec61g	2.97E-34	5.301E-30	0.43	0.70	0.276	B cells	aPD-L1 vs PBS
mt-Atp8	3.53E-34	6.289E-30	-0.32	0.40	0.651	T cells	aPD-L1 + aTGF-β vs aPD-L1
mt-Nd3	5.05E-34	9.005E-30	-0.26	0.37	0.613	B cells	aPD-L1 + aTGF-β vs aPD-L1
Iglc3	6.56E-34	1.17E-29	-0.33	0.54	0.696	B cells	aPD-L1 + aTGF-β vs aTGF-β
Atp5e	8.82E-34	1.573E-29	0.26	0.94	0.849	Macrophages	aPD-L1 + aTGF-β vs PBS
Fos	8.87E-34	1.58E-29	-0.61	0.89	0.969	B cells	aPD-L1 vs PBS
AY036118	9.43E-34	1.681E-29	0.91	1.00	0.937	Monocytes	aPD-L1 vs PBS
Pim1	9.91E-34	1.766E-29	0.37	0.54	0.33	B cells	aPD-L1 + aTGF-β vs aTGF-β
Nfkbia	1.93E-33	3.441E-29	0.32	0.92	0.808	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Dcn	2.26E-33	4.027E-29	0.38	0.25	0.106	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rplp1	2.35E-33	4.186E-29	-0.37	0.95	0.973	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rps27l	2.44E-33	4.342E-29	0.27	0.83	0.689	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rps27	2.90E-33	5.172E-29	0.81	1.00	0.94	Monocytes	aPD-L1 vs PBS
Rpl39	3.32E-33	5.915E-29	0.50	0.99	0.98	Macrophages	aPD-L1 vs PBS
Ifit2	4.10E-33	7.305E-29	0.65	0.35	0.139	Neutrophils	aTGF-β vs PBS
Cyr61	4.40E-33	7.838E-29	-0.33	0.49	0.605	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Crip1	5.46E-33	9.741E-29	0.47	0.92	0.83	Macrophages	aPD-L1 + aTGF-β vs PBS
Actg1	6.01E-33	1.071E-28	-0.32	0.97	0.992	Tumor_cells	aPD-L1 vs PBS
Isg15	1.06E-32	1.886E-28	0.44	0.97	0.916	Neutrophils	aTGF-β vs PBS
Ifi47	1.45E-32	2.588E-28	0.43	0.51	0.272	Neutrophils	aTGF-β vs PBS
Atp5e	1.71E-32	3.048E-28	0.44	0.87	0.513	B cells	aPD-L1 vs PBS
Ifitm3	2.62E-32	4.664E-28	0.45	0.99	0.975	Neutrophils	aTGF-β vs PBS
Ccnl1	2.82E-32	5.034E-28	0.32	0.51	0.285	Tumor_cells	aPD-L1 vs PBS
Cthrc1	3.06E-32	5.457E-28	-0.47	0.42	0.635	Tumor_cells	aPD-L1 vs PBS
Rps15a	4.08E-32	7.268E-28	-0.35	0.88	0.939	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
H2-Ab1	4.38E-32	7.805E-28	0.70	0.86	0.586	Macrophages	aPD-L1 vs PBS
Iglc2	6.11E-32	1.089E-27	-0.26	0.77	0.876	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rps27	6.90E-32	1.23E-27	0.29	0.99	0.972	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Txn1	6.97E-32	1.242E-27	0.36	0.97	0.944	Macrophages	aPD-L1 + aTGF-β vs PBS
Cxcl1	1.01E-31	1.796E-27	0.41	0.80	0.607	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Tmsb10	1.06E-31	1.882E-27	0.38	0.98	0.972	B cells	aPD-L1 vs PBS
Irf1	1.24E-31	2.205E-27	0.54	0.54	0.22	Macrophages	aPD-L1 vs PBS
Rpl36a	1.60E-31	2.856E-27	0.34	0.98	0.954	B cells	aPD-L1 + aTGF-β vs PBS
Lars2	1.98E-31	3.525E-27	-0.27	0.18	0.364	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Tnfaip2	2.13E-31	3.79E-27	0.39	0.32	0.072	Macrophages	aPD-L1 vs PBS
Hmgb2	2.16E-31	3.843E-27	-0.32	0.57	0.782	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rps28	2.18E-31	3.889E-27	0.41	0.98	0.946	Macrophages	aPD-L1 vs PBS
Lars2	2.19E-31	3.913E-27	0.48	0.57	0.283	Neutrophils	aPD-L1 vs PBS
Rps20	2.38E-31	4.238E-27	-0.34	0.91	0.948	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Gm10076	2.64E-31	4.704E-27	0.46	0.79	0.446	Monocytes	aPD-L1 + aTGF-β vs PBS
Ndufa4	2.69E-31	4.792E-27	0.26	0.87	0.746	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Zfand5	3.08E-31	5.496E-27	0.37	0.66	0.473	Tumor_cells	aPD-L1 vs PBS
Lars2	4.12E-31	7.352E-27	0.27	0.36	0.156	Tumor_cells	aPD-L1 vs PBS
Ubb	4.85E-31	8.638E-27	0.28	1.00	0.99	Tumor_cells	aPD-L1 vs PBS
Snrpg	8.82E-31	1.573E-26	0.37	0.53	0.246	T cells	aPD-L1 vs PBS
Hspa1a	1.18E-30	2.099E-26	-0.48	0.38	0.576	B cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl39	1.43E-30	2.555E-26	-0.38	0.91	0.938	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Cd74	1.57E-30	2.793E-26	0.70	0.87	0.805	Macrophages	aPD-L1 + aTGF-β vs PBS

H2-Aa	3.48E-30	6.201E-26	0.70	0.71	0.537	Macrophages	aPD-L1 + aTGF-β vs PBS
Actb	4.02E-30	7.161E-26	-0.36	1.00	1	T cells	aPD-L1 vs PBS
mt-Nd3	7.21E-30	1.284E-25	0.40	0.56	0.277	T cells	aPD-L1 vs PBS
Cd274	7.33E-30	1.306E-25	0.55	0.74	0.475	Neutrophils	aPD-L1 vs PBS
Atp5f1	8.27E-30	1.475E-25	-0.26	0.89	0.961	Tumor_cells	aPD-L1 vs PBS
Rps27	8.46E-30	1.507E-25	0.52	0.99	0.94	Monocytes	aPD-L1 + aTGF-β vs PBS
Pfn1	1.13E-29	2.008E-25	-0.38	0.98	0.976	T cells	aPD-L1 vs PBS
Jun	1.22E-29	2.169E-25	-0.52	0.92	0.994	B cells	aPD-L1 + aTGF-β vs PBS
Klf2	1.48E-29	2.647E-25	0.34	0.43	0.272	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Rpl37a	1.58E-29	2.813E-25	-0.39	0.91	0.954	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Klf2	1.95E-29	3.477E-25	0.39	0.43	0.272	Tumor_cells	aTGF-β vs PBS
Vps37b	2.23E-29	3.974E-25	0.45	0.74	0.53	T cells	aPD-L1 + aTGF-β vs aTGF-β
Irgm1	2.90E-29	5.169E-25	0.40	0.44	0.226	Neutrophils	aTGF-β vs PBS
Gbp4	3.00E-29	5.347E-25	0.30	0.23	0.071	Tumor_cells	aPD-L1 vs PBS
Rpl18	4.26E-29	7.585E-25	-0.33	0.99	0.994	Macrophages	aPD-L1 vs PBS
Gbp2	9.16E-29	1.633E-24	0.41	0.55	0.266	Neutrophils	aPD-L1 vs PBS
Cdkn1a	1.16E-28	2.071E-24	-0.56	0.70	0.817	Neutrophils	aPD-L1 vs PBS
mt-Nd4l	1.45E-28	2.585E-24	0.35	0.63	0.326	T cells	aPD-L1 vs PBS
Cytip	1.57E-28	2.807E-24	0.26	0.75	0.562	B cells	aPD-L1 + aTGF-β vs aTGF-β
Cmpk2	2.69E-28	4.793E-24	0.43	0.30	0.117	Neutrophils	aTGF-β vs PBS
Pfn1	3.77E-28	6.728E-24	0.25	0.94	0.908	B cells	aPD-L1 + aTGF-β vs aPD-L1
H2-T23	5.75E-28	1.025E-23	0.43	0.72	0.44	Macrophages	aPD-L1 vs PBS
Snrpg	6.35E-28	1.133E-23	0.35	0.56	0.194	B cells	aPD-L1 vs PBS
Rpl35	8.38E-28	1.494E-23	-0.26	0.99	0.996	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl41	8.69E-28	1.549E-23	0.32	1.00	0.999	Macrophages	aPD-L1 vs PBS
Sub1	8.72E-28	1.555E-23	0.27	0.82	0.672	B cells	aPD-L1 + aTGF-β vs aTGF-β
Uba52	9.90E-28	1.765E-23	0.31	0.62	0.362	T cells	aPD-L1 + aTGF-β vs PBS
H2-K1	1.03E-27	1.835E-23	0.32	1.00	0.989	Neutrophils	aTGF-β vs PBS
Rps21	1.13E-27	2.007E-23	0.42	0.90	0.904	Neutrophils	aPD-L1 vs PBS
Lars2	1.41E-27	2.516E-23	0.46	0.67	0.381	T cells	aPD-L1 vs PBS
Igkc	1.57E-27	2.793E-23	0.87	0.16	0.025	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps29	1.94E-27	3.457E-23	0.48	1.00	1	Monocytes	aPD-L1 vs PBS
H2-Ab1	1.95E-27	3.481E-23	0.67	0.73	0.586	Macrophages	aPD-L1 + aTGF-β vs PBS
Slfn4	1.97E-27	3.507E-23	0.42	0.85	0.754	Neutrophils	aTGF-β vs PBS
mt-Atp8	2.00E-27	3.573E-23	0.41	0.63	0.291	B cells	aPD-L1 vs PBS
Ifi47	2.67E-27	4.758E-23	0.35	0.50	0.272	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl27	4.29E-27	7.64E-23	0.41	0.82	0.493	B cells	aPD-L1 vs PBS
Tnf	4.36E-27	7.779E-23	0.41	0.50	0.28	Macrophages	aPD-L1 + aTGF-β vs PBS
Srgn	4.85E-27	8.643E-23	-0.33	1.00	1	Neutrophils	aPD-L1 vs PBS
Zbp1	5.06E-27	9.026E-23	0.41	0.47	0.208	Neutrophils	aPD-L1 vs PBS
Rpl35a	5.27E-27	9.4E-23	0.25	1.00	0.995	T cells	aPD-L1 + aTGF-β vs PBS
Rac2	5.63E-27	1.004E-22	0.31	0.86	0.749	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl36a	6.73E-27	1.199E-22	0.29	0.97	0.954	T cells	aPD-L1 + aTGF-β vs PBS
mt-Nd2	6.74E-27	1.201E-22	-0.25	0.97	0.999	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl22l1	7.02E-27	1.252E-22	0.35	0.98	0.894	T cells	aPD-L1 vs PBS
Oasl1	8.49E-27	1.514E-22	0.49	0.48	0.264	Macrophages	aPD-L1 + aTGF-β vs PBS
AY036118	1.12E-26	1.998E-22	-0.48	0.73	0.836	Macrophages	aTGF-β vs PBS
Fam26f	1.16E-26	2.062E-22	0.27	0.30	0.11	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl31	1.24E-26	2.211E-22	0.31	0.98	0.814	T cells	aPD-L1 vs PBS
Gbp5	1.37E-26	2.44E-22	0.33	0.31	0.118	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl37	1.69E-26	3.015E-22	0.35	0.99	0.939	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
mt-Atp8	1.81E-26	3.221E-22	0.40	0.65	0.375	Macrophages	aPD-L1 vs PBS
Tnfaip2	1.98E-26	3.538E-22	0.59	0.63	0.386	Neutrophils	aPD-L1 vs PBS
B2m	1.99E-26	3.55E-22	0.30	1.00	0.998	Neutrophils	aTGF-β vs PBS
Rpl13	2.27E-26	4.05E-22	-0.32	1.00	1	Macrophages	aPD-L1 vs PBS
Gm42418	2.42E-26	4.307E-22	-0.41	1.00	1	T cells	aPD-L1 + aTGF-β vs PBS
Ifi27l2a	3.04E-26	5.419E-22	0.37	0.53	0.353	B cells	aPD-L1 + aTGF-β vs aTGF-β
Bola2	3.09E-26	5.501E-22	0.32	0.54	0.261	T cells	aPD-L1 vs PBS
Atp5e	3.96E-26	7.055E-22	0.36	0.92	0.849	Macrophages	aPD-L1 vs PBS
Acod1	5.12E-26	9.123E-22	0.34	0.36	0.148	Macrophages	aPD-L1 + aTGF-β vs PBS
Ifi27l2a	6.98E-26	1.245E-21	0.58	0.72	0.495	Neutrophils	aPD-L1 vs PBS
Rplp1	7.09E-26	1.264E-21	0.38	0.97	0.965	Neutrophils	aPD-L1 vs PBS
Gadd45g	7.49E-26	1.335E-21	-0.25	0.32	0.441	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl39	8.56E-26	1.525E-21	0.63	0.98	0.943	Monocytes	aPD-L1 vs PBS
Fos	9.83E-26	1.752E-21	-0.47	0.92	0.969	B cells	aPD-L1 + aTGF-β vs PBS
Rpl35	1.01E-25	1.808E-21	0.30	0.99	0.986	B cells	aPD-L1 + aTGF-β vs PBS
Slamf8	1.11E-25	1.982E-21	0.26	0.36	0.162	Macrophages	aPD-L1 + aTGF-β vs PBS
Spp1	1.49E-25	2.65E-21	-0.63	0.50	0.794	Macrophages	aPD-L1 vs PBS
Gbp2b	1.69E-25	3.021E-21	0.41	0.45	0.169	Macrophages	aPD-L1 vs PBS
Tuba1b	1.88E-25	3.354E-21	0.26	0.65	0.452	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl13	2.04E-25	3.638E-21	-0.33	0.92	0.958	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Ifit3	2.17E-25	3.873E-21	0.46	0.33	0.143	Neutrophils	aTGF-β vs PBS
Gm10260	2.97E-25	5.297E-21	0.25	0.97	0.934	T cells	aPD-L1 + aTGF-β vs aTGF-β
Cxcl10	3.96E-25	7.056E-21	0.63	0.59	0.37	Macrophages	aPD-L1 + aTGF-β vs PBS
Actb	4.05E-25	7.22E-21	-0.26	1.00	1	T cells	aPD-L1 + aTGF-β vs aTGF-β
Mgp	4.19E-25	7.476E-21	0.52	0.34	0.199	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Arg1	4.46E-25	7.946E-21	-0.74	0.22	0.42	Macrophages	aTGF-β vs PBS
Sem1	4.64E-25	8.277E-21	0.32	0.94	0.847	Macrophages	aPD-L1 vs PBS
mt-Nd3	4.75E-25	8.47E-21	0.38	0.61	0.279	B cells	aPD-L1 vs PBS
Rps26	5.02E-25	8.95E-21	0.30	0.99	0.978	T cells	aPD-L1 vs PBS
Rps27rt	5.23E-25	9.329E-21	0.30	0.48	0.224	T cells	aPD-L1 vs PBS
Tomm7	6.24E-25	1.113E-20	0.35	0.67	0.384	Macrophages	aPD-L1 vs PBS
Rpl35a	8.17E-25	1.457E-20	0.37	0.98	0.981	Macrophages	aPD-L1 vs PBS
Gm11808	8.72E-25	1.554E-20	0.26	0.45	0.186	T cells	aPD-L1 vs PBS
Rpl37	1.12E-24	2.001E-20	0.52	0.99	0.94	Monocytes	aPD-L1 vs PBS
Gbp4	1.13E-24	2.008E-20	0.42	0.20	0.052	Neutrophils	aPD-L1 + aTGF-β vs PBS

Rps27rt	1.31E-24	2.342E-20	0.33	0.50	0.177	B cells	aPD-L1 vs PBS
Jund	1.50E-24	2.673E-20	-0.37	0.99	1	B cells	aTGF-β vs PBS
Rpl22l1	2.41E-24	4.3E-20	0.36	0.97	0.909	B cells	aPD-L1 vs PBS
Icam1	2.49E-24	4.44E-20	0.44	0.27	0.099	Neutrophils	aPD-L1 + aTGF-β vs PBS
Zbp1	2.52E-24	4.486E-20	0.34	0.41	0.208	Neutrophils	aPD-L1 + aTGF-β vs PBS
Gbp2b	2.93E-24	5.224E-20	0.44	0.48	0.293	Tumor_cells	aPD-L1 vs PBS
Rpl21	3.03E-24	5.401E-20	0.26	1.00	1	B cells	aPD-L1 vs PBS
Rpl35	3.34E-24	5.946E-20	0.36	0.97	0.968	Macrophages	aPD-L1 vs PBS
Rpl15	3.44E-24	6.134E-20	-0.34	0.97	0.993	Macrophages	aPD-L1 vs PBS
Jun	3.62E-24	6.444E-20	-0.31	0.92	0.954	B cells	aPD-L1 + aTGF-β vs aTGF-β
Adamts1	4.42E-24	7.873E-20	0.26	0.39	0.206	Tumor_cells	aPD-L1 vs PBS
Rpl37a	5.16E-24	9.207E-20	0.39	0.99	0.962	Monocytes	aPD-L1 + aTGF-β vs PBS
Igkc	5.32E-24	9.491E-20	1.12	0.18	0.025	Macrophages	aPD-L1 vs PBS
Rps21	5.75E-24	1.025E-19	0.53	0.99	0.943	Monocytes	aPD-L1 vs PBS
Gm42418	6.35E-24	1.131E-19	-1.10	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gbp2b	8.39E-24	1.495E-19	0.33	0.37	0.169	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl37	8.47E-24	1.51E-19	0.34	0.94	0.929	Neutrophils	aPD-L1 vs PBS
Eno1	9.79E-24	1.744E-19	-0.28	0.70	0.777	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl23	1.00E-23	1.791E-19	0.37	0.97	0.965	Neutrophils	aPD-L1 vs PBS
Gbp4	1.02E-23	1.813E-19	0.38	0.22	0.052	Neutrophils	aPD-L1 vs PBS
Ndufa1	1.02E-23	1.822E-19	0.32	0.56	0.281	Macrophages	aPD-L1 vs PBS
Pfn1	1.09E-23	1.944E-19	-0.37	0.91	0.966	B cells	aPD-L1 vs PBS
Cfl1	1.15E-23	2.051E-19	0.27	0.93	0.902	T cells	aPD-L1 + aTGF-β vs aPD-L1
Spp1	1.23E-23	2.191E-19	0.28	0.99	0.979	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Atp5e	1.61E-23	2.877E-19	0.29	0.88	0.642	T cells	aPD-L1 vs PBS
Rpl37a	1.72E-23	3.074E-19	0.47	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Gbp3	2.16E-23	3.847E-19	0.27	0.24	0.082	Neutrophils	aTGF-β vs PBS
Dusp6	2.39E-23	4.257E-19	0.25	0.37	0.188	Tumor_cells	aPD-L1 vs PBS
Samsn1	2.58E-23	4.594E-19	0.50	0.56	0.262	B cells	aPD-L1 vs PBS
Ly6a	2.87E-23	5.119E-19	0.28	0.17	0.049	B cells	aPD-L1 + aTGF-β vs aTGF-β
Mt2	3.73E-23	6.656E-19	0.28	0.74	0.561	Tumor_cells	aPD-L1 vs PBS
Myl9	3.76E-23	6.704E-19	-0.25	0.24	0.354	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Irf1	3.77E-23	6.722E-19	0.44	0.56	0.375	Neutrophils	aTGF-β vs PBS
H2-D1	4.06E-23	7.231E-19	0.38	1.00	0.993	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
AY036118	4.28E-23	7.633E-19	1.10	1.00	0.71	ILC	aPD-L1 vs PBS
Cox7c	5.05E-23	9.007E-19	0.35	0.74	0.396	B cells	aPD-L1 vs PBS
Acod1	5.38E-23	9.587E-19	0.35	0.86	0.75	Neutrophils	aTGF-β vs PBS
Brd2	5.64E-23	1.005E-18	0.25	0.47	0.282	Tumor_cells	aPD-L1 vs PBS
B2m	5.77E-23	1.028E-18	0.27	1.00	1	Macrophages	aPD-L1 vs PBS
Ifit1	6.02E-23	1.073E-18	-0.62	0.38	0.525	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rps29	6.07E-23	1.082E-18	-0.28	1.00	1	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Gm42418	6.63E-23	1.183E-18	-0.50	1.00	1	Macrophages	aPD-L1 + aTGF-β vs PBS
Pmepa1	7.28E-23	1.298E-18	-0.54	0.38	0.701	Macrophages	aPD-L1 vs PBS
Gm10076	8.50E-23	1.516E-18	0.47	0.82	0.446	Monocytes	aPD-L1 vs PBS
Rps27	9.99E-23	1.782E-18	0.39	0.99	0.934	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Sub1	1.05E-22	1.88E-18	0.42	0.93	0.709	B cells	aPD-L1 vs PBS
Cxcl10	1.13E-22	2.006E-18	0.30	0.18	0.088	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Sgk1	1.16E-22	2.065E-18	0.36	0.67	0.501	Tumor_cells	aPD-L1 vs PBS
Lars2	1.30E-22	2.31E-18	-0.71	0.54	0.842	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
H2-DMb1	1.32E-22	2.353E-18	0.49	0.64	0.356	Macrophages	aPD-L1 vs PBS
Rps21	1.37E-22	2.447E-18	-0.34	0.88	0.902	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Peli1	1.52E-22	2.702E-18	0.28	0.45	0.25	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl41	1.53E-22	2.72E-18	0.33	0.97	0.959	Neutrophils	aPD-L1 vs PBS
Dcn	1.85E-22	3.295E-18	0.42	0.22	0.106	Tumor_cells	aTGF-β vs PBS
Klf2	1.92E-22	3.422E-18	-0.50	0.89	0.966	B cells	aPD-L1 + aTGF-β vs PBS
Rpl35a	2.18E-22	3.884E-18	0.38	0.90	0.904	Neutrophils	aPD-L1 vs PBS
AC160336.1	2.24E-22	3.996E-18	-0.38	0.27	0.458	T cells	aPD-L1 + aTGF-β vs aPD-L1
Ifi27l2a	2.25E-22	4.017E-18	0.31	0.88	0.799	Macrophages	aTGF-β vs PBS
Smad7	2.49E-22	4.433E-18	-0.43	0.58	0.762	T cells	aTGF-β vs PBS
Rpl36al	2.56E-22	4.56E-18	0.31	0.47	0.16	B cells	aPD-L1 vs PBS
Cst3	2.84E-22	5.064E-18	-0.36	0.65	0.835	B cells	aPD-L1 vs PBS
Ostc	2.92E-22	5.202E-18	-0.25	0.64	0.774	Tumor_cells	aPD-L1 vs PBS
Egr1	3.29E-22	5.867E-18	0.38	0.75	0.649	Tumor_cells	aPD-L1 vs PBS
Lars2	3.72E-22	6.624E-18	0.37	0.61	0.276	B cells	aPD-L1 vs PBS
Rpl8	4.02E-22	7.167E-18	-0.33	1.00	0.996	Macrophages	aPD-L1 vs PBS
Tnfaip2	4.24E-22	7.563E-18	0.40	0.56	0.386	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl36	4.62E-22	8.233E-18	0.32	1.00	0.992	Macrophages	aPD-L1 vs PBS
Ccl4	5.02E-22	8.943E-18	0.47	0.82	0.653	Macrophages	aPD-L1 + aTGF-β vs PBS
Lgals1	5.64E-22	1.005E-17	-0.38	0.97	0.987	Macrophages	aPD-L1 vs PBS
Rpl37	5.72E-22	1.02E-17	0.33	0.99	0.94	Monocytes	aPD-L1 + aTGF-β vs PBS
Plac8	5.87E-22	1.047E-17	0.46	0.37	0.197	Neutrophils	aTGF-β vs PBS
AW112010	7.08E-22	1.261E-17	0.57	0.70	0.544	Macrophages	aPD-L1 + aTGF-β vs PBS
Cox7c	7.70E-22	1.373E-17	0.32	0.89	0.773	Macrophages	aPD-L1 vs PBS
Rps23	9.16E-22	1.633E-17	-0.30	0.91	0.939	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Sec61g	9.22E-22	1.643E-17	0.34	0.79	0.616	Macrophages	aPD-L1 vs PBS
Lars2	1.14E-21	2.027E-17	-0.63	0.48	0.728	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Igtp	1.16E-21	2.062E-17	0.31	0.39	0.209	Neutrophils	aPD-L1 + aTGF-β vs PBS
Irf1	1.18E-21	2.101E-17	0.54	0.81	0.562	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Rpl5	1.20E-21	2.136E-17	-0.28	0.97	0.994	T cells	aPD-L1 + aTGF-β vs PBS
Ifi27l2a	1.35E-21	2.399E-17	0.33	0.89	0.799	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl39	1.37E-21	2.442E-17	0.41	0.98	0.943	Monocytes	aPD-L1 + aTGF-β vs PBS
Tmsb10	1.47E-21	2.619E-17	0.36	0.97	0.938	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Gbp4	1.75E-21	3.127E-17	0.29	0.34	0.158	Macrophages	aPD-L1 + aTGF-β vs PBS
Fgl2	1.90E-21	3.394E-17	0.33	0.47	0.277	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps20	2.04E-21	3.638E-17	0.27	1.00	0.998	T cells	aPD-L1 vs PBS
Tnfaip3	2.09E-21	3.726E-17	0.38	0.44	0.178	Macrophages	aPD-L1 vs PBS

Samhd1	2.35E-21	4.183E-17	0.35	0.65	0.476	Neutrophils	aTGF-β vs PBS
Gm47283	2.71E-21	4.827E-17	-0.44	0.32	0.601	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Fcgr4	2.71E-21	4.829E-17	0.31	0.39	0.215	Neutrophils	aTGF-β vs PBS
Dab2	2.71E-21	4.831E-17	-0.41	0.64	0.834	Macrophages	aPD-L1 vs PBS
Igtp	2.91E-21	5.18E-17	0.33	0.43	0.209	Neutrophils	aPD-L1 vs PBS
Pkm	2.97E-21	5.295E-17	-0.26	0.38	0.675	B cells	aPD-L1 vs PBS
Il4i1	3.11E-21	5.546E-17	-0.26	0.13	0.259	B cells	aPD-L1 + aTGF-β vs aTGF-β
Ccrl2	3.15E-21	5.621E-17	0.33	0.90	0.794	Neutrophils	aTGF-β vs PBS
Ifit2	3.45E-21	6.152E-17	-0.54	0.20	0.349	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Dab2	3.65E-21	6.504E-17	-0.28	0.71	0.834	Macrophages	aPD-L1 + aTGF-β vs PBS
Ahnak	3.80E-21	6.772E-17	0.30	0.73	0.584	Tumor_cells	aPD-L1 vs PBS
Nampt	4.35E-21	7.749E-17	0.35	0.48	0.299	Neutrophils	aPD-L1 + aTGF-β vs PBS
Irf7	4.56E-21	8.125E-17	0.39	0.57	0.404	Neutrophils	aTGF-β vs PBS
Gm10260	4.58E-21	8.173E-17	0.30	0.96	0.843	B cells	aPD-L1 vs PBS
Acta2	5.73E-21	1.021E-16	-0.32	0.62	0.722	Tumor_cells	aTGF-β vs PBS
Gm10076	6.23E-21	1.11E-16	0.33	0.79	0.544	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Rsad2	6.31E-21	1.124E-16	0.53	0.43	0.232	Macrophages	aPD-L1 + aTGF-β vs PBS
Dusp10	6.36E-21	1.134E-16	0.39	0.63	0.392	T cells	aPD-L1 vs PBS
Irf1	6.40E-21	1.142E-16	0.41	0.48	0.197	B cells	aPD-L1 + aTGF-β vs PBS
Rps21	7.21E-21	1.285E-16	0.42	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Gbp2b	7.98E-21	1.423E-16	0.33	0.56	0.312	Neutrophils	aPD-L1 vs PBS
Fcgr4	8.35E-21	1.488E-16	0.32	0.39	0.215	Neutrophils	aPD-L1 + aTGF-β vs PBS
Klf4	9.33E-21	1.663E-16	0.25	0.48	0.29	Tumor_cells	aPD-L1 vs PBS
Rpl10a	1.06E-20	1.891E-16	-0.36	0.92	0.976	Macrophages	aPD-L1 vs PBS
Rnf213	1.15E-20	2.059E-16	0.27	0.32	0.151	Neutrophils	aTGF-β vs PBS
Rps5	1.16E-20	2.069E-16	-0.37	0.98	0.989	Macrophages	aPD-L1 vs PBS
Hist1h1c	1.18E-20	2.099E-16	-0.53	0.39	0.601	B cells	aPD-L1 + aTGF-β vs PBS
Acod1	1.20E-20	2.143E-16	0.33	0.86	0.75	Neutrophils	aPD-L1 + aTGF-β vs PBS
Socs1	1.49E-20	2.649E-16	0.31	0.34	0.168	Neutrophils	aPD-L1 + aTGF-β vs PBS
Jun	1.62E-20	2.889E-16	-0.43	0.92	0.994	B cells	aPD-L1 vs PBS
Trafd1	1.76E-20	3.134E-16	0.32	0.42	0.254	Neutrophils	aTGF-β vs PBS
Ddx60	1.97E-20	3.507E-16	0.32	0.40	0.221	Neutrophils	aTGF-β vs PBS
Cox7c	2.16E-20	3.845E-16	0.26	0.76	0.469	T cells	aPD-L1 vs PBS
Sec61g	2.38E-20	4.248E-16	0.27	0.63	0.378	T cells	aPD-L1 vs PBS
Rps23	2.44E-20	4.346E-16	0.34	0.94	0.923	Neutrophils	aPD-L1 vs PBS
Fam26f	2.45E-20	4.369E-16	0.33	0.33	0.11	Macrophages	aPD-L1 vs PBS
Stat1	2.51E-20	4.477E-16	0.27	0.55	0.353	Macrophages	aPD-L1 + aTGF-β vs PBS
Igtp	2.76E-20	4.924E-16	0.27	0.39	0.209	Neutrophils	aTGF-β vs PBS
Irf1	3.61E-20	6.438E-16	0.35	0.57	0.374	T cells	aPD-L1 + aTGF-β vs PBS
Slfn5	4.66E-20	8.304E-16	0.35	0.47	0.298	Neutrophils	aTGF-β vs PBS
Apoe	5.16E-20	9.192E-16	-1.07	0.54	0.769	Monocytes	aPD-L1 + aTGF-β vs PBS
Gm47283	5.27E-20	9.402E-16	0.38	0.84	0.587	B cells	aPD-L1 vs PBS
Hspa1a	7.30E-20	1.302E-15	0.39	0.61	0.445	Macrophages	aTGF-β vs PBS
Tmsb10	7.79E-20	1.388E-15	0.54	1.00	0.981	Monocytes	aPD-L1 vs PBS
Trim30a	8.87E-20	1.581E-15	0.31	0.59	0.424	Neutrophils	aTGF-β vs PBS
Rps27	8.94E-20	1.594E-15	0.44	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Rps19	9.75E-20	1.738E-15	0.37	0.91	0.909	Neutrophils	aPD-L1 vs PBS
Cd274	1.10E-19	1.962E-15	0.33	0.65	0.475	Neutrophils	aTGF-β vs PBS
Ier5	1.17E-19	2.088E-15	-0.26	0.66	0.838	T cells	aPD-L1 + aTGF-β vs aPD-L1
Acod1	1.46E-19	2.609E-15	0.41	0.38	0.148	Macrophages	aPD-L1 vs PBS
Parp14	1.59E-19	2.831E-15	0.32	0.51	0.324	Neutrophils	aPD-L1 + aTGF-β vs PBS
Actb	1.67E-19	2.985E-15	0.25	1.00	1	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rps4x	1.74E-19	3.108E-15	-0.34	0.98	0.993	Macrophages	aPD-L1 vs PBS
Usp18	2.37E-19	4.225E-15	0.29	0.32	0.157	Neutrophils	aTGF-β vs PBS
Ppp1r3b	2.52E-19	4.483E-15	-0.30	0.30	0.472	Neutrophils	aPD-L1 + aTGF-β vs PBS
Arpc1b	3.00E-19	5.353E-15	-0.27	0.96	0.991	Macrophages	aPD-L1 vs PBS
Usp18	3.01E-19	5.363E-15	-0.30	0.18	0.318	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Irf1	3.15E-19	5.621E-15	0.34	0.60	0.374	T cells	aPD-L1 vs PBS
Gm42418	3.16E-19	5.625E-15	-0.56	1.00	1	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
H2-Q7	3.22E-19	5.737E-15	0.34	0.62	0.405	Neutrophils	aPD-L1 vs PBS
Tspo	3.42E-19	6.105E-15	-0.27	0.88	0.925	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl34	3.77E-19	6.72E-15	0.34	0.94	0.922	Neutrophils	aPD-L1 vs PBS
Socs1	4.26E-19	7.592E-15	0.33	0.37	0.168	Neutrophils	aPD-L1 vs PBS
Rpl41	4.37E-19	7.782E-15	0.38	1.00	0.987	Monocytes	aPD-L1 vs PBS
Serpina3g	4.55E-19	8.111E-15	0.39	0.27	0.083	Macrophages	aPD-L1 vs PBS
Irf1	4.70E-19	8.383E-15	0.80	0.71	0.396	Monocytes	aPD-L1 vs PBS
Rps27	5.64E-19	1.005E-14	0.37	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Herc6	6.59E-19	1.174E-14	0.31	0.38	0.218	Neutrophils	aTGF-β vs PBS
H2-T23	6.91E-19	1.232E-14	0.31	0.62	0.402	Neutrophils	aPD-L1 vs PBS
Rpl30	7.36E-19	1.312E-14	-0.32	0.90	0.926	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Samd9l	8.01E-19	1.428E-14	0.25	0.43	0.251	Neutrophils	aTGF-β vs PBS
Oasl1	8.34E-19	1.486E-14	-0.33	0.40	0.537	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl35a	8.59E-19	1.532E-14	0.48	0.99	0.934	Monocytes	aPD-L1 vs PBS
Rps19	8.65E-19	1.542E-14	-0.28	0.89	0.914	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Gbp7	8.83E-19	1.574E-14	0.31	0.43	0.258	Neutrophils	aPD-L1 + aTGF-β vs PBS
Serpina3g	9.02E-19	1.609E-14	0.32	0.31	0.136	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Ldha	9.11E-19	1.624E-14	-0.42	0.83	0.937	Neutrophils	aPD-L1 vs PBS
Sppl2a	1.16E-18	2.075E-14	0.27	0.31	0.157	Neutrophils	aTGF-β vs PBS
Rpl14	1.25E-18	2.232E-14	-0.28	0.95	0.984	Macrophages	aPD-L1 vs PBS
Clec2d	1.32E-18	2.346E-14	0.29	0.35	0.19	Neutrophils	aTGF-β vs PBS
Fos	1.36E-18	2.422E-14	-0.31	0.99	0.993	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl39	1.46E-18	2.595E-14	0.34	0.98	0.946	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Rpl31	1.47E-18	2.615E-14	0.29	0.95	0.778	B cells	aPD-L1 vs PBS
Blvrb	1.66E-18	2.967E-14	0.31	0.62	0.464	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl13	1.66E-18	2.968E-14	0.36	0.96	0.939	Neutrophils	aPD-L1 vs PBS
H2-Eb1	1.69E-18	3.012E-14	0.57	0.71	0.559	Macrophages	aPD-L1 + aTGF-β vs aTGF-β

Rpl27a	1.69E-18	3.021E-14	-0.28	0.92	0.949	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Myh9	1.79E-18	3.182E-14	-0.25	0.44	0.578	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Slfn1	1.87E-18	3.332E-14	0.30	0.59	0.426	Neutrophils	aTGF-β vs PBS
Cox17	1.95E-18	3.467E-14	0.30	0.42	0.219	Neutrophils	aPD-L1 vs PBS
Gm31243	1.96E-18	3.499E-14	0.33	0.61	0.353	B cells	aPD-L1 vs PBS
Plac8	2.22E-18	3.964E-14	0.34	0.36	0.197	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl23	2.48E-18	4.428E-14	-0.28	0.96	0.968	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Ly6a	2.63E-18	4.688E-14	0.62	0.56	0.42	Macrophages	aPD-L1 + aTGF-β vs PBS
Irf1	2.64E-18	4.706E-14	0.28	0.69	0.563	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
9930111J21Rik	2.66E-18	4.736E-14	0.29	0.35	0.196	Neutrophils	aTGF-β vs PBS
Hk3	2.76E-18	4.923E-14	0.39	0.55	0.325	Macrophages	aPD-L1 vs PBS
Slc7a11	2.77E-18	4.941E-14	0.41	0.72	0.532	Neutrophils	aPD-L1 vs PBS
Zbp1	2.84E-18	5.054E-14	0.30	0.38	0.208	Neutrophils	aTGF-β vs PBS
Rpl38	2.84E-18	5.069E-14	0.43	0.96	0.956	Monocytes	aPD-L1 vs PBS
Gapdh	2.95E-18	5.264E-14	-0.35	0.96	0.995	Macrophages	aPD-L1 vs PBS
Rpl32	3.06E-18	5.455E-14	-0.33	0.88	0.9	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Mcl1	3.58E-18	6.374E-14	-0.26	1.00	1	Neutrophils	aPD-L1 vs PBS
Cdc42ep2	3.58E-18	6.378E-14	0.27	0.27	0.121	Neutrophils	aPD-L1 + aTGF-β vs PBS
Gbp2	3.58E-18	6.385E-14	0.42	0.59	0.468	Tumor_cells	aPD-L1 vs PBS
Rpl37a	3.61E-18	6.432E-14	0.29	0.99	0.984	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Neat1	3.80E-18	6.77E-14	0.41	0.75	0.639	Tumor_cells	aPD-L1 vs PBS
Rpl5	3.87E-18	6.893E-14	-0.31	0.92	0.964	Macrophages	aPD-L1 vs PBS
Cd274	4.68E-18	8.34E-14	0.52	0.67	0.373	Monocytes	aPD-L1 + aTGF-β vs PBS
Rpl12	4.90E-18	8.729E-14	-0.34	0.93	0.986	Macrophages	aPD-L1 vs PBS
Tmsb10	4.91E-18	8.755E-14	0.27	0.99	0.972	B cells	aPD-L1 + aTGF-β vs PBS
Isg20	5.02E-18	8.941E-14	0.42	0.62	0.486	Neutrophils	aTGF-β vs PBS
Smad7	5.32E-18	9.477E-14	-0.35	0.65	0.762	T cells	aPD-L1 + aTGF-β vs PBS
Rpl3	5.35E-18	9.533E-14	-0.33	0.95	0.989	Macrophages	aPD-L1 vs PBS
Ier5	5.61E-18	1.001E-13	-0.31	0.79	0.906	B cells	aPD-L1 + aTGF-β vs PBS
Atp5k	6.02E-18	1.074E-13	0.32	0.73	0.547	Macrophages	aPD-L1 vs PBS
Fos	6.16E-18	1.097E-13	0.34	0.84	0.694	Tumor_cells	aPD-L1 vs PBS
H2-D1	6.96E-18	1.241E-13	0.28	1.00	1	Macrophages	aPD-L1 vs PBS
Irf1	6.97E-18	1.242E-13	0.32	0.49	0.197	B cells	aPD-L1 vs PBS
Klf2	7.05E-18	1.257E-13	0.32	0.75	0.626	Macrophages	aTGF-β vs PBS
Ifit3	8.08E-18	1.44E-13	-0.43	0.19	0.326	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl35a	8.23E-18	1.467E-13	-0.28	0.89	0.9	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rps28	8.56E-18	1.526E-13	0.46	0.94	0.848	Monocytes	aPD-L1 vs PBS
Rpl37	8.77E-18	1.564E-13	-0.27	0.92	0.941	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Tmsb10	8.89E-18	1.585E-13	0.47	0.99	0.981	Monocytes	aPD-L1 + aTGF-β vs PBS
Clic1	8.96E-18	1.597E-13	-0.30	0.61	0.718	T cells	aPD-L1 vs PBS
Rpl34	9.47E-18	1.689E-13	-0.29	0.91	0.941	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rpl30	1.00E-17	1.784E-13	0.35	0.93	0.918	Neutrophils	aPD-L1 vs PBS
Srgn	1.06E-17	1.887E-13	0.25	1.00	1	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Tnf	1.06E-17	1.893E-13	0.53	0.31	0.137	Neutrophils	aPD-L1 vs PBS
Rpl37a	1.08E-17	1.932E-13	0.43	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Cxcl2	1.13E-17	2.013E-13	0.42	0.48	0.321	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Psmb8	1.21E-17	2.163E-13	0.26	0.82	0.759	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rps29	1.24E-17	2.218E-13	-0.33	1.00	1	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Nampt	1.26E-17	2.241E-13	0.27	0.47	0.299	Neutrophils	aTGF-β vs PBS
Rpl39	1.28E-17	2.275E-13	0.45	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
S100a10	1.33E-17	2.38E-13	-0.40	0.63	0.757	T cells	aPD-L1 vs PBS
Cxcl10	1.69E-17	3.012E-13	1.27	0.51	0.081	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Gramd3	1.85E-17	3.291E-13	0.26	0.44	0.256	T cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl27a	1.86E-17	3.312E-13	0.32	0.95	0.938	Neutrophils	aPD-L1 vs PBS
Rpl37	2.03E-17	3.617E-13	0.40	1.00	0.991	ILC	aPD-L1 + aTGF-β vs PBS
Klf2	2.05E-17	3.651E-13	-0.33	0.97	0.979	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Nlrp3	2.05E-17	3.655E-13	0.38	0.71	0.59	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rps21	2.14E-17	3.821E-13	0.32	0.96	0.943	Monocytes	aPD-L1 + aTGF-β vs PBS
Ifit1	2.17E-17	3.869E-13	0.32	0.26	0.113	Macrophages	aPD-L1 + aTGF-β vs PBS
Hspa8	2.42E-17	4.318E-13	-0.32	0.99	1	B cells	aTGF-β vs PBS
Dusp10	3.10E-17	5.526E-13	0.36	0.52	0.338	T cells	aPD-L1 + aTGF-β vs aTGF-β
Itgb7	3.30E-17	5.876E-13	0.30	0.51	0.258	Macrophages	aPD-L1 vs PBS
Gbp7	3.48E-17	6.197E-13	0.29	0.42	0.258	Neutrophils	aTGF-β vs PBS
Gm47283	3.62E-17	6.455E-13	-0.39	0.41	0.785	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Malat1	3.70E-17	6.6E-13	-0.59	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Pmepa1	3.79E-17	6.754E-13	-0.30	0.53	0.701	Macrophages	aPD-L1 + aTGF-β vs PBS
Crip1	3.87E-17	6.892E-13	0.36	0.92	0.871	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Rpl18	4.13E-17	7.356E-13	0.26	1.00	0.985	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Cxcl10	4.16E-17	7.418E-13	1.03	0.51	0.124	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Rpl41	4.42E-17	7.881E-13	0.30	1.00	1	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
H2-Aa	4.52E-17	8.064E-13	0.55	0.71	0.588	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Tgfbi	4.59E-17	8.178E-13	-0.33	0.82	0.874	Macrophages	aPD-L1 + aTGF-β vs PBS
Gbp7	5.48E-17	9.766E-13	0.36	0.45	0.309	Tumor_cells	aPD-L1 vs PBS
Pid1	5.77E-17	1.029E-12	-0.54	0.69	0.835	Monocytes	aPD-L1 + aTGF-β vs PBS
Rpl38	5.92E-17	1.055E-12	0.29	0.89	0.878	Neutrophils	aPD-L1 vs PBS
Cd274	7.23E-17	1.29E-12	0.43	0.42	0.199	Macrophages	aPD-L1 vs PBS
Rpl35a	7.51E-17	1.338E-12	0.31	0.97	0.934	Monocytes	aPD-L1 + aTGF-β vs PBS
Rpl36al	7.57E-17	1.35E-12	0.26	0.57	0.317	Macrophages	aPD-L1 vs PBS
Oasl1	7.64E-17	1.361E-12	0.32	0.54	0.386	Neutrophils	aTGF-β vs PBS
Tra2b	7.93E-17	1.413E-12	-0.25	0.73	0.822	T cells	aPD-L1 + aTGF-β vs aPD-L1
H2-Ab1	8.14E-17	1.451E-12	0.53	0.73	0.613	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Ly6a	8.24E-17	1.468E-12	0.55	0.64	0.42	Macrophages	aPD-L1 vs PBS
Tra2b	8.43E-17	1.503E-12	0.29	0.82	0.638	T cells	aPD-L1 vs PBS
Rpl36	9.54E-17	1.701E-12	0.43	0.98	0.927	Monocytes	aPD-L1 vs PBS
H2-DMb1	9.58E-17	1.708E-12	0.32	0.52	0.356	Macrophages	aPD-L1 + aTGF-β vs PBS
Fcgr4	9.75E-17	1.738E-12	0.47	0.69	0.496	Macrophages	aPD-L1 vs PBS

Tomm7	1.05E-16	1.88E-12	0.26	0.48	0.202	B cells	aPD-L1 vs PBS
Rpl32	1.08E-16	1.928E-12	0.39	0.90	0.912	Neutrophils	aPD-L1 vs PBS
Cd52	1.20E-16	2.136E-12	0.37	0.92	0.855	B cells	aTGF-β vs PBS
Crip1	1.21E-16	2.159E-12	0.25	0.70	0.575	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Nr4a1	1.24E-16	2.208E-12	-0.40	0.45	0.672	B cells	aTGF-β vs PBS
Rpl37	1.35E-16	2.404E-12	0.36	1.00	0.972	ILC	aPD-L1 + aTGF-β vs aTGF-β
Gm10076	1.40E-16	2.496E-12	0.61	0.85	0.495	ILC	aPD-L1 + aTGF-β vs PBS
Cmpk2	1.56E-16	2.78E-12	-0.35	0.18	0.303	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Nfkbia	1.59E-16	2.843E-12	0.28	0.84	0.711	Macrophages	aPD-L1 + aTGF-β vs PBS
Cdkn1a	1.77E-16	3.153E-12	-0.28	0.78	0.836	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Pfn1	1.77E-16	3.157E-12	-0.36	0.99	0.994	Monocytes	aPD-L1 vs PBS
Erp29	2.11E-16	3.757E-12	-0.29	0.77	0.888	Macrophages	aPD-L1 vs PBS
Cd274	2.11E-16	3.766E-12	0.27	0.36	0.199	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl5	2.12E-16	3.787E-12	-0.27	0.96	0.991	B cells	aPD-L1 + aTGF-β vs PBS
Rpl12	2.68E-16	4.784E-12	0.26	0.90	0.902	Neutrophils	aPD-L1 vs PBS
Fos	2.76E-16	4.913E-12	-0.38	0.99	0.994	Neutrophils	aPD-L1 + aTGF-β vs PBS
Psap	2.81E-16	5.002E-12	0.34	0.98	0.978	Macrophages	aPD-L1 vs PBS
Vps37b	3.06E-16	5.453E-12	0.35	0.79	0.627	T cells	aPD-L1 vs PBS
Ighg1	3.19E-16	5.691E-12	0.83	0.19	0.009	B cells	aPD-L1 vs PBS
Rgs10	4.33E-16	7.726E-12	-0.32	0.46	0.707	Macrophages	aPD-L1 vs PBS
Ccrl2	4.41E-16	7.862E-12	0.27	0.90	0.794	Neutrophils	aPD-L1 + aTGF-β vs PBS
Ubc	5.37E-16	9.575E-12	0.29	0.83	0.719	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps3a1	6.04E-16	1.076E-11	-0.26	0.90	0.909	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Arg2	8.17E-16	1.457E-11	0.44	0.60	0.326	Monocytes	aPD-L1 + aTGF-β vs PBS
Tmsb4x	8.65E-16	1.542E-11	-0.38	0.10	0.184	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Klf2	9.01E-16	1.606E-11	0.62	0.88	0.743	Epithelial cell:	aPD-L1 + aTGF-β vs aTGF-β
Rps28	9.37E-16	1.671E-11	-0.30	0.95	0.981	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Gapdh	9.41E-16	1.678E-11	0.34	0.88	0.842	T cells	aPD-L1 + aTGF-β vs aPD-L1
Pfn1	9.80E-16	1.747E-11	0.26	1.00	0.996	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Gbp2	1.03E-15	1.838E-11	0.28	0.33	0.135	Macrophages	aPD-L1 vs PBS
Slc7a11	1.13E-15	2.015E-11	0.32	0.67	0.532	Neutrophils	aPD-L1 + aTGF-β vs PBS
Gm47283	1.19E-15	2.115E-11	0.42	0.60	0.389	Macrophages	aPD-L1 vs PBS
Hspb1	1.19E-15	2.129E-11	-0.29	0.03	0.296	ILC	aPD-L1 + aTGF-β vs aPD-L1
Ifit3b	1.23E-15	2.193E-11	-0.37	0.19	0.308	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Gapdh	1.26E-15	2.248E-11	-0.34	0.94	0.981	Neutrophils	aPD-L1 vs PBS
Rpl27	1.31E-15	2.334E-11	0.27	0.69	0.473	Macrophages	aPD-L1 vs PBS
Sod2	1.41E-15	2.51E-11	0.31	0.33	0.185	Neutrophils	aPD-L1 + aTGF-β vs PBS
Actg1	1.45E-15	2.578E-11	-0.36	1.00	1	Neutrophils	aPD-L1 vs PBS
Rpsa	1.52E-15	2.704E-11	-0.26	0.89	0.909	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Gm42418	1.55E-15	2.762E-11	-0.54	1.00	1	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Stat1	1.57E-15	2.79E-11	0.36	0.57	0.353	Macrophages	aPD-L1 vs PBS
Rpl36	1.60E-15	2.846E-11	0.28	0.98	0.918	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
AW112010	1.72E-15	3.072E-11	0.53	0.63	0.517	T cells	aPD-L1 + aTGF-β vs aPD-L1
Dnaja1	1.89E-15	3.375E-11	0.29	0.91	0.818	T cells	aPD-L1 + aTGF-β vs aTGF-β
mt-Nd4l	2.27E-15	4.05E-11	0.29	0.66	0.37	B cells	aPD-L1 vs PBS
Atp5g2	2.43E-15	4.336E-11	-0.27	0.69	0.854	Macrophages	aPD-L1 vs PBS
H2-K1	2.44E-15	4.348E-11	0.32	1.00	0.978	Epithelial cell:	aPD-L1 + aTGF-β vs aTGF-β
Upp1	3.22E-15	5.734E-11	0.33	0.69	0.547	Neutrophils	aPD-L1 + aTGF-β vs PBS
Pfn1	3.29E-15	5.869E-11	-0.59	0.98	0.991	ILC	aPD-L1 vs PBS
mt-Atp8	3.35E-15	5.97E-11	-0.33	0.45	0.649	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Gramd3	3.52E-15	6.27E-11	0.29	0.50	0.312	T cells	aPD-L1 vs PBS
Ubc	3.69E-15	6.571E-11	0.41	0.86	0.719	Macrophages	aPD-L1 vs PBS
Son	3.87E-15	6.896E-11	0.26	0.78	0.582	T cells	aPD-L1 vs PBS
Rpl39	4.99E-15	8.89E-11	0.44	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Rps21	5.22E-15	9.3E-11	0.27	0.96	0.953	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Rps2	5.32E-15	9.483E-11	-0.29	0.96	0.984	Macrophages	aPD-L1 vs PBS
Uba52	5.85E-15	1.043E-10	0.28	0.52	0.279	B cells	aPD-L1 + aTGF-β vs PBS
Cox6c	5.89E-15	1.05E-10	0.26	0.65	0.359	B cells	aPD-L1 vs PBS
Pid1	5.97E-15	1.065E-10	-0.28	0.68	0.772	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps3	6.07E-15	1.081E-10	-0.26	0.98	0.991	Macrophages	aPD-L1 vs PBS
Rpl34	6.64E-15	1.184E-10	0.30	0.99	0.975	Monocytes	aPD-L1 + aTGF-β vs PBS
Nampt	7.39E-15	1.317E-10	0.30	0.51	0.294	Macrophages	aPD-L1 vs PBS
AY036118	7.61E-15	1.356E-10	-0.65	0.84	0.937	Monocytes	aPD-L1 + aTGF-β vs PBS
Acta2	9.36E-15	1.669E-10	-0.36	0.58	0.722	Tumor_cells	aPD-L1 vs PBS
Gnai2	1.11E-14	1.975E-10	-0.34	0.93	0.978	Monocytes	aPD-L1 vs PBS
Cd74	1.16E-14	2.067E-10	0.47	0.87	0.836	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Plac8	1.21E-14	2.162E-10	0.28	0.34	0.214	B cells	aPD-L1 + aTGF-β vs aTGF-β
Pfn1	1.23E-14	2.198E-10	0.48	0.99	0.978	ILC	aPD-L1 + aTGF-β vs aPD-L1
Rpl22l1	1.29E-14	2.298E-10	0.32	0.80	0.602	Macrophages	aPD-L1 vs PBS
Cxcl9	1.35E-14	2.402E-10	0.48	0.34	0.192	Macrophages	aPD-L1 + aTGF-β vs PBS
Psme2	1.41E-14	2.518E-10	0.31	0.72	0.466	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
mt-Atp8	1.54E-14	2.74E-10	0.37	0.60	0.272	Monocytes	aPD-L1 vs PBS
Gm26825	1.55E-14	2.758E-10	0.28	0.50	0.304	T cells	aPD-L1 vs PBS
Igkc	1.68E-14	2.99E-10	1.93	0.30	0.044	Monocytes	aPD-L1 vs PBS
Eid1	1.68E-14	2.998E-10	-0.27	0.37	0.617	Macrophages	aPD-L1 vs PBS
Apoe	1.69E-14	3.017E-10	-0.78	0.54	0.725	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Ifitm3	1.75E-14	3.119E-10	0.26	0.96	0.947	Macrophages	aPD-L1 + aTGF-β vs PBS
Samhd1	1.75E-14	3.125E-10	0.37	0.65	0.476	Neutrophils	aPD-L1 vs PBS
Nfkbia	1.77E-14	3.148E-10	0.39	0.94	0.807	Monocytes	aPD-L1 + aTGF-β vs PBS
Rps21	1.82E-14	3.248E-10	0.39	1.00	0.981	ILC	aPD-L1 + aTGF-β vs PBS
Hcst	1.83E-14	3.256E-10	0.26	0.64	0.454	T cells	aPD-L1 vs PBS
Arg2	1.85E-14	3.306E-10	0.49	0.64	0.326	Monocytes	aPD-L1 vs PBS
Ms4a6d	1.95E-14	3.477E-10	-0.35	0.83	0.896	Macrophages	aPD-L1 vs PBS
Jun	1.99E-14	3.546E-10	-0.33	0.86	0.926	T cells	aPD-L1 + aTGF-β vs PBS
Igkc	2.17E-14	3.868E-10	0.31	0.11	0.008	T cells	aPD-L1 + aTGF-β vs PBS
Atp5e	2.23E-14	3.978E-10	0.29	0.70	0.513	B cells	aPD-L1 + aTGF-β vs PBS

Psme2	2.35E-14	4.182E-10	0.41	0.79	0.571	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Samhd1	2.45E-14	4.371E-10	0.39	0.57	0.361	Macrophages	aPD-L1 vs PBS
Lgals1	2.69E-14	4.789E-10	0.41	0.65	0.34	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Rpsa	2.80E-14	4.997E-10	0.33	0.91	0.91	Neutrophils	aPD-L1 vs PBS
Lgals1	2.84E-14	5.059E-10	-0.33	0.38	0.6	T cells	aPD-L1 vs PBS
Crem	3.34E-14	5.946E-10	0.29	0.32	0.125	B cells	aPD-L1 + aTGF-β vs PBS
Psmb8	3.38E-14	6.02E-10	-0.27	0.76	0.818	T cells	aPD-L1 vs PBS
AY036118	3.42E-14	6.1E-10	-0.31	0.65	0.789	T cells	aPD-L1 + aTGF-β vs PBS
Ms4a7	3.94E-14	7.025E-10	-0.35	0.53	0.681	Macrophages	aPD-L1 + aTGF-β vs PBS
Upp1	4.06E-14	7.246E-10	0.27	0.69	0.547	Neutrophils	aTGF-β vs PBS
Rsad2	4.70E-14	8.379E-10	-0.54	0.67	0.716	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
S100a8	4.74E-14	8.447E-10	0.37	0.95	0.935	Neutrophils	aPD-L1 + aTGF-β vs PBS
Gm47283	5.15E-14	9.184E-10	-0.51	0.38	0.663	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Cd83	5.81E-14	1.035E-09	-0.36	0.83	0.872	B cells	aTGF-β vs PBS
Kdm6b	5.82E-14	1.037E-09	0.35	0.67	0.44	Monocytes	aPD-L1 + aTGF-β vs PBS
Nampt	6.18E-14	1.101E-09	0.30	0.48	0.299	Neutrophils	aPD-L1 vs PBS
Rplp2	6.36E-14	1.134E-09	-0.27	0.90	0.912	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rpl37a	6.44E-14	1.148E-09	0.54	1.00	1	ILC	aPD-L1 vs PBS
Tmsb10	6.67E-14	1.189E-09	0.63	0.95	0.724	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gm26825	6.69E-14	1.192E-09	-0.25	0.36	0.497	T cells	aPD-L1 + aTGF-β vs aPD-L1
Gbp4	6.92E-14	1.234E-09	0.35	0.34	0.158	Macrophages	aPD-L1 vs PBS
Rplp2	7.32E-14	1.305E-09	0.29	0.91	0.909	Neutrophils	aPD-L1 vs PBS
Rpl36	7.34E-14	1.308E-09	0.29	0.98	0.927	Monocytes	aPD-L1 + aTGF-β vs PBS
Cxcl10	7.55E-14	1.345E-09	-0.81	0.17	0.282	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
H2-D1	7.85E-14	1.399E-09	0.50	1.00	1	Epithelial cell	aPD-L1 + aTGF-β vs PBS
Gadd45g	7.98E-14	1.423E-09	-0.25	0.32	0.41	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Gm10260	8.30E-14	1.479E-09	0.36	0.71	0.513	Monocytes	aPD-L1 + aTGF-β vs PBS
Nfkbia	8.45E-14	1.505E-09	-0.43	0.82	0.886	B cells	aTGF-β vs PBS
Psme2	1.02E-13	1.827E-09	0.25	0.54	0.424	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rps3a1	1.20E-13	2.147E-09	-0.28	0.98	0.985	Macrophages	aPD-L1 vs PBS
Plaur	1.22E-13	2.169E-09	0.49	0.72	0.43	Monocytes	aPD-L1 vs PBS
Rps6	1.24E-13	2.219E-09	-0.26	0.93	0.98	Macrophages	aPD-L1 vs PBS
Rpl39	1.25E-13	2.235E-09	0.30	1.00	0.992	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Sqstm1	1.26E-13	2.249E-09	0.26	0.45	0.299	Macrophages	aPD-L1 + aTGF-β vs PBS
Cfl1	1.27E-13	2.269E-09	-0.35	0.94	0.994	Monocytes	aPD-L1 vs PBS
Rpl19	1.30E-13	2.323E-09	0.27	0.93	0.924	Neutrophils	aPD-L1 vs PBS
Oasl1	1.41E-13	2.519E-09	0.38	0.48	0.325	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Ier3	1.44E-13	2.559E-09	-0.34	0.99	0.999	Neutrophils	aPD-L1 vs PBS
Junb	1.52E-13	2.715E-09	-0.32	0.96	0.986	B cells	aTGF-β vs PBS
Klf2	1.58E-13	2.815E-09	0.30	0.76	0.626	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl38	1.60E-13	2.845E-09	0.35	1.00	0.993	ILC	aPD-L1 + aTGF-β vs aTGF-β
Rps4x	1.71E-13	3.047E-09	0.29	0.99	0.981	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Klf2	1.77E-13	3.153E-09	-0.34	0.83	0.901	T cells	aPD-L1 + aTGF-β vs PBS
Lars2	1.86E-13	3.31E-09	-0.34	0.16	0.422	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Acod1	1.87E-13	3.341E-09	0.32	0.86	0.75	Neutrophils	aPD-L1 vs PBS
Slfn2	1.88E-13	3.35E-09	0.27	0.68	0.587	Neutrophils	aTGF-β vs PBS
Ifit3b	1.91E-13	3.405E-09	0.33	0.31	0.179	Neutrophils	aTGF-β vs PBS
Sec61g	1.92E-13	3.426E-09	0.27	0.49	0.276	B cells	aPD-L1 + aTGF-β vs PBS
Atf3	1.97E-13	3.505E-09	0.27	0.39	0.248	Tumor_cells	aPD-L1 vs PBS
Slc38a2	2.06E-13	3.676E-09	-0.26	0.67	0.793	T cells	aPD-L1 + aTGF-β vs aPD-L1
Trim30a	2.11E-13	3.753E-09	-0.25	0.48	0.586	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Nfkb1	2.21E-13	3.933E-09	0.27	0.49	0.322	T cells	aPD-L1 + aTGF-β vs PBS
Ly6a	2.25E-13	4.009E-09	0.41	0.72	0.639	Tumor_cells	aPD-L1 vs PBS
Ldha	2.35E-13	4.197E-09	-0.29	0.91	0.937	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl35a	2.48E-13	4.423E-09	0.31	1.00	0.98	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Rpl15	2.58E-13	4.598E-09	0.25	0.99	0.966	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Shisa5	2.74E-13	4.878E-09	-0.27	0.79	0.824	T cells	aPD-L1 vs PBS
Lars2	2.96E-13	5.268E-09	0.53	0.84	0.608	Monocytes	aPD-L1 vs PBS
Tnfaip2	3.10E-13	5.523E-09	0.41	0.50	0.193	Monocytes	aPD-L1 vs PBS
Fcgr4	3.16E-13	5.625E-09	0.40	0.59	0.496	Macrophages	aPD-L1 + aTGF-β vs PBS
Atf3	3.18E-13	5.674E-09	0.47	0.90	0.768	Epithelial cell	aPD-L1 + aTGF-β vs aTGF-β
Gnai2	3.21E-13	5.727E-09	-0.27	0.70	0.739	T cells	aPD-L1 vs PBS
Dusp1	3.28E-13	5.851E-09	-0.27	0.64	0.806	B cells	aPD-L1 + aTGF-β vs PBS
Ccl4	3.35E-13	5.972E-09	0.45	0.76	0.591	Neutrophils	aPD-L1 vs PBS
Gbp2b	3.47E-13	6.184E-09	0.27	0.37	0.215	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Hspa1b	3.53E-13	6.285E-09	0.30	0.51	0.373	Macrophages	aTGF-β vs PBS
Rpl5	3.88E-13	6.918E-09	-0.25	0.99	0.996	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Mirt1	3.94E-13	7.03E-09	0.30	0.55	0.422	Neutrophils	aPD-L1 + aTGF-β vs PBS
Fdps	4.01E-13	7.143E-09	-0.27	0.41	0.508	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
AY036118	4.20E-13	7.481E-09	-1.44	0.65	1	DC	aPD-L1 + aTGF-β vs aPD-L1
H2-D1	4.27E-13	7.614E-09	0.53	1.00	0.946	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Isg20	4.35E-13	7.748E-09	-0.39	0.55	0.618	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl34	4.42E-13	7.87E-09	0.26	0.99	0.967	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Srrm2	4.70E-13	8.376E-09	-0.26	0.71	0.784	T cells	aPD-L1 vs PBS
Rps21	5.25E-13	9.355E-09	0.80	1.00	1	DC	aPD-L1 vs PBS
mt-Nd2	5.27E-13	9.387E-09	-0.48	0.93	0.978	ILC	aPD-L1 + aTGF-β vs aPD-L1
B2m	5.27E-13	9.397E-09	0.32	0.99	0.975	Epithelial cell	aPD-L1 + aTGF-β vs aTGF-β
Sod2	5.27E-13	9.398E-09	0.31	0.31	0.185	Neutrophils	aTGF-β vs PBS
Itm2b	5.29E-13	9.425E-09	-0.26	0.80	0.851	T cells	aPD-L1 vs PBS
Eif5a	5.77E-13	1.028E-08	-0.38	0.66	0.858	Monocytes	aPD-L1 vs PBS
Hist1h1c	5.95E-13	1.062E-08	-0.35	0.40	0.601	B cells	aTGF-β vs PBS
Ier2	6.49E-13	1.158E-08	-0.31	0.71	0.855	B cells	aPD-L1 + aTGF-β vs PBS
Sod2	6.64E-13	1.183E-08	0.33	0.35	0.185	Neutrophils	aPD-L1 vs PBS
Lst1	7.00E-13	1.248E-08	0.43	0.74	0.631	Macrophages	aPD-L1 vs PBS
Nfkb1	7.34E-13	1.308E-08	0.27	0.51	0.322	T cells	aPD-L1 vs PBS
Park7	7.62E-13	1.359E-08	-0.27	0.47	0.673	Macrophages	aPD-L1 vs PBS

mt-Nd3	8.45E-13	1.507E-08	0.31	0.61	0.436	Macrophages	aPD-L1 vs PBS
Marcks	8.67E-13	1.546E-08	-0.69	0.64	0.897	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ms4a7	8.76E-13	1.561E-08	-0.45	0.46	0.681	Macrophages	aPD-L1 vs PBS
Igfbp4	9.59E-13	1.709E-08	0.30	0.60	0.486	Tumor_cells	aPD-L1 vs PBS
Prelid1	9.78E-13	1.744E-08	-0.38	0.37	0.649	Monocytes	aPD-L1 vs PBS
Ccl4	9.79E-13	1.745E-08	0.33	0.72	0.591	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rplp0	1.04E-12	1.852E-08	-0.25	0.90	0.926	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Socs1	1.09E-12	1.94E-08	0.42	0.45	0.218	Monocytes	aPD-L1 + aTGF-β vs PBS
Ubc	1.11E-12	1.984E-08	0.40	0.93	0.826	Monocytes	aPD-L1 vs PBS
Vps37b	1.12E-12	1.997E-08	0.38	0.59	0.396	B cells	aPD-L1 + aTGF-β vs PBS
Cdkn1a	1.17E-12	2.084E-08	-0.27	0.78	0.817	Neutrophils	aPD-L1 + aTGF-β vs PBS
Nfkbia	1.34E-12	2.383E-08	-0.37	0.78	0.886	B cells	aPD-L1 + aTGF-β vs PBS
Rps5	1.37E-12	2.447E-08	0.30	0.99	0.978	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Fth1	1.41E-12	2.516E-08	-0.26	1.00	1	Neutrophils	aPD-L1 vs PBS
Pid1	1.42E-12	2.534E-08	-0.57	0.63	0.835	Monocytes	aPD-L1 vs PBS
Ier2	1.46E-12	2.605E-08	-0.31	0.68	0.855	B cells	aTGF-β vs PBS
Klf2	1.56E-12	2.776E-08	0.87	0.88	0.5	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Cxcl10	1.60E-12	2.856E-08	0.31	0.17	0.07	Neutrophils	aPD-L1 + aTGF-β vs PBS
Ppia	1.76E-12	3.13E-08	-0.26	0.99	0.998	Macrophages	aPD-L1 vs PBS
Ccl12	1.77E-12	3.155E-08	0.35	0.59	0.451	Macrophages	aTGF-β vs PBS
H2-K1	1.93E-12	3.446E-08	0.47	0.99	0.913	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Ighg1	1.97E-12	3.516E-08	1.40	0.16	0.003	Monocytes	aPD-L1 vs PBS
Cox5a	2.02E-12	3.609E-08	0.27	0.81	0.608	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Tnfaip2	2.05E-12	3.656E-08	0.34	0.44	0.193	Monocytes	aPD-L1 + aTGF-β vs PBS
Dusp5	2.07E-12	3.686E-08	0.39	0.55	0.31	Monocytes	aPD-L1 + aTGF-β vs PBS
Lars2	2.10E-12	3.746E-08	0.46	0.73	0.59	Macrophages	aPD-L1 vs PBS
Gbp2b	2.18E-12	3.889E-08	0.39	0.65	0.396	Monocytes	aPD-L1 + aTGF-β vs PBS
Dusp2	2.28E-12	4.065E-08	-0.34	0.61	0.715	B cells	aPD-L1 + aTGF-β vs PBS
Gbp3	2.35E-12	4.197E-08	0.26	0.39	0.26	Tumor_cells	aPD-L1 vs PBS
Ifitm2	2.43E-12	4.332E-08	0.27	0.96	0.905	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Irf1	2.52E-12	4.5E-08	0.60	0.63	0.295	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Fstl1	2.73E-12	4.866E-08	-0.68	0.94	0.954	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gm42418	2.75E-12	4.9E-08	-0.48	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Rpl34	2.78E-12	4.951E-08	0.36	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
H2-D1	2.95E-12	5.256E-08	0.48	1.00	0.985	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Il1a	3.03E-12	5.396E-08	0.32	0.18	0.095	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl18	3.05E-12	5.434E-08	0.33	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Marcksl1	3.08E-12	5.49E-08	0.31	0.59	0.479	Neutrophils	aPD-L1 + aTGF-β vs PBS
Htra3	3.17E-12	5.652E-08	-0.65	0.57	0.874	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Cxcl2	3.50E-12	6.241E-08	0.26	0.44	0.176	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Ppp1r3b	3.61E-12	6.443E-08	-0.30	0.33	0.472	Neutrophils	aPD-L1 vs PBS
Pde4b	3.62E-12	6.444E-08	0.35	0.52	0.291	Monocytes	aPD-L1 + aTGF-β vs PBS
Cxcl14	3.62E-12	6.446E-08	-0.35	0.42	0.633	Macrophages	aPD-L1 vs PBS
Socs1	3.82E-12	6.813E-08	0.31	0.45	0.228	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Adgre5	4.00E-12	7.135E-08	0.29	0.33	0.157	Macrophages	aPD-L1 vs PBS
Tnfaip3	4.12E-12	7.343E-08	0.39	0.60	0.304	Monocytes	aPD-L1 vs PBS
Crip1	4.22E-12	7.523E-08	0.64	0.87	0.83	Macrophages	aPD-L1 vs PBS
Rps27	4.38E-12	7.807E-08	-0.29	0.99	0.993	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Prkca	4.39E-12	7.819E-08	0.28	0.46	0.29	T cells	aPD-L1 vs PBS
Cd36	4.84E-12	8.636E-08	0.39	0.35	0.17	Macrophages	aPD-L1 vs PBS
Icam1	4.90E-12	8.742E-08	0.28	0.20	0.099	Neutrophils	aTGF-β vs PBS
Gm47283	4.92E-12	8.766E-08	-0.62	0.57	0.778	ILC	aPD-L1 + aTGF-β vs aPD-L1
Arhgdib	5.23E-12	9.316E-08	-0.26	0.67	0.762	T cells	aPD-L1 vs PBS
Rpl22	5.25E-12	9.363E-08	0.32	0.98	0.969	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Col14a1	5.45E-12	9.715E-08	-0.66	0.63	0.908	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rpl36	6.04E-12	1.076E-07	0.29	0.89	0.908	Neutrophils	aPD-L1 vs PBS
Spp1	6.24E-12	1.112E-07	0.95	0.68	0.5	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Pf4	6.69E-12	1.193E-07	-0.60	0.24	0.483	Macrophages	aPD-L1 vs PBS
Rpl37	7.08E-12	1.263E-07	0.48	1.00	0.991	ILC	aPD-L1 vs PBS
Ppp1r14b	7.18E-12	1.279E-07	-0.28	0.42	0.613	Macrophages	aPD-L1 vs PBS
Samhd1	7.31E-12	1.303E-07	0.27	0.50	0.361	Macrophages	aPD-L1 + aTGF-β vs PBS
Rps29	7.35E-12	1.311E-07	0.52	1.00	1	ILC	aPD-L1 vs PBS
Fn1	7.41E-12	1.322E-07	-0.71	0.92	0.954	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rpl37	7.46E-12	1.33E-07	0.76	1.00	1	DC	aPD-L1 vs PBS
Rpl39	7.52E-12	1.341E-07	0.95	1.00	1	DC	aPD-L1 vs PBS
Serf2	7.55E-12	1.345E-07	0.32	0.92	0.762	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Ifrd1	7.75E-12	1.381E-07	0.34	0.84	0.623	Monocytes	aPD-L1 + aTGF-β vs PBS
Btg2	7.75E-12	1.381E-07	-0.28	0.91	0.926	B cells	aPD-L1 vs PBS
Rpl41	7.88E-12	1.404E-07	0.36	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Igfbp5	7.88E-12	1.405E-07	1.15	0.67	0.242	Fibroblasts	aPD-L1 vs PBS
Marcksl1	8.12E-12	1.447E-07	0.30	0.59	0.479	Neutrophils	aTGF-β vs PBS
Rps8	8.21E-12	1.464E-07	0.28	0.93	0.928	Neutrophils	aPD-L1 vs PBS
Tnfaip3	8.29E-12	1.478E-07	0.28	0.75	0.554	T cells	aPD-L1 vs PBS
Rps27	8.32E-12	1.482E-07	0.60	1.00	1	ILC	aPD-L1 vs PBS
Dusp1	8.70E-12	1.551E-07	-0.26	0.67	0.806	B cells	aPD-L1 vs PBS
Rplp0	8.75E-12	1.559E-07	0.29	0.93	0.926	Neutrophils	aPD-L1 vs PBS
Rgs10	9.02E-12	1.609E-07	0.26	0.70	0.455	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Rpl22l1	9.05E-12	1.613E-07	0.43	0.75	0.513	Monocytes	aPD-L1 vs PBS
Il1rn	9.06E-12	1.616E-07	0.27	0.75	0.652	Neutrophils	aPD-L1 + aTGF-β vs PBS
Arpc1b	9.63E-12	1.717E-07	-0.31	0.94	0.991	Monocytes	aPD-L1 vs PBS
Junb	9.71E-12	1.732E-07	-0.30	0.98	0.986	B cells	aPD-L1 + aTGF-β vs PBS
Jun	9.87E-12	1.76E-07	-0.34	0.97	0.988	Neutrophils	aPD-L1 + aTGF-β vs PBS
Smad7	9.92E-12	1.768E-07	-0.57	0.66	0.83	ILC	aPD-L1 + aTGF-β vs aPD-L1
Nfe2l2	1.00E-11	1.783E-07	0.40	0.55	0.316	Monocytes	aPD-L1 + aTGF-β vs PBS
H2-DMb1	1.18E-11	2.095E-07	0.27	0.52	0.374	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Gm10076	1.19E-11	2.125E-07	0.53	0.87	0.495	ILC	aPD-L1 vs PBS

Tgfbi	1.28E-11	2.274E-07	-0.35	0.76	0.874	Macrophages	aPD-L1 vs PBS
Rpl37a	1.30E-11	2.319E-07	-0.29	0.99	0.995	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Rel	1.31E-11	2.333E-07	0.37	0.53	0.291	Monocytes	aPD-L1 + aTGF-β vs PBS
Ccl3	1.31E-11	2.34E-07	0.30	0.62	0.461	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl37a	1.39E-11	2.477E-07	0.71	1.00	1	DC	aPD-L1 vs PBS
Rps27	1.40E-11	2.502E-07	0.86	1.00	1	DC	aPD-L1 vs PBS
B2m	1.44E-11	2.56E-07	0.61	0.99	0.882	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Ifitm2	1.46E-11	2.6E-07	-0.32	0.91	0.965	Neutrophils	aPD-L1 vs PBS
Rpl36	1.58E-11	2.823E-07	0.34	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Gatm	1.62E-11	2.883E-07	-0.36	0.64	0.792	Macrophages	aPD-L1 vs PBS
AC160336.1	1.68E-11	2.99E-07	-0.27	0.53	0.648	B cells	aPD-L1 + aTGF-β vs aPD-L1
Zfp36	1.72E-11	3.066E-07	-0.30	0.71	0.823	B cells	aPD-L1 + aTGF-β vs PBS
Rpl10a	1.74E-11	3.099E-07	0.28	0.96	0.918	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Fst	1.78E-11	3.181E-07	0.28	0.39	0.27	Tumor_cells	aPD-L1 vs PBS
Slfn4	1.83E-11	3.255E-07	-0.26	0.85	0.853	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Cryab	1.84E-11	3.272E-07	-0.26	0.44	0.505	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
Cr2	1.90E-11	3.381E-07	0.26	0.47	0.265	B cells	aTGF-β vs PBS
Hsp90aa1	1.95E-11	3.482E-07	-0.30	0.98	0.989	B cells	aTGF-β vs PBS
Ltb	1.99E-11	3.545E-07	-0.35	0.62	0.704	B cells	aPD-L1 vs PBS
Sdf4	2.01E-11	3.582E-07	0.25	0.46	0.331	T cells	aPD-L1 + aTGF-β vs aPD-L1
Pkm	2.05E-11	3.651E-07	-0.30	0.65	0.73	T cells	aPD-L1 vs PBS
mt-Atp6	2.17E-11	3.869E-07	-0.40	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Cd34	2.20E-11	3.925E-07	-0.60	0.48	0.828	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rplp2	2.29E-11	4.091E-07	0.28	0.99	0.981	Monocytes	aPD-L1 vs PBS
Btg2	2.55E-11	4.538E-07	-0.26	0.84	0.926	B cells	aTGF-β vs PBS
Fbn1	2.61E-11	4.661E-07	-0.76	0.78	0.92	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Cmah	2.73E-11	4.874E-07	-0.39	0.17	0.54	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
B2m	2.95E-11	5.262E-07	0.49	1.00	0.919	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Ccl4	3.05E-11	5.431E-07	0.32	0.76	0.653	Macrophages	aTGF-β vs PBS
F10	3.23E-11	5.762E-07	0.32	0.44	0.203	Monocytes	aPD-L1 + aTGF-β vs PBS
C1qa	3.25E-11	5.797E-07	0.44	0.82	0.69	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Hspa1b	3.32E-11	5.913E-07	-0.60	0.45	0.593	B cells	aPD-L1 vs PBS
Cyr61	3.42E-11	6.101E-07	-0.28	0.49	0.543	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Hspa1b	3.45E-11	6.149E-07	-0.29	0.61	0.721	T cells	aPD-L1 + aTGF-β vs aTGF-β
Psmb8	3.63E-11	6.466E-07	-0.47	0.84	0.953	ILC	aPD-L1 vs PBS
Rpl35a	3.76E-11	6.705E-07	0.70	1.00	1	DC	aPD-L1 vs PBS
Rps29	3.93E-11	7.009E-07	0.27	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Lrrn4cl	4.02E-11	7.172E-07	-0.47	0.22	0.598	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rps21	4.03E-11	7.182E-07	0.51	1.00	0.981	ILC	aPD-L1 vs PBS
Ifi27l2a	4.23E-11	7.537E-07	-0.36	0.59	0.716	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Srgn	4.23E-11	7.541E-07	-0.31	0.89	0.905	Macrophages	aTGF-β vs PBS
Lst1	4.42E-11	7.882E-07	0.32	0.56	0.412	Neutrophils	aPD-L1 vs PBS
Selenom	4.44E-11	7.915E-07	0.50	0.42	0.316	Macrophages	aPD-L1 + aTGF-β vs PBS
Crem	4.54E-11	8.098E-07	0.26	0.30	0.125	B cells	aPD-L1 vs PBS
Icam1	4.68E-11	8.343E-07	0.33	0.22	0.099	Neutrophils	aPD-L1 vs PBS
Igfbp5	4.74E-11	8.451E-07	-1.17	0.32	0.667	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Hist1h2bc	4.75E-11	8.474E-07	-0.27	0.17	0.278	B cells	aPD-L1 + aTGF-β vs aPD-L1
Csf1	5.08E-11	9.053E-07	0.27	0.44	0.279	Neutrophils	aPD-L1 vs PBS
Klf2	5.20E-11	9.276E-07	-0.43	0.97	0.976	Neutrophils	aPD-L1 + aTGF-β vs PBS
Ltb	5.26E-11	9.377E-07	-0.30	0.75	0.822	T cells	aPD-L1 vs PBS
Lars2	5.44E-11	9.701E-07	-0.51	0.34	0.747	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Bst2	5.91E-11	1.053E-06	-0.44	0.63	0.767	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Cd52	6.39E-11	1.14E-06	0.25	0.82	0.757	Neutrophils	aPD-L1 vs PBS
Ms4a6c	6.41E-11	1.143E-06	-0.39	0.83	0.905	Monocytes	aPD-L1 vs PBS
Rps5	6.48E-11	1.156E-06	0.33	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Igfbp6	6.49E-11	1.157E-06	-0.76	0.71	0.897	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
AY036118	6.71E-11	1.196E-06	-1.55	0.70	1	NK cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl17	6.87E-11	1.225E-06	-0.25	1.00	1	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Spag9	6.87E-11	1.225E-06	0.30	0.72	0.519	Monocytes	aPD-L1 + aTGF-β vs PBS
Bst2	6.88E-11	1.227E-06	-0.37	0.63	0.785	Monocytes	aPD-L1 + aTGF-β vs PBS
Slfn5	7.02E-11	1.252E-06	-0.28	0.38	0.474	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Irf1	7.17E-11	1.278E-06	0.47	0.44	0.221	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Ccl4	7.26E-11	1.294E-06	0.38	0.70	0.591	Neutrophils	aTGF-β vs PBS
Socs3	7.66E-11	1.366E-06	-0.31	0.69	0.754	Neutrophils	aTGF-β vs PBS
Pfn1	8.14E-11	1.451E-06	0.28	1.00	0.985	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Uba52	8.56E-11	1.526E-06	0.28	0.45	0.199	Monocytes	aPD-L1 vs PBS
Cd274	8.71E-11	1.552E-06	0.47	0.63	0.373	Monocytes	aPD-L1 vs PBS
Rpl38	8.76E-11	1.562E-06	-0.29	0.96	0.964	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Pf4	8.92E-11	1.591E-06	-0.63	0.35	0.483	Macrophages	aPD-L1 + aTGF-β vs PBS
Dennd4a	9.43E-11	1.681E-06	-0.29	0.53	0.684	B cells	aTGF-β vs PBS
Sh3bgrl3	1.00E-10	1.785E-06	-0.25	0.72	0.749	T cells	aPD-L1 vs PBS
Cytip	1.01E-10	1.797E-06	0.36	0.67	0.468	Monocytes	aPD-L1 + aTGF-β vs PBS
Tgfbi	1.03E-10	1.836E-06	-0.43	0.77	0.877	Monocytes	aPD-L1 + aTGF-β vs PBS
Nr4a1	1.03E-10	1.842E-06	0.26	0.30	0.14	Macrophages	aPD-L1 vs PBS
Atrx	1.04E-10	1.849E-06	-0.28	0.37	0.506	T cells	aPD-L1 vs PBS
Icam1	1.06E-10	1.887E-06	0.30	0.44	0.247	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Dennd4a	1.11E-10	1.979E-06	0.41	0.51	0.256	Monocytes	aPD-L1 vs PBS
Gm10260	1.13E-10	2.02E-06	-0.26	0.79	0.914	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
H2-K1	1.14E-10	2.032E-06	0.47	1.00	0.956	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Samsn1	1.20E-10	2.138E-06	0.31	0.44	0.262	B cells	aPD-L1 + aTGF-β vs PBS
Cfl1	1.22E-10	2.176E-06	0.29	0.97	0.944	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Lgals1	1.27E-10	2.27E-06	-0.40	0.84	0.911	Monocytes	aPD-L1 + aTGF-β vs PBS
Tmx4	1.32E-10	2.348E-06	-0.27	0.24	0.376	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Cd274	1.32E-10	2.354E-06	0.38	0.67	0.478	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Hspa1b	1.33E-10	2.379E-06	-0.32	0.41	0.593	B cells	aPD-L1 + aTGF-β vs PBS
Rps3a1	1.37E-10	2.45E-06	0.26	0.91	0.926	Neutrophils	aPD-L1 vs PBS

Rpl36	1.45E-10	2.59E-06	0.44	1.00	1	ILC	aPD-L1 vs PBS
Hist1h2bc	1.50E-10	2.68E-06	-0.40	0.16	0.305	B cells	aTGF-β vs PBS
Ly6a	1.53E-10	2.734E-06	0.34	0.69	0.428	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Iglc2	1.55E-10	2.759E-06	-0.27	0.77	0.858	B cells	aPD-L1 + aTGF-β vs PBS
Thbs1	1.55E-10	2.76E-06	0.27	0.14	0.056	Neutrophils	aTGF-β vs PBS
Scara3	1.71E-10	3.051E-06	-0.47	0.26	0.621	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Clec3b	1.71E-10	3.053E-06	-0.67	0.68	0.897	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rpl22	1.75E-10	3.117E-06	0.44	0.96	0.885	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ifi27l2a	1.79E-10	3.19E-06	0.34	0.67	0.55	T cells	aPD-L1 + aTGF-β vs PBS
Hal	1.82E-10	3.24E-06	0.26	0.29	0.172	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Tnf	1.83E-10	3.266E-06	0.31	0.24	0.137	Neutrophils	aPD-L1 + aTGF-β vs PBS
Rpl38	1.98E-10	3.531E-06	0.31	1.00	0.991	ILC	aPD-L1 + aTGF-β vs PBS
Nfix	2.14E-10	3.811E-06	-0.30	0.33	0.594	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Ly6e	2.27E-10	4.042E-06	-0.26	0.66	0.723	Neutrophils	aPD-L1 + aTGF-β vs aTGF-β
Rpl34	2.40E-10	4.274E-06	0.34	0.97	0.975	Monocytes	aPD-L1 vs PBS
Nfkbia	2.42E-10	4.309E-06	-0.38	0.80	0.886	B cells	aPD-L1 vs PBS
H2-Q7	2.43E-10	4.33E-06	0.25	0.53	0.356	Macrophages	aPD-L1 vs PBS
Pamr1	2.46E-10	4.392E-06	-0.45	0.17	0.529	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ccl2	2.64E-10	4.712E-06	0.29	0.69	0.565	Macrophages	aPD-L1 + aTGF-β vs PBS
Ccr2	2.67E-10	4.76E-06	-0.28	0.38	0.491	Macrophages	aPD-L1 + aTGF-β vs PBS
Gas7	2.71E-10	4.826E-06	-0.73	0.33	0.678	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Hmgb2	2.73E-10	4.874E-06	0.26	0.78	0.564	B cells	aPD-L1 vs PBS
Ndel1	2.83E-10	5.038E-06	-0.29	0.50	0.611	Neutrophils	aPD-L1 vs PBS
Rpl18a	2.83E-10	5.05E-06	0.29	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Ly6e	2.98E-10	5.307E-06	0.31	0.85	0.759	Macrophages	aPD-L1 vs PBS
Rps28	3.20E-10	5.706E-06	-0.64	0.94	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Rpl35	3.72E-10	6.635E-06	0.33	0.92	0.816	Monocytes	aPD-L1 vs PBS
Fth1	3.91E-10	6.969E-06	-0.29	1.00	1	Macrophages	aPD-L1 vs PBS
Dpt	3.95E-10	7.049E-06	-0.61	0.70	0.908	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gapdh	4.13E-10	7.364E-06	0.27	0.99	0.955	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Pgam1	4.28E-10	7.632E-06	-0.30	0.85	0.923	Neutrophils	aPD-L1 vs PBS
Sem1	4.29E-10	7.644E-06	0.31	0.94	0.902	Monocytes	aPD-L1 vs PBS
Sh3bgrl3	4.31E-10	7.687E-06	-0.32	0.85	0.908	Monocytes	aPD-L1 vs PBS
Ifrd1	4.31E-10	7.69E-06	0.44	0.87	0.623	Monocytes	aPD-L1 vs PBS
Vps37b	4.32E-10	7.696E-06	0.34	0.60	0.396	B cells	aPD-L1 vs PBS
Rpl34	4.41E-10	7.869E-06	0.66	1.00	1	DC	aPD-L1 vs PBS
Atf3	4.55E-10	8.111E-06	0.39	0.91	0.826	Monocytes	aTGF-β vs PBS
Rpl38	4.66E-10	8.304E-06	0.63	1.00	1	DC	aPD-L1 vs PBS
Lgals1	4.68E-10	8.35E-06	0.43	0.50	0.377	T cells	aPD-L1 + aTGF-β vs aPD-L1
Ubald2	4.82E-10	8.593E-06	0.28	0.48	0.346	T cells	aPD-L1 + aTGF-β vs PBS
AW112010	4.90E-10	8.726E-06	0.53	0.92	0.748	ILC	aPD-L1 + aTGF-β vs aPD-L1
Rpl38	4.91E-10	8.755E-06	0.44	1.00	0.991	ILC	aPD-L1 vs PBS
Clec4e	5.02E-10	8.953E-06	0.32	0.79	0.669	Neutrophils	aPD-L1 vs PBS
Rps29	5.09E-10	9.07E-06	0.64	1.00	1	DC	aPD-L1 vs PBS
Tnfaip3	5.25E-10	9.357E-06	0.29	0.57	0.396	Neutrophils	aPD-L1 vs PBS
Wfdc17	5.29E-10	9.426E-06	1.30	0.41	0.259	Macrophages	aPD-L1 vs PBS
Cox8a	5.33E-10	9.499E-06	0.29	0.97	0.895	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Plaur	5.36E-10	9.556E-06	0.38	0.63	0.43	Monocytes	aPD-L1 + aTGF-β vs PBS
Scara5	5.52E-10	9.835E-06	-0.46	0.21	0.563	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Fos	5.96E-10	1.062E-05	-0.39	0.97	0.994	Neutrophils	aPD-L1 vs PBS
Dusp2	5.96E-10	1.062E-05	0.26	0.26	0.119	Macrophages	aPD-L1 vs PBS
Rps28	6.14E-10	1.095E-05	-0.30	0.92	0.944	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Rpl22l1	6.17E-10	1.101E-05	0.26	0.71	0.513	Monocytes	aPD-L1 + aTGF-β vs PBS
Il1b	6.45E-10	1.15E-05	0.49	0.82	0.699	Monocytes	aPD-L1 + aTGF-β vs PBS
Actb	6.49E-10	1.158E-05	-0.35	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Rpl35	6.62E-10	1.18E-05	0.29	0.79	0.824	Neutrophils	aPD-L1 vs PBS
Slfn4	6.71E-10	1.196E-05	-0.53	0.36	0.529	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
mt-Co3	6.75E-10	1.202E-05	-0.37	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Ccl5	7.23E-10	1.288E-05	0.37	0.18	0.083	Macrophages	aPD-L1 + aTGF-β vs PBS
Selenom	7.25E-10	1.293E-05	0.43	0.47	0.316	Macrophages	aPD-L1 vs PBS
Nfkbia	7.40E-10	1.319E-05	0.37	0.91	0.807	Monocytes	aPD-L1 vs PBS
Irf1	7.48E-10	1.333E-05	0.61	0.68	0.295	Fibroblasts	aPD-L1 vs PBS
Adgre5	7.74E-10	1.38E-05	0.32	0.52	0.291	Monocytes	aPD-L1 + aTGF-β vs PBS
Rps29	7.93E-10	1.414E-05	0.28	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Rpl30	8.13E-10	1.448E-05	0.25	1.00	0.992	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Fgl2	8.18E-10	1.458E-05	0.32	0.44	0.277	Macrophages	aPD-L1 vs PBS
Fos	8.20E-10	1.461E-05	-0.37	0.86	0.872	T cells	aPD-L1 vs PBS
AY036118	8.25E-10	1.471E-05	1.22	1.00	0.792	DC	aPD-L1 vs PBS
Arg2	8.30E-10	1.48E-05	0.31	0.60	0.44	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Actb	8.54E-10	1.522E-05	-0.42	1.00	1	ILC	aPD-L1 vs PBS
C1qc	8.74E-10	1.557E-05	0.39	0.81	0.69	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Rsad2	9.17E-10	1.635E-05	0.48	0.40	0.232	Macrophages	aPD-L1 vs PBS
Gatm	9.22E-10	1.644E-05	-0.27	0.71	0.792	Macrophages	aPD-L1 + aTGF-β vs PBS
Ubc	9.24E-10	1.647E-05	0.39	0.90	0.866	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Rpl34	9.27E-10	1.653E-05	0.29	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Gm42418	9.53E-10	1.699E-05	0.49	1.00	1	Fibroblasts	aPD-L1 vs PBS
Rilpl2	9.68E-10	1.725E-05	0.25	0.45	0.234	Monocytes	aPD-L1 + aTGF-β vs PBS
Cxcl9	1.04E-09	1.856E-05	0.79	0.35	0.192	Macrophages	aPD-L1 vs PBS
Ccr7	1.05E-09	1.871E-05	-0.26	0.58	0.735	B cells	aTGF-β vs PBS
Ly6a	1.05E-09	1.871E-05	0.25	0.17	0.088	B cells	aPD-L1 + aTGF-β vs aPD-L1
Rps4x	1.05E-09	1.876E-05	0.33	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Lgals1	1.08E-09	1.932E-05	-0.47	0.78	0.911	Monocytes	aPD-L1 vs PBS
Ltb	1.09E-09	1.941E-05	-0.28	0.60	0.704	B cells	aPD-L1 + aTGF-β vs PBS
Dnaja1	1.11E-09	1.977E-05	0.28	0.94	0.862	T cells	aPD-L1 vs PBS
mt-Atp6	1.16E-09	2.067E-05	-0.37	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Rac2	1.24E-09	2.216E-05	0.40	0.88	0.719	ILC	aPD-L1 + aTGF-β vs aPD-L1

Rpl35a	1.26E-09	2.241E-05	0.46	1.00	0.972	ILC	aPD-L1 vs PBS
Mt1	1.38E-09	2.451E-05	0.84	0.79	0.412	Epithelial cell	aPD-L1 + aTGF-β vs PBS
Rpl37	1.38E-09	2.461E-05	-0.48	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Fcgr3	1.40E-09	2.495E-05	-0.29	0.66	0.743	Neutrophils	aPD-L1 vs PBS
Gm42418	1.43E-09	2.55E-05	-0.45	1.00	1	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Malt1	1.43E-09	2.557E-05	0.38	0.62	0.361	Monocytes	aPD-L1 vs PBS
Jun	1.44E-09	2.571E-05	0.26	0.89	0.834	Tumor_cells	aPD-L1 vs PBS
Cxcl10	1.45E-09	2.592E-05	0.71	0.41	0.081	Fibroblasts	aPD-L1 vs PBS
Zfp36	1.46E-09	2.598E-05	-0.28	0.71	0.823	B cells	aTGF-β vs PBS
Ldha	1.55E-09	2.769E-05	-0.26	0.60	0.682	T cells	aPD-L1 vs PBS
AW112010	1.60E-09	2.845E-05	0.46	0.71	0.544	Macrophages	aPD-L1 vs PBS
H2-D1	1.63E-09	2.899E-05	0.39	1.00	1	Epithelial cell	aPD-L1 vs PBS
Slc11a1	1.63E-09	2.912E-05	0.28	0.53	0.378	Macrophages	aPD-L1 vs PBS
Gm10076	1.64E-09	2.932E-05	0.36	0.85	0.667	ILC	aPD-L1 + aTGF-β vs aTGF-β
Rpl28	1.68E-09	3.002E-05	0.25	0.91	0.925	Neutrophils	aPD-L1 vs PBS
Polr2l	1.70E-09	3.024E-05	0.34	0.40	0.174	Monocytes	aPD-L1 vs PBS
Hsp90aa1	1.75E-09	3.112E-05	-0.27	0.94	0.969	Neutrophils	aTGF-β vs PBS
Cxcl10	1.76E-09	3.129E-05	0.46	0.59	0.481	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Wfdc17	1.77E-09	3.16E-05	0.57	0.37	0.259	Macrophages	aPD-L1 + aTGF-β vs PBS
Pid1	1.78E-09	3.179E-05	-0.33	0.69	0.772	Macrophages	aPD-L1 vs PBS
AC160336.1	1.81E-09	3.232E-05	0.28	0.46	0.304	T cells	aPD-L1 vs PBS
Tspo	1.83E-09	3.261E-05	-0.35	0.90	0.953	Monocytes	aPD-L1 vs PBS
Cd83	1.83E-09	3.268E-05	0.34	0.57	0.373	Monocytes	aPD-L1 + aTGF-β vs PBS
Mgp	1.86E-09	3.312E-05	0.30	0.34	0.266	Tumor_cells	aPD-L1 + aTGF-β vs aTGF-β
P4hb	1.88E-09	3.345E-05	-0.27	0.41	0.498	Neutrophils	aPD-L1 + aTGF-β vs PBS
Ppia	1.88E-09	3.35E-05	-0.35	0.94	0.962	Monocytes	aPD-L1 vs PBS
Ntpcr	1.89E-09	3.369E-05	-0.25	0.37	0.557	Macrophages	aPD-L1 vs PBS
Rps15a	1.91E-09	3.411E-05	0.37	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Klf2	1.92E-09	3.417E-05	-0.31	0.93	0.966	B cells	aTGF-β vs PBS
Bsg	1.92E-09	3.418E-05	-0.25	0.60	0.73	Neutrophils	aPD-L1 vs PBS
S100a10	1.98E-09	3.532E-05	0.38	0.67	0.625	T cells	aPD-L1 + aTGF-β vs aPD-L1
Hist1h1c	1.99E-09	3.548E-05	-0.25	0.39	0.496	B cells	aPD-L1 + aTGF-β vs aPD-L1
Mt1	2.06E-09	3.68E-05	0.48	0.79	0.641	Epithelial cell	aPD-L1 + aTGF-β vs aTGF-β
Arg1	2.09E-09	3.723E-05	-0.44	0.29	0.42	Macrophages	aPD-L1 + aTGF-β vs PBS
Dennd4a	2.35E-09	4.191E-05	0.36	0.44	0.256	Monocytes	aPD-L1 + aTGF-β vs PBS
mt-Co3	2.37E-09	4.228E-05	-0.34	1.00	0.995	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Cdkn1a	2.39E-09	4.259E-05	0.28	0.78	0.699	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rpl36	2.42E-09	4.316E-05	0.28	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Ifrd1	2.43E-09	4.324E-05	0.37	0.60	0.445	Macrophages	aPD-L1 vs PBS
Zfp36	2.45E-09	4.364E-05	0.35	0.84	0.69	Macrophages	aPD-L1 vs PBS
Malat1	2.46E-09	4.383E-05	0.54	1.00	0.991	ILC	aPD-L1 vs PBS
Socs3	2.56E-09	4.567E-05	0.30	0.77	0.589	Monocytes	aPD-L1 + aTGF-β vs PBS
Hist1h2bc	2.58E-09	4.602E-05	-0.38	0.17	0.305	B cells	aPD-L1 + aTGF-β vs PBS
mt-Co3	2.81E-09	5.003E-05	-0.37	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Timp2	2.91E-09	5.19E-05	-0.54	0.88	0.954	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Fcgr4	2.93E-09	5.22E-05	0.31	0.59	0.504	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Junb	3.02E-09	5.39E-05	-0.27	0.98	0.986	B cells	aPD-L1 vs PBS
Ftl1	3.10E-09	5.524E-05	-0.26	0.98	0.994	B cells	aPD-L1 vs PBS
H2-K1	3.39E-09	6.05E-05	0.39	0.99	0.946	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Tmsb10	3.55E-09	6.329E-05	0.29	0.86	0.879	Neutrophils	aPD-L1 vs PBS
Dusp2	3.63E-09	6.462E-05	-0.30	0.61	0.715	B cells	aTGF-β vs PBS
Klf2	3.68E-09	6.56E-05	0.86	0.79	0.5	Epithelial cell	aPD-L1 vs PBS
Nfkbia	3.78E-09	6.742E-05	0.27	0.87	0.711	Macrophages	aPD-L1 vs PBS
Nr4a1	3.85E-09	6.871E-05	0.49	0.62	0.386	Monocytes	aPD-L1 vs PBS
Pmepa1	3.86E-09	6.887E-05	-0.27	0.06	0.199	Monocytes	aTGF-β vs PBS
Rps21	4.01E-09	7.157E-05	-0.45	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Lgals1	4.02E-09	7.172E-05	0.29	0.99	0.966	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Adamts5	4.12E-09	7.345E-05	-0.62	0.53	0.816	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ccl6	4.17E-09	7.433E-05	-0.38	0.50	0.586	Neutrophils	aPD-L1 + aTGF-β vs PBS
Fth1	4.25E-09	7.576E-05	0.27	1.00	1	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Ly6a	4.39E-09	7.825E-05	0.38	0.56	0.46	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Dnaja1	4.49E-09	7.996E-05	0.65	0.96	0.841	ILC	aPD-L1 vs PBS
Polr2l	4.51E-09	8.038E-05	0.25	0.36	0.203	Macrophages	aPD-L1 vs PBS
Klf2	4.55E-09	8.106E-05	0.27	0.80	0.626	Macrophages	aPD-L1 vs PBS
Rel	5.00E-09	8.908E-05	0.31	0.54	0.291	Monocytes	aPD-L1 vs PBS
Timp2	5.12E-09	9.135E-05	0.55	0.95	0.866	Fibroblasts	aPD-L1 vs PBS
S100a6	5.19E-09	9.256E-05	0.49	0.97	0.887	Epithelial cell	aPD-L1 + aTGF-β vs aPD-L1
Fos	5.37E-09	9.576E-05	-0.27	0.81	0.872	T cells	aPD-L1 + aTGF-β vs PBS
mt-Co2	5.38E-09	9.597E-05	-0.35	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Rps15a	5.42E-09	9.654E-05	0.29	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Spp1	6.05E-09	0.0001078	0.30	0.97	0.968	Tumor_cells	aPD-L1 vs PBS
Cxcr4	6.53E-09	0.0001164	-0.29	0.50	0.624	B cells	aTGF-β vs PBS
Emilin2	6.62E-09	0.000118	-0.50	0.38	0.69	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gng11	6.68E-09	0.0001191	-0.29	0.30	0.362	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Btg1	6.77E-09	0.0001207	-0.38	0.74	0.866	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Ifitm2	6.84E-09	0.0001219	-0.37	0.90	0.962	Monocytes	aPD-L1 vs PBS
Rpl39	7.05E-09	0.0001256	0.50	1.00	1	ILC	aPD-L1 vs PBS
Jun	7.05E-09	0.0001257	-0.30	0.98	0.988	Neutrophils	aTGF-β vs PBS
Smc6	7.06E-09	0.0001259	-0.26	0.66	0.709	T cells	aPD-L1 + aTGF-β vs PBS
Oaz1	7.14E-09	0.0001272	-0.27	0.87	0.953	Monocytes	aPD-L1 vs PBS
Marcks	7.24E-09	0.0001291	0.56	0.90	0.745	Fibroblasts	aPD-L1 vs PBS
Mmp2	7.37E-09	0.0001314	0.29	0.32	0.223	Tumor_cells	aPD-L1 vs PBS
Mdm2	7.44E-09	0.0001327	0.42	0.51	0.291	Monocytes	aPD-L1 vs PBS
Zfand5	7.52E-09	0.0001341	0.29	0.75	0.573	Monocytes	aPD-L1 + aTGF-β vs PBS
AW112010	7.73E-09	0.0001379	0.41	0.70	0.65	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Sept1	8.03E-09	0.0001431	0.36	0.75	0.474	ILC	aPD-L1 + aTGF-β vs aPD-L1

Tmsb10	8.04E-09	0.0001433	0.37	0.82	0.66	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl39	8.18E-09	0.0001458	0.49	1.00	1	DC	aPD-L1 + aTGF-β vs PBS
Lgmn	8.42E-09	0.0001501	-0.27	0.85	0.921	Macrophages	aPD-L1 vs PBS
Sema3c	8.50E-09	0.0001514	-0.62	0.31	0.632	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Slc2a1	9.20E-09	0.000164	-0.28	0.49	0.592	Neutrophils	aPD-L1 vs PBS
mt-Co2	9.30E-09	0.0001657	-0.34	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Lars2	9.38E-09	0.0001672	-0.42	0.34	0.585	ILC	aPD-L1 + aTGF-β vs aPD-L1
Gm42418	9.70E-09	0.0001728	-0.74	0.99	1	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Samhd1	9.96E-09	0.0001776	0.33	0.87	0.772	Monocytes	aPD-L1 + aTGF-β vs PBS
Dcn	1.01E-08	0.0001805	-0.44	0.96	0.989	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Atp5k	1.03E-08	0.0001845	-0.28	0.49	0.673	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Spp1	1.04E-08	0.0001858	-0.82	0.32	0.494	Monocytes	aPD-L1 + aTGF-β vs PBS
Ier2	1.07E-08	0.00019	-0.25	0.78	0.855	B cells	aPD-L1 vs PBS
Akr1a1	1.07E-08	0.0001908	-0.26	0.62	0.791	Monocytes	aPD-L1 vs PBS
Pde4b	1.08E-08	0.0001926	0.33	0.52	0.291	Monocytes	aPD-L1 vs PBS
Ms4a7	1.08E-08	0.0001931	-0.55	0.11	0.269	Monocytes	aPD-L1 + aTGF-β vs PBS
Man1a	1.08E-08	0.0001933	-0.44	0.32	0.655	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Itm2b	1.09E-08	0.0001951	-0.35	0.89	0.953	Monocytes	aPD-L1 vs PBS
H3f3b	1.17E-08	0.0002088	-0.29	1.00	1	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Dcn	1.19E-08	0.0002121	0.37	0.19	0.106	Tumor_cells	aPD-L1 vs PBS
Rps29	1.20E-08	0.0002131	-0.47	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Ddr2	1.20E-08	0.0002138	-0.42	0.37	0.655	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Irf7	1.20E-08	0.0002139	-0.50	0.74	0.816	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Ctla4	1.21E-08	0.0002151	0.36	0.32	0.21	T cells	aPD-L1 + aTGF-β vs aPD-L1
Gm42418	1.30E-08	0.0002318	-0.45	1.00	1	Monocytes	aPD-L1 + aTGF-β vs PBS
Gm10260	1.31E-08	0.0002343	0.27	0.71	0.614	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Scara5	1.33E-08	0.0002363	0.45	0.56	0.228	Fibroblasts	aPD-L1 vs PBS
Plau	1.34E-08	0.0002385	-0.36	0.37	0.536	Macrophages	aPD-L1 vs PBS
Rpl36a	1.39E-08	0.0002479	0.29	0.77	0.62	Monocytes	aPD-L1 + aTGF-β vs PBS
Sec61g	1.42E-08	0.0002527	0.30	0.81	0.633	Monocytes	aPD-L1 vs PBS
Rps15a	1.44E-08	0.0002569	0.29	0.96	0.934	Monocytes	aPD-L1 + aTGF-β vs PBS
Nos2	1.47E-08	0.0002616	0.29	0.18	0.032	Monocytes	aPD-L1 vs PBS
B2m	1.54E-08	0.0002744	0.53	0.98	0.882	Epithelial cells	aPD-L1 vs PBS
Fndc1	1.54E-08	0.0002744	-0.51	0.42	0.724	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Efemp1	1.55E-08	0.0002765	-0.57	0.54	0.782	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Zfand5	1.68E-08	0.0002991	0.28	0.61	0.494	Macrophages	aPD-L1 vs PBS
Dnaja1	1.70E-08	0.0003026	0.26	0.91	0.862	T cells	aPD-L1 + aTGF-β vs PBS
Klf2	1.81E-08	0.0003226	-0.26	0.86	0.901	T cells	aTGF-β vs PBS
Nr4a1	1.83E-08	0.0003262	0.31	0.60	0.386	Monocytes	aPD-L1 + aTGF-β vs PBS
mt-Co2	1.84E-08	0.0003277	-0.31	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Rpl41	1.88E-08	0.0003352	0.51	1.00	1	DC	aPD-L1 vs PBS
Rpl35a	1.95E-08	0.000347	0.30	1.00	0.972	ILC	aPD-L1 + aTGF-β vs PBS
Nampt	1.95E-08	0.000348	0.29	0.63	0.462	Monocytes	aPD-L1 + aTGF-β vs PBS
Antxr2	1.97E-08	0.0003514	-0.33	0.19	0.506	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Zfp36l2	2.05E-08	0.0003646	0.29	0.64	0.499	Macrophages	aPD-L1 vs PBS
Cxcl16	2.06E-08	0.0003676	-0.36	0.38	0.554	Monocytes	aPD-L1 + aTGF-β vs PBS
Slfn2	2.09E-08	0.0003724	0.26	0.87	0.775	Monocytes	aPD-L1 + aTGF-β vs PBS
Rpl36	2.25E-08	0.0004019	0.53	1.00	1	DC	aPD-L1 vs PBS
Eef1a1	2.30E-08	0.0004093	0.30	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Nov	2.31E-08	0.000411	-0.55	0.24	0.54	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Cxcl9	2.35E-08	0.0004189	0.71	0.32	0.099	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Cd44	2.38E-08	0.0004246	0.25	0.78	0.614	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Blvrb	2.41E-08	0.0004303	0.31	0.60	0.464	Macrophages	aPD-L1 vs PBS
Fos	2.48E-08	0.0004421	-0.28	0.93	0.965	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Txn1	2.55E-08	0.0004537	0.29	0.96	0.944	Macrophages	aPD-L1 vs PBS
Elob	2.59E-08	0.0004621	0.25	0.75	0.574	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
Psmb8	2.66E-08	0.0004745	0.50	0.94	0.75	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Ifitm2	2.70E-08	0.0004812	0.34	0.93	0.903	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Creb5	2.76E-08	0.0004916	-0.50	0.27	0.563	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Pcsk6	2.92E-08	0.0005207	-0.33	0.09	0.345	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Itm2b	3.01E-08	0.0005371	-0.32	0.96	0.986	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Ppia	3.10E-08	0.000553	-0.32	0.99	1	ILC	aPD-L1 vs PBS
AY036118	3.11E-08	0.0005546	-0.47	0.77	0.899	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Socs3	3.18E-08	0.0005668	0.29	0.77	0.619	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Socs1	3.19E-08	0.0005693	0.41	0.36	0.124	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
AY036118	3.30E-08	0.0005878	1.29	1.00	0.788	NK cells	aPD-L1 vs PBS
Gm10260	3.30E-08	0.0005879	0.34	0.94	0.832	ILC	aPD-L1 + aTGF-β vs PBS
Jun	3.37E-08	0.0006008	0.26	1.00	0.975	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Ms4a6d	3.50E-08	0.000624	-0.35	0.88	0.924	Monocytes	aPD-L1 vs PBS
Itgb2	3.53E-08	0.0006301	0.28	0.68	0.586	Macrophages	aPD-L1 vs PBS
Klf2	3.54E-08	0.0006314	-0.26	0.92	0.966	B cells	aPD-L1 vs PBS
Gm42418	3.67E-08	0.0006537	-0.61	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Gadd45g	3.70E-08	0.0006593	-0.27	0.32	0.41	Tumor_cells	aPD-L1 + aTGF-β vs aPD-L1
Phlda1	3.72E-08	0.000664	0.28	0.81	0.772	Tumor_cells	aPD-L1 vs PBS
Rab20	3.82E-08	0.0006805	0.27	0.56	0.38	Monocytes	aPD-L1 + aTGF-β vs PBS
Tmsb4x	3.83E-08	0.0006825	-0.28	1.00	1	Monocytes	aPD-L1 vs PBS
Tnxb	3.86E-08	0.0006887	-0.50	0.57	0.862	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Psmb9	3.96E-08	0.0007058	0.55	0.62	0.279	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Cstb	3.97E-08	0.000707	-0.26	0.69	0.744	Neutrophils	aTGF-β vs PBS
Rpl36a	4.09E-08	0.0007284	0.35	0.77	0.62	Monocytes	aPD-L1 vs PBS
Rel	4.09E-08	0.0007299	0.26	0.53	0.355	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Ier2	4.13E-08	0.0007369	-0.29	0.71	0.782	T cells	aTGF-β vs PBS
Zfp36	4.14E-08	0.0007383	0.25	0.98	0.989	Neutrophils	aPD-L1 vs PBS
Klf6	4.17E-08	0.0007442	0.31	0.93	0.851	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
C1qb	4.31E-08	0.0007685	0.33	0.82	0.683	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Hsp90ab1	4.39E-08	0.0007819	0.45	1.00	1	ILC	aPD-L1 vs PBS

Rps11	4.39E-08	0.0007823	0.26	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Rpl35a	4.52E-08	0.0008055	0.44	1.00	1	DC	aPD-L1 + aTGF-β vs PBS
Csrnp1	4.54E-08	0.0008097	0.25	0.59	0.408	Monocytes	aPD-L1 + aTGF-β vs PBS
mt-Atp8	4.59E-08	0.0008176	-0.25	0.38	0.597	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Rpl36	4.74E-08	0.0008447	0.35	0.98	0.954	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Clic1	4.76E-08	0.0008486	-0.27	0.86	0.946	Monocytes	aPD-L1 vs PBS
Ly6a	4.83E-08	0.0008617	0.28	0.67	0.639	Tumor_cells	aPD-L1 + aTGF-β vs PBS
Jund	4.86E-08	0.0008666	0.36	0.88	0.817	Macrophages	aPD-L1 vs PBS
Psmb9	4.94E-08	0.00088	0.28	0.62	0.428	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Hexb	4.96E-08	0.0008843	-0.25	0.48	0.635	Macrophages	aPD-L1 vs PBS
Rpl27a	5.50E-08	0.00098	0.29	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Dnajb1	5.59E-08	0.0009967	0.45	0.69	0.522	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Phlda1	5.67E-08	0.0010112	0.53	0.65	0.362	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Osr1	5.77E-08	0.0010281	-0.34	0.23	0.54	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Psme2	5.79E-08	0.0010319	-0.32	0.57	0.737	Monocytes	aPD-L1 vs PBS
Rpl30	5.80E-08	0.0010335	0.27	1.00	0.981	ILC	aPD-L1 + aTGF-β vs PBS
Arid5a	5.94E-08	0.0010585	0.28	0.49	0.256	Monocytes	aPD-L1 vs PBS
Egr1	5.96E-08	0.001062	-0.34	0.42	0.544	B cells	aPD-L1 + aTGF-β vs PBS
Isg20	6.04E-08	0.0010761	-0.34	0.21	0.36	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Gm10260	6.06E-08	0.0010797	0.31	0.94	0.861	ILC	aPD-L1 + aTGF-β vs aTGF-β
Isg15	6.09E-08	0.0010858	0.26	0.52	0.417	Macrophages	aPD-L1 + aTGF-β vs PBS
Crip1	6.11E-08	0.0010891	0.28	0.49	0.288	B cells	aPD-L1 vs PBS
Antxr1	6.17E-08	0.0010991	-0.41	0.31	0.621	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rpl39	6.18E-08	0.0011023	-0.46	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Tshz2	6.48E-08	0.0011548	-0.31	0.34	0.604	Fibroblasts	aTGF-β vs PBS
Timp3	6.50E-08	0.0011595	-0.74	0.29	0.575	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ubc	6.63E-08	0.0011822	0.31	0.91	0.826	Monocytes	aPD-L1 + aTGF-β vs PBS
Nampt	6.65E-08	0.0011848	0.33	0.63	0.462	Monocytes	aPD-L1 vs PBS
Wfdc17	6.79E-08	0.0012098	0.56	0.37	0.265	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Samsn1	6.82E-08	0.001215	0.27	0.41	0.262	B cells	aTGF-β vs PBS
Rpl41	6.85E-08	0.0012212	0.25	1.00	1	ILC	aPD-L1 + aTGF-β vs aTGF-β
Btg1	6.86E-08	0.0012237	0.27	0.98	0.953	Monocytes	aPD-L1 vs PBS
Ccl5	7.01E-08	0.0012504	0.39	0.19	0.083	Macrophages	aPD-L1 vs PBS
Cxcl10	7.09E-08	0.0012635	0.32	0.13	0.051	T cells	aPD-L1 + aTGF-β vs PBS
Rhob	7.25E-08	0.0012916	-0.34	0.73	0.777	Neutrophils	aPD-L1 vs PBS
Ly6a	7.37E-08	0.0013133	0.63	0.69	0.324	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Plaur	7.40E-08	0.0013185	0.31	0.63	0.475	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Osr2	7.54E-08	0.0013446	-0.40	0.14	0.425	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Igfbp5	7.57E-08	0.0013492	-0.76	0.36	0.691	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Fn1	7.62E-08	0.0013576	-0.27	0.35	0.488	Macrophages	aPD-L1 + aTGF-β vs PBS
Cxcl16	7.75E-08	0.0013808	-0.32	0.39	0.554	Monocytes	aTGF-β vs PBS
Rpl27	7.77E-08	0.0013849	0.56	0.93	0.521	DC	aPD-L1 vs PBS
Tnfaip2	7.79E-08	0.0013884	0.26	0.44	0.264	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Ifit3	7.79E-08	0.0013892	-0.34	0.19	0.348	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Slfn5	7.82E-08	0.0013933	-0.29	0.43	0.572	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Pi16	7.87E-08	0.0014036	-0.58	0.67	0.885	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Igkc	8.52E-08	0.0015191	0.30	0.18	0.044	Monocytes	aPD-L1 + aTGF-β vs PBS
Grn	9.16E-08	0.0016329	-0.27	0.69	0.804	Monocytes	aPD-L1 + aTGF-β vs PBS
Gapdh	9.19E-08	0.0016382	-0.26	0.84	0.878	T cells	aPD-L1 vs PBS
Rpl34	9.33E-08	0.0016635	0.31	0.98	0.966	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
G0s2	9.44E-08	0.0016822	-0.37	0.84	0.865	Neutrophils	aPD-L1 vs PBS
Junb	9.53E-08	0.0016989	0.27	0.90	0.798	Macrophages	aPD-L1 vs PBS
Bcl2a1d	9.71E-08	0.0017304	0.26	0.51	0.336	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Il1rn	9.76E-08	0.0017399	0.26	0.75	0.652	Neutrophils	aPD-L1 vs PBS
AY036118	9.84E-08	0.0017545	-0.35	0.84	0.861	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Prelid1	9.89E-08	0.0017622	0.26	0.57	0.372	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Klf6	1.00E-07	0.0017892	0.31	0.93	0.873	Monocytes	aTGF-β vs PBS
Cthrc1	1.03E-07	0.0018415	-0.57	0.42	0.658	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Gbp2	1.04E-07	0.0018475	0.25	0.57	0.37	Monocytes	aPD-L1 + aTGF-β vs PBS
Fos	1.04E-07	0.0018539	0.25	1.00	0.975	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Tsc22d3	1.06E-07	0.0018959	-0.27	0.67	0.761	B cells	aTGF-β vs PBS
Wls	1.09E-07	0.0019447	-0.27	0.26	0.537	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Lgals1	1.10E-07	0.0019659	0.47	0.98	1	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Egr1	1.13E-07	0.0020223	0.27	0.34	0.198	Macrophages	aPD-L1 vs PBS
AY036118	1.14E-07	0.0020399	-0.60	0.65	0.838	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Thbs3	1.15E-07	0.0020473	-0.42	0.40	0.69	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ccl5	1.15E-07	0.0020487	0.42	0.18	0.092	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Celsr2	1.16E-07	0.0020593	-0.33	0.14	0.397	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Bcl2a1b	1.16E-07	0.0020762	-0.28	0.25	0.421	Monocytes	aTGF-β vs PBS
Rps28	1.17E-07	0.0020785	0.55	1.00	0.938	DC	aPD-L1 vs PBS
Wnt2	1.17E-07	0.0020881	-0.43	0.19	0.471	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Inhba	1.17E-07	0.0020882	0.57	0.11	0.036	Macrophages	aPD-L1 vs PBS
Hsp90ab1	1.19E-07	0.0021209	0.36	1.00	1	ILC	aTGF-β vs PBS
Nfil3	1.24E-07	0.0022086	-0.25	0.38	0.487	Neutrophils	aPD-L1 vs PBS
Atp5f1	1.32E-07	0.0023484	-0.26	0.50	0.709	Monocytes	aPD-L1 vs PBS
Mx1	1.36E-07	0.0024211	-0.30	0.24	0.395	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Col1a2	1.41E-07	0.002518	-0.39	0.99	0.98	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Irf1	1.46E-07	0.0025983	0.34	0.56	0.396	Monocytes	aTGF-β vs PBS
Sh3bgrl3	1.47E-07	0.0026129	-0.43	0.88	0.935	ILC	aPD-L1 vs PBS
Nfkbia	1.50E-07	0.0026662	0.27	0.94	0.868	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Apoe	1.50E-07	0.0026756	-0.77	0.16	0.337	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Il1a	1.52E-07	0.0027069	0.27	0.20	0.107	Neutrophils	aPD-L1 vs PBS
Rps5	1.53E-07	0.0027287	-0.35	1.00	1	ILC	aPD-L1 vs PBS
Tmsb4x	1.56E-07	0.0027873	0.33	1.00	1	ILC	aPD-L1 + aTGF-β vs aPD-L1
Rpl30	1.58E-07	0.002818	0.35	0.98	0.989	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Pim1	1.59E-07	0.0028351	-0.27	0.33	0.462	B cells	aTGF-β vs PBS

Dnaja1	1.62E-07	0.0028796	0.59	0.90	0.841	ILC	aPD-L1 + aTGF-β vs PBS
Igkc	1.63E-07	0.0028974	0.26	0.31	0.037	ILC	aPD-L1 vs PBS
Uba52	1.66E-07	0.0029562	0.28	0.59	0.326	ILC	aPD-L1 + aTGF-β vs aTGF-β
Ppp1r14b	1.68E-07	0.0029991	-0.26	0.24	0.486	ILC	aPD-L1 + aTGF-β vs aTGF-β
Ccl4	1.72E-07	0.0030656	0.34	0.79	0.653	Macrophages	aPD-L1 vs PBS
Rps15a	1.81E-07	0.0032216	0.30	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Cldn3	1.82E-07	0.003238	-0.26	0.74	0.82	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
mt-Nd1	1.85E-07	0.0032913	-0.35	0.89	0.956	ILC	aPD-L1 + aTGF-β vs aPD-L1
Nfix	2.02E-07	0.0036076	-0.37	0.33	0.647	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Cxcl9	2.04E-07	0.0036422	0.79	0.32	0.094	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Rpl22	2.04E-07	0.0036427	0.26	0.98	0.981	ILC	aPD-L1 + aTGF-β vs PBS
Gm42418	2.13E-07	0.0037945	-0.34	1.00	1	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Arhgdib	2.19E-07	0.0039003	0.36	0.80	0.57	ILC	aPD-L1 + aTGF-β vs aPD-L1
Ms4a6b	2.24E-07	0.003987	-0.31	0.58	0.747	Monocytes	aPD-L1 vs PBS
Aprt	2.27E-07	0.0040492	-0.31	0.65	0.791	Monocytes	aPD-L1 vs PBS
Fxyd3	2.30E-07	0.0041009	-0.46	0.74	0.882	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Klf6	2.30E-07	0.004108	0.26	0.93	0.814	Macrophages	aPD-L1 vs PBS
Ikzf2	2.39E-07	0.0042635	0.28	0.21	0.116	T cells	aPD-L1 + aTGF-β vs aPD-L1
Fn1	2.43E-07	0.0043359	-0.45	0.24	0.408	Monocytes	aPD-L1 + aTGF-β vs PBS
Ptgs2	2.44E-07	0.0043463	0.26	0.25	0.126	Macrophages	aPD-L1 vs PBS
Zfp385a	2.55E-07	0.0045455	-0.28	0.11	0.368	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gadd45b	2.56E-07	0.0045705	0.28	0.40	0.287	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Prnp	2.64E-07	0.0047029	-0.34	0.44	0.691	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Fosb	2.68E-07	0.0047822	0.33	0.63	0.492	Macrophages	aPD-L1 vs PBS
Lmna	2.69E-07	0.0047873	0.30	0.89	0.793	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
S100a8	2.79E-07	0.0049686	0.39	0.93	0.935	Neutrophils	aPD-L1 vs PBS
Grb10	2.83E-07	0.0050468	-0.31	0.21	0.477	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Rpl18	2.84E-07	0.0050625	-0.33	1.00	1	ILC	aPD-L1 vs PBS
Gng11	2.86E-07	0.0050963	-0.29	0.31	0.362	Tumor_cells	aTGF-β vs PBS
Klf2	2.86E-07	0.0051015	0.33	0.74	0.579	Monocytes	aTGF-β vs PBS
Ifi44	2.88E-07	0.0051308	-0.32	0.53	0.631	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Tcim	2.95E-07	0.0052624	-0.54	0.23	0.515	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Rplp2	2.99E-07	0.0053269	0.51	1.00	1	DC	aPD-L1 vs PBS
Prss23	3.02E-07	0.0053848	-0.46	0.45	0.736	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rps27	3.07E-07	0.0054689	-0.45	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Rpl35	3.07E-07	0.0054804	0.54	1.00	0.979	DC	aPD-L1 vs PBS
Zfp36	3.14E-07	0.0056015	-0.25	0.98	0.978	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Cd83	3.17E-07	0.0056527	0.35	0.60	0.373	Monocytes	aPD-L1 vs PBS
Hk2	3.22E-07	0.0057345	0.36	0.53	0.329	Monocytes	aPD-L1 vs PBS
H2-K1	3.24E-07	0.0057676	0.37	0.99	0.956	Epithelial cells	aPD-L1 vs PBS
Igkc	3.24E-07	0.0057802	0.64	0.16	0.081	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Park7	3.38E-07	0.0060265	-0.25	0.26	0.468	Monocytes	aPD-L1 vs PBS
P3h4	3.43E-07	0.0061165	-0.25	0.18	0.423	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Ccl6	3.53E-07	0.0062944	-0.39	0.54	0.586	Neutrophils	aTGF-β vs PBS
Tshz2	3.55E-07	0.0063275	-0.27	0.33	0.604	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Cd83	3.59E-07	0.0063922	0.26	0.57	0.419	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Iigp1	3.65E-07	0.0065142	0.32	0.26	0.101	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Ifrd1	3.70E-07	0.0065883	0.42	0.71	0.463	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Tspan5	3.70E-07	0.0065908	-0.28	0.11	0.368	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Cd248	3.88E-07	0.006916	-0.47	0.57	0.793	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Snx3	4.07E-07	0.0072614	0.26	0.51	0.252	ILC	aPD-L1 + aTGF-β vs aPD-L1
Ltbp4	4.09E-07	0.0072847	-0.36	0.12	0.336	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Krt8	4.15E-07	0.0074031	0.31	0.91	0.851	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Ifitm3	4.20E-07	0.0074797	-0.28	0.99	0.997	Monocytes	aPD-L1 vs PBS
Psmb8	4.35E-07	0.007761	0.28	0.88	0.837	ILC	aPD-L1 + aTGF-β vs aPD-L1
Gm47283	4.42E-07	0.0078852	0.35	0.66	0.475	Monocytes	aPD-L1 vs PBS
Tmed9	4.57E-07	0.0081522	-0.26	0.32	0.509	Monocytes	aPD-L1 vs PBS
Ifitm3	4.62E-07	0.0082349	0.40	1.00	1	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Upp1	4.63E-07	0.0082508	0.41	0.51	0.354	Monocytes	aPD-L1 + aTGF-β vs PBS
Hilpda	4.69E-07	0.0083647	0.62	0.52	0.316	Monocytes	aPD-L1 vs PBS
Cxcr4	4.78E-07	0.0085263	-0.27	0.56	0.624	B cells	aPD-L1 + aTGF-β vs PBS
Nlrp3	4.79E-07	0.0085401	0.32	0.54	0.329	Monocytes	aPD-L1 vs PBS
F10	4.81E-07	0.0085724	0.25	0.41	0.203	Monocytes	aPD-L1 vs PBS
Col1a1	4.93E-07	0.0087881	-0.53	0.97	0.946	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Lmna	4.96E-07	0.0088352	0.70	0.75	0.495	ILC	aPD-L1 vs PBS
Tnf	5.03E-07	0.0089742	0.26	0.42	0.28	Macrophages	aPD-L1 vs PBS
Gm42418	5.20E-07	0.0092618	-0.61	1.00	1	Fibroblasts	aTGF-β vs PBS
Klf4	5.32E-07	0.0094888	-0.48	0.52	0.805	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Tgfbr2	5.35E-07	0.0095305	-0.44	0.58	0.805	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Ier2	5.35E-07	0.0095392	-0.26	0.73	0.782	T cells	aPD-L1 + aTGF-β vs PBS
Srgn	5.40E-07	0.009621	0.26	0.89	0.906	T cells	aPD-L1 + aTGF-β vs aPD-L1
Rpl36	5.46E-07	0.0097411	0.26	0.98	0.98	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Hsp90aa1	5.57E-07	0.0099212	0.29	0.97	0.964	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Ahnak	5.70E-07	0.0101526	-0.43	0.78	0.931	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
mt-Atp8	5.91E-07	0.0105421	-0.33	0.35	0.541	ILC	aPD-L1 + aTGF-β vs aPD-L1
Ablim1	6.74E-07	0.0120214	-0.27	0.18	0.483	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gsn	7.00E-07	0.0124863	-0.26	0.46	0.614	Monocytes	aPD-L1 + aTGF-β vs PBS
Fosb	7.36E-07	0.0131202	-0.37	0.86	0.948	ILC	aPD-L1 + aTGF-β vs aPD-L1
Tmsb4x	7.38E-07	0.0131584	0.58	0.99	0.971	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Scara3	7.45E-07	0.0132828	0.35	0.62	0.295	Fibroblasts	aPD-L1 vs PBS
Rpl41	7.46E-07	0.0132904	0.26	1.00	1	ILC	aPD-L1 + aTGF-β vs PBS
Irf1	7.46E-07	0.0132937	0.36	0.63	0.431	Fibroblasts	aPD-L1 + aTGF-β vs aTGF-β
Rpl38	7.51E-07	0.0133876	-0.36	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Pid1	7.60E-07	0.0135437	-0.29	0.70	0.835	Monocytes	aTGF-β vs PBS
Ccr2	7.62E-07	0.0135758	-0.27	0.66	0.804	Monocytes	aPD-L1 + aTGF-β vs PBS
Nfe2l2	7.67E-07	0.0136779	0.27	0.55	0.402	Monocytes	aPD-L1 + aTGF-β vs aTGF-β

AY036118	8.02E-07	0.0142933	-0.35	0.65	0.779	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Emilin2	8.12E-07	0.0144751	0.44	0.69	0.45	Fibroblasts	aPD-L1 vs PBS
Tmx4	8.28E-07	0.0147567	-0.25	0.22	0.374	Macrophages	aPD-L1 vs PBS
Ctsc	8.35E-07	0.0148774	-0.27	0.85	0.934	Monocytes	aTGF-β vs PBS
Grb10	8.62E-07	0.0153691	-0.35	0.21	0.494	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Gda	8.76E-07	0.0156075	-0.32	0.32	0.632	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Lrg1	8.76E-07	0.0156131	-0.36	0.17	0.319	Epithelial cells	aPD-L1 + aTGF-β vs aTGF-β
Chchd2	8.92E-07	0.0159036	0.33	0.91	0.885	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Upp1	8.92E-07	0.0159065	0.25	0.69	0.596	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Rsad2	8.96E-07	0.0159781	0.32	0.43	0.322	Macrophages	aPD-L1 + aTGF-β vs aTGF-β
Iglc1	9.25E-07	0.0164929	0.49	0.21	0.284	B cells	aPD-L1 + aTGF-β vs aTGF-β
Tppp3	9.30E-07	0.0165751	-0.47	0.35	0.632	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Csrp2	9.30E-07	0.0165826	-0.55	0.63	0.799	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Socs3	9.67E-07	0.017246	0.33	0.76	0.589	Monocytes	aPD-L1 vs PBS
AW112010	9.95E-07	0.0177385	-0.55	0.75	0.916	ILC	aPD-L1 vs PBS
Klf4	9.97E-07	0.017767	0.28	0.47	0.332	Macrophages	aPD-L1 vs PBS
Hspa1a	1.01E-06	0.0179672	0.35	0.58	0.451	T cells	aTGF-β vs PBS
Rpl35	1.02E-06	0.0182682	0.40	0.98	0.916	ILC	aPD-L1 vs PBS
Tnfrsf4	1.03E-06	0.0183983	0.39	0.23	0.141	T cells	aPD-L1 + aTGF-β vs aPD-L1
Ly6a	1.05E-06	0.0187173	0.34	0.69	0.539	Epithelial cells	aPD-L1 + aTGF-β vs aPD-L1
C4b	1.14E-06	0.020278	-0.47	0.80	0.897	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Klf2	1.14E-06	0.0203505	0.43	0.71	0.409	Fibroblasts	aPD-L1 vs PBS
Mmp2	1.14E-06	0.0203674	-0.46	0.82	0.885	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Isg20	1.15E-06	0.0204356	0.25	0.55	0.458	Neutrophils	aPD-L1 + aTGF-β vs aPD-L1
Ccl6	1.16E-06	0.0206265	-0.34	0.49	0.586	Neutrophils	aPD-L1 vs PBS
mt-Nd3	1.18E-06	0.021051	0.26	0.48	0.291	Monocytes	aPD-L1 vs PBS
Acta2	1.19E-06	0.0212694	-1.31	0.02	0.162	Epithelial cells	aPD-L1 vs PBS
Hcst	1.19E-06	0.0212808	0.33	0.81	0.617	ILC	aPD-L1 + aTGF-β vs PBS
Rps27	1.20E-06	0.0214621	0.41	1.00	1	DC	aPD-L1 + aTGF-β vs PBS
Hspa8	1.23E-06	0.0220127	0.40	1.00	0.981	ILC	aPD-L1 vs PBS
Il1f9	1.25E-06	0.0222762	0.28	0.52	0.407	Neutrophils	aPD-L1 vs PBS
Mmp23	1.26E-06	0.0223835	-0.28	0.43	0.678	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Htra3	1.26E-06	0.0225122	0.42	0.87	0.685	Fibroblasts	aPD-L1 vs PBS
Cd55	1.28E-06	0.0228867	-0.60	0.32	0.563	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rpl37	1.33E-06	0.0236715	0.29	0.99	0.954	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Clic1	1.34E-06	0.023864	-0.30	0.88	0.944	ILC	aPD-L1 vs PBS
Rpl36	1.34E-06	0.0238903	-0.36	0.99	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Ccl7	1.38E-06	0.0246127	0.25	0.51	0.399	Macrophages	aPD-L1 + aTGF-β vs PBS
Lama4	1.41E-06	0.0251135	-0.35	0.44	0.736	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Pdpn	1.42E-06	0.0253097	-0.33	0.48	0.793	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Sept1	1.43E-06	0.025467	-0.39	0.47	0.71	ILC	aPD-L1 vs PBS
Mt1	1.43E-06	0.0255408	0.40	0.96	0.832	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Gadd45b	1.48E-06	0.0264515	0.26	0.40	0.303	Macrophages	aPD-L1 + aTGF-β vs PBS
Rpl37a	1.49E-06	0.0265288	-0.34	0.99	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Fbn1	1.53E-06	0.027336	-0.43	0.78	0.879	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Ccdc80	1.54E-06	0.0273643	-0.34	0.63	0.819	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Rpl27	1.55E-06	0.0276639	0.29	0.79	0.688	ILC	aPD-L1 + aTGF-β vs aTGF-β
Hspa8	1.57E-06	0.0280162	0.38	0.99	0.981	ILC	aPD-L1 + aTGF-β vs PBS
Isg15	1.59E-06	0.0283515	-0.51	0.76	0.814	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Apoe	1.64E-06	0.0292935	-0.29	0.45	0.561	B cells	aPD-L1 vs PBS
Rpl34	1.67E-06	0.0297307	-0.36	1.00	1	DC	aPD-L1 + aTGF-β vs aPD-L1
Gm10076	1.67E-06	0.0298528	0.60	0.85	0.625	DC	aPD-L1 vs PBS
Ifit2	1.69E-06	0.0300915	-0.40	0.24	0.369	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Ms4a7	1.72E-06	0.0306353	-0.46	0.14	0.269	Monocytes	aTGF-β vs PBS
Lgmn	1.77E-06	0.0315931	-0.28	0.60	0.725	Monocytes	aPD-L1 + aTGF-β vs PBS
Gja1	1.78E-06	0.0317818	-0.31	0.18	0.416	Fibroblasts	aPD-L1 + aTGF-β vs PBS
Gng11	1.83E-06	0.0326816	-0.31	0.28	0.362	Tumor_cells	aPD-L1 vs PBS
Hist1h1c	1.86E-06	0.0332186	-0.27	0.50	0.601	B cells	aPD-L1 vs PBS
Vps37b	1.86E-06	0.0332257	-0.26	0.53	0.627	T cells	aTGF-β vs PBS
Ninj1	1.88E-06	0.0335369	0.26	0.67	0.522	Monocytes	aPD-L1 + aTGF-β vs PBS
Rpl30	1.89E-06	0.0336273	0.46	1.00	0.979	DC	aPD-L1 vs PBS
Dmkn	1.91E-06	0.0340191	-0.63	0.13	0.356	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rpl22	1.94E-06	0.0345917	-0.30	0.97	0.985	Epithelial cells	aPD-L1 vs PBS
Supt4a	1.97E-06	0.0351251	0.26	0.65	0.4	ILC	aPD-L1 + aTGF-β vs aPD-L1
Hal	2.00E-06	0.0356797	0.35	0.40	0.278	Macrophages	aPD-L1 vs PBS
Atf3	2.02E-06	0.0359388	0.56	0.77	0.497	Fibroblasts	aPD-L1 vs PBS
Rps28	2.05E-06	0.03654	0.38	0.99	0.916	ILC	aPD-L1 vs PBS
Cfl1	2.09E-06	0.0372058	-0.37	0.96	0.981	ILC	aPD-L1 vs PBS
Ets2	2.10E-06	0.0374884	0.27	0.56	0.364	Monocytes	aPD-L1 vs PBS
Pcolce	2.13E-06	0.0380111	-0.53	0.76	0.879	Fibroblasts	aPD-L1 vs PBS
Alox5ap	2.16E-06	0.0384706	-0.27	0.44	0.528	Neutrophils	aPD-L1 vs PBS
Fn1	2.18E-06	0.0388733	-0.42	0.25	0.408	Monocytes	aTGF-β vs PBS
Uba52	2.21E-06	0.0394255	0.50	0.66	0.188	DC	aPD-L1 vs PBS
Tmsb10	2.23E-06	0.0398207	0.31	0.95	0.94	Fibroblasts	aTGF-β vs PBS
mt-Cytb	2.25E-06	0.0401059	-0.33	0.97	0.97	ILC	aPD-L1 + aTGF-β vs aPD-L1
Atp5g2	2.34E-06	0.041682	-0.31	0.80	0.86	ILC	aPD-L1 vs PBS
Cap1	2.36E-06	0.0421483	-0.26	0.56	0.706	Monocytes	aPD-L1 vs PBS
Atp6v1b1	2.43E-06	0.0433536	-0.27	0.11	0.324	Epithelial cells	aPD-L1 + aTGF-β vs PBS
Dusp2	2.48E-06	0.0442446	0.31	0.38	0.235	Monocytes	aPD-L1 + aTGF-β vs aTGF-β
Cavin1	2.49E-06	0.0443414	-0.34	0.45	0.724	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Malat1	2.51E-06	0.0446877	-0.26	1.00	1	Monocytes	aPD-L1 + aTGF-β vs aPD-L1
Rpl35	2.51E-06	0.0447681	0.30	0.98	0.916	ILC	aPD-L1 + aTGF-β vs PBS
Cxcl14	2.60E-06	0.0462715	0.25	0.56	0.418	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Cdkn1c	2.60E-06	0.0464031	-0.47	0.23	0.494	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Kdm6b	2.65E-06	0.0472485	0.30	0.60	0.44	Monocytes	aPD-L1 vs PBS
Fosb	2.66E-06	0.0473527	-0.25	0.83	0.858	Neutrophils	aPD-L1 + aTGF-β vs PBS

Prelp	2.68E-06	0.0476924	-0.35	0.44	0.713	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Rnase4	2.68E-06	0.0478187	-0.42	0.72	0.839	Fibroblasts	aPD-L1 + aTGF-β vs aPD-L1
Zfand5	2.70E-06	0.0481123	0.35	0.72	0.573	Monocytes	aPD-L1 vs PBS
Myl12b	2.74E-06	0.0487754	0.28	0.74	0.541	ILC	aPD-L1 + aTGF-β vs aPD-L1
AC160336.1	2.74E-06	0.0488647	-0.28	0.29	0.422	Macrophages	aPD-L1 + aTGF-β vs aPD-L1
Man1a	2.75E-06	0.0490332	0.40	0.66	0.403	Fibroblasts	aPD-L1 vs PBS
Cfp	2.76E-06	0.049246	-0.33	0.49	0.636	Monocytes	aPD-L1 vs PBS

Table 2

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	comparison	genes_used	cells
BP	GO:0009617	response to bacterium	39/180	453/13307	7.2043646640	2.2290304270	1.5834435177	Rpl39/Cxcl9/Ly6a	39	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002237	response to molecule of bacterial origin	28/180	243/13307	1.9466728175	3.0115028486	2.1392909699	Cxcl9/Cd274/Tnf,	28	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032496	response to lipopolysaccharide	27/180	226/13307	3.2523756566	3.3542834272	2.3827931126	Cxcl9/Cd274/Tnf,	27	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071222	cellular response to lipopolysaccharide	21/180	160/13307	3.3197630230	2.5678366983	1.8241224189	Cxcl9/Cd274/Tnf,	21	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071219	cellular response to molecule of bacterial origin	21/180	167/13307	7.9904965376	4.9445192575	3.5124540569	Cxcl9/Cd274/Tnf,	21	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002181	cytoplasmic translation	15/180	76/13307	7.1445687566	3.6842159555	2.6171683445	Rpl39/Rps21/Rpl	15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071216	cellular response to biotic stimulus	21/180	188/13307	8.7794585628	3.8805206847	2.7566179668	Cxcl9/Cd274/Tnf,	21	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002819	regulation of adaptive immune response	20/180	176/13307	2.5521539982	9.7785968084	6.9464532834	Cd74/Irf1/H2-Ab1	20	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001819	positive regulation of cytokine production	28/180	385/13307	2.8444528531	9.7785968084	6.9464532834	Cd74/Irf1/Hilpda,	28	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002821	positive regulation of adaptive immune response	16/180	120/13307	5.8664929083	1.8150929058	1.2893933886	Cd74/Irf1/H2-Ab1	16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034341	response to interferon-gamma	16/180	123/13307	8.6354865462	2.4289268521	1.7254445845	H2-Eb1/H2-Aa/Ir	16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002824	positive regulation of adaptive immune response base	15/180	113/13307	2.9498284072	7.1558111661	5.0832966063	Irf1/H2-Ab1/Cd2	15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0098542	defense response to other organism	25/180	370/13307	3.0066433471	7.1558111661	5.0832966063	Rpl39/Irf1/Cxcl9/	25	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071396	cellular response to lipid	25/180	375/13307	4.0157949339	8.8749068040	6.3044961068	Cxcl9/Dnaja1/Inh	25	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0007159	leukocyte cell-cell adhesion	22/180	288/13307	4.7981750999	9.8543686650	7.0002795810	H2-Aa/Cd74/Irf1,	22	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002822	regulation of adaptive immune response based on som	17/180	160/13307	5.0959889670	9.8543686650	7.0002795810	Irf1/H2-Ab1/Cd2	17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002697	regulation of immune effector process	24/180	354/13307	7.2205821380	1.3099163074	9.3052946278	Cd74/Irf1/Tnf/Rs	24	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048002	antigen processing and presentation of peptide antige	11/180	52/13307	7.6207154280	1.3099163074	9.3052946278	H2-Eb1/H2-Aa/Cd	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002250	adaptive immune response	24/180	356/13307	8.1146041984	1.3213992310	9.3868662417	Cd74/Irf1/H2-Ab1	24	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019882	antigen processing and presentation	13/180	87/13307	1.4065177561	2.1758829687	1.5456889867	H2-Eb1/H2-Aa/Cd	13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022407	regulation of cell-cell adhesion	23/180	339/13307	1.8319660120	2.6990965910	1.9173659313	H2-Aa/Cd74/Irf1,	23	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002460	adaptive immune response based on somatic recombi	20/180	260/13307	3.4146525898	4.8022432332	3.4113849797	Cd74/Irf1/H2-Ab1	20	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	20/180	261/13307	3.6551907007	4.9170260992	3.4929236536	H2-Aa/Cd74/Irf1,	20	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002478	antigen processing and presentation of exogenous pep	8/180	24/13307	5.8641383905	7.5598517417	5.3703162102	H2-Eb1/H2-Aa/Cd	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071346	cellular response to interferon-gamma	13/180	104/13307	1.3772962879	1.7045418859	1.2108609049	Irf1/H2-Ab1/Irgm	13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002711	positive regulation of T cell mediated immunity	10/180	54/13307	2.2833373542	2.7171714516	1.9302058282	Rsad2/H2-T23/B2	10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0014070	response to organic cyclic compound	25/180	458/13307	2.6604686768	3.0487000319	2.1657148527	Dnaja1/Inhba/Tn	25	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019884	antigen processing and presentation of exogenous ant	8/180	29/13307	3.2302876974	3.5694679057	2.5356544031	H2-Eb1/H2-Aa/Cd	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042742	defense response to bacterium	15/180	158/13307	3.5341236224	3.7705443061	2.6784936928	Rpl39/Tnf/Arg2/I	15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002456	T cell mediated immunity	13/180	113/13307	3.8891964247	4.0110579127	2.8493481175	Rsad2/H2-T23/B2	13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002699	positive regulation of immune effector process	17/180	212/13307	4.1382738667	4.1302643044	2.9340291456	Cd74/Irf1/Tnf/Rs	17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	16/180	186/13307	4.4019680666	4.2561528744	3.0234570142	H2-Aa/Cd74/Irf1,	16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002718	regulation of cytokine production involved in immune	11/180	75/13307	4.7207335376	4.3053002263	3.0583699767	Cd74/Tnf/Rsad2/	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002367	cytokine production involved in immune response	12/180	94/13307	4.7310991498	4.3053002263	3.0583699767	Cd74/Tnf/Rsad2/	12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022409	positive regulation of cell-cell adhesion	17/180	215/13307	5.1214617370	4.5273721755	3.2161239419	H2-Aa/Cd74/Irf1,	17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002440	production of molecular mediator of immune response	16/180	190/13307	5.9891018801	5.1473003380	3.6565043057	Cd74/H2-Ab1/Tn	16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002709	regulation of T cell mediated immunity	11/180	77/13307	6.2905518529	5.2602614683	3.7367488674	Rsad2/H2-T23/B2	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042110	T cell activation	23/180	426/13307	1.4987198037	1.2202734401	8.6684957067	H2-Aa/Cd74/Irf1,	23	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002720	positive regulation of cytokine production involved in i	9/180	49/13307	1.6007941611	1.2699633678	9.0214796448	Cd74/Rsad2/H2-	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903706	regulation of hemopoiesis	21/180	362/13307	1.9404277064	1.5009208309	1.0662139608	H2-Aa/Cd74/Irf1,	21	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903428	positive regulation of reactive oxygen species biosynth	9/180	52/13307	2.7685052934	2.0892086287	1.4841178569	Tnf/Cd36/Sod2/I	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002449	lymphocyte mediated immunity	17/180	243/13307	3.1911473676	2.3429997327	1.6644042602	Cd74/H2-Ab1/Tn	17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019221	cytokine-mediated signaling pathway	18/180	274/13307	3.2562698290	2.3429997327	1.6644042602	Cd74/Irf1/Cxcl9/I	18	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903708	positive regulation of hemopoiesis	15/180	190/13307	4.3458632871	3.0559320478	2.1708522831	H2-Aa/Cd74/Irf1,	15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002443	leukocyte mediated immunity	19/180	313/13307	4.7015293347	3.2325626136	2.2963259066	Cd74/H2-Ab1/Tn	19	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	8/180	41/13307	6.2612478598	4.2113697561	2.9916442863	Tnf/Cd36/Sod2/I	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045785	positive regulation of cell adhesion	20/180	356/13307	7.3413249034	4.8327785641	3.4330764610	H2-Aa/Cd74/Irf1,	20	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904407	positive regulation of nitric oxide metabolic process	8/180	42/13307	7.6458083038	4.9283606025	3.5009753812	Tnf/Cd36/Sod2/I	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045088	regulation of innate immune response	17/180	259/13307	8.1084279376	5.1198930691	3.6370349159	Cd74/Irf1/Irgm1/	17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001818	negative regulation of cytokine production	16/180	234/13307	1.1343501647	7.0193588196	4.9863645138	Cd274/Tnf/Arg2/	16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0044419	interspecies interaction between organisms	19/180	333/13307	1.2487499778	7.4483088705	5.2910791418	Cd74/Irgm1/Tnf/	19	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903409	reactive oxygen species biosynthetic process	11/180	102/13307	1.2518166169	7.4483088705	5.2910791418	Tnf/Arg2/Cd36/S	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0097530	granulocyte migration	12/180	127/13307	1.4467149283	8.4455396004	5.9994851446	Cd74/Cxcl9/Ccl4/	12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1990266	neutrophil migration	11/180	104/13307	1.5310163573	8.7721566844	6.2315051737	Cd74/Cxcl9/Ccl4/	11	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:0001660	fever generation	5/180	11/13307	1.85307035531.03433215157.34761859107	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002700	regulation of production of molecular mediator of imm	12/180	130/13307	1.87209439197.03433215157.34761859107	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071621	granulocyte chemotaxis	11/180	107/13307	2.05350688887.11146579498.91823154917	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	8/180	48/13307	2.28105511167.21682491647.64399831787	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0030593	neutrophil chemotaxis	10/180	87/13307	2.59754811717.36217184317.67650395827	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006809	nitric oxide biosynthetic process	9/180	67/13307	2.70335507617.39403010097.90281649947	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050777	negative regulation of immune response	12/180	136/13307	3.07085548737.15757817667.10646182187	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903426	regulation of reactive oxygen species biosynthetic proc	10/180	89/13307	3.22544246737.60959983777.14341666167	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	11/180	113/13307	3.59193255067.76403798607.25312534097	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046209	nitric oxide metabolic process	9/180	70/13307	3.97110319567.91978020117.36376043957	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048660	regulation of smooth muscle cell proliferation	12/180	140/13307	4.21063616837.98632034567.41102877617	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031349	positive regulation of defense response	18/180	325/13307	4.23714100887.98632034567.41102877617	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002705	positive regulation of leukocyte mediated immunity	12/180	141/13307	4.54870079817.21005492397.49217396177	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000379	positive regulation of reactive oxygen species metabol	10/180	93/13307	4.89135552017.22556676167.58098302267	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019886	antigen processing and presentation of exogenous pep	5/180	13/13307	5.04974283187.26433395967.60852220187	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048659	smooth muscle cell proliferation	12/180	143/13307	5.29807239037.34174799657.66351506037	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001057	reactive nitrogen species metabolic process	9/180	74/13307	6.44291705657.80765991167.99448640687	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901652	response to peptide	17/180	302/13307	7.20420061787.05521958387.21703461677	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002521	leukocyte differentiation	22/180	488/13307	7.20850128057.05521958387.21703461677	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009615	response to virus	15/180	237/13307	7.72928381207.23167623167.29569624467	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	18/180	339/13307	7.83765845587.23329536837.29684643587	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046634	regulation of alpha-beta T cell activation	10/180	98/13307	7.99920262167.25651748837.31334280807	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002369	T cell cytokine production	7/180	40/13307	9.43054718687.78936532417.69186363997	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0097529	myeloid leukocyte migration	13/180	180/13307	9.90004357677.92701728547.78964790667	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009636	response to toxic substance	15/180	242/13307	1.00641506407.94158001017.79993287627	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0010035	response to inorganic substance	18/180	348/13307	1.14392534217.42413126077.14278436107	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0030217	T cell differentiation	15/180	245/13307	1.17526073627.48920582457.18901158837	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902107	positive regulation of leukocyte differentiation	12/180	155/13307	1.25708900127.70063294567.33920375277	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042136	neurotransmitter biosynthetic process	9/180	80/13307	1.26099720267.70063294567.33920375277	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045089	positive regulation of innate immune response	14/180	215/13307	1.30528605457.80780363427.41533493967	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045428	regulation of nitric oxide biosynthetic process	8/180	60/13307	1.34701625147.90313915517.48305874057	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0097237	cellular response to toxic substance	11/180	130/13307	1.47190342487.29542929827.76173115187	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042274	ribosomal small subunit biogenesis	8/180	61/13307	1.53259614817.38846873007.82782387247	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	8/180	61/13307	1.53259614817.38846873007.82782387247	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002706	regulation of lymphocyte mediated immunity	12/180	159/13307	1.64699149417.63796998997.00506288537	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022408	negative regulation of cell-cell adhesion	12/180	159/13307	1.64699149417.63796998997.00506288537	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031649	heat generation	5/180	16/13307	1.65822646767.63796998997.00506288537	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0070555	response to interleukin-1	9/180	85/13307	2.11280674147.10546093267.04752914897	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0035458	cellular response to interferon-beta	7/180	46/13307	2.52851630727.81002185037.97425428627	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002724	regulation of T cell cytokine production	6/180	30/13307	2.55508097587.81002185037.97425428627	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050727	regulation of inflammatory response	16/180	296/13307	2.63186205687.51838727457.05123418137	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0030098	lymphocyte differentiation	17/180	332/13307	2.64306780337.51838727457.05123418137	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050900	leukocyte migration	16/180	297/13307	2.74922386127.76917384207.22938624247	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051250	negative regulation of lymphocyte activation	11/180	139/13307	2.84801759177.99159839667.38739068907	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902105	regulation of leukocyte differentiation	15/180	264/13307	2.97632680977.21297478207.54465054437	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071236	cellular response to antibiotic	10/180	113/13307	2.97769062127.21297478207.54465054437	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050865	regulation of cell activation	21/180	491/13307	3.03023686347.28272559947.59419965697	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050830	defense response to Gram-positive bacterium	8/180	67/13307	3.16802372627.46631393977.67246158977	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0000028	ribosomal small subunit assembly	5/180	18/13307	3.18195426547.46631393977.67246158977	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002495	antigen processing and presentation of peptide antigen	5/180	18/13307	3.18195426547.46631393977.67246158977	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002683	negative regulation of immune system process	19/180	413/13307	3.23970712867.54633700597.78146214007	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050870	positive regulation of T cell activation	12/180	171/13307	3.53268020357.00010198437.24469196807	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071347	cellular response to interleukin-1	8/180	68/13307	3.54936299757.00010198437.24469196807	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051249	regulation of lymphocyte activation	18/180	377/13307	3.55998174297.00010198437.24469196807	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002702	positive regulation of production of molecular mediato	9/180	91/13307	3.75183195327.00010649697.56525844367	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002694	regulation of leukocyte activation	20/180	459/13307	4.00905926167.00011206597.96086465767	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046631	alpha-beta T cell activation	11/180	144/13307	4.02046541257.00011206597.96086465767	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:0002428	antigen processing and presentation of peptide antigen	5/180	19/13307	4.271181436	0.000115921	3.234743157	6 H2-T23/B2m/H2-5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002504	antigen processing and presentation of peptide or poly	5/180	19/13307	4.271181436	0.000115921	3.234743157	6 H2-Eb1/H2-Aa/Cr5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002726	positive regulation of T cell cytokine production	5/180	19/13307	4.271181436	0.000115921	3.234743157	6 Rsad2/B2m/Malt5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	9/180	93/13307	4.498798378	9.000121037	2.598161112	3 Irf1/Cd274/Arg2/9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	6/180	33/13307	4.608155323	8.000122910	6.731241666	1 H2-T23/B2m/H2-6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002703	regulation of leukocyte mediated immunity	13/180	207/13307	4.707556741	7.000123830	7.796607336	1 Tnf/Rsad2/H2-T23	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	10/180	119/13307	4.758367556	0.000123830	7.796607336	1 H2-Aa/Cd74/Irf1,10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000377	regulation of reactive oxygen species metabolic proces	12/180	176/13307	4.762722506	4.000123830	7.796607336	1 Tnf/Arg2/Acod1/12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050863	regulation of T cell activation	15/180	275/13307	4.905104190	6.000126469	9.984085570	2 H2-Aa/Cd74/Irf1,15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	12/180	177/13307	5.049620231	2.000129120	9.172341924	9 Cd74/Irf1/Tnf/Tn12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071407	cellular response to organic cyclic compound	16/180	312/13307	5.173227237	0.000131196	4.319843374	3 Dnaja1/Inhba/Tn16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1900407	regulation of cellular response to oxidative stress	8/180	72/13307	5.488688861	8.000138065	9.807772651	7 Tnf/Slc7a11/Cd3i8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031348	negative regulation of defense response	12/180	179/13307	5.669382964	8.000141460	2.000100489	5 Arg2/H2-T23/Du12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0060326	cell chemotaxis	14/180	244/13307	5.752610978	8.000142388	6.000101149	0 Cd74/Cxcl9/Nr4a14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043901	negative regulation of multi-organism process	11/180	150/13307	5.967925626	5.000146545	7.000104102	1 Tnf/Arg2/Rsad2/11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0044403	symbiont process	16/180	318/13307	6.588052518	1.000160499	4.000114014	5 Cd74/Irgm1/Tnf/16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071356	cellular response to tumor necrosis factor	10/180	124/13307	6.885298220	7.000166430	5.000118227	8 Irf1/Tnf/Ccl4/Acc10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	9/180	99/13307	7.553156886	1.000181158	6.000128690	2 Tnf/Mdm2/Ccl5/9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901031	regulation of response to reactive oxygen species	6/180	36/13307	7.835766277	3.000186491	2.000132478	3 Tnf/Cd36/Hk3/Nr6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0035690	cellular response to drug	14/180	251/13307	7.958462586	2.000187965	5.000133525	6 Tnf/Ccl4/Acod1/14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0035456	response to interferon-beta	7/180	55/13307	8.652735247	3.000202814	8.000144074	2 Irf1/Irgm1/Gbp2/7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0030595	leukocyte chemotaxis	12/180	187/13307	8.868906369	5.000204779	0.000145469	5 Cd74/Cxcl9/Ccl4/12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0033002	muscle cell proliferation	12/180	187/13307	8.868906369	5.000204779	0.000145469	5 Tnf/Mdm2/Tnfaip12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002475	antigen processing and presentation via MHC class Ib	5/180	22/13307	9.359507665	9.000213015	9.000151320	8 H2-T23/B2m/H2-5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046677	response to antibiotic	12/180	188/13307	9.363339520	0.000213015	9.000151320	8 Crip1/Mdm2/Tnf12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001914	regulation of T cell mediated cytotoxicity	6/180	38/13307	1.085961749	6.000245252	9.000174221	1 H2-T23/B2m/H2-6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902882	regulation of response to oxidative stress	8/180	79/13307	1.103881061	5.000247493	3.000175812	6 Slc7a11/Cd3i8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002695	negative regulation of leukocyte activation	11/180	162/13307	1.244464764	6.000277005	3.000196777	1 H2-Aa/Cd74/Irf1,11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042255	ribosome assembly	7/180	59/13307	1.389942234	9.000307177	2.000218210	4 Rps27/Rpl38/Rps7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002483	antigen processing and presentation of endogenous pe	5/180	24/13307	1.477864016	1.000320196	8.000227459	2 H2-T23/B2m/H2-5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019885	antigen processing and presentation of endogenous pe	5/180	24/13307	1.477864016	1.000320196	8.000227459	2 H2-T23/B2m/H2-5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045619	regulation of lymphocyte differentiation	11/180	165/13307	1.479901203	5.000320196	8.000227459	2 H2-Aa/Cd74/Irf1,11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045580	regulation of T cell differentiation	10/180	136/13307	1.559898839	5.000335161	5.000238089	8 H2-Aa/Cd74/Irf1,10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050868	negative regulation of T cell activation	9/180	109/13307	1.657011807	6.000350079	0.000248686	7 H2-Aa/Cd74/Irf1,9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051607	defense response to virus	12/180	199/13307	1.661998861	2.000350079	0.000248686	7 Irf1/Cxcl9/Rsad2,12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001906	cell killing	10/180	137/13307	1.663271552	5.000350079	0.000248686	7 Rpl30/Hsp90ab1,10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006953	acute-phase response	5/180	25/13307	1.827177184	3.000381978	7.000271347	5 Tnf/Ccl5/Il1a/Il1r5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072593	reactive oxygen species metabolic process	13/180	235/13307	1.848049627	2.000383749	3.000272605	2 Tnf/Arg2/Acod1/13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002526	acute inflammatory response	8/180	85/13307	1.900661407	5.000392043	0.000278496	9 Tnf/H2-T23/Ccl5/8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034113	heterotypic cell-cell adhesion	6/180	42/13307	1.973053543	0.000401620	2.000285300	2 Tnf/Tnfaip3/Itgb6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903202	negative regulation of oxidative stress-induced cell de	6/180	42/13307	1.973053543	0.000401620	2.000285300	2 Slc7a11/Hk3/Nr4 6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032870	cellular response to hormone stimulus	17/180	387/13307	1.991729254	8.000402771	9.000286118	3 Irf1/Dnaja1/Inhb17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0044406	adhesion of symbiont to host	4/180	13/13307	2.104624653	7.000422838	2.000300372	9 Hsp90ab1/Gbp2/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034612	response to tumor necrosis factor	10/180	141/13307	2.137924088	1.000426757	2.000303156	9 Irf1/Tnf/Ccl4/Acc10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042133	neurotransmitter metabolic process	9/180	113/13307	2.215409058	5.000438470	9.000311477	9 Tnf/Cd36/Sod2/Ir9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019883	antigen processing and presentation of endogenous ar	5/180	26/13307	2.237547081	2.000438470	9.000311477	9 H2-T23/B2m/H2-5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002286	T cell activation involved in immune response	8/180	87/13307	2.255424355	4.000438470	9.000311477	9 Irf1/Malt1/Icam18	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045582	positive regulation of T cell differentiation	8/180	87/13307	2.255424355	4.000438470	9.000311477	9 H2-Aa/Cd74/Irf1,8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1900408	negative regulation of cellular response to oxidative st	6/180	43/13307	2.267464258	8.000438470	9.000311477	9 Slc7a11/Hk3/Nr4 6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032623	interleukin-2 production	7/180	64/13307	2.391170390	6.000459520	5.000326431	1 Tnfaip3/Malt1/Cr7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019730	antimicrobial humoral response	6/180	44/13307	2.596242907	0.000495850	3.000352238	8 Rpl39/Cxcl9/Rpl36	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046635	positive regulation of alpha-beta T cell activation	7/180	65/13307	2.649482940	7.000502611	0.000357041	4 Irf1/H2-Ab1/H2-17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045639	positive regulation of myeloid cell differentiation	8/180	89/13307	2.664130851	0.000502611	0.000357041	4 Cd74/Inhba/Tnf/8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050866	negative regulation of cell activation	11/180	177/13307	2.851229901	0.000534648	8.000379800	1 H2-Aa/Cd74/Irf1,11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 product	4/180	14/13307	2.915397662	3.000543387	9.000386008	2 Cd74/Tnf/Ccl5/Kl4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002696	positive regulation of leukocyte activation	14/180	282/13307	2.942599486	4.000545173	8.000387276	8 H2-Aa/Cd74/Irf1,14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di	5/180	28/13307	3.270561172	1.000598764	2.000425346	1 Irf1/Malt1/Cd83/5	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:2001024	negative regulation of response to drug	5/180	28/13307	3.2705611721	0.0005987642	0.0004253461	Tnf/Hk3/Nr4a3/F5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902883	negative regulation of response to oxidative stress	6/180	46/13307	3.3687245704	0.0006131078	0.0004355354	Slc7a11/Hk3/Nr4 6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentia	6/180	47/13307	3.8187229610	0.0006909432	0.0004908275	Irf1/Malt1/Cd83/6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072567	chemokine (C-X-C motif) ligand 2 production	4/180	15/13307	3.9336282674	0.0007075956	0.0005026570	Cd74/Tnf/Ccl5/Kl 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002262	myeloid cell homeostasis	10/180	152/13307	4.0851241530	0.0007305996	0.0005189984	Inhba/Rps24/B2r 10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045824	negative regulation of innate immune response	6/180	48/13307	4.3156846614	0.0007673981	0.0005451391	H2-T23/Dusp10/.6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042035	regulation of cytokine biosynthetic process	8/180	96/13307	4.6159691585	0.0008161033	0.0005797379	Irf1/Tnf/Zfp36/R 8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050867	positive regulation of cell activation	14/180	296/13307	4.9980278516	0.0008743272	0.0006210986	H2-Aa/Cd74/Irf1/ 14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071417	cellular response to organonitrogen compound	16/180	375/13307	5.0018073684	0.0008743272	0.0006210986	Irf1/Tnf/Nr4a1/N 16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045637	regulation of myeloid cell differentiation	11/180	189/13307	5.2063040153	0.0009049609	0.0006428600	Cd74/Inhba/Tnf/ 11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002828	regulation of type 2 immune response	5/180	31/13307	5.4715027314	0.0009404905	0.0006680992	Cd74/Irf1/Arg2/F5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0061756	leukocyte adhesion to vascular endothelial cell	5/180	31/13307	5.4715027314	0.0009404905	0.0006680992	Tnf/Icam1/Itgb7/5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042254	ribosome biogenesis	13/180	261/13307	5.5163554879	0.0009942615	0.0006698546	Rps27/Rps21/Rpl13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902532	negative regulation of intracellular signal transduction	18/180	464/13307	5.8156079673	0.0009886533	0.0007023128	Cd74/Irf1/Dnaja118	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901699	cellular response to nitrogen compound	17/180	422/13307	5.9258629889	0.0010018918	0.0007117171	Irf1/Tnf/Nr4a1/N 17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045621	positive regulation of lymphocyte differentiation	8/180	100/13307	6.1874968647	0.0010404410	0.0007391014	H2-Aa/Cd74/Irf1/8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031341	regulation of cell killing	8/180	101/13307	6.6431644282	0.0010922823	0.0007759281	Hsp90ab1/H2-T2 8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904018	positive regulation of vasculature development	10/180	161/13307	6.6546259214	0.0010922823	0.0007759281	Cd5l/Hk2/Sod2/K 10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034614	cellular response to reactive oxygen species	9/180	130/13307	6.7128787112	0.0010922823	0.0007759281	Tnf/Tnfaip3/Cd3 9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002486	antigen processing and presentation of endogenous pe	4/180	17/13307	6.7148607768	0.0010922823	0.0007759281	H2-T23/H2-D1/H 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	4/180	17/13307	6.7148607768	0.0010922823	0.0007759281	Irf1/Cd274/H2-T: 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031343	positive regulation of cell killing	7/180	75/13307	6.7429194883	0.0010922823	0.0007759281	H2-T23/B2m/H2- 7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	7/180	75/13307	6.7429194883	0.0010922823	0.0007759281	Irf1/Rsad2/Malt17	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002474	antigen processing and presentation of peptide antigen	5/180	33/13307	7.4772282053	0.0012049241	0.0008559458	H2-T23/B2m/H2- 5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006979	response to oxidative stress	15/180	349/13307	7.9751270160	0.0012737106	0.0009048099	Tnf/Slc7a11/ND3 15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032642	regulation of chemokine production	7/180	77/13307	7.9864209609	0.0012737106	0.0009048099	Cd74/Tnf/Arg2/C7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901653	cellular response to peptide	12/180	234/13307	8.1193487240	0.0012882699	0.0009151525	Irf1/Nr4a1/Mdm 12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0060759	regulation of response to cytokine stimulus	8/180	104/13307	8.1807127006	0.0012913839	0.0009173645	Cd74/Irgm1/Zbp 8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002476	antigen processing and presentation of endogenous pe	4/180	18/13307	8.5424794483	0.0013215215	0.0009387735	H2-T23/H2-D1/H 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002484	antigen processing and presentation of endogenous pe	4/180	18/13307	8.5424794483	0.0013215215	0.0009387735	H2-T23/H2-D1/H 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002577	regulation of antigen processing and presentation	4/180	18/13307	8.5424794483	0.0013215215	0.0009387735	Cd74/H2-Ab1/Fgl 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904994	regulation of leukocyte adhesion to vascular endotheli	4/180	18/13307	8.5424794483	0.0013215215	0.0009387735	Tnf/Icam1/Klf4/I4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	5/180	34/13307	8.6710058988	0.0013347309	0.0009481571	Irf1/Malt1/Cd83/5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0007162	negative regulation of cell adhesion	12/180	236/13307	8.8063087818	0.0013422029	0.0009534650	H2-Aa/Cd74/Irf1/12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051251	positive regulation of lymphocyte activation	12/180	236/13307	8.8063087818	0.0013422029	0.0009534650	H2-Aa/Cd74/Irf1/12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901342	regulation of vasculature development	13/180	274/13307	9.0423900136	0.0013714291	0.0009742265	Cd5l/Cd36/Stat1/13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009144	purine nucleoside triphosphate metabolic process	12/180	237/13307	9.1681744851	0.0013837235	0.0009829601	ATP8/Atp5e/Hsp 12	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001913	T cell mediated cytotoxicity	6/180	55/13307	9.4275593615	0.0014159644	0.0010058632	H2-T23/B2m/H2-6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002831	regulation of response to biotic stimulus	9/180	136/13307	9.5220158161	0.0014232423	0.0010110332	Cd274/Arg2/Aco9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048872	homeostasis of number of cells	13/180	276/13307	9.7295297703	0.0014472675	0.0010281001	Cd74/Inhba/Rps2 13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042089	cytokine biosynthetic process	8/180	107/13307	0.0001000253	0.0014807585	0.0010518912	Irf1/Tnf/Zfp36/R 8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032663	regulation of interleukin-2 production	6/180	56/13307	0.0001044154	0.0015383873	0.0010928291	Tnfaip3/Malt1/Ci 6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046034	ATP metabolic process	11/180	205/13307	0.0001081368	0.0015781864	0.0011211014	ATP8/Atp5e/Hsp 11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001234	negative regulation of apoptotic signaling pathway	11/180	205/13307	0.0001081368	0.0015781864	0.0011211014	Cd74/Lmna/Dnaj 11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022613	ribonucleoprotein complex biogenesis	16/180	401/13307	0.0001100150	0.0015955592	0.0011334425	Rps27/Rps21/Rpl16	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032602	chemokine production	7/180	81/13307	0.0001103586	0.0015955592	0.0011334425	Cd74/Tnf/Arg2/C7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045123	cellular extravasation	6/180	57/13307	0.0001154031	0.0016607320	0.0011797395	Tnf/Ccl5/Icam1/I 6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032635	interleukin-6 production	9/180	140/13307	0.0001189625	0.0017040278	0.0012104957	Tnf/Tnfaip3/Cd3 9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042107	cytokine metabolic process	8/180	111/13307	0.0001294263	0.0018209774	0.0012935736	Irf1/Tnf/Zfp36/R 8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042092	type 2 immune response	5/180	37/13307	0.0001314499	0.0018209774	0.0012935736	Cd74/Irf1/Arg2/F5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0015985	energy coupled proton transport, down electrochemic	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	ATP8/Atp5e/ATP 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0015986	ATP synthesis coupled proton transport	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	ATP8/Atp5e/ATP 4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034114	regulation of heterotypic cell-cell adhesion	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	Tnf/Tnfaip3/Klf4/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0060333	interferon-gamma-mediated signaling pathway	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	Irf1/Irgm1/Stat1/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901032	negative regulation of response to reactive oxygen spe	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	Hk3/Nr4a3/Psap/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903206	negative regulation of hydrogen peroxide-induced cell	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	Hk3/Nr4a3/Psap/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001039	negative regulation of cellular response to drug	4/180	20/13307	0.0001324240	0.0018209774	0.0012935736	Hk3/Nr4a3/Psap/4	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:0000302	response to reactive oxygen species	10/180	175/13307	0.0001332827	0.0018246759	0.0012962009	Tnf/Tnfaip3/Cd3	Up-regulated genes
BP	GO:0050663	cytokine secretion	11/180	212/13307	0.0001455260	0.0019835136	0.0014090349	Cd274/Tnf/Arg2/	Up-regulated genes
BP	GO:0006959	humoral immune response	8/180	113/13307	0.0001466063	0.0019894742	0.0014132692	Rpl39/Cxcl9/H2-r	Up-regulated genes
BP	GO:0002791	regulation of peptide secretion	16/180	413/13307	0.0001545087	0.0020875550	0.0014829431	Cd74/Cd274/Tnf,	Up-regulated genes
BP	GO:0016032	viral process	12/180	251/13307	0.0001575057	0.0021187940	0.0015051345	Cd74/Tnf/Rsad2/	Up-regulated genes
BP	GO:0010742	macrophage derived foam cell differentiation	4/180	21/13307	0.0001618621	0.0021586264	0.0015334304	Cd36/Nfkbia/Sta	Up-regulated genes
BP	GO:2000316	regulation of T-helper 17 type immune response	4/180	21/13307	0.0001618621	0.0021586264	0.0015334304	Malt1/Nlrp3/Aric	Up-regulated genes
BP	GO:0009141	nucleoside triphosphate metabolic process	12/180	253/13307	0.0001696059	0.0022521924	0.0015998972	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	11/180	217/13307	0.0001785243	0.0023604889	0.0016768281	Cd74/Irf1/Tnf/Sa	Up-regulated genes
BP	GO:0046637	regulation of alpha-beta T cell differentiation	6/180	62/13307	0.0001848857	0.0024341982	0.0017291892	Irf1/Malt1/Cd83/	Up-regulated genes
BP	GO:0046636	negative regulation of alpha-beta T cell activation	5/180	40/13307	0.0001920311	0.0025175608	0.0017884077	Irf1/Cd274/Arg2/	Up-regulated genes
BP	GO:0002827	positive regulation of T-helper 1 type immune respons	4/180	22/13307	0.0001957515	0.0025447703	0.0018077367	Irf1/H2-Ab1/Slc1	Up-regulated genes
BP	GO:0090077	foam cell differentiation	4/180	22/13307	0.0001957515	0.0025447703	0.0018077367	Cd36/Nfkbia/Sta	Up-regulated genes
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	6/180	63/13307	0.0002020800	0.0026051492	0.0018506282	H2-T23/B2m/H2-	Up-regulated genes
BP	GO:1903201	regulation of oxidative stress-induced cell death	6/180	63/13307	0.0002020800	0.0026051492	0.0018506282	Slc7a11/Hk3/Nr4	Up-regulated genes
BP	GO:0050707	regulation of cytokine secretion	10/180	185/13307	0.0002098964	0.0026946876	0.0019142339	Cd274/Tnf/Arg2/	Up-regulated genes
BP	GO:0032103	positive regulation of response to external stimulus	12/180	260/13307	0.0002184278	0.0027926274	0.0019838077	Cd74/Tnf/Ccl4/H	Up-regulated genes
BP	GO:0050729	positive regulation of inflammatory response	8/180	120/13307	0.0002222035	0.0028292092	0.0020097944	Tnf/H2-T23/Ccl5/	Up-regulated genes
BP	GO:0002366	leukocyte activation involved in immune response	11/180	223/13307	0.0002263154	0.0028697543	0.0020385966	Irf1/Tnfaip3/Mal	Up-regulated genes
BP	GO:0032943	mononuclear cell proliferation	12/180	262/13307	0.0002344046	0.0029346726	0.0020847128	H2-Aa/Cd74/Irf1,	Up-regulated genes
BP	GO:0002675	positive regulation of acute inflammatory response	4/180	23/13307	0.0002344721	0.0029346726	0.0020847128	Tnf/H2-T23/Ccl5/	Up-regulated genes
BP	GO:0002698	negative regulation of immune effector process	8/180	121/13307	0.0002352290	0.0029346726	0.0020847128	Irf1/Tnf/H2-T23/	Up-regulated genes
BP	GO:0034101	erythrocyte homeostasis	8/180	121/13307	0.0002352290	0.0029346726	0.0020847128	Inhba/Rps24/B2r	Up-regulated genes
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	10/180	188/13307	0.0002390613	0.0029705058	0.0021101678	Cd74/Tnf/Rsad2/	Up-regulated genes
BP	GO:0042098	T cell proliferation	10/180	190/13307	0.0002603352	0.0032219091	0.0022887579	H2-Aa/Irf1/H2-Ab	Up-regulated genes
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	7/180	93/13307	0.0002624652	0.0032268044	0.0022922354	Cd74/Irgm1/Zbp	Up-regulated genes
BP	GO:0050728	negative regulation of inflammatory response	8/180	123/13307	0.0002631608	0.0032268044	0.0022922354	Dusp10/Acod1/T	Up-regulated genes
BP	GO:0002263	cell activation involved in immune response	11/180	227/13307	0.0002638595	0.0032268044	0.0022922354	Irf1/Tnfaip3/Mal	Up-regulated genes
BP	GO:0002468	dendritic cell antigen processing and presentation	3/180	10/13307	0.0002723667	0.0032484284	0.0023075965	Cd74/Fgl2/Slc11	Up-regulated genes
BP	GO:0002579	positive regulation of antigen processing and presenta	3/180	10/13307	0.0002723667	0.0032484284	0.0023075965	Cd74/H2-Ab1/Slc	Up-regulated genes
BP	GO:0031652	positive regulation of heat generation	3/180	10/13307	0.0002723667	0.0032484284	0.0023075965	Tnf/Ccl5/Ptgs2	Up-regulated genes
BP	GO:0042090	interleukin-12 biosynthetic process	3/180	10/13307	0.0002723667	0.0032484284	0.0023075965	Irf1/Rel/Nfkb1	Up-regulated genes
BP	GO:0045075	regulation of interleukin-12 biosynthetic process	3/180	10/13307	0.0002723667	0.0032484284	0.0023075965	Irf1/Rel/Nfkb1	Up-regulated genes
BP	GO:0070586	cell-cell adhesion involved in gastrulation	3/180	10/13307	0.0002723667	0.0032484284	0.0023075965	Tnfaip3/Klf4/Il1r	Up-regulated genes
BP	GO:0009126	purine nucleoside monophosphate metabolic process	11/180	228/13307	0.0002740270	0.0032484284	0.0023075965	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0009167	purine ribonucleoside monophosphate metabolic proc	11/180	228/13307	0.0002740270	0.0032484284	0.0023075965	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0002292	T cell differentiation involved in immune response	6/180	67/13307	0.0002838585	0.0033472092	0.0023777677	Irf1/Malt1/Fgl2/C	Up-regulated genes
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	11/180	229/13307	0.0002845236	0.0033472092	0.0023777677	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0050792	regulation of viral process	9/180	158/13307	0.0002959913	0.0034689290	0.0024642343	Cd74/Tnf/Rsad2/	Up-regulated genes
BP	GO:0045581	negative regulation of T cell differentiation	5/180	44/13307	0.0003033966	0.0035422994	0.0025163546	Cd74/Irf1/Socs1/	Up-regulated genes
BP	GO:0030099	myeloid cell differentiation	14/180	352/13307	0.0003081974	0.0035848223	0.0025465618	Cd74/Inhba/Tnf/	Up-regulated genes
BP	GO:0009161	ribonucleoside monophosphate metabolic process	11/180	232/13307	0.0003180725	0.0036858290	0.0026183142	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0036037	CD8-positive, alpha-beta T cell activation	4/180	25/13307	0.0003279611	0.0037862379	0.0026896420	Irf1/Cd274/H2-T	Up-regulated genes
BP	GO:0009199	ribonucleoside triphosphate metabolic process	11/180	233/13307	0.0003299711	0.0037952820	0.0026960667	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0045444	fat cell differentiation	10/180	196/13307	0.0003339054	0.0038263087	0.0027181072	Tnf/Nr4a1/Dusp	Up-regulated genes
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	5/180	45/13307	0.0003376183	0.0038545804	0.0027381907	Irf1/Malt1/Cd83/	Up-regulated genes
BP	GO:0002224	toll-like receptor signaling pathway	7/180	97/13307	0.0003401601	0.0038553339	0.0027387259	Irf1/Tnf/Rsad2/A	Up-regulated genes
BP	GO:0002285	lymphocyte activation involved in immune response	9/180	161/13307	0.0003401765	0.0038553339	0.0027387259	Irf1/Tnfaip3/Mal	Up-regulated genes
BP	GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2	3/180	11/13307	0.0003707835	0.0041868764	0.0029742449	Cd74/Tnf/Ccl5	Up-regulated genes
BP	GO:0045646	regulation of erythrocyte differentiation	5/180	46/13307	0.0003746831	0.0042155262	0.0029945969	Inhba/B2m/Stat1	Up-regulated genes
BP	GO:0002221	pattern recognition receptor signaling pathway	8/180	130/13307	0.0003831137	0.0042947603	0.0030508827	Irf1/Tnf/Rsad2/A	Up-regulated genes
BP	GO:0001933	negative regulation of protein phosphorylation	14/180	360/13307	0.0003866237	0.0043184617	0.0030677195	Irf1/Dnaja1/Sam	Up-regulated genes
BP	GO:0008015	blood circulation	13/180	318/13307	0.0003898857	0.0043392321	0.0030824742	Tnf/Ccl4/Mdm2/	Up-regulated genes
BP	GO:0070661	leukocyte proliferation	12/180	278/13307	0.0004020176	0.0044582171	0.0031669980	H2-Aa/Cd74/Irf1,	Up-regulated genes
BP	GO:0009123	nucleoside monophosphate metabolic process	11/180	239/13307	0.0004095227	0.0045252266	0.0032145998	ATP8/Atp5e/Hsp	Up-regulated genes
BP	GO:0002758	innate immune response-activating signal transductior	8/180	132/13307	0.0004245462	0.0046579647	0.0033088934	Irf1/Tnf/Rsad2/A	Up-regulated genes
BP	GO:0032675	regulation of interleukin-6 production	8/180	132/13307	0.0004245462	0.0046579647	0.0033088934	Tnf/Tnfaip3/Cd3	Up-regulated genes

BP	GO:0046632	alpha-beta T cell differentiation	7/180	102/13307	0.0004621253	0.0050523533	0.0035890564	Irf1/Rsad2/Malt1	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0003013	circulatory system process	13/180	325/13307	0.0004793527	0.0052222438	0.0037097421	Tnf/Ccl4/Mdm2/	13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031650	regulation of heat generation	3/180	12/13307	0.0004894693	0.0053036388	0.0037675630	Tnf/Ccl5/Ptgs2	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006754	ATP biosynthetic process	7/180	103/13307	0.0004902523	0.0053036388	0.0037675630	ATP8/Atp5e/Hk3	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022618	ribonucleoprotein complex assembly	10/180	206/13307	0.0004948186	0.0053343860	0.0037894049	Rps27/Rpl38/Rps	10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002673	regulation of acute inflammatory response	5/180	49/13307	0.0005044632	0.0054194767	0.0038498511	Tnf/H2-T23/Ccl5/	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043281	regulation of cysteine-type endopeptidase activity involv	9/180	170/13307	0.0005065755	0.0054216325	0.0038513825	Tnf/Nr4a1/Plaur/	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001233	regulation of apoptotic signaling pathway	14/180	370/13307	0.0005081685	0.0054216325	0.0038513825	Cd74/Lmna/Dnaj1	14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002507	tolerance induction	4/180	28/13307	0.0005142966	0.0054494313	0.0038711301	Cd274/H2-T23/A	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903205	regulation of hydrogen peroxide-induced cell death	4/180	28/13307	0.0005142966	0.0054494313	0.0038711301	Hk3/Nr4a3/Psap/	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043434	response to peptide hormone	11/180	246/13307	0.0005221135	0.0054946237	0.0039032335	Irf1/Nr4a1/Serpii	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0070371	ERK1 and ERK2 cascade	11/180	246/13307	0.0005221135	0.0054946237	0.0039032335	Cd74/Ccl4/Atf3/I	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001659	temperature homeostasis	8/180	137/13307	0.0005442503	0.0057081715	0.0040549321	Tnf/Ccl5/Cd36/Kl	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045765	regulation of angiogenesis	11/180	248/13307	0.0005586703	0.0058396154	0.0041483064	Ccl5/Cd36/Stat1/	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001023	regulation of response to drug	6/180	76/13307	0.0005625352	0.0058602158	0.0041629403	Tnf/Arg2/Hk3/Nr	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002825	regulation of T-helper 1 type immune response	4/180	29/13307	0.0005903299	0.0061291307	0.0043539703	Irf1/H2-Ab1/Slc1	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032479	regulation of type I interferon production	6/180	77/13307	0.0006033243	0.0062430956	0.0044349279	Irf1/Acod1/Gbp4	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006801	superoxide metabolic process	5/180	51/13307	0.0006080510	0.0062501990	0.0044399740	Tnf/Cd36/Sod2/N	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045620	negative regulation of lymphocyte differentiation	5/180	51/13307	0.0006080510	0.0062501990	0.0044399740	Cd74/Irf1/Socs1/	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042542	response to hydrogen peroxide	7/180	107/13307	0.0006167119	0.0063182340	0.0044883042	Tnfaip3/Hk3/Nr4	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904950	negative regulation of establishment of protein localiz	9/180	175/13307	0.0006247198	0.0063791529	0.0045315793	Dnaja1/Tnf/Arg2,	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STA	3/180	13/13307	0.0006299963	0.0064118704	0.0045548210	Irf1/Socs3/Socs1	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902600	proton transmembrane transport	6/180	78/13307	0.0006463723	0.0065569705	0.0046578962	ATP8/Atp5e/ATP	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009612	response to mechanical stimulus	7/180	108/13307	0.0006520525	0.0065929758	0.0046834734	Tnf/Cd36/Nfkbia,	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072538	T-helper 17 type immune response	4/180	30/13307	0.0006740122	0.0067707592	0.0048097660	Malt1/Nlrp3/Aric	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001038	regulation of cellular response to drug	4/180	30/13307	0.0006740122	0.0067707592	0.0048097660	Hk3/Nr4a3/Psap/	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0070301	cellular response to hydrogen peroxide	6/180	79/13307	0.0006917638	0.0069265930	0.0049204661	Tnfaip3/Hk3/Nr4	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0036473	cell death in response to oxidative stress	6/180	80/13307	0.0007395848	0.0073759426	0.0052396721	Slc7a11/Rpl38/Nr4	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071826	ribonucleoprotein complex subunit organization	10/180	217/13307	0.0007414085	0.0073759426	0.0052396721	Rps27/Rpl38/Rps	10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032743	positive regulation of interleukin-2 production	4/180	31/13307	0.0007657599	0.0075415793	0.0053573359	Malt1/Cd83/Pde4	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0036474	cell death in response to hydrogen peroxide	4/180	31/13307	0.0007657599	0.0075415793	0.0053573359	Hk3/Nr4a3/Psap/	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000515	negative regulation of CD4-positive, alpha-beta T cell a	4/180	31/13307	0.0007657599	0.0075415793	0.0053573359	Irf1/Cd274/Arg2/	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0030218	erythrocyte differentiation	7/180	111/13307	0.0007678078	0.0075415793	0.0053573359	Inhba/B2m/Rps1	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032606	type I interferon production	6/180	81/13307	0.0007899229	0.0077342456	0.0054942009	Irf1/Acod1/Gbp4	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001505	regulation of neurotransmitter levels	11/180	259/13307	0.0008001601	0.0078052208	0.0055446198	Tnf/Slc7a11/Cd3i	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006935	chemotaxis	15/180	433/13307	0.0008022172	0.0078052208	0.0055446198	Cd74/Cxcl9/Nr4a	15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050708	regulation of protein secretion	14/180	388/13307	0.0008096435	0.0078298375	0.0055621068	Cd274/Tnf/Arg2/	14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic proce	7/180	112/13307	0.0008098086	0.0078298375	0.0055621068	ATP8/Atp5e/Hk3	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046651	lymphocyte proliferation	11/180	260/13307	0.0008258591	0.0079601501	0.0056546774	H2-Aa/Cd74/Irf1,	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	6/180	82/13307	0.0008428669	0.0080988520	0.0057532076	H2-T23/B2m/H2-	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	7/180	113/13307	0.0008536050	0.0081766377	0.0058084644	ATP8/Atp5e/Hk3	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042330	taxis	15/180	436/13307	0.0008604440	0.0082148348	0.0058355986	Cd74/Cxcl9/Nr4a	15	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045766	positive regulation of angiogenesis	8/180	147/13307	0.0008655579	0.0082148348	0.0058355986	Ccl5/Hk2/Klf4/Itg	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokir	8/180	147/13307	0.0008655579	0.0082148348	0.0058355986	Cd274/Arg2/Ccl4	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0018108	peptidyl-tyrosine phosphorylation	11/180	264/13307	0.0009356128	0.0088330564	0.0062747667	Cd74/Irf1/Tnf/Sa	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051384	response to glucocorticoid	5/180	56/13307	0.0009364067	0.0088330564	0.0062747667	Tnf/ND3/Zfp36/Z	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009201	ribonucleoside triphosphate biosynthetic process	7/180	115/13307	0.0009468006	0.0089039554	0.0063251314	ATP8/Atp5e/Hk3	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048525	negative regulation of viral process	6/180	84/13307	0.0009569348	0.0089719888	0.0063734606	Tnf/Rsad2/Ccl4/C	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904996	positive regulation of leukocyte adhesion to vascular e	3/180	15/13307	0.0009824939	0.0091837954	0.0065239223	Tnf/Icam1/Itgb2	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	8/180	150/13307	0.0009870780	0.0091988539	0.0065346195	Cd74/Tnf/Tnfaip:	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042326	negative regulation of phosphorylation	14/180	397/13307	0.0010099314	0.0093763211	0.0066606874	Irf1/Dnaja1/Sam:	14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031960	response to corticosteroid	5/180	57/13307	0.0010153494	0.0093763211	0.0066606874	Tnf/ND3/Zfp36/Z	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032722	positive regulation of chemokine production	5/180	57/13307	0.0010153494	0.0093763211	0.0066606874	Cd74/Tnf/Ccl5/Eg	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032755	positive regulation of interleukin-6 production	6/180	85/13307	0.0010182430	0.0093763211	0.0066606874	Tnf/Cd36/Il1f9/A	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0018212	peptidyl-tyrosine modification	11/180	267/13307	0.0010256332	0.0094163484	0.0066891217	Cd74/Irf1/Tnf/Sa	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	8/180	151/13307	0.0010304911	0.0094329573	0.0067009202	Cd274/Arg2/Ccl4	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048871	multicellular organismal homeostasis	13/180	354/13307	0.0010585327	0.0096610631	0.0068629605	Tnf/Fcgr4/Ccl5/C	13	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:0044057	regulation of system process	14/180	400/13307	0.0010853465	0.0070161102	Up-regulated genes	CD45+
BP	GO:0009611	response to wounding	13/180	356/13307	0.0011140692	0.0071806656	Up-regulated genes	CD45+
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	9/180	190/13307	0.0011208477	0.0072032321	Up-regulated genes	CD45+
BP	GO:0002763	positive regulation of myeloid leukocyte differentiation	5/180	59/13307	0.0011879252	0.0075615625	Up-regulated genes	CD45+
BP	GO:0002830	positive regulation of type 2 immune response	3/180	16/13307	0.0011972474	0.0075615625	Up-regulated genes	CD45+
BP	GO:0019430	removal of superoxide radicals	3/180	16/13307	0.0011972474	0.0075615625	Up-regulated genes	CD45+
BP	GO:0071157	negative regulation of cell cycle arrest	3/180	16/13307	0.0011972474	0.0075615625	Up-regulated genes	CD45+
BP	GO:0071498	cellular response to fluid shear stress	3/180	16/13307	0.0011972474	0.0075615625	Up-regulated genes	CD45+
BP	GO:2000319	regulation of T-helper 17 cell differentiation	3/180	16/13307	0.0011972474	0.0075615625	Up-regulated genes	CD45+
BP	GO:0045622	regulation of T-helper cell differentiation	4/180	35/13307	0.0012217761	0.0108005011	Up-regulated genes	CD45+
BP	GO:0061844	antimicrobial humoral immune response mediated by	4/180	35/13307	0.0012217761	0.0108005011	Up-regulated genes	CD45+
BP	GO:0002218	activation of innate immune response	8/180	156/13307	0.0012710513	0.0111773671	Up-regulated genes	CD45+
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	10/180	233/13307	0.0012737252	0.0111773671	Up-regulated genes	CD45+
BP	GO:0007369	gastrulation	7/180	121/13307	0.0012752458	0.0111773671	Up-regulated genes	CD45+
BP	GO:0034121	regulation of toll-like receptor signaling pathway	5/180	60/13307	0.0012819214	0.0112041383	Up-regulated genes	CD45+
BP	GO:2000106	regulation of leukocyte apoptotic process	6/180	89/13307	0.0012941800	0.0112366705	Up-regulated genes	CD45+
BP	GO:0006163	purine nucleotide metabolic process	13/180	362/13307	0.0012955153	0.0112366705	Up-regulated genes	CD45+
BP	GO:0046942	carboxylic acid transport	9/180	194/13307	0.0012965389	0.0112366705	Up-regulated genes	CD45+
BP	GO:0015849	organic acid transport	9/180	195/13307	0.0013437636	0.0116134208	Up-regulated genes	CD45+
BP	GO:0034599	cellular response to oxidative stress	10/180	235/13307	0.0013579943	0.0116895715	Up-regulated genes	CD45+
BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via	4/180	36/13307	0.0013601311	0.0116895715	Up-regulated genes	CD45+
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	5/180	61/13307	0.0013813012	0.0118386318	Up-regulated genes	CD45+
BP	GO:0000188	inactivation of MAPK activity	3/180	17/13307	0.0014394114	0.0122349972	Up-regulated genes	CD45+
BP	GO:0010743	regulation of macrophage derived foam cell differentia	3/180	17/13307	0.0014394114	0.0122349972	Up-regulated genes	CD45+
BP	GO:0061081	positive regulation of myeloid leukocyte cytokine prod	3/180	17/13307	0.0014394114	0.0122349972	Up-regulated genes	CD45+
BP	GO:0009127	purine nucleoside monophosphate biosynthetic proce	7/180	124/13307	0.0014698397	0.0124253663	Up-regulated genes	CD45+
BP	GO:0009168	purine ribonucleoside monophosphate biosynthetic pr	7/180	124/13307	0.0014698397	0.0124253663	Up-regulated genes	CD45+
BP	GO:0046640	regulation of alpha-beta T cell proliferation	4/180	37/13307	0.0015090621	0.0127221754	Up-regulated genes	CD45+
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pat	6/180	92/13307	0.0015361057	0.0129149756	Up-regulated genes	CD45+
BP	GO:0002757	immune response-activating signal transduction	11/180	282/13307	0.0015899825	0.0133179960	Up-regulated genes	CD45+
BP	GO:0008625	extrinsic apoptotic signaling pathway via death domair	5/180	63/13307	0.0015969542	0.0133179960	Up-regulated genes	CD45+
BP	GO:0042108	positive regulation of cytokine biosynthetic process	5/180	63/13307	0.0015969542	0.0133179960	Up-regulated genes	CD45+
BP	GO:0009142	nucleoside triphosphate biosynthetic process	7/180	126/13307	0.0016119315	0.0134067642	Up-regulated genes	CD45+
BP	GO:0048545	response to steroid hormone	8/180	162/13307	0.0016166380	0.0134098609	Up-regulated genes	CD45+
BP	GO:0002832	negative regulation of response to biotic stimulus	4/180	38/13307	0.0016689846	0.0138070548	Up-regulated genes	CD45+
BP	GO:0031664	regulation of lipopolysaccharide-mediated signaling pa	3/180	18/13307	0.0017102087	0.0139983754	Up-regulated genes	CD45+
BP	GO:0032656	regulation of interleukin-13 production	3/180	18/13307	0.0017102087	0.0139983754	Up-regulated genes	CD45+
BP	GO:0071450	cellular response to oxygen radical	3/180	18/13307	0.0017102087	0.0139983754	Up-regulated genes	CD45+
BP	GO:0071451	cellular response to superoxide	3/180	18/13307	0.0017102087	0.0139983754	Up-regulated genes	CD45+
BP	GO:0009156	ribonucleoside monophosphate biosynthetic process	7/180	128/13307	0.0017645020	0.0144046683	Up-regulated genes	CD45+
BP	GO:0032944	regulation of mononuclear cell proliferation	9/180	204/13307	0.0018343798	0.0148737328	Up-regulated genes	CD45+
BP	GO:0007260	tyrosine phosphorylation of STAT protein	5/180	65/13307	0.0018363820	0.0148737328	Up-regulated genes	CD45+
BP	GO:0042273	ribosomal large subunit biogenesis	5/180	65/13307	0.0018363820	0.0148737328	Up-regulated genes	CD45+
BP	GO:0010563	negative regulation of phosphorus metabolic process	15/180	471/13307	0.0018508693	0.0149129942	Up-regulated genes	CD45+
BP	GO:0045936	negative regulation of phosphate metabolic process	15/180	471/13307	0.0018508693	0.0149129942	Up-regulated genes	CD45+
BP	GO:0052548	regulation of endopeptidase activity	10/180	246/13307	0.0019065604	0.0153218132	Up-regulated genes	CD45+
BP	GO:0050715	positive regulation of cytokine secretion	7/180	130/13307	0.0019280675	0.0154545104	Up-regulated genes	CD45+
BP	GO:0098869	cellular oxidant detoxification	3/180	19/13307	0.0020107980	0.0160759929	Up-regulated genes	CD45+
BP	GO:0051090	regulation of DNA-binding transcription factor activity	12/180	335/13307	0.0020217784	0.0160940017	Up-regulated genes	CD45+
BP	GO:0046633	alpha-beta T cell proliferation	4/180	40/13307	0.0020234540	0.0160940017	Up-regulated genes	CD45+
BP	GO:0035821	modification of morphology or physiology of other org	6/180	98/13307	0.0021217461	0.0168325192	Up-regulated genes	CD45+
BP	GO:0009306	protein secretion	15/180	479/13307	0.0021777642	0.0172327432	Up-regulated genes	CD45+
BP	GO:0051224	negative regulation of protein transport	8/180	170/13307	0.0021888965	0.0172766479	Up-regulated genes	CD45+
BP	GO:0009124	nucleoside monophosphate biosynthetic process	7/180	133/13307	0.0021951862	0.0172822043	Up-regulated genes	CD45+
BP	GO:0002764	immune response-regulating signaling pathway	11/180	294/13307	0.0022059370	0.0173227642	Up-regulated genes	CD45+
BP	GO:0030490	maturation of SSU-rRNA	4/180	41/13307	0.0022188191	0.0173798134	Up-regulated genes	CD45+
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	7/180	134/13307	0.0022903000	0.0178944150	Up-regulated genes	CD45+

BP	GO:0032616	interleukin-13 production	3/180	20/13307	0.00234227581	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032897	negative regulation of viral transcription	3/180	20/13307	0.00234227581	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045624	positive regulation of T-helper cell differentiation	3/180	20/13307	0.00234227581	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0070498	interleukin-1-mediated signaling pathway	3/180	20/13307	0.00234227581	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032649	regulation of interferon-gamma production	6/180	100/13307	0.00235019691	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signa	6/180	100/13307	0.00235019691	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0070663	regulation of leukocyte proliferation	9/180	212/13307	0.00238231081	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043154	negative regulation of cysteine-type endopeptidase ac	5/180	69/13307	0.00239263351	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050702	interleukin-1 beta secretion	4/180	42/13307	0.00242681121	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051591	response to cAMP	4/180	42/13307	0.00242681121	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072521	purine-containing compound metabolic process	13/180	389/13307	0.00244516941	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019058	viral life cycle	8/180	174/13307	0.00252922661	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001961	positive regulation of cytokine-mediated signaling pat	4/180	43/13307	0.00264783081	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032102	negative regulation of response to external stimulus	10/180	258/13307	0.00269647771	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0000303	response to superoxide	3/180	21/13307	0.00270567811	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046823	negative regulation of nucleocytoplasmic transport	3/180	21/13307	0.00270567811	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031397	negative regulation of protein ubiquitination	5/180	71/13307	0.00271252241	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032088	negative regulation of NF-kappaB transcription factor	5/180	71/13307	0.00271252241	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032729	positive regulation of interferon-gamma production	5/180	71/13307	0.00271252241	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006364	rRNA processing	8/180	177/13307	0.00281064691	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002437	inflammatory response to antigenic stimulus	4/180	44/13307	0.00288227421	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0015807	L-amino acid transport	4/180	44/13307	0.00288227421	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006913	nucleocytoplasmic transport	10/180	261/13307	0.00293011831	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051169	nuclear transport	10/180	261/13307	0.00293011831	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045598	regulation of fat cell differentiation	6/180	105/13307	0.00300222891	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903707	negative regulation of hemopoiesis	7/180	141/13307	0.00304822061	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0000305	response to oxygen radical	3/180	22/13307	0.00310198231	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034405	response to fluid shear stress	3/180	22/13307	0.00310198231	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1902042	negative regulation of extrinsic apoptotic signaling pat	3/180	22/13307	0.00310198231	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0090257	regulation of muscle system process	8/180	180/13307	0.00311595961	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050829	defense response to Gram-negative bacterium	4/180	45/13307	0.00313053331	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904705	regulation of vascular smooth muscle cell proliferation	4/180	45/13307	0.00313053331	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1990874	vascular smooth muscle cell proliferation	4/180	45/13307	0.00313053331	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0048514	blood vessel morphogenesis	15/180	498/13307	0.00315075591	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051348	negative regulation of transferase activity	9/180	222/13307	0.00324224471	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032611	interleukin-1 beta production	5/180	74/13307	0.00324886901	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0097193	intrinsic apoptotic signaling pathway	10/180	266/13307	0.00335527241	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042088	T-helper 1 type immune response	4/180	46/13307	0.00339299521	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2000117	negative regulation of cysteine-type endopeptidase ac	5/180	75/13307	0.00344353711	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0035743	CD4-positive, alpha-beta T cell cytokine production	3/180	23/13307	0.00353210881	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046426	negative regulation of JAK-STAT cascade	3/180	23/13307	0.00353210881	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1904893	negative regulation of STAT cascade	3/180	23/13307	0.00353210881	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032680	regulation of tumor necrosis factor production	7/180	145/13307	0.00355994061	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045333	cellular respiration	7/180	145/13307	0.00355994061	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071887	leukocyte apoptotic process	6/180	109/13307	0.00361438441	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0007498	mesoderm development	5/180	76/13307	0.00364642451	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043618	regulation of transcription from RNA polymerase II pro	4/180	47/13307	0.00367004201	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001909	leukocyte mediated cytotoxicity	6/180	110/13307	0.00378093261	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006164	purine nucleotide biosynthetic process	8/180	187/13307	0.00392887511	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002377	immunoglobulin production	6/180	111/13307	0.00395311111	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045661	regulation of myoblast differentiation	4/180	48/13307	0.00396205041	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050701	interleukin-1 secretion	4/180	48/13307	0.00396205041	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032640	tumor necrosis factor production	7/180	148/13307	0.00398481051	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045648	positive regulation of erythrocyte differentiation	3/180	24/13307	0.00399692281	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045730	respiratory burst	3/180	24/13307	0.00399692281	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903792	negative regulation of anion transport	3/180	24/13307	0.00399692281	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022904	respiratory electron transport chain	5/180	78/13307	0.00407770831	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:0009165	nucleotide biosynthetic process	9/180	230/13307	0.0040926083	0.0278910356	0.0198130447	ATP8/Atp5e/Hk3	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0010951	negative regulation of endopeptidase activity	6/180	112/13307	0.0041310339	0.0280294277	0.0199113547	Nr4a1/Plaur/Mdr	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032609	interferon-gamma production	6/180	112/13307	0.0041310339	0.0280294277	0.0199113547	Cd274/Tnf/H2-Q	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009117	nucleotide metabolic process	14/180	464/13307	0.0042336493	0.0286510193	0.0203529168	ATP8/Atp5e/Hsp	14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0001525	angiogenesis	13/180	415/13307	0.0042411657	0.0286510193	0.0203529168	Tnfaip2/Nr4a1/C	13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051051	negative regulation of transport	13/180	417/13307	0.0044147542	0.0297587140	0.0211397934	Cd74/Tnf/Arg2/R	13	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043902	positive regulation of multi-organism process	7/180	151/13307	0.0044471170	0.0299116960	0.0212484678	Cd74/Inhba/Acod	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050678	regulation of epithelial cell proliferation	10/180	277/13307	0.0044639070	0.0299594978	0.0212824249	Tnf/Nr4a1/Dusp1	10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032480	negative regulation of type I interferon production	3/180	25/13307	0.0044972358	0.0299880338	0.0213026961	Acod1/Gbp4/Rel	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032673	regulation of interleukin-4 production	3/180	25/13307	0.0044972358	0.0299880338	0.0213026961	H2-T23/Cd83/Nlr	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046639	negative regulation of alpha-beta T cell differentiation	3/180	25/13307	0.0044972358	0.0299880338	0.0213026961	Irf1/Socs1/Smad	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1903321	negative regulation of protein modification by small pr	5/180	80/13307	0.0045442820	0.0302365774	0.0214792548	Dnaja1/Tnfaip3/C	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylati	4/180	50/13307	0.0045924306	0.0304260820	0.0216138737	Irf1/Samsn1/Socs	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0060760	positive regulation of response to cytokine stimulus	4/180	50/13307	0.0045924306	0.0304260820	0.0216138737	Cd74/Irgm1/Zbp1	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072522	purine-containing compound biosynthetic process	8/180	192/13307	0.0046034231	0.0304337418	0.0216193151	ATP8/Atp5e/Hk3	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0062013	positive regulation of small molecule metabolic proces	6/180	115/13307	0.0047004090	0.0310086683	0.0220277275	Tnf/Nr4a3/Nfkb1	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0006753	nucleoside phosphate metabolic process	14/180	470/13307	0.0047369251	0.0311830775	0.0221516231	ATP8/Atp5e/Hsp	14	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0071375	cellular response to peptide hormone stimulus	8/180	193/13307	0.0047484073	0.0311922978	0.0221581730	Irf1/Nr4a1/Nr4a3	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046328	regulation of JNK cascade	7/180	153/13307	0.0047771209	0.0312088804	0.0221699528	Dnaja1/Tnf/Dusp	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0022900	electron transport chain	5/180	81/13307	0.0047912793	0.0312088804	0.0221699528	Cox7c/ND4L/CYT	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0044070	regulation of anion transport	5/180	81/13307	0.0047912793	0.0312088804	0.0221699528	Tnf/Arg2/Il1a/Il1	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pat	5/180	81/13307	0.0047912793	0.0312088804	0.0221699528	Lmna/Tnf/Tnfaip	5	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:1901293	nucleoside phosphate biosynthetic process	9/180	236/13307	0.0048378822	0.0314462347	0.0223385629	ATP8/Atp5e/Hk3	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072539	T-helper 17 cell differentiation	3/180	26/13307	0.0050338072	0.0326511519	0.0231945038	Malt1/Nlrp3/Sma	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0052547	regulation of peptidase activity	10/180	282/13307	0.0050549491	0.0327196915	0.0232431926	Tnf/Nr4a1/Plaur/	10	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0007259	JAK-STAT cascade	6/180	117/13307	0.0051108083	0.0329434189	0.0234021225	Irf1/Tnf/Ccl5/Sta	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051092	positive regulation of NF-kappaB transcription factor a	6/180	117/13307	0.0051108083	0.0329434189	0.0234021225	Tnf/Cd36/Malt1/	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042129	regulation of T cell proliferation	7/180	155/13307	0.0051252715	0.0329679628	0.0234195578	H2-Aa/Irf1/H2-Ab	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032655	regulation of interleukin-12 production	4/180	52/13307	0.0052870328	0.0337279990	0.0239594672	Irf1/Cd36/Rel/Nf	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032890	regulation of organic acid transport	4/180	52/13307	0.0052870328	0.0337279990	0.0239594672	Tnf/Arg2/Il1a/Il1	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043620	regulation of DNA-templated transcription in response	4/180	52/13307	0.0052870328	0.0337279990	0.0239594672	Atf3/Cd36/Egr1/I	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050810	regulation of steroid biosynthetic process	4/180	52/13307	0.0052870328	0.0337279990	0.0239594672	Tnf/Nfkb1/Egr1/I	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0072594	establishment of protein localization to organelle	11/180	332/13307	0.0055312596	0.0351726757	0.0249857268	Lmna/Dnaja1/Hs	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0034504	protein localization to nucleus	9/180	241/13307	0.0055362291	0.0351726757	0.0249857268	Lmna/Mdm2/Gb	9	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0010470	regulation of gastrulation	3/180	27/13307	0.0056073458	0.0352624554	0.0250495039	Tnfaip3/Klf4/Il1rn	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042036	negative regulation of cytokine biosynthetic process	3/180	27/13307	0.0056073458	0.0352624554	0.0250495039	Zfp36/Nfkb1/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0042119	neutrophil activation	3/180	27/13307	0.0056073458	0.0352624554	0.0250495039	Fcgr4/Ccl5/Itgb2	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0051955	regulation of amino acid transport	3/180	27/13307	0.0056073458	0.0352624554	0.0250495039	Tnf/Arg2/Il1rn	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0061082	myeloid leukocyte cytokine production	3/180	27/13307	0.0056073458	0.0352624554	0.0250495039	Cd74/Cd36/Nr4a	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0014911	positive regulation of smooth muscle cell migration	4/180	53/13307	0.0056592951	0.0353734529	0.0251283535	Mdm2/Ccl5/Nr4a	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0033627	cell adhesion mediated by integrin	4/180	53/13307	0.0056592951	0.0353734529	0.0251283535	Ccl5/Icam1/Itgb7	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0043388	positive regulation of DNA binding	4/180	53/13307	0.0056592951	0.0353734529	0.0251283535	Plaur/Txn1/Klf4/I	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0097191	extrinsic apoptotic signaling pathway	8/180	199/13307	0.0056933594	0.0355146252	0.0252286386	Lmna/Inhba/Tnf/	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0097696	STAT cascade	6/180	120/13307	0.0057749212	0.0359509179	0.0255385692	Irf1/Tnf/Ccl5/Sta	6	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0032615	interleukin-12 production	4/180	54/13307	0.0060486533	0.0375793844	0.0266953882	Irf1/Cd36/Rel/Nf	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	7/180	160/13307	0.0060790482	0.0376171507	0.0267222164	Cd74/Ccl4/Ccl5/C	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	7/180	160/13307	0.0060790482	0.0376171507	0.0267222164	Cd74/Dnaja1/Pla	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0050670	regulation of lymphocyte proliferation	8/180	202/13307	0.0062165377	0.0380238643	0.0270111348	H2-Aa/Cd74/Irf1/	8	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0000027	ribosomal large subunit assembly	3/180	28/13307	0.0062185117	0.0380238643	0.0270111348	Rpl38/Rplp0/Rpl	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0031640	killing of cells of other organism	3/180	28/13307	0.0062185117	0.0380238643	0.0270111348	Rpl30/Rps19/Nos	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0044364	disruption of cells of other organism	3/180	28/13307	0.0062185117	0.0380238643	0.0270111348	Rpl30/Rps19/Nos	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0045589	regulation of regulatory T cell differentiation	3/180	28/13307	0.0062185117	0.0380238643	0.0270111348	Irf1/Dusp10/Socs	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0046885	regulation of hormone biosynthetic process	3/180	28/13307	0.0062185117	0.0380238643	0.0270111348	Tnf/Nfkb1/Egr1	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0007254	JNK cascade	7/180	162/13307	0.0064955310	0.0396393945	0.0281587642	Dnaja1/Tnf/Dusp	7	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0002253	activation of immune response	11/180	341/13307	0.0067204239	0.0408506712	0.0290192228	Irf1/Tnf/Rsad2/A	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009150	purine ribonucleotide metabolic process	11/180	341/13307	0.0067204239	0.0408506712	0.0290192228	ATP8/Atp5e/Hsp	11	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0019233	sensory perception of pain	5/180	88/13307	0.0067937436	0.0412153783	0.0292783009	Tnf/Fcgr4/Il1a/Il1	5	aPD-L1 vs PBS	Up-regulated genes	CD45+

BP	GO:0002931	response to ischemia	3/180	29/13307	0.0068679173	0.0412608471	0.0293106007	Hk2/Egr1/Csf1	3
BP	GO:0060142	regulation of syncytium formation by plasma membrar	3/180	29/13307	0.0068679173	0.0412608471	0.0293106007	Cxcl9/Stat1/Il1f9	3
BP	GO:0071385	cellular response to glucocorticoid stimulus	3/180	29/13307	0.0068679173	0.0412608471	0.0293106007	ND3/Zfp36/Zfp3t	3
BP	GO:0090322	regulation of superoxide metabolic process	3/180	29/13307	0.0068679173	0.0412608471	0.0293106007	Tnf/Cd36/Itgb2	3
BP	GO:1990748	cellular detoxification	3/180	29/13307	0.0068679173	0.0412608471	0.0293106007	Tnf/Cd36/Sod2	3
BP	GO:0016072	rRNA metabolic process	8/180	206/13307	0.0069700370	0.0417932067	0.0296887747	Rps21/Rpl35a/Rp	8
BP	GO:1903900	regulation of viral life cycle	6/180	125/13307	0.0070187656	0.0420039864	0.0298385070	Cd74/Tnf/Rsad2/	6
BP	GO:0032612	interleukin-1 production	5/180	89/13307	0.0071210986	0.0425341298	0.0302151066	Arg2/Tnfaip3/Cd	5
BP	GO:0045672	positive regulation of osteoclast differentiation	3/180	30/13307	0.0075561290	0.0440928050	0.0313223478	Tnf/Ccl5/Csf1	3
BP	GO:0071384	cellular response to corticosteroid stimulus	3/180	30/13307	0.0075561290	0.0440928050	0.0313223478	ND3/Zfp36/Zfp3t	3
BP	GO:0002792	negative regulation of peptide secretion	6/180	127/13307	0.0075669040	0.0440928050	0.0313223478	Cd74/Tnf/Arg2/R	6
BP	GO:0051403	stress-activated MAPK cascade	8/180	209/13307	0.0075790570	0.0440928050	0.0313223478	Dnaja1/Tnf/Dusp	8
BP	GO:0002676	regulation of chronic inflammatory response	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Tnf/Tnfaip3	2
BP	GO:0002679	respiratory burst involved in defense response	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Dusp10/Rps19	2
BP	GO:0010744	positive regulation of macrophage derived foam cell di	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Cd36/Csf1	2
BP	GO:0015802	basic amino acid transport	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Arg2/Slc11a1	2
BP	GO:0032769	negative regulation of monooxygenase activity	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Arg2/Nfkb1	2
BP	GO:0042359	vitamin D metabolic process	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Tnf/Nfkb1	2
BP	GO:0045080	positive regulation of chemokine biosynthetic process	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Tnf/Egr1	2
BP	GO:0045414	regulation of interleukin-8 biosynthetic process	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Tnf/Klf4	2
BP	GO:0047484	regulation of response to osmotic stress	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Prkca/Ptgs2	2
BP	GO:0048333	mesodermal cell differentiation	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Inhba/Kdm6b	2
BP	GO:0051956	negative regulation of amino acid transport	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Tnf/Il1rn	2
BP	GO:0097709	connective tissue replacement	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Il1a/Klf6	2
BP	GO:2000551	regulation of T-helper 2 cell cytokine production	2/180	10/13307	0.0076243214	0.0440928050	0.0313223478	Rsad2/Nlrp3	2
BP	GO:0043410	positive regulation of MAPK cascade	12/180	396/13307	0.0076435546	0.0441215637	0.0313427772	Cd74/Tnf/Ccl4/Cı	12
BP	GO:0019915	lipid storage	4/180	58/13307	0.0077835923	0.0448053019	0.0318284865	Hilpda/Tnf/Cd36,	4
BP	GO:0045786	negative regulation of cell cycle	12/180	397/13307	0.0077909671	0.0448053019	0.0318284865	Irf1/Inhba/Tnf/N	12
BP	GO:0006091	generation of precursor metabolites and energy	10/180	302/13307	0.0080580286	0.0462551774	0.0328584392	Hk3/Nr4a3/ND1/	10
BP	GO:0002687	positive regulation of leukocyte migration	6/180	129/13307	0.0081453114	0.0465994009	0.0331029664	Cd74/Ccl4/Ccl5/I	6
BP	GO:1902106	negative regulation of leukocyte differentiation	5/180	92/13307	0.0081690747	0.0465994009	0.0331029664	Cd74/Irf1/Socs1/	5
BP	GO:0042093	T-helper cell differentiation	4/180	59/13307	0.0082632772	0.0465994009	0.0331029664	Irf1/Malt1/Nlrp3,	4
BP	GO:0042773	ATP synthesis coupled electron transport	4/180	59/13307	0.0082632772	0.0465994009	0.0331029664	Cox7c/ND4L/CYT	4
BP	GO:0009259	ribonucleotide metabolic process	11/180	351/13307	0.0082678601	0.0465994009	0.0331029664	ATP8/Atp5e/Hsp	11
BP	GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcr	3/180	31/13307	0.0082836685	0.0465994009	0.0331029664	Rps21/Rps19/Rp:	3
BP	GO:0032633	interleukin-4 production	3/180	31/13307	0.0082836685	0.0465994009	0.0331029664	H2-T23/Cd83/Nlr	3
BP	GO:0045066	regulatory T cell differentiation	3/180	31/13307	0.0082836685	0.0465994009	0.0331029664	Irf1/Dusp10/Socs	3
BP	GO:0051085	chaperone cofactor-dependent protein refolding	3/180	31/13307	0.0082836685	0.0465994009	0.0331029664	Cd74/H2-DMb1/I	3
BP	GO:0060337	type I interferon signaling pathway	3/180	31/13307	0.0082836685	0.0465994009	0.0331029664	Zbp1/Samhd1/St	3
BP	GO:0071357	cellular response to type I interferon	3/180	31/13307	0.0082836685	0.0465994009	0.0331029664	Zbp1/Samhd1/St	3
BP	GO:0006606	protein import into nucleus	6/180	130/13307	0.0084461458	0.0474271784	0.0336909973	Lmna/Hspa8/Cd3	6
BP	GO:0002294	CD4-positive, alpha-beta T cell differentiation involved	4/180	60/13307	0.0087619455	0.0489340424	0.0347614332	Irf1/Malt1/Nlrp3,	4
BP	GO:0050710	negative regulation of cytokine secretion	4/180	60/13307	0.0087619455	0.0489340424	0.0347614332	Tnf/Arg2/Tnfaip3	4
BP	GO:0070228	regulation of lymphocyte apoptotic process	4/180	60/13307	0.0087619455	0.0489340424	0.0347614332	Cd74/Cd274/Arg	4
BP	GO:0009152	purine ribonucleotide biosynthetic process	7/180	172/13307	0.0089039092	0.0496372884	0.0352610003	ATP8/Atp5e/Hk3	7
CC	GO:0022626	cytosolic ribosome	39/181	104/13541	3.2715172295	9.8799820332	8.0238264683	Rpl39/Rps27/Rps	39
CC	GO:0044391	ribosomal subunit	39/181	184/13541	3.1623237767	4.7751089028	3.8780075788	Rpl39/Rps27/Rps	39
CC	GO:0044445	cytosolic part	42/181	233/13541	6.3639957752	6.4064224137	5.2028456688	Rpl39/Rps27/Rps	42
CC	GO:0005840	ribosome	40/181	215/13541	9.1687432784	6.9224011752	5.6218873259	Rpl39/Rps27/Rps	40
CC	GO:0022625	cytosolic large ribosomal subunit	26/181	58/13541	4.5584050701	2.7532766623	2.2360176449	Rpl39/Rpl37/Rpl	26
CC	GO:0015934	large ribosomal subunit	26/181	118/13541	9.8477147477	4.9566830897	4.0254693618	Rpl39/Rpl37/Rpl	26
CC	GO:0022627	cytosolic small ribosomal subunit	15/181	42/13541	3.1138310677	1.3433956892	1.0910114869	Rps27/Rps21/Rp:	15
CC	GO:0015935	small ribosomal subunit	15/181	72/13541	2.5759440708	9.7241888676	7.8973022173	Rps27/Rps21/Rp:	15
CC	GO:0042611	MHC protein complex	10/181	21/13541	4.4059464436	1.4784398066	1.2006848203	H2-Eb1/H2-Aa/Cı	10
CC	GO:0042788	polysomal ribosome	10/181	28/13541	1.5119489110	4.5660857112	3.7082536448	Rpl39/Rps21/Rps	10
CC	GO:0005844	polysome	10/181	68/13541	2.1112396570	5.7963125130	4.7073573215	Rpl39/Rps21/Rps	10
CC	GO:0042612	MHC class I protein complex	5/181	11/13541	1.7479780388	4.3990780643	3.5726217810	H2-T23/B2m/H2-	5

aPD-L1 vs PBS	Up-regulated genes	CD45+	

CC	GO:0009897	external side of plasma membrane	16/181	313/13541	4.65348301311	0.000108103911	8.77944568481	H2-Aa/Cd74/Cxcl16	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0042824	MHC class I peptide loading complex	4/181	14/13541	2.78393566711	0.000600534611	0.000487712011	B2m/H2-D1/H2-K1	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0098800	inner mitochondrial membrane protein complex	9/181	125/13541	4.51252813821	0.000908522311	0.000737837911	ATP8/Atp5e/ND3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0098797	plasma membrane protein complex	15/181	344/13541	5.94987988721	0.001123039811	0.000912053911	H2-Eb1/H2-Aa/Cd1	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0005753	mitochondrial proton-transporting ATP synthase comp	4/181	18/13541	8.16133290511	0.001144983611	0.001177454911	ATP8/Atp5e/ATP4	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0045259	proton-transporting ATP synthase complex	4/181	19/13541	0.000102303311	0.001716391111	0.001393930511	ATP8/Atp5e/ATP4	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0044455	mitochondrial membrane part	10/181	206/13541	0.000451693311	0.006800146111	0.005522600311	ATP8/ATP6/Atp5e/ND3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0098552	side of membrane	16/181	460/13541	0.000453047111	0.006800146111	0.005522600311	H2-Aa/Cd74/Cxcl16	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0045263	proton-transporting ATP synthase complex, coupling fa	3/181	12/13541	0.000472857811	0.006800146111	0.005522600311	ATP8/ATP6/Atp5 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0098803	respiratory chain complex	6/181	76/13541	0.000528837411	0.007259495311	0.005895651411	ND3/ND1/ND4L/6	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0019866	organelle inner membrane	15/181	429/13541	0.000647773111	0.008505543311	0.006907604011	Rsad2/ATP8/Atp5 15	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0070469	respiratory chain	6/181	83/13541	0.000845442411	0.010638484611	0.008639828911	ND3/ND1/ND4L/6	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0005743	mitochondrial inner membrane	14/181	396/13541	0.000881251411	0.010645517311	0.008645540411	Rsad2/ATP8/Atp5 14	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0016469	proton-transporting two-sector ATPase complex	4/181	41/13541	0.002125810611	0.024692108411	0.020053193611	ATP8/Atp5e/ATP4	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0033177	proton-transporting two-sector ATPase complex, proto	3/181	20/13541	0.002264892511	0.025333242311	0.020573877511	ATP8/ATP6/Atp5 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0098798	mitochondrial protein complex	10/181	257/13541	0.002409683411	0.025990157411	0.021107377711	ATP8/Atp5e/ND3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0005797	Golgi medial cisterna	3/181	22/13541	0.003000194011	0.031243400211	0.025373692011	H2-D1/H2-K1/H2 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0005667	transcription factor complex	11/181	313/13541	0.003264261611	0.031901981211	0.025908545211	Nr4a1/Hsp90ab1 11	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0005746	mitochondrial respiratory chain	5/181	75/13541	0.003274706611	0.031901981211	0.025908545211	ND3/ND1/ND4L/5	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0005747	mitochondrial respiratory chain complex I	4/181	48/13541	0.003799188711	0.033745735411	0.027405912711	ND3/ND1/ND4L/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0030964	NADH dehydrogenase complex	4/181	48/13541	0.003799188711	0.033745735411	0.027405912711	ND3/ND1/ND4L/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0045271	respiratory chain complex I	4/181	48/13541	0.003799188711	0.033745735411	0.027405912711	ND3/ND1/ND4L/4	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0043230	extracellular organelle	5/181	82/13541	0.004804359111	0.040861206111	0.033184597511	Cd274/Gbp2/Gbp5	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0070971	endoplasmic reticulum exit site	3/181	26/13541	0.004870872211	0.040861206111	0.033184597511	H2-D1/H2-K1/H2 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0003735	structural constituent of ribosome	36/175	147/13229	4.32234000661	1.66842324251	1.37859897051	Rpl39/Rps27/Rps36	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0005198	structural molecule activity	37/175	428/13229	3.19003226321	6.15676226801	5.08726197771	Rpl39/Rps27/Rps37	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0042277	peptide binding	15/175	209/13229	1.13866859241	1.46508692221	1.21058450351	H2-Aa/Cd74/H2-K1	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0042605	peptide antigen binding	6/175	23/13229	4.11920674071	3.32268267491	2.74549454731	H2-Aa/H2-Ab1/H6	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0033218	amide binding	16/175	264/13229	4.30399310231	3.32268267491	2.74549454731	H2-Aa/Cd74/H2-K1	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0005125	cytokine activity	10/175	129/13229	8.03527293051	0.000500817311	0.000413819611	Cxcl9/Inhba/Tnf/10	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0030881	beta-2-microglobulin binding	4/175	11/13229	9.08218002451	0.000500817311	0.000413819611	H2-T23/H2-D1/H4	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0003823	antigen binding	6/175	39/13229	1.11703725131	0.000538970411	0.000445345111	H2-Aa/H2-Ab1/H6	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0042608	T cell receptor binding	4/175	14/13229	2.67057018231	0.001145377811	0.000946412511	H2-T23/H2-D1/H4	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0019843	rRNA binding	7/175	69/13229	3.40047940181	0.001312585011	0.001084573911	Rpl37/Rpl37a/Mt7	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0015078	proton transmembrane transporter activity	8/175	96/13229	3.93626755381	0.001381272011	0.001141329211	ATP8/Atp5e/Cox8	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0001228	DNA-binding transcription activator activity, RNA polyr	13/175	277/13229	8.03050083041	0.002583144411	0.002134422511	Irf1/Nr4a1/Sub1/13	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0005126	cytokine receptor binding	11/175	217/13229	0.000146572311	0.004352072711	0.003596067711	Cxcl9/Inhba/Tnf/11	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0031072	heat shock protein binding	8/175	126/13229	0.000266536811	0.007348800911	0.006072229811	Dnaja1/Hsp90ab1/8	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0030545	receptor regulator activity	12/175	276/13229	0.000306945111	0.007446768811	0.006153179611	Cxcl9/Inhba/Tnf/12	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0031386	protein tag	3/175	11/13229	0.000347258611	0.007446768811	0.006153179611	Uba52/Ubc/Uba1/3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0042610	CD8 receptor binding	3/175	11/13229	0.000347258611	0.007446768811	0.006153179611	H2-D1/H2-K1/H2 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0046977	TAP binding	3/175	11/13229	0.000347258611	0.007446768811	0.006153179611	H2-D1/H2-K1/H2 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0048018	receptor ligand activity	11/175	255/13229	0.000583895511	0.011784751011	0.009737604511	Cxcl9/Inhba/Tnf/11	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0044389	ubiquitin-like protein ligase binding	12/175	298/13229	0.000610608811	0.011784751011	0.009737604511	H2-Ab1/Dnaja1/Ub12	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0005149	interleukin-1 receptor binding	3/175	14/13229	0.000749395011	0.013675338411	0.011299775111	Il1f9/Il1a/Il1rn 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0000981	DNA-binding transcription factor activity, RNA polymer	16/175	493/13229	0.000846565611	0.014853379411	0.012273176911	Irf1/Nr4a1/Sub1/16	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0030547	receptor inhibitor activity	3/175	15/13229	0.000920983411	0.015456505211	0.012771532811	Cd5/Ly6e/Il1rn 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0031625	ubiquitin protein ligase binding	11/175	280/13229	0.001254802911	0.020181413711	0.016675670411	H2-Ab1/Dnaja1/11	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0035014	phosphatidylinositol 3-kinase regulator activity	3/175	18/13229	0.001604211511	0.024769026411	0.020466362111	Socs3/Socs1/Klf4 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0035259	glucocorticoid receptor binding	3/175	19/13229	0.001886590111	0.026234321411	0.021677118611	Nr4a1/Nr4a3/Ets 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0050998	nitric-oxide synthase binding	3/175	19/13229	0.001886590111	0.026234321411	0.021677118611	Cd74/Arg2/Nos2 3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0019207	kinase regulator activity	8/175	170/13229	0.001903007711	0.026234321411	0.021677118611	Hsp90ab1/Ccl5/N8	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0000978	RNA polymerase II proximal promoter sequence-specif	13/175	390/13229	0.002052464111	0.027319005711	0.022573380811	Irf1/Nr4a1/Atf3/13	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0004129	cytochrome-c oxidase activity	3/175	21/13229	0.002539674111	0.029923906411	0.024725780311	Cox7c/Cox6c/Co3	aPD-L1 vs PBS	Up-regulated genes	CD45+
CC	GO:0015002	heme-copper terminal oxidase activity	3/175	21/13229	0.002539674111	0.029923906411	0.024725780311	Cox7c/Cox6c/Co3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0016676	oxidoreductase activity, acting on a heme group of dor	3/175	21/13229	0.002539674111	0.029923906411	0.024725780311	Cox7c/Cox6c/Co3	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0000987	proximal promoter sequence-specific DNA binding	13/175	400/13229	0.002558261411	0.029923906411	0.024725780311	Irf1/Nr4a1/Atf3/13	aPD-L1 vs PBS	Up-regulated genes	CD45+

MF	GO:0033293	monocarboxylic acid binding	4/175	45/13229	0.0028888018	0.0312264181	0.0258020308	Hspa8/Cd36/S10	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0042379	chemokine receptor binding	4/175	45/13229	0.0028888018	0.0312264181	0.0258020308	Cxcl9/Ccl4/Ccl5/S	4	aPD-L1 vs PBS	Up-regulated genes	CD45+
MF	GO:0016675	oxidoreductase activity, acting on a heme group of dor	3/175	22/13229	0.0029123084	0.0312264181	0.0258020308	Cox7c/Cox6c/CO	3	aPD-L1 vs PBS	Up-regulated genes	CD45+
BP	GO:0009617	response to bacterium	13/47	430/13403	1.6596196766	2.2321884650	1.7923892507	Cxcl10/B2m/Gbp	13	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0042832	defense response to protozoan	5/47	27/13403	3.2460044595	2.1829379990	1.7528424081	Gbp2b/Iigp1/Gbp	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001562	response to protozoan	5/47	30/13403	5.6851273522	2.5488320962	2.0466458467	Gbp2b/Iigp1/Gbp	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0044406	adhesion of symbiont to host	4/47	15/13403	1.7610108773	5.9213990749	4.7547293687	Gbp2b/Gbp2/Gbp	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0035458	cellular response to interferon-beta	5/47	44/13403	4.1767828989	0.0001123554	9.0218510618	Irf1/Gbp2b/Iigp1	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048660	regulation of smooth muscle cell proliferation	7/47	147/13403	7.2073742222	0.0001611031	0.0001293616	Igfbp5/Egr1/Trib	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048659	smooth muscle cell proliferation	7/47	152/13403	9.0336542433	0.0001611031	0.0001293616	Igfbp5/Egr1/Trib	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071346	cellular response to interferon-gamma	6/47	97/13403	1.0387111215	0.0001611031	0.0001293616	Irf1/Gbp2b/Gbp2	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0035456	response to interferon-beta	5/47	53/13403	1.0780139427	0.0001611031	0.0001293616	Irf1/Gbp2b/Iigp1	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0098542	defense response to other organism	9/47	325/13403	1.5704560188	0.0002112263	0.0001696092	Cxcl10/Irf1/Gbp2	9	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0034341	response to interferon-gamma	6/47	115/13403	2.8209383753	0.0003449238	0.0002769648	Irf1/Gbp2b/Gbp2	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1904707	positive regulation of vascular smooth muscle cell prol	4/47	34/13403	5.6981014966	0.0006386622	0.0005128291	Igfbp5/Mmp2/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0033002	muscle cell proliferation	7/47	207/13403	7.0528846450	0.0007297022	0.0005859319	Igfbp5/Egr1/Trib	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0042742	defense response to bacterium	6/47	137/13403	7.7764541238	0.0007470950	0.0005998978	Gbp2b/Iigp1/Gbp	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0016525	negative regulation of angiogenesis	5/47	92/13403	1.6683502612	0.0014959540	0.0012012121	Klf2/Cxcl10/Dcn/	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0043618	regulation of transcription from RNA polymerase II pro	4/47	46/13403	1.9442058711	0.0016235700	0.0013036845	Klf2/Atf3/Egr1/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:2000181	negative regulation of blood vessel morphogenesis	5/47	96/13403	2.0520959730	0.0016235700	0.0013036845	Klf2/Cxcl10/Dcn/	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071498	cellular response to fluid shear stress	3/47	16/13403	2.1919727634	0.0016378907	0.0013151836	Klf2/Spp1/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	5/47	99/13403	2.3824745292	0.0016603475	0.0013332158	Igfbp5/Egr1/Mm	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002428	antigen processing and presentation of peptide antige	3/47	17/13403	2.6551353349	0.0016603475	0.0013332158	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1904705	regulation of vascular smooth muscle cell proliferation	4/47	50/13403	2.7158100507	0.0016603475	0.0013332158	Igfbp5/Mmp2/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1990874	vascular smooth muscle cell proliferation	4/47	50/13403	2.7158100507	0.0016603475	0.0013332158	Igfbp5/Mmp2/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0043620	regulation of DNA-templated transcription in response	4/47	51/13403	2.9393933397	0.0017189061	0.0013802368	Klf2/Atf3/Egr1/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1901343	negative regulation of vasculature development	5/47	107/13403	3.4679594607	0.0019435022	0.0015605817	Klf2/Cxcl10/Dcn/	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002475	antigen processing and presentation via MHC class Ib	3/47	20/13403	4.4185030326	0.0022857256	0.0018353781	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071276	cellular response to cadmium ion	3/47	20/13403	4.4185030326	0.0022857256	0.0018353781	Fos/Mt2/Jun	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071248	cellular response to metal ion	5/47	117/13403	5.3248369989	0.0025769968	0.0020692614	B2m/Fosb/Fos/M	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0050830	defense response to Gram-positive bacterium	4/47	60/13403	5.6048341715	0.0025769968	0.0020692614	Gbp2b/Gbp2/Gbp	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002483	antigen processing and presentation of endogenous pe	3/47	22/13403	5.9395467468	0.0025769968	0.0020692614	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0019885	antigen processing and presentation of endogenous pe	3/47	22/13403	5.9395467468	0.0025769968	0.0020692614	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0034405	response to fluid shear stress	3/47	22/13403	5.9395467468	0.0025769968	0.0020692614	Klf2/Spp1/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0019883	antigen processing and presentation of endogenous ar	3/47	24/13403	7.7679394238	0.0032649620	0.0026216795	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002237	response to molecule of bacterial origin	6/47	219/13403	0.0001090612	0.0043301696	0.0034770135	Cxcl10/B2m/Gbp	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	3/47	27/13403	0.0001114336	0.0043301696	0.0034770135	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071241	cellular response to inorganic substance	5/47	137/13403	0.0001126809	0.0043301696	0.0034770135	B2m/Fosb/Fos/M	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0046686	response to cadmium ion	3/47	29/13403	0.0001385232	0.0051753832	0.0041556980	Fos/Mt2/Jun	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002474	antigen processing and presentation of peptide antige	3/47	30/13403	0.0001535367	0.0054343928	0.0043636760	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048730	epidermis morphogenesis	3/47	30/13403	0.0001535367	0.0054343928	0.0043636760	Igfbp5/Fst/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001914	regulation of T cell mediated cytotoxicity	3/47	31/13403	0.0001695696	0.0058479805	0.0046957762	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0014910	regulation of smooth muscle cell migration	4/47	82/13403	0.0001900158	0.0063892818	0.0051304270	Igfbp5/Egr1/Trib	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002824	positive regulation of adaptive immune response base	4/47	86/13403	0.0002283495	0.0074676359	0.0059963173	Irf1/B2m/H2-D1/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001933	negative regulation of protein phosphorylation	7/47	360/13403	0.0002370781	0.0074676359	0.0059963173	Irf1/Atf3/Trib1/G	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0008585	female gonad development	4/47	87/13403	0.0002387422	0.0074676359	0.0059963173	Mmp2/Fst/Ubb/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0014909	smooth muscle cell migration	4/47	89/13403	0.0002605433	0.0077873517	0.0062530408	Igfbp5/Egr1/Trib	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0046545	development of primary female sexual characteristics	4/47	89/13403	0.0002605433	0.0077873517	0.0062530408	Mmp2/Fst/Ubb/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0045087	innate immune response	8/47	494/13403	0.0002849402	0.0083314052	0.0066899015	Irf1/Gbp2b/Iigp1	8	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002821	positive regulation of adaptive immune response	4/47	93/13403	0.0003083880	0.0088251467	0.0070863632	Irf1/B2m/H2-D1/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1901342	regulation of vasculature development	6/47	277/13403	0.0003890044	0.0109002275	0.0087525991	Klf2/Cxcl10/Egr1,	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0031103	axon regeneration	3/47	42/13403	0.0004215244	0.0113654591	0.0091261679	Mmp2/Jun/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0046660	female sex differentiation	4/47	101/13403	0.0004225077	0.0113654591	0.0091261679	Mmp2/Fst/Ubb/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0014812	muscle cell migration	4/47	102/13403	0.0004386293	0.0115677750	0.0092886223	Igfbp5/Egr1/Trib	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0042326	negative regulation of phosphorylation	7/47	400/13403	0.0004487228	0.0116063896	0.0093196288	Irf1/Atf3/Trib1/G	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	3/47	45/13403	0.0005172071	0.0128822898	0.0103441435	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002711	positive regulation of T cell mediated immunity	3/47	45/13403	0.0005172071	0.0128822898	0.0103441435	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-

BP	GO:0043568	positive regulation of insulin-like growth factor recept	2/47	10/13403	0.0005320055	0.0130099538	0.0104466544	Igfbp5/Igfbp4	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048002	antigen processing and presentation of peptide antige	3/47	46/13403	0.0005519349	0.0130237287	0.0104577152	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048662	negative regulation of smooth muscle cell proliferation	3/47	46/13403	0.0005519349	0.0130237287	0.0104577152	Igfbp5/Trib1/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001913	T cell mediated cytotoxicity	3/47	47/13403	0.0005881217	0.0136383396	0.0109512318	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002763	positive regulation of myeloid leukocyte differentiation	3/47	48/13403	0.0006257922	0.0140281759	0.0112642602	Fos/Trib1/Jun	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	3/47	48/13403	0.0006257922	0.0140281759	0.0112642602	Fos/Jun/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0031102	neuron projection regeneration	3/47	50/13403	0.0007056825	0.0149153289	0.0119766210	Mmp2/Jun/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001525	angiogenesis	7/47	432/13403	0.0007095961	0.0149153289	0.0119766210	Klf2/Cxcl10/Dcn/	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0010038	response to metal ion	5/47	204/13403	0.0007097256	0.0149153289	0.0119766210	B2m/Fosb/Fos/M	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0032496	response to lipopolysaccharide	5/47	204/13403	0.0007097256	0.0149153289	0.0119766210	Cxcl10/Gbp2/Trit	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0014745	negative regulation of muscle adaptation	2/47	12/13403	0.0007767918	0.0160736166	0.0129066959	Igfbp5/Klf4	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0031343	positive regulation of cell killing	3/47	52/13403	0.0007917988	0.0161359017	0.0129567092	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071277	cellular response to calcium ion	3/47	54/13403	0.0008843295	0.0177525850	0.0142548638	Fosb/Fos/Jun	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1902107	positive regulation of leukocyte differentiation	4/47	125/13403	0.0009431908	0.0186557611	0.0149800907	Irf1/Fos/Trib1/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002822	regulation of adaptive immune response based on som	4/47	128/13403	0.0010303115	0.0198974091	0.0159771017	Irf1/B2m/H2-D1/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0048678	response to axon injury	3/47	57/13403	0.0010355528	0.0198974091	0.0159771017	Mmp2/Jun/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	3/47	59/13403	0.0011449131	0.0216888481	0.0174155806	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0014911	positive regulation of smooth muscle cell migration	3/47	60/13403	0.0012022218	0.0220139694	0.0176766446	Igfbp5/Egr1/Ada	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0035914	skeletal muscle cell differentiation	3/47	60/13403	0.0012022218	0.0220139694	0.0176766446	Atf3/Egr1/Fos	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002486	antigen processing and presentation of endogenous pe	2/47	15/13403	0.0012275447	0.0220139694	0.0176766446	H2-D1/H2-K1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0035994	response to muscle stretch	2/47	15/13403	0.0012275447	0.0220139694	0.0176766446	Fos/Jun	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002709	regulation of T cell mediated immunity	3/47	61/13403	0.0012613111	0.0223218887	0.0179238958	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0010563	negative regulation of phosphorus metabolic process	7/47	481/13403	0.0013294763	0.0229249439	0.0184081334	Irf1/Atf3/Trib1/G	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0045936	negative regulation of phosphate metabolic process	7/47	481/13403	0.0013294763	0.0229249439	0.0184081334	Irf1/Atf3/Trib1/G	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0070373	negative regulation of ERK1 and ERK2 cascade	3/47	63/13403	0.0013849151	0.0232432092	0.0186636922	Atf3/Dusp6/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002476	antigen processing and presentation of endogenous pe	2/47	16/13403	0.0013997769	0.0232432092	0.0186636922	H2-D1/H2-K1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002484	antigen processing and presentation of endogenous pe	2/47	16/13403	0.0013997769	0.0232432092	0.0186636922	H2-D1/H2-K1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0010035	response to inorganic substance	6/47	355/13403	0.0014209640	0.0233072764	0.0187151364	B2m/Fosb/Fos/M	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002819	regulation of adaptive immune response	4/47	141/13403	0.0014740010	0.0238859209	0.0191797729	Irf1/B2m/H2-D1/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071363	cellular response to growth factor stimulus	7/47	493/13403	0.0015321750	0.0245330405	0.0196993931	Htra3/Egr1/Dcn/	7	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0045765	regulation of angiogenesis	5/47	247/13403	0.0016654072	0.0263526201	0.0211604682	Klf2/Cxcl10/Dcn/	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0071396	cellular response to lipid	6/47	379/13403	0.0019806802	0.0302833038	0.0243167049	Cxcl10/Gbp2/Sgk	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0043567	regulation of insulin-like growth factor receptor signali	2/47	19/13403	0.0019813611	0.0302833038	0.0243167049	Igfbp5/Igfbp4	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1904754	positive regulation of vascular associated smooth mus	2/47	19/13403	0.0019813611	0.0302833038	0.0243167049	Igfbp5/Adamts1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0031341	regulation of cell killing	3/47	72/13403	0.0020346031	0.0307476548	0.0246895667	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0019882	antigen processing and presentation	3/47	73/13403	0.0021166146	0.0316316293	0.0253993752	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0008406	gonad development	4/47	160/13403	0.0023403366	0.0342147035	0.0274735166	Mmp2/Fst/Ubb/A	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1903708	positive regulation of hemopoiesis	4/47	160/13403	0.0023403366	0.0342147035	0.0274735166	Irf1/Fos/Trib1/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0042035	regulation of cytokine biosynthetic process	3/47	76/13403	0.0023749098	0.0342962456	0.0275389928	Irf1/Egr1/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0007178	transmembrane receptor protein serine/threonine kin	5/47	269/13403	0.0024175555	0.0342962456	0.0275389928	Htra3/Egr1/Fos/F	5	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0014912	negative regulation of smooth muscle cell migration	2/47	21/13403	0.0024224114	0.0342962456	0.0275389928	Igfbp5/Trib1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0045137	development of primary sexual characteristics	4/47	163/13403	0.0025034047	0.0350737436	0.0281633034	Mmp2/Fst/Ubb/A	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0045639	positive regulation of myeloid cell differentiation	3/47	78/13403	0.0025574966	0.0354621962	0.0284752207	Fos/Trib1/Jun	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002478	antigen processing and presentation of exogenous pep	2/47	22/13403	0.0026587129	0.0364894794	0.0293001024	B2m/H2-K1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0001909	leukocyte mediated cytotoxicity	3/47	81/13403	0.0028472957	0.0386829572	0.0310614080	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0060343	trabecula formation	2/47	23/13403	0.0029054345	0.0390780944	0.0313786929	Mmp2/Adamts1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	3/47	83/13403	0.0030512955	0.0393808395	0.0316217893	B2m/H2-D1/H2-K	3	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0045637	regulation of myeloid cell differentiation	4/47	173/13403	0.0031033699	0.0393808395	0.0316217893	B2m/Fos/Trib1/Ju	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0036003	positive regulation of transcription from RNA polymera	2/47	24/13403	0.0031625031	0.0393808395	0.0316217893	Klf2/Atf3	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0044342	type B pancreatic cell proliferation	2/47	24/13403	0.0031625031	0.0393808395	0.0316217893	Igfbp5/Igfbp4	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1903671	negative regulation of sprouting angiogenesis	2/47	24/13403	0.0031625031	0.0393808395	0.0316217893	Klf2/Klf4	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1904738	vascular associated smooth muscle cell migration	2/47	24/13403	0.0031625031	0.0393808395	0.0316217893	Igfbp5/Adamts1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:1904752	regulation of vascular associated smooth muscle cell m	2/47	24/13403	0.0031625031	0.0393808395	0.0316217893	Igfbp5/Adamts1	2	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002699	positive regulation of immune effector process	4/47	174/13403	0.0031683079	0.0393808395	0.0316217893	Irf1/B2m/H2-D1/	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0002521	leukocyte differentiation	6/47	417/13403	0.0031914583	0.0393808395	0.0316217893	Irf1/B2m/Egr1/Fc	6	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0051607	defense response to virus	4/47	177/13403	0.0033686946	0.0408808068	0.0328262241	Cxcl10/Irf1/Gbp2	4	aPD-L1 vs PBS	Up-regulated genes	CD45-
BP	GO:0042089	cytokine biosynthetic process	3/47	86/13403	0.0033738063	0.0408808068	0.0328262241	Irf1/Egr1/Klf4	3	aPD-L1 vs PBS	Up-regulated genes	CD45-

BP	GO:0042107	cytokine metabolic process	3/47	88/13403	0.0035999953	0.0432320870	0.0347142408	Irf1/Egr1/Klf4	3
BP	GO:0002697	regulation of immune effector process	5/47	297/13403	0.0037008183	0.0437407256	0.0351226644	Irf1/B2m/H2-D1/	5
BP	GO:0031069	hair follicle morphogenesis	2/47	26/13403	0.0037073923	0.0437407256	0.0351226644	Igfbp5/Fst	2
BP	GO:0002456	T cell mediated immunity	3/47	90/13403	0.0038352645	0.0448559198	0.0360181364	B2m/H2-D1/H2-K	3
BP	GO:0019884	antigen processing and presentation of exogenous ant	2/47	27/13403	0.0039950690	0.0463221369	0.0371954705	B2m/H2-K1	2
BP	GO:0051592	response to calcium ion	3/47	93/13403	0.0042054366	0.0483445498	0.0388194154	Fosb/Fos/Jun	3
CC	GO:0020005	symbiont-containing vacuole membrane	5/46	11/13620	1.5983390008	1.2467044206	7.5710794778	Gbp2b/Iigp1/Gbp	5
CC	GO:0020003	symbiont-containing vacuole	5/46	13/13620	4.4301980840	1.7277772527	1.0492574409	Gbp2b/Iigp1/Gbp	5
CC	GO:0065010	extracellular membrane-bounded organelle	5/46	14/13620	6.8741265778	1.7872729102	1.0853884070	Gbp2b/Iigp1/Gbp	5
CC	GO:0030430	host cell cytoplasm	5/46	16/13620	1.4922920297	2.3279755664	1.4137503439	Gbp2b/Iigp1/Gbp	5
CC	GO:0033655	host cell cytoplasm part	5/46	16/13620	1.4922920297	2.3279755664	1.4137503439	Gbp2b/Iigp1/Gbp	5
CC	GO:0033646	host intracellular part	5/46	19/13620	3.9427832030	4.3933869977	2.6680487840	Gbp2b/Iigp1/Gbp	5
CC	GO:0043656	intracellular region of host	5/46	19/13620	3.9427832030	4.3933869977	2.6680487840	Gbp2b/Iigp1/Gbp	5
CC	GO:0033643	host cell part	5/46	21/13620	6.8652884447	6.6936562336	4.0649734212	Gbp2b/Iigp1/Gbp	5
CC	GO:0018995	host	5/46	23/13620	1.1295507912	8.8104961717	5.3505037480	Gbp2b/Iigp1/Gbp	5
CC	GO:0043657	host cell	5/46	23/13620	1.1295507912	8.8104961717	5.3505037480	Gbp2b/Iigp1/Gbp	5
CC	GO:0044215	other organism	5/46	26/13620	2.1915651177	1.3149390706	7.9854599433	Gbp2b/Iigp1/Gbp	5
CC	GO:0044216	other organism cell	5/46	26/13620	2.1915651177	1.3149390706	7.9854599433	Gbp2b/Iigp1/Gbp	5
CC	GO:0044217	other organism part	5/46	26/13620	2.1915651177	1.3149390706	7.9854599433	Gbp2b/Iigp1/Gbp	5
CC	GO:0043230	extracellular organelle	6/46	86/13620	4.0638264133	2.2641318588	1.3749788616	Gbp2b/Iigp1/Gbp	6
CC	GO:0042612	MHC class I protein complex	3/46	11/13620	5.8376209843	3.0355629118	1.8434592582	B2m/H2-D1/H2-K	3
CC	GO:0042824	MHC class I peptide loading complex	3/46	14/13620	1.2786943852	6.2336351281	3.7856083773	B2m/H2-D1/H2-K	3
CC	GO:0042611	MHC protein complex	3/46	19/13620	3.3639299135	0.0001543450	9.3731793256	B2m/H2-D1/H2-K	3
CC	GO:0031012	extracellular matrix	6/46	353/13620	0.0011340023	0.0049140101	0.0029842167	Timp2/Emilin2/D	6
CC	GO:0005581	collagen trimer	3/46	64/13620	0.0013005400	0.0053390593	0.0032423437	Emilin2/Dcn/Scar	3
CC	GO:0009897	external side of plasma membrane	5/46	246/13620	0.0013827380	0.0053926783	0.0032749058	Cxcl10/B2m/Ly6c	5
CC	GO:0005797	Golgi medial cisterna	2/46	23/13620	0.0026986395	0.0100235183	0.0060871569	H2-D1/H2-K1	2
CC	GO:0070971	endoplasmic reticulum exit site	2/46	26/13620	0.0034443849	0.0122119101	0.0074161397	H2-D1/H2-K1	2
CC	GO:0005719	nuclear euchromatin	2/46	31/13620	0.0048755689	0.0165345382	0.0100412175	Jun/Klf4	2
CC	GO:0000791	euchromatin	2/46	39/13620	0.0076375091	0.0248219046	0.0150740311	Jun/Klf4	2
CC	GO:0030176	integral component of endoplasmic reticulum membra	3/46	128/13620	0.0091692375	0.0286080210	0.0173732921	B2m/H2-D1/H2-K	3
CC	GO:0098552	side of membrane	5/46	393/13620	0.0101202882	0.0303608648	0.0184377721	Cxcl10/B2m/Ly6c	5
CC	GO:0031227	intrinsic component of endoplasmic reticulum membra	3/46	135/13620	0.0105957081	0.0306098235	0.0185889616	B2m/H2-D1/H2-K	3
CC	GO:0062023	collagen-containing extracellular matrix	4/46	284/13620	0.0152005069	0.0423442694	0.0257151433	Timp2/Emilin2/D	4
CC	GO:0031985	Golgi cisterna	2/46	57/13620	0.0158298850	0.0425769321	0.0258564365	H2-D1/H2-K1	2
MF	GO:0005520	insulin-like growth factor binding	3/47	25/13297	9.0139026798	0.0128898808	0.0083497203	Igfbp5/Htra3/Igfl	3
MF	GO:0030881	beta-2-microglobulin binding	2/47	11/13297	0.0006590554	0.0155180266	0.0100521629	H2-D1/H2-K1	2
MF	GO:0031386	protein tag	2/47	11/13297	0.0006590554	0.0155180266	0.0100521629	Ubc/Ubb	2
MF	GO:0031994	insulin-like growth factor I binding	2/47	11/13297	0.0006590554	0.0155180266	0.0100521629	Igfbp5/Igfbp4	2
MF	GO:0042610	CD8 receptor binding	2/47	11/13297	0.0006590554	0.0155180266	0.0100521629	H2-D1/H2-K1	2
MF	GO:0046977	TAP binding	2/47	11/13297	0.0006590554	0.0155180266	0.0100521629	H2-D1/H2-K1	2
MF	GO:0001228	DNA-binding transcription activator activity, RNA polyr	6/47	312/13297	0.0007596236	0.0155180266	0.0100521629	Irf1/Fosb/Egr1/Fo	6
MF	GO:0042608	T cell receptor binding	2/47	15/13297	0.0012469055	0.0222884375	0.0144378542	H2-D1/H2-K1	2
MF	GO:0003924	GTPase activity	5/47	256/13297	0.0020167915	0.0320445772	0.0207576209	Gbp2b/Iigp1/Gbp	5
MF	GO:0042605	peptide antigen binding	2/47	21/13297	0.0024603554	0.0351040367	0.0227394569	H2-D1/H2-K1	2
MF	GO:0070412	R-SMAD binding	2/47	22/13297	0.0027003105	0.0351040367	0.0227394569	Fos/Jun	2
MF	GO:0000978	RNA polymerase II proximal promoter sequence-specif	6/47	427/13297	0.0037286344	0.0391398207	0.0253537300	Irf1/Atf3/Fosb/Fo	6
MF	GO:0000987	proximal promoter sequence-specific DNA binding	6/47	437/13297	0.0041755891	0.0391398207	0.0253537300	Irf1/Atf3/Fosb/Fo	6
MF	GO:0005525	GTP binding	5/47	311/13297	0.0046522044	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0001968	fibronectin binding	2/47	30/13297	0.0049944134	0.0391398207	0.0253537300	Igfbp5/Mmp2	2
MF	GO:0032550	purine ribonucleoside binding	5/47	317/13297	0.0050418867	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0001883	purine nucleoside binding	5/47	319/13297	0.0051768018	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0032549	ribonucleoside binding	5/47	322/13297	0.0053839715	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0019001	guanyl nucleotide binding	5/47	325/13297	0.0055969756	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0032561	guanyl ribonucleotide binding	5/47	325/13297	0.0055969756	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0001882	nucleoside binding	5/47	330/13297	0.0059651857	0.0391398207	0.0253537300	Gbp2b/Iigp1/Gbp	5
MF	GO:0001102	RNA polymerase II activating transcription factor bindi	2/47	33/13297	0.0060215108	0.0391398207	0.0253537300	Fos/Jun	2

MF	GO:0000979	RNA polymerase II core promoter sequence-specific DI	2/47	35/13297	0.0067552361	0.0402499487	0.0260728412	Egr1/Fos	2	aPD-L1 vs PBS	Up-regulated genes CD45-
MF	GO:0003823	antigen binding	2/47	35/13297	0.0067552361	0.0402499487	0.0260728412	H2-D1/H2-K1	2	aPD-L1 vs PBS	Up-regulated genes CD45-
BP	GO:0043902	positive regulation of multi-organism process	10/105	151/13307	3.01293756596	0.00036117466	0.00029740956	Park7/Ppia/Apoe	10	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0051651	maintenance of location in cell	8/105	84/13307	3.04788692326	0.00036117466	0.00029740956	Park7/Fth1/Ftl1/	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:2000379	positive regulation of reactive oxygen species metabol	8/105	93/13307	6.71581760036	0.00053054956	0.00043688166	Park7/Klf2/Gnai2	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009126	purine nucleoside monophosphate metabolic process	11/105	228/13307	1.77896614836	0.00057869506	0.00047652706	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009167	purine ribonucleoside monophosphate metabolic proc	11/105	228/13307	1.77896614836	0.00057869506	0.00047652706	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	11/105	229/13307	1.85657228206	0.00057869506	0.00047652706	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0016052	carbohydrate catabolic process	8/105	107/13307	1.96266311736	0.00057869506	0.00047652706	Hexb/Akr1a1/Pkı	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009161	ribonucleoside monophosphate metabolic process	11/105	232/13307	2.10754066596	0.00057869506	0.00047652706	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009199	ribonucleoside triphosphate metabolic process	11/105	233/13307	2.19757632326	0.00057869506	0.00047652706	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009144	purine nucleoside triphosphate metabolic process	11/105	237/13307	2.59241248036	0.00060590386	0.00049893216	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009123	nucleoside monophosphate metabolic process	11/105	239/13307	2.81221175266	0.00060590386	0.00049893216	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009141	nucleoside triphosphate metabolic process	11/105	253/13307	4.86401434966	0.00089106266	0.00073374646	Park7/Atp5f1/Pkı	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0046034	ATP metabolic process	10/105	205/13307	4.88768552766	0.00089106266	0.00073374646	Park7/Atp5f1/Pkı	10	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009127	purine nucleoside monophosphate biosynthetic proce	8/105	124/13307	5.93639372786	0.00093795026	0.00077235606	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009168	purine ribonucleoside monophosphate biosynthetic pr	8/105	124/13307	5.93639372786	0.00093795026	0.00077235606	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009156	ribonucleoside monophosphate biosynthetic process	8/105	128/13307	7.51188155746	0.00111269746	0.00091625186	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009124	nucleoside monophosphate biosynthetic process	8/105	133/13307	9.96571010716	0.00134409136	0.00110679336	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:2000377	regulation of reactive oxygen species metabolic proce	9/105	176/13307	1.02082883566	0.00134409136	0.00110679336	Park7/Klf2/Gnai2	9	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0043900	regulation of multi-organism process	12/105	339/13307	1.43380142576	0.00177884786	0.00147272456	Park7/Ppia/Ifitm2	12	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009150	purine ribonucleotide metabolic process	12/105	341/13307	1.52048217516	0.00180177136	0.00148367056	Park7/Atp5f1/Pkı	12	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0006754	ATP biosynthetic process	7/105	103/13307	1.65787450546	0.00186637196	0.00153686586	Atp5f1/Pkm/Atp	7	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	9/105	188/13307	1.73249714456	0.00186637196	0.00153686586	Ppia/Ifitm3/Apoe	9	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009259	ribonucleotide metabolic process	12/105	351/13307	2.02630410816	0.00208797426	0.00171934456	Park7/Atp5f1/Pkı	12	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0006163	purine nucleotide metabolic process	12/105	362/13307	2.74699998456	0.00271187996	0.00223310036	Park7/Atp5f1/Pkı	12	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic proce	7/105	112/13307	2.86063281996	0.00271187996	0.00223310036	Atp5f1/Pkm/Atp	7	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	7/105	113/13307	3.02997196316	0.00273160996	0.00249347406	Atp5f1/Pkm/Atp	7	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0048524	positive regulation of viral process	6/105	77/13307	3.14821651796	0.00273160996	0.00249347406	Ppia/Apoe/Pfn1/	6	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0019693	ribose phosphate metabolic process	12/105	368/13307	3.22721846116	0.00273160996	0.00249347406	Park7/Atp5f1/Pkı	12	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009201	ribonucleoside triphosphate biosynthetic process	7/105	115/13307	3.39345459016	0.00274888106	0.00226356896	Atp5f1/Pkm/Atp	7	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0050792	regulation of viral process	8/105	158/13307	3.47959629306	0.00274888106	0.00226356896	Ppia/Ifitm3/Apoe	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0051235	maintenance of location	10/105	260/13307	3.85617151006	0.00294810536	0.00242762036	Park7/Hexb/Fth1	10	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0044403	symbiont process	11/105	318/13307	4.11902699086	0.00305065436	0.00251206446	Ppia/Ifitm3/Apoe	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0032370	positive regulation of lipid transport	5/105	50/13307	4.44114975176	0.00318955306	0.00262644076	Apoe/Prelid1/Nfl	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0072521	purine-containing compound metabolic process	12/105	389/13307	5.53045319316	0.00385505116	0.00317444586	Park7/Atp5f1/Pkı	12	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009142	nucleoside triphosphate biosynthetic process	7/105	126/13307	6.09243313066	0.00407475676	0.00335536266	Atp5f1/Pkm/Atp	7	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0044419	interspecies interaction between organisms	11/105	333/13307	6.25005692336	0.00407475676	0.00335536266	Ppia/Ifitm3/Apoe	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009152	purine ribonucleotide biosynthetic process	8/105	172/13307	6.36143462746	0.00407475676	0.00335536266	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0071277	cellular response to calcium ion	5/105	55/13307	7.06756018596	0.00440793556	0.00362971906	Lgmn/Alox5ap/Il	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009260	ribonucleotide biosynthetic process	8/105	181/13307	9.10021706776	0.00553013196	0.00455379286	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0072593	reactive oxygen species metabolic process	9/105	235/13307	9.88752396746	0.00573438586	0.00472198596	Park7/Klf2/Gnai2	9	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0042255	ribosome assembly	5/105	59/13307	9.92024549026	0.00573438586	0.00472198596	Rpl5/Rps2/Rpl3/1	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0015850	organic hydroxy compound transport	7/105	138/13307	0.00010822866	0.00061060166	0.00502800586	Park7/Fcgr3/Apo	7	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0006164	purine nucleotide biosynthetic process	8/105	187/13307	0.00011420756	0.00061060166	0.00502800586	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0045185	maintenance of protein location	6/105	97/13307	0.00011553886	0.00061060166	0.00502800586	Park7/Tmsb4x/Pf	6	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0051851	modification by host of symbiont morphology or physi	5/105	61/13307	0.00011642096	0.00061060166	0.00502800586	Apoe/Gapdh/Cfl1	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0046390	ribose phosphate biosynthetic process	8/105	188/13307	0.00011851346	0.00061060166	0.00502800586	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0035821	modification of morphology or physiology of other org	6/105	98/13307	0.00012229436	0.00061665696	0.00507802246	Apoe/Gapdh/Cfl1	6	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0072522	purine-containing compound biosynthetic process	8/105	192/13307	0.00013710376	0.00076949916	0.00557435106	Atp5f1/Pkm/Atp	8	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0042273	ribosomal large subunit biogenesis	5/105	65/13307	0.00015765626	0.00076254166	0.00627915736	Rpl5/Rpl14/Rpl3/	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0051702	interaction with symbiont	5/105	66/13307	0.00016951826	0.00080351646	0.00661656616	Apoe/Gapdh/Cfl1	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:1905954	positive regulation of lipid localization	5/105	67/13307	0.00018205016	0.00845997926	0.00696637866	Apoe/Prelid1/Nfl	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0046031	ADP metabolic process	5/105	70/13307	0.00022391846	0.01020551506	0.00840374196	Pkm/Pgam1/Ier3	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0032870	cellular response to hormone stimulus	11/105	387/13307	0.00023485716	0.01050210236	0.00864796696	Park7/Pkm/Junb/	11	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0051881	regulation of mitochondrial membrane potential	5/105	72/13307	0.00025565146	0.01122025896	0.00923933386	Park7/Clic1/Prdx1,	5	aPD-L1 vs PBS	Down-regulated genes CD45+
BP	GO:0009117	nucleotide metabolic process	12/105	464/13307	0.00028893826	0.01181652316	0.00973032826	Park7/Atp5f1/Pkı	12	aPD-L1 vs PBS	Down-regulated genes CD45+

BP	GO:0009135	purine nucleoside diphosphate metabolic process	5/105	74/13307	0.0002906916	0.011816523	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	5/105	74/13307	0.0002906916	0.011816523	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1903578	regulation of ATP metabolic process	9/105	272/13307	0.0002906916	0.011816523	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0046394	carboxylic acid biosynthetic process	9/105	272/13307	0.0002960302	0.011816523	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0035994	response to muscle stretch	3/105	17/13307	0.0002995288	0.011816523	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0016053	organic acid biosynthetic process	9/105	273/13307	0.0003041383	0.011816523	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006753	nucleoside phosphate metabolic process	12/105	470/13307	0.0003247331	0.012070628	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0002181	cytoplasmic translation	5/105	76/13307	0.0003292610	0.012070628	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0010563	negative regulation of phosphorus metabolic process	12/105	471/13307	0.0003310509	0.012070628	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0045936	negative regulation of phosphate metabolic process	12/105	471/13307	0.0003310509	0.012070628	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0009185	ribonucleoside diphosphate metabolic process	5/105	78/13307	0.0003715874	0.013343366	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0052547	regulation of peptidase activity	9/105	282/13307	0.0003857494	0.013645168	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0010035	response to inorganic substance	10/105	348/13307	0.0004190956	0.014606716	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0032368	regulation of lipid transport	5/105	81/13307	0.0004426346	0.014986344	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0051817	modification of morphology or physiology of other org	5/105	81/13307	0.0004426346	0.014986344	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0009165	nucleotide biosynthetic process	8/105	230/13307	0.0004660168	0.015419895	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1900542	regulation of purine nucleotide metabolic process	5/105	82/13307	0.0004684525	0.015419895	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006090	pyruvate metabolic process	5/105	84/13307	0.0005234756	0.016995032	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1901293	nucleoside phosphate biosynthetic process	8/105	236/13307	0.0005525905	0.017635124	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0034614	cellular response to reactive oxygen species	6/105	130/13307	0.0005655145	0.017635124	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0097237	cellular response to toxic substance	6/105	130/13307	0.0005655145	0.017635124	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006140	regulation of nucleotide metabolic process	5/105	86/13307	0.0005832243	0.017951190	aPD-L1 vs PBS	Down-regulated genes
BP	GO:2001233	regulation of apoptotic signaling pathway	10/105	370/13307	0.0006755245	0.020461087	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0034404	nucleobase-containing small molecule biosynthetic prc	6/105	135/13307	0.0006901444	0.020461087	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0030595	leukocyte chemotaxis	7/105	187/13307	0.0006906696	0.020461087	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0009132	nucleoside diphosphate metabolic process	5/105	90/13307	0.0007179232	0.020969890	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0052548	regulation of endopeptidase activity	8/105	246/13307	0.0007255405	0.020969890	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0002675	positive regulation of acute inflammatory response	3/105	23/13307	0.0007537088	0.021015176	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1900543	negative regulation of purine nucleotide metabolic prc	3/105	23/13307	0.0007537088	0.021015176	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1903579	negative regulation of ATP metabolic process	3/105	23/13307	0.0007537088	0.021015176	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0051592	response to calcium ion	5/105	92/13307	0.0007933976	0.021694243	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006081	cellular aldehyde metabolic process	4/105	53/13307	0.0007963709	0.021694243	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0016032	viral process	8/105	251/13307	0.0008270797	0.022274760	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0045980	negative regulation of nucleotide metabolic process	3/105	24/13307	0.0008564613	0.022806891	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0046596	regulation of viral entry into host cell	3/105	25/13307	0.0009676941	0.025482611	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0010038	response to metal ion	7/105	199/13307	0.0009953323	0.025922391	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0042254	ribosome biogenesis	8/105	261/13307	0.0010644570	0.027129023	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0070997	neuron death	9/105	325/13307	0.0010645566	0.027129023	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0042326	negative regulation of phosphorylation	10/105	397/13307	0.0011554603	0.029132350	aPD-L1 vs PBS	Down-regulated genes
BP	GO:2001234	negative regulation of apoptotic signaling pathway	7/105	205/13307	0.0011829300	0.029510992	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0043467	regulation of generation of precursor metabolites and	5/105	101/13307	0.0012084430	0.029833437	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0009166	nucleotide catabolic process	5/105	103/13307	0.0013190939	0.031792545	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0000027	ribosomal large subunit assembly	3/105	28/13307	0.0013548722	0.031792545	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0031640	killing of cells of other organism	3/105	28/13307	0.0013548722	0.031792545	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0044364	disruption of cells of other organism	3/105	28/13307	0.0013548722	0.031792545	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0071353	cellular response to interleukin-4	3/105	28/13307	0.0013548722	0.031792545	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DN	5/105	105/13307	0.0014370593	0.033390495	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1905952	regulation of lipid localization	5/105	106/13307	0.0014988754	0.034426900	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006096	glycolytic process	4/105	63/13307	0.0015252424	0.034426900	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006757	ATP generation from ADP	4/105	63/13307	0.0015252424	0.034426900	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0062012	regulation of small molecule metabolic process	8/105	278/13307	0.0015908031	0.035567957	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0031099	regeneration	5/105	108/13307	0.0016283569	0.036067344	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0070670	response to interleukin-4	3/105	30/13307	0.0016600233	0.036428898	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0042176	regulation of protein catabolic process	9/105	347/13307	0.0016759999	0.036441466	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0042866	pyruvate biosynthetic process	4/105	65/13307	0.0017128679	0.036904518	aPD-L1 vs PBS	Down-regulated genes
BP	GO:0006979	response to oxidative stress	9/105	349/13307	0.0017432703	0.037221177	aPD-L1 vs PBS	Down-regulated genes
BP	GO:1901292	nucleoside phosphate catabolic process	5/105	112/13307	0.0019117458	0.040453908	aPD-L1 vs PBS	Down-regulated genes

BP	GO:0045862	positive regulation of proteolysis	8/105	288/13307	0.0019857925	0.0416489232	0.0342958488	Rps3/Lgmn/Apoe	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0032507	maintenance of protein location in cell	4/105	69/13307	0.0021351456	0.0438336570	0.0360948701	Park7/Tmsb4x/Pl	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0071248	cellular response to metal ion	5/105	115/13307	0.0021468271	0.0438336570	0.0360948701	Lgmn/Alox5ap/Ls	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0001933	negative regulation of protein phosphorylation	9/105	360/13307	0.0021530896	0.0438336570	0.0360948701	Park7/Dusp1/Apo	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0009991	response to extracellular stimulus	8/105	292/13307	0.0021639400	0.0438336570	0.0360948701	Slc2a1/Apoe/Gat	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0051345	positive regulation of hydrolase activity	10/105	434/13307	0.0022353020	0.0448954730	0.0369692236	Rps3/Lgmn/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0010810	regulation of cell-substrate adhesion	6/105	171/13307	0.0023253644	0.0463118797	0.0381355652	S100a10/Cfl1/Lg	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0031397	negative regulation of protein ubiquitination	4/105	71/13307	0.0023710726	0.0468286848	0.0385611289	Park7/Rps3/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0051402	neuron apoptotic process	7/105	234/13307	0.0025134661	0.0492307015	0.0405390720	Park7/Mcl1/Lgmn	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0034599	cellular response to oxidative stress	7/105	235/13307	0.0025741373	0.0497273266	0.0409480184	Park7/Rps3/Mcl1	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0061844	antimicrobial humoral immune response mediated by	3/105	35/13307	0.0026007411	0.0497273266	0.0409480184	Gapdh/Pglyrp1/P	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0000302	response to reactive oxygen species	6/105	175/13307	0.0026101971	0.0497273266	0.0409480184	Park7/Rps3/Rhok	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0043471	regulation of cellular carbohydrate catabolic process	2/105	10/13307	0.0026629773	0.0497273266	0.0409480184	Ppp1r3b/Pgam1	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0006091	generation of precursor metabolites and energy	8/105	302/13307	0.0026647132	0.0497273266	0.0409480184	Park7/Pkm/Ppp1	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:1901652	response to peptide	8/105	302/13307	0.0026647132	0.0497273266	0.0409480184	Pkm/Lgmn/Ndel1	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0022626	cytosolic ribosome	15/106	104/13541	2.4574490056	6.5122398650	5.4581235810	Rps6/Rps3/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0044391	ribosomal subunit	15/106	184/13541	1.2358757631	1.6375353862	1.3724725580	Rps6/Rps3/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0005840	ribosome	15/106	215/13541	1.1428808653	1.0095447643	8.4613285115	Rps6/Rps3/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0044445	cytosolic part	15/106	233/13541	3.5398781255	2.3451692581	1.9655639065	Rps6/Rps3/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0022625	cytosolic large ribosomal subunit	9/106	58/13541	6.0536409988	3.2084297294	2.6890910542	Rpl5/Rpl14/Rpl1	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0015934	large ribosomal subunit	9/106	118/13541	3.4471630295	1.5224970047	1.2760550863	Rpl5/Rpl14/Rpl1	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0022627	cytosolic small ribosomal subunit	6/106	42/13541	8.3266805245	3.1522433414	2.6419993844	Rps6/Rps3/Rps3	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0005844	polysome	6/106	68/13541	1.4737037607	0.0004881643	0.0004091467	Rps6/Rps3/Rpl18	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0015935	small ribosomal subunit	6/106	72/13541	2.0510985381	0.0006039345	0.0005061775	Rps6/Rps3/Rps3	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0043209	myelin sheath	7/106	188/13541	0.0006812887	0.0180541524	0.0151317822	Ppia/Atp5f1/Pkm	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0099572	postsynaptic specialization	9/106	315/13541	0.0008095399	0.0195025526	0.0163457343	Rps3/Rpl5/Rpl14	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0042788	polysomal ribosome	3/106	28/13541	0.0013247395	0.0329546642	0.0245193015	Rpl18/Rpl8/Rpl1	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0031012	extracellular matrix	8/106	279/13541	0.0015504992	0.0316063313	0.0264903114	Pkm/S100a6/Apc	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0005635	nuclear envelope	9/106	362/13541	0.0021225764	0.0364900960	0.0305835561	Shisa5/Clic1/Alox	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0062023	collagen-containing extracellular matrix	7/106	229/13541	0.0021321442	0.0364900960	0.0305835561	Pkm/S100a6/S107	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0014069	postsynaptic density	8/106	296/13541	0.0022452181	0.0364900960	0.0305835561	Rps3/Rpl5/Rpl14	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0032279	asymmetric synapse	8/106	298/13541	0.0023408740	0.0364900960	0.0305835561	Rps3/Rpl5/Rpl14	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0000276	mitochondrial proton-transporting ATP synthase comp	2/106	10/13541	0.0026220276	0.0386027043	0.0323536750	Atp5f1/Atp5g2	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0098984	neuron to neuron synapse	8/106	311/13541	0.0030433853	0.0410458862	0.0344019145	Rps3/Rpl5/Rpl14	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0044754	autolysosome	2/106	11/13541	0.0031883668	0.0410458862	0.0344019145	Fth1/Ftl1	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0005938	cell cortex	7/106	247/13541	0.0032526928	0.0410458862	0.0344019145	Cap1/Slc2a1/Pfn	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0005767	secondary lysosome	2/106	12/13541	0.0038065512	0.0438580909	0.0367589163	Fth1/Ftl1	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0045263	proton-transporting ATP synthase complex, coupling fa	2/106	12/13541	0.0038065512	0.0438580909	0.0367589163	Atp5f1/Atp5g2	aPD-L1 vs PBS	Down-regulated genes	CD45+
CC	GO:0098685	Schaffer collateral - CA1 synapse	4/106	83/13541	0.0040588984	0.0448170035	0.0375626127	Pfn1/Srgn/Actb/	aPD-L1 vs PBS	Down-regulated genes	CD45+
MF	GO:0003735	structural constituent of ribosome	15/101	147/13229	3.0971476924	9.8799011389	9.1610368587	Rps6/Rps3/Rpl5/	aPD-L1 vs PBS	Down-regulated genes	CD45+
MF	GO:0005198	structural molecule activity	19/101	428/13229	4.6497901584	7.4164153026	6.8767949185	Rps6/Rps3/Arpc1	aPD-L1 vs PBS	Down-regulated genes	CD45+
MF	GO:0019843	rRNA binding	7/101	69/13229	8.9760669076	9.5445511451	8.8500870212	Rps3/Rpl5/Rpl3/	aPD-L1 vs PBS	Down-regulated genes	CD45+
MF	GO:0005125	cytokine activity	6/101	129/13229	0.0004549735	0.0331664990	0.0307532955	Ltb/Ccl6/Cxcl14/	aPD-L1 vs PBS	Down-regulated genes	CD45+
MF	GO:0070412	R-SMAD binding	3/101	21/13229	0.0005198510	0.0331664990	0.0307532955	Fos/Jun/Pmepa1	aPD-L1 vs PBS	Down-regulated genes	CD45+
BP	GO:0009617	response to bacterium	24/68	453/13307	1.2111348740	1.8009575576	1.4520869700	Cxcl10/Ifit1/Gbp	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0098542	defense response to other organism	22/68	370/13307	3.9591418608	2.9436219735	2.3734013576	Cxcl10/Rsad2/Ifit	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0009615	response to virus	18/68	237/13307	9.8313975772	4.0239928749	3.2444893530	Cxcl10/Rsad2/Ifit	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051607	defense response to virus	17/68	199/13307	1.0824459650	4.0239928749	3.2444893530	Cxcl10/Rsad2/Ifit	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035456	response to interferon-beta	11/68	55/13307	2.6683626784	7.9357106057	6.3984528226	Ifit1/Gbp2b/Gbp	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035458	cellular response to interferon-beta	11/68	46/13307	2.1481601872	5.3238569972	4.2925516723	Ifit1/Gbp2b/Gbp	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034341	response to interferon-gamma	12/68	123/13307	1.0601628042	2.2520886998	1.8158277203	Gbp2b/Parp14/G	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071346	cellular response to interferon-gamma	11/68	104/13307	4.0990584019	7.6191248045	6.1431941049	Gbp2b/Parp14/G	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044406	adhesion of symbiont to host	6/68	13/13307	2.3709235250	3.9172925352	3.1584583567	Gbp2b/Gbp2/Hsj	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044403	symbiont process	15/68	318/13307	4.8199481107	7.1672628407	5.7788641033	Rsad2/Gbp2b/Gt	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044419	interspecies interaction between organisms	15/68	333/13307	9.2286343897	1.2475435761	1.0058769923	Rsad2/Gbp2b/Gt	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045088	regulation of innate immune response	13/68	259/13307	5.1548256125	6.3876880715	5.1503038357	Rsad2/Parp14/G	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019221	cytokine-mediated signaling pathway	11/68	274/13307	1.2511100113	1.4310773745	1.1538577351	Cxcl10/Parp14/If	aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:0016032	viral process	10/68	251/13307	5.30288098031	5.6324171555	4.5413394260	Rsad2/Ifitm3/Isg:10	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034340	response to type I interferon	5/68	36/13307	1.00063953391	9.5592730175	7.7075085598	Ifitm3/Isg15/Irf7,5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002683	negative regulation of immune system process	12/68	413/13307	1.02857006241	9.5592730175	7.7075085598	Parp14/Irf1/Sam\12	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045089	positive regulation of innate immune response	9/68	215/13307	1.36922759611	0.0001197671	9.6566577837	Rsad2/Gbp5/Irf1,9	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019058	viral life cycle	8/68	174/13307	2.75715918441	0.0002277191	0.0001836493	Rsad2/Ifitm3/Isg:8	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002819	regulation of adaptive immune response	8/68	176/13307	3.00253815841	0.0002349881	0.0001894676	Rsad2/Irf1/Irf7/C8	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048525	negative regulation of viral process	6/68	84/13307	4.22766164101	0.0003069354	0.0002474777	Rsad2/Ifitm3/Isg:6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045824	negative regulation of innate immune response	5/68	48/13307	4.33466338961	0.0003069354	0.0002474777	Parp14/Samhd1/5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035455	response to interferon-alpha	4/68	23/13307	5.13231916221	0.0003468981	0.0002796991	Ifit1/Ifit2/Ifit3/Ifi 4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050777	negative regulation of immune response	7/68	136/13307	5.75407060781	0.0003641058	0.0002935734	Parp14/Irf1/Sam\7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045071	negative regulation of viral genome replication	5/68	51/13307	5.87662244351	0.0003641058	0.0002935734	Rsad2/Ifitm3/Isg:5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002460	adaptive immune response based on somatic recombi	9/68	260/13307	6.50972409671	0.0003871983	0.0003121926	Rsad2/Irf1/Irf7/C9	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043901	negative regulation of multi-organism process	7/68	150/13307	1.09610487251	0.0006268876	0.0005054507	Rsad2/Ifitm3/Isg:7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002250	adaptive immune response	10/68	356/13307	1.21018909851	0.0006665004	0.0005373900	Rsad2/Irf1/Irf7/C10	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034121	regulation of toll-like receptor signaling pathway	5/68	60/13307	1.31865064481	0.0007002976	0.0005646402	Rsad2/Irf1/Irf7/A5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042742	defense response to bacterium	7/68	158/13307	1.53820114751	0.0007624350	0.0006147407	Gbp2b/Gbp2/Pla 7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050792	regulation of viral process	7/68	158/13307	1.53820114751	0.0007624350	0.0006147407	Rsad2/Ifitm3/Isg:7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071222	cellular response to lipopolysaccharide	7/68	160/13307	1.66918078861	0.0007968607	0.0006424976	Cxcl10/Gbp2/Cm 7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060337	type I interferon signaling pathway	4/68	31/13307	1.76841985961	0.0007968607	0.0006424976	Ifitm3/Irf7/Samh 4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071357	cellular response to type I interferon	4/68	31/13307	1.76841985961	0.0007968607	0.0006424976	Ifitm3/Irf7/Samh 4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071219	cellular response to molecule of bacterial origin	7/68	167/13307	2.20248164111	0.0009632618	0.0007766645	Cxcl10/Gbp2/Cm 7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042832	defense response to protozoan	4/68	33/13307	2.28219702401	0.0009666689	0.0007794117	Gbp2b/Gbp2/Gbp4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002824	positive regulation of adaptive immune response base	6/68	113/13307	2.34028801621	0.0009666689	0.0007794117	Rsad2/Irf1/Cd27 6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035457	cellular response to interferon-alpha	3/68	12/13307	2.71687488811	0.0010918899	0.0008803756	Ifit1/Ifit2/Ifit3 3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001562	response to protozoan	4/68	35/13307	2.89786202661	0.0011339791	0.0009143115	Gbp2b/Gbp2/Gbp4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903901	negative regulation of viral life cycle	5/68	71/13307	3.01017927311	0.0011477273	0.0009253965	Rsad2/Ifitm3/Isg:5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002237	response to molecule of bacterial origin	8/68	243/13307	3.16621917921	0.0011483336	0.0009258854	Cxcl10/Gbp2/Cm 8	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002449	lymphocyte mediated immunity	8/68	243/13307	3.16621917921	0.0011483336	0.0009258854	Rsad2/Irf7/H2-D18	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002821	positive regulation of adaptive immune response	6/68	120/13307	3.29017073791	0.0011648771	0.0009392241	Rsad2/Irf1/Cd27 6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031349	positive regulation of defense response	9/68	325/13307	3.84003009351	0.0013279359	0.0010706962	Rsad2/Gbp5/Irf1,9	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903900	regulation of viral life cycle	6/68	125/13307	4.14151770821	0.0013996447	0.0011285140	Rsad2/Ifitm3/Isg:6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	7/68	188/13307	4.70540077741	0.0015210719	0.0012264191	Rsad2/Ifitm3/Isg:7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071216	cellular response to biotic stimulus	7/68	188/13307	4.70540077741	0.0015210719	0.0012264191	Cxcl10/Gbp2/Cm 7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002221	pattern recognition receptor signaling pathway	6/68	130/13307	5.16124581271	0.0016329303	0.0013166089	Rsad2/Irf1/Irf7/A6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	9/68	339/13307	5.32966948711	0.0016510871	0.0013312485	Rsad2/Ifitm3/Isg:9	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002758	innate immune response-activating signal transductior	6/68	132/13307	5.62149653941	0.0016936412	0.0013655592	Rsad2/Irf1/Irf7/A6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045069	regulation of viral genome replication	5/68	81/13307	5.69482587671	0.0016936412	0.0013655592	Rsad2/Ifitm3/Isg:5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001961	positive regulation of cytokine-mediated signaling patl	4/68	43/13307	6.62334489049	0.0019311607	0.0015570679	Parp14/Irgm1/Irf 4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019882	antigen processing and presentation	5/68	87/13307	8.02094864421	0.0022936828	0.0018493644	H2-D1/H2-K1/B2 5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	5/68	93/13307	0.00011018401	0.0030341424	0.0024463867	Parp14/Irgm1/Irf 5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000379	positive regulation of reactive oxygen species metabol	5/68	93/13307	0.00011018401	0.0030341424	0.0024463867	Acod1/Klf2/Sod2 5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002428	antigen processing and presentation of peptide antigei	3/68	19/13307	0.00011663671	0.0030427880	0.0024533575	H2-D1/H2-K1/B2 3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060338	regulation of type I interferon-mediated signaling path	3/68	19/13307	0.00011663671	0.0030427880	0.0024533575	Irf7/Samhd1/Zbp 3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1901623	regulation of lymphocyte chemotaxis	3/68	19/13307	0.00011663671	0.0030427880	0.0024533575	Cxcl10/Ccl4/Ccl1 3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060760	positive regulation of response to cytokine stimulus	4/68	50/13307	0.00012032291	0.0030848320	0.0024872570	Parp14/Irgm1/Irf 4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002224	toll-like receptor signaling pathway	5/68	97/13307	0.00013449771	0.0033327923	0.0026871840	Rsad2/Irf1/Irf7/A5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019079	viral genome replication	5/68	97/13307	0.00013449771	0.0033327923	0.0026871840	Rsad2/Ifitm3/Isg:5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060333	interferon-gamma-mediated signaling pathway	3/68	20/13307	0.00013671841	0.0033327923	0.0026871840	Parp14/Irf1/Irgm 3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001819	positive regulation of cytokine production	9/68	385/13307	0.00014096211	0.0033444775	0.0026966055	Rsad2/Gbp5/Irf1,9	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002218	activation of innate immune response	6/68	156/13307	0.00014169601	0.0033444775	0.0026966055	Rsad2/Irf1/Irf7/A6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032496	response to lipopolysaccharide	7/68	226/13307	0.00014939701	0.0034705412	0.0027982489	Cxcl10/Gbp2/Cm 7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002711	positive regulation of T cell mediated immunity	4/68	54/13307	0.00016271221	0.0036116554	0.0029120274	Rsad2/H2-D1/H2 4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031341	regulation of cell killing	5/68	101/13307	0.00016272611	0.0036116554	0.0029120274	Hsp90ab1/H2-D15	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002822	regulation of adaptive immune response based on son	6/68	160/13307	0.00016273091	0.0036116554	0.0029120274	Rsad2/Irf1/Cd27 6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002475	antigen processing and presentation via MHC class Ib	3/68	22/13307	0.00018334321	0.0039662772	0.0031979540	H2-D1/H2-K1/B2 3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002443	leukocyte mediated immunity	8/68	313/13307	0.00018574611	0.0039662772	0.0031979540	Rsad2/Irf7/H2-D18	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060759	regulation of response to cytokine stimulus	5/68	104/13307	0.00018671111	0.0039662772	0.0031979540	Parp14/Irgm1/Irf5	aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:0002483	antigen processing and presentation of endogenous pe	3/68	24/13307	0.000239209	0.004940332	0.003983321	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019885	antigen processing and presentation of endogenous pe	3/68	24/13307	0.000239209	0.004940332	0.003983321	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000377	regulation of reactive oxygen species metabolic proce	6/68	176/13307	0.000272837	0.005527474	0.004456725	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002456	T cell mediated immunity	5/68	113/13307	0.000275072	0.005527474	0.004456725	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019883	antigen processing and presentation of endogenous ar	3/68	26/13307	0.000305045	0.006048038	0.004876448	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050830	defense response to Gram-positive bacterium	4/68	67/13307	0.000375183	0.007340769	0.005918759	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071347	cellular response to interleukin-1	4/68	68/13307	0.000397108	0.007668394	0.006183278	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071674	mononuclear cell migration	4/68	69/13307	0.000419934	0.007981464	0.006435343	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042026	protein refolding	3/68	29/13307	0.000424032	0.007981464	0.006435343	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002687	positive regulation of leukocyte migration	5/68	129/13307	0.000506514	0.009414830	0.007591046	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	3/68	33/13307	0.000623965	0.011315077	0.009123189	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002474	antigen processing and presentation of peptide antige	3/68	33/13307	0.000623965	0.011315077	0.009123189	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002709	regulation of T cell mediated immunity	4/68	77/13307	0.000637529	0.011421768	0.009209212	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001906	cell killing	5/68	137/13307	0.000666219	0.011793666	0.009509069	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002699	positive regulation of immune effector process	6/68	212/13307	0.000732767	0.012819127	0.010335883	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via	3/68	36/13307	0.000807661	0.013816670	0.011140188	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	4/68	82/13307	0.000808372	0.013816670	0.011140188	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070555	response to interleukin-1	4/68	85/13307	0.000925131	0.015632626	0.012604368	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001914	regulation of T cell mediated cytotoxicity	3/68	38/13307	0.000947325	0.015827794	0.012761729	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072676	lymphocyte migration	4/68	86/13307	0.000966557	0.015969685	0.012876134	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	3/68	41/13307	0.001184049	0.019348150	0.015600143	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001818	negative regulation of cytokine production	6/68	234/13307	0.001222253	0.019755344	0.015928458	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072593	reactive oxygen species metabolic process	6/68	235/13307	0.001249298	0.019975347	0.016105843	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1904407	positive regulation of nitric oxide metabolic process	3/68	42/13307	0.001270491	0.020098094	0.016204813	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002706	regulation of lymphocyte mediated immunity	5/68	159/13307	0.001300184	0.020351310	0.016408977	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072608	interleukin-10 secretion	2/68	11/13307	0.001373693	0.021058584	0.016979242	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902043	positive regulation of extrinsic apoptotic signaling path	2/68	11/13307	0.001373693	0.021058584	0.016979242	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048247	lymphocyte chemotaxis	3/68	44/13307	0.001455071	0.021855473	0.017621763	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000351	regulation of endothelial cell apoptotic process	3/68	44/13307	0.001455071	0.021855473	0.017621763	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002548	monocyte chemotaxis	3/68	45/13307	0.001553337	0.022869434	0.018439306	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070098	chemokine-mediated signaling pathway	3/68	45/13307	0.001553337	0.022869434	0.018439306	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006968	cellular defense response	2/68	12/13307	0.001642998	0.023672891	0.019087122	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060340	positive regulation of type I interferon-mediated signal	2/68	12/13307	0.001642998	0.023672891	0.019087122	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072577	endothelial cell apoptotic process	3/68	46/13307	0.001655669	0.023672891	0.019087122	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002688	regulation of leukocyte chemotaxis	4/68	100/13307	0.001691847	0.023959781	0.019318438	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002253	activation of immune response	7/68	341/13307	0.001730327	0.024273551	0.019571425	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002833	positive regulation of response to biotic stimulus	3/68	48/13307	0.001872774	0.026026314	0.020984654	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STA	2/68	13/13307	0.001935327	0.026402130	0.021287669	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1900225	regulation of NLRP3 inflammasome complex assembly	2/68	13/13307	0.001935327	0.026402130	0.021287669	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006986	response to unfolded protein	4/68	104/13307	0.001953851	0.026412520	0.021296046	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032103	positive regulation of response to external stimulus	6/68	260/13307	0.002087562	0.027965816	0.022548447	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylati	3/68	50/13307	0.002106856	0.027972286	0.022553664	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002697	regulation of immune effector process	7/68	354/13307	0.002139079	0.028148775	0.022695965	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071621	granulocyte chemotaxis	4/68	107/13307	0.002167914	0.028277976	0.022800139	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031348	negative regulation of defense response	5/68	179/13307	0.002189653	0.028313168	0.022828513	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044546	NLRP3 inflammasome complex assembly	2/68	14/13307	0.002250444	0.028359420	0.022865805	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060330	regulation of response to interferon-gamma	2/68	14/13307	0.002250444	0.028359420	0.022865805	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060334	regulation of interferon-gamma-mediated signaling pa	2/68	14/13307	0.002250444	0.028359420	0.022865805	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002685	regulation of leukocyte migration	5/68	182/13307	0.002353832	0.028982592	0.023368260	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048002	antigen processing and presentation of peptide antige	3/68	52/13307	0.002358368	0.028982592	0.023368260	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903428	positive regulation of reactive oxygen species biosynth	3/68	52/13307	0.002358368	0.028982592	0.023368260	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001909	leukocyte mediated cytotoxicity	4/68	110/13307	0.002397667	0.029224027	0.023562926	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	4/68	113/13307	0.002643677	0.031960550	0.025769346	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001913	T cell mediated cytotoxicity	3/68	55/13307	0.002769257	0.032424304	0.026143264	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1990868	response to chemokine	3/68	55/13307	0.002769257	0.032424304	0.026143264	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1990869	cellular response to chemokine	3/68	55/13307	0.002769257	0.032424304	0.026143264	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000401	regulation of lymphocyte migration	3/68	55/13307	0.002769257	0.032424304	0.026143264	aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:0071396	cellular response to lipid	7/68	375/13307	0.0029534376	0.0343106394	0.0276641902	Cxcl10/Gbp2/Cm	7	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002757	immune response-activating signal transduction	6/68	282/13307	0.0031284387	0.0360619255	0.0290762278	Rsad2/Irf1/Irf7/A	6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002486	antigen processing and presentation of endogenous pe	2/68	17/13307	0.0033302004	0.0378015884	0.0304788937	H2-D1/H2-K1	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	2/68	17/13307	0.0033302004	0.0378015884	0.0304788937	Irf1/Cd274	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0007050	cell cycle arrest	4/68	121/13307	0.0033834369	0.0381149295	0.0307315362	Irf1/Hsp90ab1/Sl	4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045428	regulation of nitric oxide biosynthetic process	3/68	60/13307	0.0035471021	0.0396582017	0.0319758551	Klf2/Sod2/Icam1	3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071356	cellular response to tumor necrosis factor	4/68	124/13307	0.0036938150	0.0402368507	0.0324424118	Irf1/Ccl4/Acod1/	4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002476	antigen processing and presentation of endogenous pe	2/68	18/13307	0.0037341529	0.0402368507	0.0324424118	H2-D1/H2-K1	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002484	antigen processing and presentation of endogenous pe	2/68	18/13307	0.0037341529	0.0402368507	0.0324424118	H2-D1/H2-K1	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0009200	deoxyribonucleoside triphosphate metabolic process	2/68	18/13307	0.0037341529	0.0402368507	0.0324424118	Cmpk2/Samhd1	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048245	eosinophil chemotaxis	2/68	18/13307	0.0037341529	0.0402368507	0.0324424118	Ccl4/Ccl12	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002764	immune response-regulating signaling pathway	6/68	294/13307	0.0038387404	0.0410662375	0.0331111348	Rsad2/Irf1/Irf7/A	6	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035966	response to topologically incorrect protein	4/68	126/13307	0.0039111572	0.0415420773	0.0334947978	Hspa1a/Atf3/Hsp	4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0097530	granulocyte migration	4/68	127/13307	0.0040230143	0.0420784893	0.0339272993	Cxcl10/Ccl4/Ccl1	4	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	3/68	63/13307	0.0040716941	0.0420784893	0.0339272993	H2-D1/H2-K1/B2	3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0008625	extrinsic apoptotic signaling pathway via death domair	3/68	63/13307	0.0040716941	0.0420784893	0.0339272993	Atf3/Icam1/Thbs	3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002703	regulation of leukocyte mediated immunity	5/68	207/13307	0.0040903062	0.0420784893	0.0339272993	Rsad2/H2-D1/H2	5	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002726	positive regulation of T cell cytokine production	2/68	19/13307	0.0041597430	0.0420784893	0.0339272993	Rsad2/B2m	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002755	MyD88-dependent toll-like receptor signaling pathway	2/68	19/13307	0.0041597430	0.0420784893	0.0339272993	Irf1/Irf7	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000353	positive regulation of endothelial cell apoptotic proces	2/68	19/13307	0.0041597430	0.0420784893	0.0339272993	Ccl12/Thbs1	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032897	negative regulation of viral transcription	2/68	20/13307	0.0046067458	0.0462853446	0.0373192280	Ifitm3/Ccl4	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006809	nitric oxide biosynthetic process	3/68	67/13307	0.0048410977	0.0483135052	0.0389545057	Klf2/Sod2/Icam1	3	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072677	eosinophil migration	2/68	21/13307	0.0050749377	0.0499763737	0.0402952534	Ccl4/Ccl12	2	aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1901673	regulation of mitotic spindle assembly	2/68	21/13307	0.0050749377	0.0499763737	0.0402952534	Hspa1a/Hspa1b	2	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0009897	external side of plasma membrane	12/67	313/13541	3.6244629662	5.0380035231	4.0441376255	Cxcl10/Cd274/Cc	12	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0020005	symbiont-containing vacuole membrane	4/67	11/13541	1.7598638262	1.2231053592	9.8181876623	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0098552	side of membrane	13/67	460/13541	3.2223397389	1.3151896363	1.0557372317	Cxcl10/Cd274/Cc	13	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0020003	symbiont-containing vacuole	4/67	13/13541	3.7847183779	1.3151896363	1.0557372317	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0065010	extracellular membrane-bounded organelle	4/67	15/13541	7.1717179531	1.8917356269	1.5185458269	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0030430	host cell cytoplasm	4/67	16/13541	9.5267261787	1.8917356269	1.5185458269	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0033655	host cell cytoplasm part	4/67	16/13541	9.5267261787	1.8917356269	1.5185458269	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0033646	host intracellular part	4/67	19/13541	2.0063293825	3.0986642685	2.4873791175	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0043656	intracellular region of host	4/67	19/13541	2.0063293825	3.0986642685	2.4873791175	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0043230	extracellular organelle	6/67	82/13541	3.0452731315	3.8857032569	3.1191559654	Gbp2b/Gbp2/Cd	6	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0033643	host cell part	4/67	21/13541	3.0750169659	3.8857032569	3.1191559654	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0018995	host	4/67	23/13541	4.5158286283	4.8284629180	3.8759338834	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0043657	host cell	4/67	23/13541	4.5158286283	4.8284629180	3.8759338834	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044215	other organism	4/67	25/13541	6.4033253546	5.5628889018	4.4654768920	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044216	other organism cell	4/67	25/13541	6.4033253546	5.5628889018	4.4654768920	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044217	other organism part	4/67	25/13541	6.4033253546	5.5628889018	4.4654768920	Gbp2b/Gbp2/Gb	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042612	MHC class I protein complex	3/67	11/13541	1.8570658304	0.0001518424	0.0001218879	H2-D1/H2-K1/B2	3	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042824	MHC class I peptide loading complex	3/67	14/13541	4.0534473369	0.0003130162	0.0002512663	H2-D1/H2-K1/B2	3	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042611	MHC protein complex	3/67	21/13541	0.0001444787	0.0010569764	0.0008484627	H2-D1/H2-K1/B2	3	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0008180	COP9 signalosome	3/67	34/13541	0.0006208377	0.0043148222	0.0034636210	Hspa1a/Hsp90ab	3	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0005789	endoplasmic reticulum membrane	8/67	439/13541	0.0013975149	0.0092502180	0.0074253927	Rsad2/Ifi47/Irgm	8	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0098827	endoplasmic reticulum subcompartment	8/67	452/13541	0.0016809586	0.0106206021	0.0085254359	Rsad2/Ifi47/Irgm	8	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042175	nuclear outer membrane-endoplasmic reticulum mem	8/67	457/13541	0.0018014279	0.0108868907	0.0087391929	Rsad2/Ifi47/Irgm	8	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0030176	integral component of endoplasmic reticulum membra	4/67	132/13541	0.0041157776	0.0238372124	0.0191347559	H2-D1/H2-K1/B2	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0031227	intrinsic component of endoplasmic reticulum membra	4/67	139/13541	0.0049436096	0.0274864696	0.0220641104	H2-D1/H2-K1/B2	4	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0005797	Golgi medial cisterna	2/67	22/13541	0.0052264724	0.0279415255	0.0224293957	H2-D1/H2-K1	2	aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0070971	endoplasmic reticulum exit site	2/67	26/13541	0.0072602738	0.0373769652	0.0300034707	H2-D1/H2-K1	2	aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0003924	GTPase activity	8/65	263/13229	4.1554441655	0.0053744411	0.0045946080	Gbp2b/Gbp2/Gb	8	aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0042379	chemokine receptor binding	4/65	45/13229	6.7980433526	0.0053744411	0.0045946080	Cxcl10/Ccl4/Ccl1	4	aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0005525	GTP binding	8/65	324/13229	0.0001778549	0.0053744411	0.0045946080	Gbp2b/Gbp2/Gb	8	aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0032550	purine ribonucleoside binding	8/65	330/13229	0.0002015873	0.0053744411	0.0045946080	Gbp2b/Gbp2/Gb	8	aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0001883	purine nucleoside binding	8/65	333/13229	0.0002143972	0.0053744411	0.0045946080	Gbp2b/Gbp2/Gb	8	aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0032549	ribonucleoside binding	8/65	335/13229	0.0002233036	0.0053744411	0.0045946080	Gbp2b/Gbp2/Gb	8	aTGFb vs PBS	Up-regulated genes	CD45+

MF	GO:0019001	guanyl nucleotide binding	8/65	340/13229	0.000246909	3	0.005374441	1	0.004594608
MF	GO:0032561	guanyl ribonucleotide binding	8/65	340/13229	0.000246909	3	0.005374441	1	0.004594608
MF	GO:0001882	nucleoside binding	8/65	344/13229	0.000267237	4	0.005374441	1	0.004594608
MF	GO:0048020	CCR chemokine receptor binding	3/65	29/13229	0.000377605	8	0.006834665	9	0.005842953
MF	GO:0003725	double-stranded RNA binding	4/65	75/13229	0.000496639	6	0.008171980	1	0.006986223
MF	GO:0008009	chemokine activity	3/65	35/13229	0.000662291	2	0.009989559	7	0.008540071
MF	GO:0030881	beta-2-microglobulin binding	2/65	11/13229	0.001270635	2	0.015332331	8	0.013107605
MF	GO:0042610	CD8 receptor binding	2/65	11/13229	0.001270635	2	0.015332331	8	0.013107605
MF	GO:0046977	TAP binding	2/65	11/13229	0.001270635	2	0.015332331	8	0.013107605
MF	GO:0016763	transferase activity, transferring pentosyl groups	3/65	46/13229	0.001478078	6	0.016720764	7	0.014294576
MF	GO:0042608	T cell receptor binding	2/65	14/13229	0.002082488	8	0.022171742	9	0.018954615
MF	GO:0001664	G protein-coupled receptor binding	5/65	204/13229	0.003240751	5	0.032585756	7	0.027859091
MF	GO:0005125	cytokine activity	4/65	129/13229	0.003691597	8	0.035167326	8	0.030064536
MF	GO:0044183	protein binding involved in protein folding	2/65	21/13229	0.004700342	7	0.040512478	0	0.034634104
MF	GO:0051787	misfolded protein binding	2/65	21/13229	0.004700342	7	0.040512478	0	0.034634104
MF	GO:0042605	peptide antigen binding	2/65	23/13229	0.005627129	6	0.046295930	2	0.039578375
BP	GO:0061077	chaperone-mediated protein folding	3/10	50/13403	5.755390777	6	0.002595681	2	0.001526693
BP	GO:0006457	protein folding	3/10	140/13403	0.000126860	3	0.022116057	1	0.013007922
BP	GO:0051085	chaperone cofactor-dependent protein refolding	2/10	29/13403	0.000201246	7	0.022116057	1	0.013007927
BP	GO:0051084	'de novo' posttranslational protein folding	2/10	34/13403	0.000277524	4	0.022116057	1	0.013007927
BP	GO:0006458	'de novo' protein folding	2/10	35/13403	0.000294226	9	0.022116057	1	0.013007927
BP	GO:0038084	vascular endothelial growth factor signaling pathway	2/10	35/13403	0.000294226	9	0.022116057	1	0.013007927
BP	GO:0043618	regulation of transcription from RNA polymerase II pro	2/10	46/13403	0.000509569	8	0.028794098	6	0.016935728
BP	GO:0043620	regulation of DNA-templated transcription in response	2/10	51/13403	0.000626482	5	0.028794098	6	0.016935728
BP	GO:0035924	cellular response to vascular endothelial growth factor	2/10	52/13403	0.000651282	4	0.028794098	6	0.016935728
BP	GO:0045765	regulation of angiogenesis	3/10	247/13403	0.000674181	6	0.028794098	6	0.016935728
BP	GO:0071277	cellular response to calcium ion	2/10	54/13403	0.000702295	0	0.028794098	6	0.016935728
BP	GO:1901342	regulation of vasculature development	3/10	277/13403	0.000940916	0	0.034188054	6	0.020108273
BP	GO:0032272	negative regulation of protein polymerization	2/10	64/13403	0.000985464	9	0.034188054	6	0.020108273
MF	GO:0044183	protein binding involved in protein folding	2/10	19/13297	8.645726370	1	0.005533264	8	0.003003252
BP	GO:1903706	regulation of hemopoiesis	9/36	362/13307	3.632827224	1	0.000569264	0	0.000407641
BP	GO:0032496	response to lipopolysaccharide	7/36	226/13307	2.038744853	9	0.001292770	8	0.000925733
BP	GO:0001818	negative regulation of cytokine production	7/36	234/13307	2.569144948	0	0.001292770	8	0.000925733
BP	GO:0002237	response to molecule of bacterial origin	7/36	243/13307	3.299989502	2	0.001292770	8	0.000925733
BP	GO:0009612	response to mechanical stimulus	5/36	108/13307	9.899243165	0	0.002625011	7	0.001879731
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	6/36	188/13307	1.005109796	7	0.002625011	7	0.001879731
BP	GO:0002456	T cell mediated immunity	5/36	113/13307	1.234469002	7	0.002763447	0	0.001978863
BP	GO:0002710	negative regulation of T cell mediated immunity	3/36	19/13307	1.710400945	8	0.003336455	0	0.002389185
BP	GO:0044403	symbiont process	7/36	318/13307	1.916279235	8	0.003336455	0	0.002389185
BP	GO:0009617	response to bacterium	8/36	453/13307	2.215362669	0	0.003471473	3	0.002485870
BP	GO:0044419	interspecies interaction between organisms	7/36	333/13307	2.578167235	0	0.003648687	4	0.002612770
BP	GO:0051702	interaction with symbiont	4/36	66/13307	2.885151721	5	0.003648687	4	0.002612770
BP	GO:0045580	regulation of T cell differentiation	5/36	136/13307	3.026990245	0	0.003648687	4	0.002612770
BP	GO:0034612	response to tumor necrosis factor	5/36	141/13307	3.600349051	3	0.002889219	2	0.002085693
BP	GO:0048514	blood vessel morphogenesis	8/36	498/13307	4.361246881	1	0.004443214	7	0.003181719
BP	GO:0002709	regulation of T cell mediated immunity	4/36	77/13307	5.309333399	0	0.004443214	7	0.003181719
BP	GO:1902107	positive regulation of leukocyte differentiation	5/36	155/13307	5.661310946	9	0.004443214	7	0.003181719
BP	GO:0050792	regulation of viral process	5/36	158/13307	6.202277807	0	0.004443214	7	0.003181719
BP	GO:0002460	adaptive immune response based on somatic recombi	6/36	260/13307	6.252478802	6	0.004443214	7	0.003181719
BP	GO:0032103	positive regulation of response to external stimulus	6/36	260/13307	6.252478802	6	0.004443214	7	0.003181719
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	6/36	261/13307	6.387152503	5	0.004443214	7	0.003181719
BP	GO:0002822	regulation of adaptive immune response based on son	5/36	160/13307	6.584545100	4	0.004443214	7	0.003181719
BP	GO:0032870	cellular response to hormone stimulus	7/36	387/13307	6.709975440	6	0.004443214	7	0.003181719
BP	GO:1902105	regulation of leukocyte differentiation	6/36	264/13307	6.805178958	3	0.004443214	7	0.003181719
BP	GO:0045619	regulation of lymphocyte differentiation	5/36	165/13307	7.620057546	5	0.004776252	0	0.003420202
BP	GO:0050863	regulation of T cell activation	6/36	275/13307	8.529296815	0	0.004966714	3	0.003556589
BP	GO:0045582	positive regulation of T cell differentiation	4/36	87/13307	8.557835743	6	0.004966714	3	0.003556589

BP	GO:0002819	regulation of adaptive immune response	5/36	176/13307	0.0001033904	0.0057861726	0.0041433916	Ccr7/Il7r/Hspa8/	Down-regulated genes	CD45+
BP	GO:0007159	leukocyte cell-cell adhesion	6/36	288/13307	0.0001099923	0.0059433791	0.0042559648	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:0042110	T cell activation	7/36	426/13307	0.0001224644	0.0063967269	0.0045806005	Ccr7/Hsp90aa1/C	Down-regulated genes	CD45+
BP	GO:0045621	positive regulation of lymphocyte differentiation	4/36	100/13307	0.0001470365	0.0072547247	0.0051949998	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:1903708	positive regulation of hemopoiesis	5/36	190/13307	0.0001481500	0.0072547247	0.0051949998	Ccr7/Hsp90aa1/J	Down-regulated genes	CD45+
BP	GO:0014070	response to organic cyclic compound	7/36	458/13307	0.0001917719	0.0084602646	0.0060582689	Pim1/Zfp36/Jun/	Down-regulated genes	CD45+
BP	GO:0002823	negative regulation of adaptive immune response base	3/36	42/13307	0.0001941551	0.0084602646	0.0060582689	Il7r/Smad7/Arg1	Down-regulated genes	CD45+
BP	GO:0051591	response to cAMP	3/36	42/13307	0.0001941551	0.0084602646	0.0060582689	Jun/Junb/Jund	Down-regulated genes	CD45+
BP	GO:0002694	regulation of leukocyte activation	7/36	459/13307	0.0001943647	0.0084602646	0.0060582689	Ccr7/Ctsc/Hsp90.	Down-regulated genes	CD45+
BP	GO:0002707	negative regulation of lymphocyte mediated immunity	3/36	43/13307	0.0002083295	0.0087570118	0.0062707652	Il7r/Smad7/Arg1	Down-regulated genes	CD45+
BP	GO:0001909	leukocyte mediated cytotoxicity	4/36	110/13307	0.0002123589	0.0087570118	0.0062707652	Ctsc/Il7r/Hspa8/	Down-regulated genes	CD45+
BP	GO:0048247	lymphocyte chemotaxis	3/36	44/13307	0.0002231583	0.0089663875	0.0064206959	Ccr7/Cxcl16/Ccl6	Down-regulated genes	CD45+
BP	GO:0071248	cellular response to metal ion	4/36	115/13307	0.0002518659	0.0094612392	0.0067750519	Jun/Junb/Jund/Fı	Down-regulated genes	CD45+
BP	GO:0022409	positive regulation of cell-cell adhesion	5/36	215/13307	0.0002634481	0.0094612392	0.0067750519	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:0022407	regulation of cell-cell adhesion	6/36	339/13307	0.0002669913	0.0094612392	0.0067750519	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	6/36	339/13307	0.0002669913	0.0094612392	0.0067750519	Zfp36/Cxcr4/Jun/	Down-regulated genes	CD45+
BP	GO:0002820	negative regulation of adaptive immune response	3/36	47/13307	0.0002717011	0.0094612392	0.0067750519	Il7r/Smad7/Arg1	Down-regulated genes	CD45+
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentia	3/36	47/13307	0.0002717011	0.0094612392	0.0067750519	Ccr7/Cd83/Smad	Down-regulated genes	CD45+
BP	GO:0002521	leukocyte differentiation	7/36	488/13307	0.0002829007	0.0096370755	0.0069009656	Ccr7/Hsp90aa1/J	Down-regulated genes	CD45+
BP	GO:0050865	regulation of cell activation	7/36	491/13307	0.0002936656	0.0097909366	0.0070111432	Ccr7/Ctsc/Hsp90.	Down-regulated genes	CD45+
BP	GO:0010035	response to inorganic substance	6/36	348/13307	0.0003073672	0.0100342586	0.0071853825	Ccr7/Jun/Junb/Ju	Down-regulated genes	CD45+
BP	GO:0060394	negative regulation of pathway-restricted SMAD prote	2/36	10/13307	0.0003158890	0.0100741580	0.0072139539	Pmepa1/Smad7	Down-regulated genes	CD45+
BP	GO:0030099	myeloid cell differentiation	6/36	352/13307	0.0003267881	0.0100741580	0.0072139539	Ccr7/Zfp36/Jun/	Down-regulated genes	CD45+
BP	GO:0071356	cellular response to tumor necrosis factor	4/36	124/13307	0.0003359164	0.0100741580	0.0072139539	Zfp36/Pid1/Ccl6/	Down-regulated genes	CD45+
BP	GO:0002704	negative regulation of leukocyte mediated immunity	3/36	51/13307	0.0003463654	0.0100741580	0.0072139539	Il7r/Smad7/Arg1	Down-regulated genes	CD45+
BP	GO:0002250	adaptive immune response	6/36	356/13307	0.0003471630	0.0100741580	0.0072139539	Ccr7/Ctsc/Il7r/Hs	Down-regulated genes	CD45+
BP	GO:0045785	positive regulation of cell adhesion	6/36	356/13307	0.0003471630	0.0100741580	0.0072139539	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:2000107	negative regulation of leukocyte apoptotic process	3/36	52/13307	0.0003668898	0.0103121155	0.0073843517	Ccr7/Tsc22d3/Il7	Down-regulated genes	CD45+
BP	GO:0001933	negative regulation of protein phosphorylation	6/36	360/13307	0.0003685248	0.0103121155	0.0073843517	Pmepa1/Pid1/Du	Down-regulated genes	CD45+
BP	GO:0001913	T cell mediated cytotoxicity	3/36	55/13307	0.0004331182	0.0117016598	0.0083793835	Ctsc/Il7r/Hspa8	Down-regulated genes	CD45+
BP	GO:0071277	cellular response to calcium ion	3/36	55/13307	0.0004331182	0.0117016598	0.0083793835	Jun/Junb/Jund	Down-regulated genes	CD45+
BP	GO:0060213	positive regulation of nuclear-transcribed mRNA poly(	2/36	12/13307	0.0004617288	0.0117247148	0.0083958929	Btg2/Zfp36	Down-regulated genes	CD45+
BP	GO:0002449	lymphocyte mediated immunity	5/36	243/13307	0.0004626229	0.0117247148	0.0083958929	Ctsc/Il7r/Hspa8/	Down-regulated genes	CD45+
BP	GO:0071241	cellular response to inorganic substance	4/36	135/13307	0.0004639225	0.0117247148	0.0083958929	Jun/Junb/Jund/Fı	Down-regulated genes	CD45+
BP	GO:0051249	regulation of lymphocyte activation	6/36	377/13307	0.0004711140	0.0117247148	0.0083958929	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:0060326	cell chemotaxis	5/36	244/13307	0.0004713829	0.0117247148	0.0083958929	Ccr7/Cxcr4/Cxcl1	Down-regulated genes	CD45+
BP	GO:0030217	T cell differentiation	5/36	245/13307	0.0004802678	0.0117590569	0.0084204848	Ccr7/Hsp90aa1/I	Down-regulated genes	CD45+
BP	GO:0001906	cell killing	4/36	137/13307	0.0004904683	0.0118240598	0.0084670324	Ctsc/Il7r/Hspa8/	Down-regulated genes	CD45+
BP	GO:0071774	response to fibroblast growth factor	3/36	59/13307	0.0005327282	0.0125421936	0.0089812772	Zfp36/Ier2/Nr4a	Down-regulated genes	CD45+
BP	GO:0016032	viral process	5/36	251/13307	0.0005362648	0.0125421936	0.0089812772	Zfp36/Cxcr4/Jun/	Down-regulated genes	CD45+
BP	GO:0051851	modification by host of symbiont morphology or physi	3/36	61/13307	0.0005875876	0.0133442010	0.0095555827	Jun/Hspa8/Arg1	Down-regulated genes	CD45+
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	3/36	61/13307	0.0005875876	0.0133442010	0.0095555827	Ccr7/Cd83/Smad	Down-regulated genes	CD45+
BP	GO:0046637	regulation of alpha-beta T cell differentiation	3/36	62/13307	0.0006163207	0.0136636403	0.0097843285	Ccr7/Cd83/Smad	Down-regulated genes	CD45+
BP	GO:0042326	negative regulation of phosphorylation	6/36	397/13307	0.0006190928	0.0136636403	0.0097843285	Pmepa1/Pid1/Du	Down-regulated genes	CD45+
BP	GO:0060211	regulation of nuclear-transcribed mRNA poly(A) tail sh	2/36	14/13307	0.0006344624	0.0138083699	0.0098879672	Btg2/Zfp36	Down-regulated genes	CD45+
BP	GO:0046683	response to organophosphorus	3/36	64/13307	0.0006764493	0.0145204938	0.0103979084	Jun/Junb/Jund	Down-regulated genes	CD45+
BP	GO:0043902	positive regulation of multi-organism process	4/36	151/13307	0.0007075421	0.0149826837	0.0107288757	Jun/Nps37b/Hsp	Down-regulated genes	CD45+
BP	GO:0002683	negative regulation of immune system process	6/36	413/13307	0.0007617199	0.0159148698	0.0113964002	Tsc22d3/Zfp36/Il	Down-regulated genes	CD45+
BP	GO:0001525	angiogenesis	6/36	415/13307	0.0007812053	0.0161072198	0.0115341392	Cxcr4/Btg1/Jun/	Down-regulated genes	CD45+
BP	GO:0048872	homeostasis of number of cells	5/36	276/13307	0.0008241592	0.0167721764	0.0120103046	Ccr7/Tsc22d3/Zfı	Down-regulated genes	CD45+
BP	GO:0002706	regulation of lymphocyte mediated immunity	4/36	159/13307	0.0008583097	0.0172432220	0.0123476134	Il7r/Hspa8/Smad	Down-regulated genes	CD45+
BP	GO:0002696	positive regulation of leukocyte activation	5/36	282/13307	0.0009077755	0.0180061301	0.0128939204	Ccr7/Ctsc/Hsp90.	Down-regulated genes	CD45+
BP	GO:0010818	T cell chemotaxis	2/36	17/13307	0.0009433795	0.0180277539	0.0129094050	Ccr7/Cxcl16	Down-regulated genes	CD45+
BP	GO:0035994	response to muscle stretch	2/36	17/13307	0.0009433795	0.0180277539	0.0129094050	Jun/Nfkbia	Down-regulated genes	CD45+
BP	GO:1900153	positive regulation of nuclear-transcribed mRNA catab	2/36	17/13307	0.0009433795	0.0180277539	0.0129094050	Btg2/Zfp36	Down-regulated genes	CD45+
BP	GO:0006935	chemotaxis	6/36	433/13307	0.0009745487	0.0183990114	0.0131752569	Ccr7/Cxcr4/Cxcl1	Down-regulated genes	CD45+
BP	GO:0042330	taxis	6/36	436/13307	0.0010100806	0.0188428131	0.0134930566	Ccr7/Cxcr4/Cxcl1	Down-regulated genes	CD45+

BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	3/36	75/13307	0.0010741936	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0007517	muscle organ development	5/36	295/13307	0.0011105580	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001938	positive regulation of endothelial cell proliferation	3/36	76/13307	0.0011162681	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0014074	response to purine-containing compound	3/36	76/13307	0.0011162681	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1903313	positive regulation of mRNA metabolic process	3/36	76/13307	0.0011162681	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0070848	response to growth factor	6/36	445/13307	0.0011227179	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050870	positive regulation of T cell activation	4/36	171/13307	0.0011251316	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050727	regulation of inflammatory response	5/36	296/13307	0.0011274434	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050867	positive regulation of cell activation	5/36	296/13307	0.0011274434	0.0189968166	0.0136033362	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0048524	positive regulation of viral process	3/36	77/13307	0.0011593720	0.0193269779	0.0138397598	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1900151	regulation of nuclear-transcribed mRNA catabolic proc	2/36	19/13307	0.0011821328	0.0194989709	0.0139629214	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0032897	negative regulation of viral transcription	2/36	20/13307	0.0013112493	0.0214034134	0.0153266642	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051817	modification of morphology or physiology of other org	3/36	81/13307	0.0013422734	0.0216839432	0.0155275474	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	3/36	82/13307	0.0013906675	0.0222364903	0.0159232181	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002443	leukocyte mediated immunity	5/36	313/13307	0.0014447567	0.0226715687	0.0162347713	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002719	negative regulation of cytokine production involved in	2/36	21/13307	0.0014468135	0.0226715687	0.0162347713	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0010563	negative regulation of phosphorus metabolic process	6/36	471/13307	0.0015031393	0.0229264995	0.0164173234	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0045936	negative regulation of phosphate metabolic process	6/36	471/13307	0.0015031393	0.0229264995	0.0164173234	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0014706	striated muscle tissue development	5/36	316/13307	0.0015069747	0.0229264995	0.0164173234	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	4/36	186/13307	0.0015346748	0.0231234174	0.0165583333	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0072676	lymphocyte migration	3/36	86/13307	0.0015951956	0.0238063953	0.0170474036	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0031331	positive regulation of cellular catabolic process	5/36	321/13307	0.0016150504	0.0238753205	0.0170967599	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	2/36	23/13307	0.0017371501	0.0252047623	0.0180487533	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0070233	negative regulation of T cell apoptotic process	2/36	23/13307	0.0017371501	0.0252047623	0.0180487533	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:2000106	regulation of leukocyte apoptotic process	3/36	89/13307	0.0017603414	0.0253069277	0.0181219124	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0030098	lymphocyte differentiation	5/36	332/13307	0.0018728684	0.0266798630	0.0191050509	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060537	muscle tissue development	5/36	333/13307	0.0018977218	0.0267903614	0.0191841771	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051592	response to calcium ion	3/36	92/13307	0.0019358199	0.0270841950	0.0193945870	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0010038	response to metal ion	4/36	199/13307	0.0019655070	0.0272065045	0.0194821710	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	3/36	93/13307	0.0019966483	0.0272065045	0.0194821710	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:2000379	positive regulation of reactive oxygen species metabol	3/36	93/13307	0.0019966483	0.0272065045	0.0194821710	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002703	regulation of leukocyte mediated immunity	4/36	207/13307	0.0022687871	0.0306481855	0.0219467072	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0035821	modification of morphology or physiology of other org	3/36	98/13307	0.0023186772	0.0307912481	0.0220491522	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0046634	regulation of alpha-beta T cell activation	3/36	98/13307	0.0023186772	0.0307912481	0.0220491522	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0048535	lymph node development	2/36	27/13307	0.0023937153	0.0315206047	0.0225714336	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002697	regulation of immune effector process	5/36	354/13307	0.0024777718	0.0323555712	0.0231693406	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0031341	regulation of cell killing	3/36	101/13307	0.0025264902	0.0327190930	0.0234296531	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di	2/36	28/13307	0.0025734730	0.0330543626	0.0236697347	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0046632	alpha-beta T cell differentiation	3/36	102/13307	0.0025982403	0.0331011597	0.0237032454	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0042026	protein refolding	2/36	29/13307	0.0027594111	0.0348709451	0.0249705622	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001936	regulation of endothelial cell proliferation	3/36	106/13307	0.0028978355	0.0363272666	0.0260134123	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002724	regulation of T cell cytokine production	2/36	30/13307	0.0029514966	0.0367063119	0.0262848410	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071887	leukocyte apoptotic process	3/36	109/13307	0.0031359597	0.0385591819	0.0276116534	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002701	negative regulation of production of molecular mediat	2/36	31/13307	0.0031496970	0.0385591819	0.0276116534	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071396	cellular response to lipid	5/36	375/13307	0.0031779616	0.0386036114	0.0276434687	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0006623	protein targeting to vacuole	2/36	32/13307	0.0033539795	0.0401197406	0.0287291462	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060674	placenta blood vessel development	2/36	32/13307	0.0033539795	0.0401197406	0.0287291462	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0009896	positive regulation of catabolic process	5/36	381/13307	0.0034019757	0.0403855761	0.0289195070	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051251	positive regulation of lymphocyte activation	4/36	236/13307	0.0036390467	0.0428750846	0.0307022068	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0046627	negative regulation of insulin receptor signaling pathw	2/36	34/13307	0.0037806613	0.0438836761	0.0314244441	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	2/36	34/13307	0.0037806613	0.0438836761	0.0314244441	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0045927	positive regulation of growth	4/36	240/13307	0.0038640519	0.0445218344	0.0318814197	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001935	endothelial cell proliferation	3/36	118/13307	0.0039213816	0.0448525921	0.0321182703	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0045622	regulation of T-helper cell differentiation	2/36	35/13307	0.0040029958	0.0449434877	0.0321833593	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	2/36	35/13307	0.0040029958	0.0449434877	0.0321833593	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050921	positive regulation of chemotaxis	3/36	119/13307	0.0040153722	0.0449434877	0.0321833593	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050729	positive regulation of inflammatory response	3/36	120/13307	0.0041107302	0.0456844982	0.0327139859	aTGFb vs PBS	Down-regulated genes CD45+

BP	GO:0002698	negative regulation of immune effector process	3/36	121/13307	0.0042074617	0.0464302296	0.0332479930	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0030855	epithelial cell differentiation	5/36	402/13307	0.0042765501	0.0468626164	0.0335576187	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0034341	response to interferon-gamma	3/36	123/13307	0.0044050696	0.0479357227	0.0343260541	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0031647	regulation of protein stability	4/36	250/13307	0.0044676549	0.0482814846	0.0345736490	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1903364	positive regulation of cellular protein catabolic process	3/36	124/13307	0.0045059577	0.0483618884	0.0346312250	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001774	microglial cell activation	2/36	38/13307	0.0047055892	0.0488321742	0.0349679896	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001914	regulation of T cell mediated cytotoxicity	2/36	38/13307	0.0047055892	0.0488321742	0.0349679896	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002269	leukocyte activation involved in inflammatory response	2/36	38/13307	0.0047055892	0.0488321742	0.0349679896	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0072666	establishment of protein localization to vacuole	2/36	38/13307	0.0047055892	0.0488321742	0.0349679896	aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1900077	negative regulation of cellular response to insulin stim	2/36	38/13307	0.0047055892	0.0488321742	0.0349679896	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0019957	C-C chemokine binding	3/36	21/13229	2.3800403054	0.0043792741	0.0034072155	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0019956	chemokine binding	3/36	27/13229	5.1758813128	0.0047618108	0.0037048413	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0031625	ubiquitin protein ligase binding	6/36	280/13229	9.7279179431	0.0059664563	0.0046420941	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0044389	ubiquitin-like protein ligase binding	6/36	298/13229	0.0001369238	0.0062984972	0.0049004326	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0000981	DNA-binding transcription factor activity, RNA polymer	7/36	493/13229	0.0003119315	0.0114790812	0.0089310930	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0001228	DNA-binding transcription activator activity, RNA polyr	5/36	277/13229	0.0008599775	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0046332	SMAD binding	3/36	73/13229	0.0010099911	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0016493	C-C chemokine receptor activity	2/36	20/13229	0.0013265184	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0004896	cytokine receptor activity	3/36	82/13229	0.0014141913	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0001637	G protein-coupled chemoattractant receptor activity	2/36	21/13229	0.0014636466	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0004950	chemokine receptor activity	2/36	21/13229	0.0014636466	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0070412	R-SMAD binding	2/36	21/13229	0.0014636466	0.0224425821	0.0174610479	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0051087	chaperone binding	3/36	88/13229	0.0017328699	0.0245267741	0.0190826160	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0016504	peptidase activator activity	2/36	29/13229	0.0027912926	0.0366855599	0.0285425409	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0019955	cytokine binding	3/36	110/13229	0.0032713688	0.0390152344	0.0303551023	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0097718	disordered domain specific binding	2/36	32/13229	0.0033926290	0.0390152344	0.0303551023	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0008009	chemokine activity	2/36	35/13229	0.0040490032	0.0438245057	0.0340968694	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0031072	heat shock protein binding	3/36	126/13229	0.0047893520	0.0489578214	0.0380907535	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0061134	peptidase regulator activity	3/36	129/13229	0.0051139754	0.0495248152	0.0385318928	aTGFb vs PBS	Down-regulated genes CD45+
MF	GO:0031681	G-protein beta-subunit binding	1/4	17/13297	0.0051047114	0.0209767442	0.0110403917	aTGFb vs PBS	Down-regulated genes CD45-
MF	GO:0017147	Wnt-protein binding	1/4	32/13297	0.0095926163	0.0209767442	0.0110403917	aTGFb vs PBS	Down-regulated genes CD45-
MF	GO:0005109	frizzled binding	1/4	35/13297	0.0104883721	0.0209767442	0.0110403917	aTGFb vs PBS	Down-regulated genes CD45-
BP	GO:0034341	response to interferon-gamma	22/127	123/13307	2.8071490959	6.9336582669	4.9080785771	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0009617	response to bacterium	34/127	453/13307	1.7386214388	2.1471974769	1.5199211631	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0071346	cellular response to interferon-gamma	19/127	104/13307	1.5705387595	1.2930769119	0.9.1532101036	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0098542	defense response to other organism	28/127	370/13307	8.5624131735	5.2872901346	3.7426758634	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0009615	response to virus	20/127	237/13307	8.6257574130	4.2611241620	3.0162911711	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0019221	cytokine-mediated signaling pathway	20/127	274/13307	1.3186938848	5.4286231595	3.8427202505	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0071222	cellular response to lipopolysaccharide	16/127	160/13307	2.3166185190	8.1743539170	5.7863208421	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0071219	cellular response to molecule of bacterial origin	16/127	167/13307	4.4961751460	1.3881940763	9.8265091021	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0044419	interspecies interaction between organisms	21/127	333/13307	5.7453894346	1.4689227441	1.0397957289	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0051607	defense response to virus	17/127	199/13307	5.9470556444	1.4689227441	1.0397957289	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0002237	response to molecule of bacterial origin	18/127	243/13307	1.5095811739	3.3896959087	2.3994395501	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:1990266	neutrophil migration	13/127	104/13307	1.7147528242	3.5295328966	2.4984249483	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0071216	cellular response to biotic stimulus	16/127	188/13307	2.7573449859	5.2389554732	3.7084615559	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0030593	neutrophil chemotaxis	12/127	87/13307	3.2625777335	5.7561192870	4.0745425680	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0032496	response to lipopolysaccharide	17/127	226/13307	4.5522738844	7.4960776631	5.3061943313	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0035456	response to interferon-beta	10/127	55/13307	8.9121410837	1.3758117798	9.7388594343	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0097530	granulocyte migration	13/127	127/13307	2.2172608558	3.2215495964	2.2804150350	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0007159	leukocyte cell-cell adhesion	18/127	288/13307	2.4972798572	3.4268229152	2.4257203759	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0042742	defense response to bacterium	14/127	158/13307	3.0209110711	3.9271843925	2.7799076394	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0071621	granulocyte chemotaxis	12/127	107/13307	3.8831285695	4.7476122387	3.3606579708	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0035458	cellular response to interferon-beta	9/127	46/13307	4.0364314580	4.7476122387	3.3606579708	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	17/127	261/13307	4.3401333595	4.8727860900	3.4492638805	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0044403	symbiont process	18/127	318/13307	1.2351644561	1.3264592203	0.9395110374	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0060326	cell chemotaxis	16/127	244/13307	1.3353826388	1.3743312991	9.7283796630	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+
BP	GO:0002821	positive regulation of adaptive immune response	12/127	120/13307	1.4878359628	1.4699819313	1.0405454881	aPD-L1+aTGFb vs PBS	Up-regulated genes CD45+

BP	GO:0097529	myeloid leukocyte migration	14/127	180/13307	1.6927102296	1.6080747181	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002478	antigen processing and presentation of exogenous pep	7/127	24/13307	1.8467051855	1.6893932623	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0071356	cellular response to tumor necrosis factor	12/127	124/13307	2.1762669020	1.9197783028	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0030595	leukocyte chemotaxis	14/127	187/13307	2.7851608754	2.3721887456	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0022407	regulation of cell-cell adhesion	18/127	339/13307	3.4108850914	2.8082953919	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0001819	positive regulation of cytokine production	19/127	385/13307	4.0181950754	3.2015941407	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0019730	antimicrobial humoral response	8/127	44/13307	7.3244917297	5.4436710036	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002250	adaptive immune response	18/127	356/13307	7.3548515209	5.4436710036	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0070555	response to interleukin-1	10/127	85/13307	7.4933123127	5.4436710036	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0019884	antigen processing and presentation of exogenous ant	7/127	29/13307	8.0046359809	5.6489859636	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002548	monocyte chemotaxis	8/127	45/13307	8.8374019870	5.9395370954	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0019882	antigen processing and presentation	10/127	87/13307	9.4278434240	5.9395370954	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0034612	response to tumor necrosis factor	12/127	141/13307	9.4965871442	5.9395370954	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:1903706	regulation of hemopoiesis	18/127	362/13307	9.5449614832	5.9395370954	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002824	positive regulation of adaptive immune response base	11/127	113/13307	9.8591506443	5.9395370954	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0006959	humoral immune response	11/127	113/13307	9.8591506443	5.9395370954	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002819	regulation of adaptive immune response	13/127	176/13307	1.2475044720	7.2447073830	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002683	negative regulation of immune system process	19/127	413/13307	1.2612243622	7.2447073830	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0071347	cellular response to interleukin-1	9/127	68/13307	1.5137256734	8.4975054849	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0043901	negative regulation of multi-organism process	12/127	150/13307	1.9120789481	1.0495188893	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0042110	T cell activation	19/127	426/13307	2.0775434964	1.1155505296	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050900	leukocyte migration	16/127	297/13307	2.2265076519	1.1598811900	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0043900	regulation of multi-organism process	17/127	339/13307	2.2540201263	1.1598811900	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	13/127	186/13307	2.4212004990	1.1989081996	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0045088	regulation of innate immune response	15/127	259/13307	2.4269396753	1.1989081996	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0048002	antigen processing and presentation of peptide antige	8/127	52/13307	2.9178081642	1.4131345423	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0061844	antimicrobial humoral immune response mediated by	7/127	35/13307	3.2888133598	1.5621863459	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002697	regulation of immune effector process	17/127	354/13307	4.2500118283	1.9806658898	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050863	regulation of T cell activation	15/127	275/13307	5.3775147435	2.4597150771	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050777	negative regulation of immune response	11/127	136/13307	6.8633249306	3.0822568324	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050868	negative regulation of T cell activation	10/127	109/13307	8.4199903231	3.7138171603	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0051250	negative regulation of lymphocyte activation	11/127	139/13307	8.5959197410	3.7248985544	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0019886	antigen processing and presentation of exogenous pep	5/127	13/13307	8.8567326709	3.7717464995	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0071396	cellular response to lipid	17/127	375/13307	9.7916603282	4.0992205103	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0051249	regulation of lymphocyte activation	17/127	377/13307	1.0569804781	4.3512363016	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0022409	positive regulation of cell-cell adhesion	13/127	215/13307	1.3383062549	5.4190433601	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002460	adaptive immune response based on somatic recombi	14/127	260/13307	1.8048910185	7.1904529287	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	10/127	119/13307	1.9391464352	7.6026852302	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0070098	chemokine-mediated signaling pathway	7/127	45/13307	2.0506285769	7.9141446640	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	12/127	188/13307	2.3235273814	8.8294040494	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:1903708	positive regulation of hemopoiesis	12/127	190/13307	2.6060730274	9.7530308753	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0071674	mononuclear cell migration	8/127	69/13307	2.8311653797	1.0437281325	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050792	regulation of viral process	11/127	158/13307	3.1748874172	1.1532311647	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0022408	negative regulation of cell-cell adhesion	11/127	159/13307	3.3835513900	1.2112133236	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002822	regulation of adaptive immune response based on som	11/127	160/13307	3.6042551356	1.2717871692	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002695	negative regulation of leukocyte activation	11/127	162/13307	4.0841931209	1.4208390153	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0031349	positive regulation of defense response	15/127	325/13307	4.6912153325	1.6093474821	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002495	antigen processing and presentation of peptide antige	5/127	18/13307	5.6746695164	1.9200594117	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050870	positive regulation of T cell activation	11/127	171/13307	7.0158860503	2.3417889924	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002711	positive regulation of T cell mediated immunity	7/127	54/13307	7.4533138268	2.4546246869	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002504	antigen processing and presentation of peptide or poly	5/127	19/13307	7.6425971976	2.4838440892	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0016032	viral process	13/127	251/13307	7.9144416185	2.5387884152	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0002699	positive regulation of immune effector process	12/127	212/13307	8.4416836717	2.6160500798	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:1990868	response to chemokine	7/127	55/13307	8.4730366957	2.6160500798	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:1990869	cellular response to chemokine	7/127	55/13307	8.4730366957	2.6160500798	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0050866	negative regulation of cell activation	11/127	177/13307	9.8814353688	3.0132278223	aPD-L1+aTGFb vs PBS	Up-regulated genes
BP	GO:0060333	interferon-gamma-mediated signaling pathway	5/127	20/13307	1.0112419499	3.0460580686	aPD-L1+aTGFb vs PBS	Up-regulated genes

BP	GO:0032103	positive regulation of response to external stimulus	13/127	260/13307	1.17685752673.5022145674	2.4790873200	Cd74/Cxcl10/Il1b	13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048525	negative regulation of viral process	8/127	84/13307	1.3098908950	3.8517029890	2.7264771637	Rsad2/Oasl1/Ccl	8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902105	regulation of leukocyte differentiation	13/127	264/13307	1.3963494211	4.0576271413	2.8722432055	Irf1/H2-Aa/Cd74	13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002694	regulation of leukocyte activation	17/127	459/13307	1.6657661699	4.7842353951	3.3865821399	Irf1/H2-Aa/Cd74	17	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902107	positive regulation of leukocyte differentiation	10/127	155/13307	2.2387405500	6.3559645501	4.4991507001	Irf1/H2-Aa/Cd74	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001660	fever generation	4/127	11/13307	2.4793717229	6.9591456315	4.9261201337	Il1b/Tnf/Ccl5/Il1r	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051251	positive regulation of lymphocyte activation	12/127	236/13307	2.6046953962	7.2287613805	5.1169710859	Irf1/H2-Aa/Cd74	12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903900	regulation of viral life cycle	9/127	125/13307	2.9759360865	8.1672912598	5.7813214500	Cd74/Rsad2/Oasl	9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050830	defense response to Gram-positive bacterium	7/127	67/13307	3.3027756116	8.9646766602	6.3457608918	Rpl39/Gbp2b/Gb	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0030098	lymphocyte differentiation	14/127	332/13307	3.3547919579	9.0068871044	6.3756400940	Irf1/H2-Aa/Cd74	14	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048247	lymphocyte chemotaxis	6/127	44/13307	3.5203180592	9.2620152472	6.5562358089	Cxcl10/Ccl4/Ccl5,	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002449	lymphocyte mediated immunity	12/127	243/13307	3.5257462153	9.2620152472	6.5562358089	Cd74/H2-Ab1/Rs	12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006935	chemotaxis	16/127	433/13307	3.5623135566	9.2620152472	6.5562358089	Cd74/Cxcl10/Il1b	16	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002521	leukocyte differentiation	17/127	488/13307	3.8111165137	9.7701622107	6.9159341283	Irf1/H2-Aa/Cd74	17	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0030217	T cell differentiation	12/127	245/13307	3.8368653216	9.7701622107	6.9159341283	Irf1/H2-Aa/Cd74	12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042330	taxis	16/127	436/13307	3.8914831221	9.8081258283	6.9428071599	Cd74/Cxcl10/Il1b	16	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045619	regulation of lymphocyte differentiation	10/127	165/13307	3.9321979126	9.8106351963	6.9445834481	Irf1/H2-Aa/Cd74	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050865	regulation of cell activation	17/127	491/13307	4.1365000631	10.000102171	7.2323437945	Irf1/H2-Aa/Cd74	17	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050727	regulation of inflammatory response	13/127	296/13307	4.9371325390	10.000120739	7 8.5467192780	Il1b/Tnf/Nfkbia/I	13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STA	4/127	13/13307	5.2929427204	10.000126972	8 8.9847499832	Irf1/Socs1/Parp1	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044406	adhesion of symbiont to host	4/127	13/13307	5.2929427204	10.000126972	8 8.9847499832	Gbp2b/Gbp2/Ica	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	6/127	48/13307	5.9318587986	10.000140333	5 9.9336917738	Il1b/Tnf/Nfkbia/C	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045580	regulation of T cell differentiation	9/127	136/13307	5.9655975583	10.000140333	5 9.9336917738	Irf1/H2-Aa/Cd74	9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019058	viral life cycle	10/127	174/13307	6.3138445354	10.000147124	4 10.000104143	9 Cd74/Rsad2/Oasl	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045089	positive regulation of innate immune response	11/127	215/13307	6.5468544008	10.000151128	3 10.000106978	1 Irf1/Cd74/Rsad2	11	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	10/127	177/13307	7.3461022428	10.000168008	0 10.000118926	6 Irf1/Cd74/Il1b/Tr	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045785	positive regulation of cell adhesion	14/127	356/13307	7.4900986954	10.000169729	7 10.000120145	3 Irf1/H2-Aa/Cd74	14	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002181	cytoplasmic translation	7/127	76/13307	7.7334838004	10.000173651	8 10.000122921	6 Rpl39/Rpl35a/Rp	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031348	negative regulation of defense response	10/127	179/13307	8.1127114485	10.000180526	1 10.000122787	7 Samhd1/Arg2/Nl	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002709	regulation of T cell mediated immunity	7/127	77/13307	8.4399831789	10.000185891	1 10.000131585	4 Rsad2/Il1b/H2-K	17	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045071	negative regulation of viral genome replication	6/127	51/13307	8.5043332261	10.000185891	1 10.000131585	4 Rsad2/Oasl1/Tnf,	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046631	alpha-beta T cell activation	9/127	144/13307	9.5048111890	10.000205937	5 10.000145775	5 Irf1/H2-Ab1/Rsa	9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002828	regulation of type 2 immune response	5/127	31/13307	1.0188208571	10.000218825	0 10.000154898	0 Irf1/Cd74/Rsad2/	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045069	regulation of viral genome replication	7/127	81/13307	1.1824704987	10.000251784	6 10.000178228	9 Rsad2/Oasl1/Tnf,	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002456	T cell mediated immunity	8/127	113/13307	1.2207218321	10.000255523	9 10.000180875	9 Rsad2/Il1b/H2-K	18	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	8/127	113/13307	1.2207218321	10.000255523	9 10.000180875	9 Rsad2/Il1b/H2-K	18	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031649	heat generation	4/127	16/13307	1.3176918230	10.000273504	10 10.000193603	3 Il1b/Tnf/Ccl5/Il1r	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002262	myeloid cell homeostasis	9/127	152/13307	1.4704254613	10.000302662	5 10.000214243	5 Pde4b/B2m/Slc7	9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0007162	negative regulation of cell adhesion	11/127	236/13307	1.5781432816	10.000322149	9 10.000228037	9 Irf1/H2-Aa/Cd74	11	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002696	positive regulation of leukocyte activation	12/127	282/13307	1.5978083116	10.000323496	6 10.000228987	0 Irf1/H2-Aa/Cd74	12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042129	regulation of T cell proliferation	9/127	155/13307	1.7198487917	10.000345368	0 10.000244473	1 Irf1/H2-Aa/H2-At	9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072676	lymphocyte migration	7/127	86/13307	1.7565858154	10.000349900	5 10.000247681	5 Cxcl10/Ccl4/Icam	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045582	positive regulation of T cell differentiation	7/127	87/13307	1.8952869704	10.000371671	0 10.000263092	1 Irf1/H2-Aa/Cd74	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050729	positive regulation of inflammatory response	8/127	120/13307	1.8959738478	10.000371671	0 10.000263092	1 Il1b/Tnf/Nfkbia/C	8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034340	response to type I interferon	5/127	36/13307	2.1758239550	10.000421233	1 10.000298175	2 Samhd1/Zbp1/St	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048245	eosinophil chemotaxis	4/127	18/13307	2.1829085614	10.000421233	1 10.000298175	2 Ccl4/Ccl5/Ccl2/C	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050670	regulation of lymphocyte proliferation	10/127	202/13307	2.3275395855	10.000445660	6 10.000315466	6 Irf1/H2-Aa/Cd74	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	6/127	61/13307	2.4255600581	10.000457338	4 10.000323732	8 Irf1/Socs1/Tnf/C	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	6/127	61/13307	2.4255600581	10.000457338	4 10.000323732	8 Irf1/Cd274/Arg2/	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042092	type 2 immune response	5/127	37/13307	2.4966648024	10.000467178	9 10.000330698	5 Irf1/Cd74/Rsad2/	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032944	regulation of mononuclear cell proliferation	10/127	204/13307	2.5333741093	10.000470837	10.000333037	9 Irf1/H2-Aa/Cd74	10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050867	positive regulation of cell activation	12/127	296/13307	2.5826204208	10.000476050	1 10.000336978	2 Irf1/H2-Aa/Cd74	12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042130	negative regulation of T cell proliferation	6/127	62/13307	2.6646239036	10.000487527	4 10.000345102	5 H2-Aa/H2-Ab1/C	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002726	positive regulation of T cell cytokine production	4/127	19/13307	2.7446372519	10.000498474	5 10.000352851	5 Rsad2/Il1b/Nlrp3	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035690	cellular response to drug	11/127	251/13307	2.7951344157	10.000503940	2 10.000356720	5 Il1b/Ccl4/Tnf/Nfe	11	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	7/127	93/13307	2.9308418259	10.000517084	2 10.000366024	6 Cd74/Samhd1/Irf	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	7/127	93/13307	2.9308418259	10.000517084	2 10.000366024	6 Irf1/Rsad2/Cd27	7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:2000379	positive regulation of reactive oxygen species metabol	7/127	93/13307	2.9308418259	0.0005170842	0.0003660246	Il1b/Icam1/Tnf/N	7
BP	GO:0014070	response to organic cyclic compound	15/127	458/13307	3.0483735465	0.0005340058	0.0003780028	Dnaja1/Il1b/Socs	15
BP	GO:0007260	tyrosine phosphorylation of STAT protein	6/127	65/13307	3.4976629970	0.0006081201	0.0004304655	Irf1/Socs1/Tnf/Cx	6
BP	GO:0070663	regulation of leukocyte proliferation	10/127	212/13307	3.5206954699	0.0006081201	0.0004304655	Irf1/H2-Aa/Cd74,	10
BP	GO:0019079	viral genome replication	7/127	97/13307	3.8509413970	0.0006605434	0.0004675740	Rsad2/Oasl1/Tnf,	7
BP	GO:0046634	regulation of alpha-beta T cell activation	7/127	98/13307	4.1146312017	0.0007009061	0.0004961453	Irf1/H2-Ab1/Cd2	7
BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	5/127	41/13307	4.1632596444	0.0007016517	0.0004966731	Il1b/Icam1/Tnf/S	5
BP	GO:0072677	eosinophil migration	4/127	21/13307	4.1758218723	0.0007016517	0.0004966731	Ccl4/Ccl5/Ccl2/Cx	4
BP	GO:0002443	leukocyte mediated immunity	12/127	313/13307	4.4574940408	0.0007439196	0.0005265930	Cd74/H2-Ab1/Rs	12
BP	GO:0002831	regulation of response to biotic stimulus	8/127	136/13307	4.6762522712	0.0007621176	0.0005394746	Cd274/Il1b/Arg2,	8
BP	GO:0002688	regulation of leukocyte chemotaxis	7/127	100/13307	4.6865667515	0.0007621176	0.0005394746	Cd74/Cxcl10/Il1b	7
BP	GO:0045621	positive regulation of lymphocyte differentiation	7/127	100/13307	4.6865667515	0.0007621176	0.0005394746	Irf1/H2-Aa/Cd74,	7
BP	GO:1904407	positive regulation of nitric oxide metabolic process	5/127	42/13307	4.6899545645	0.0007621176	0.0005394746	Il1b/Icam1/Tnf/S	5
BP	GO:0090025	regulation of monocyte chemotaxis	4/127	22/13307	5.0661926631	0.0008178755	0.0005789436	Cxcl10/Ccl5/Ccl2,	4
BP	GO:1903901	negative regulation of viral life cycle	6/127	71/13307	5.7881684029	0.0009283620	0.0006571529	Rsad2/Oasl1/Tnf,	6
BP	GO:0045581	negative regulation of T cell differentiation	5/127	44/13307	5.8968274853	0.0009396879	0.0006651701	Irf1/Cd74/Socs1/	5
BP	GO:0060759	regulation of response to cytokine stimulus	7/127	104/13307	6.0266334537	0.0009456842	0.0006694146	Cd74/Samhd1/Irf	7
BP	GO:0002705	positive regulation of leukocyte mediated immunity	8/127	141/13307	6.0448762954	0.0009456842	0.0006694146	Rsad2/Il1b/H2-Ki	8
BP	GO:0046426	negative regulation of JAK-STAT cascade	4/127	23/13307	6.0876031485	0.0009456842	0.0006694146	Irf1/Socs1/Parp1	4
BP	GO:1904893	negative regulation of STAT cascade	4/127	23/13307	6.0876031485	0.0009456842	0.0006694146	Irf1/Socs1/Parp1	4
BP	GO:0002718	regulation of cytokine production involved in immune	6/127	75/13307	7.8888173815	0.0012028011	0.0008514181	Cd74/Rsad2/Il1b,	6
BP	GO:0032945	negative regulation of mononuclear cell proliferation	6/127	75/13307	7.8888173815	0.0012028011	0.0008514181	H2-Aa/H2-Ab1/C	6
BP	GO:0050672	negative regulation of lymphocyte proliferation	6/127	75/13307	7.8888173815	0.0012028011	0.0008514181	H2-Aa/H2-Ab1/C	6
BP	GO:0001818	negative regulation of cytokine production	10/127	234/13307	8.0866360856	0.0012253982	0.0008674137	Cd274/Arg2/Gbp	10
BP	GO:0002440	production of molecular mediator of immune response	9/127	190/13307	8.4937745385	0.0012714923	0.0009000420	Cd74/H2-Ab1/Sa	9
BP	GO:0042098	T cell proliferation	9/127	190/13307	8.4937745385	0.0012714923	0.0009000420	Irf1/H2-Aa/H2-Al	9
BP	GO:0006953	acute-phase response	4/127	25/13307	8.5690287239	0.0012750301	0.0009025463	Il1b/Tnf/Ccl5/Il1r	4
BP	GO:0045824	negative regulation of innate immune response	5/127	48/13307	9.0183457894	0.0013338511	0.0009441835	Samhd1/Acod1/F	5
BP	GO:0031652	positive regulation of heat generation	3/127	10/13307	9.7011570609	0.0013931312	0.0009861457	Il1b/Tnf/Ccl5	3
BP	GO:0042090	interleukin-12 biosynthetic process	3/127	10/13307	9.7011570609	0.0013931312	0.0009861457	Irf1/Rel/Nfkb1	3
BP	GO:0042359	vitamin D metabolic process	3/127	10/13307	9.7011570609	0.0013931312	0.0009861457	Il1b/Tnf/Nfkb1	3
BP	GO:0045075	regulation of interleukin-12 biosynthetic process	3/127	10/13307	9.7011570609	0.0013931312	0.0009861457	Irf1/Rel/Nfkb1	3
BP	GO:0051956	negative regulation of amino acid transport	3/127	10/13307	9.7011570609	0.0013931312	0.0009861457	Il1b/Tnf/Il1rn	3
BP	GO:0070664	negative regulation of leukocyte proliferation	6/127	78/13307	9.8310645392	0.0014036259	0.0009935745	H2-Aa/H2-Ab1/C	6
BP	GO:0002720	positive regulation of cytokine production involved in i	5/127	49/13307	9.9669409609	0.0014148473	0.0010015177	Cd74/Rsad2/Il1b,	5
BP	GO:0002690	positive regulation of leukocyte chemotaxis	6/127	79/13307	0.0001055678	0.0014900152	0.0010547262	Cd74/Cxcl10/Il1b	6
BP	GO:0009636	response to toxic substance	10/127	242/13307	0.0001068466	0.0014994959	0.0010613473	Ccl4/Tnf/Nfe2l2/	10
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylatio	5/127	50/13307	0.0001099035	0.0015336817	0.0010856362	Irf1/Socs1/Parp1	5
BP	GO:0051955	regulation of amino acid transport	4/127	27/13307	0.0001171399	0.0016254806	0.0011506172	Il1b/Arg2/Tnf/Il1	4
BP	GO:0045620	negative regulation of lymphocyte differentiation	5/127	51/13307	0.0001209251	0.0016686320	0.0011811625	Irf1/Cd74/Socs1/	5
BP	GO:0007259	JAK-STAT cascade	7/127	117/13307	0.0001270182	0.0017429728	0.0012337856	Irf1/Socs1/Tnf/Cx	7
BP	GO:0072683	T cell extravasation	3/127	11/13307	0.0001324611	0.0017920963	0.0012685583	Icam1/Ccl5/Ccl2	3
BP	GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2	3/127	11/13307	0.0001324611	0.0017920963	0.0012685583	Cd74/Tnf/Ccl5	3
BP	GO:1903428	positive regulation of reactive oxygen species biosynth	5/127	52/13307	0.0001327747	0.0017920963	0.0012685583	Il1b/Icam1/Tnf/S	5
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di	4/127	28/13307	0.0001356582	0.0018194897	0.0012879490	Irf1/Socs1/Nlrp3,	4
BP	GO:1902532	negative regulation of intracellular signal transduction	14/127	464/13307	0.0001362775	0.0018194897	0.0012879490	Irf1/Cd74/Dnaja1	14
BP	GO:0002706	regulation of lymphocyte mediated immunity	8/127	159/13307	0.0001402436	0.0018623751	0.0013183060	Rsad2/Il1b/H2-Ki	8
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	8/127	160/13307	0.0001464587	0.0019345085	0.0013693666	Cd74/Il1b/Ccl4/Ix	8
BP	GO:1901652	response to peptide	11/127	302/13307	0.0001474426	0.0019371458	0.0013712334	Irf1/Il1b/Icam1/S	11
BP	GO:0097696	STAT cascade	7/127	120/13307	0.0001488033	0.0019446793	0.0013765661	Irf1/Socs1/Tnf/Cx	7
BP	GO:0002526	acute inflammatory response	6/127	85/13307	0.0001585435	0.0020610667	0.0014589524	Il1b/Icam1/Tnf/N	6
BP	GO:0030656	regulation of vitamin metabolic process	3/127	12/13307	0.0001753843	0.0022445559	0.0015888375	Il1b/Tnf/Nfkb1	3
BP	GO:0031650	regulation of heat generation	3/127	12/13307	0.0001753843	0.0022445559	0.0015888375	Il1b/Tnf/Ccl5	3
BP	GO:0042362	fat-soluble vitamin biosynthetic process	3/127	12/13307	0.0001753843	0.0022445559	0.0015888375	Il1b/Tnf/Nfkb1	3
BP	GO:0002724	regulation of T cell cytokine production	4/127	30/13307	0.0001789138	0.0022779234	0.0016124571	Rsad2/Il1b/Nlrp3	4
BP	GO:0046651	lymphocyte proliferation	10/127	260/13307	0.0001920703	0.0024328910	0.0017221529	Irf1/H2-Aa/Cd74,	10
BP	GO:0050663	cytokine secretion	9/127	212/13307	0.0001949385	0.0024566237	0.0017389524	Cd274/Il1b/Arg2,	9

aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+							

BP	GO:0060337	type I interferon signaling pathway	4/127	31/13307	0.0002039102	0.0025111528	0.0017775516	Samhd1/Zbp1/St 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071357	cellular response to type I interferon	4/127	31/13307	0.0002039102	0.0025111528	0.0017775516	Samhd1/Zbp1/St 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045639	positive regulation of myeloid cell differentiation	6/127	89/13307	0.0002042181	0.0025111528	0.0017775516	Cd74/Tnf/Ccl5/St6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903426	regulation of reactive oxygen species biosynthetic proc	6/127	89/13307	0.0002042181	0.0025111528	0.0017775516	Il1b/Arg2/Icam1/6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032943	mononuclear cell proliferation	10/127	262/13307	0.0002043488	0.0025111528	0.0017775516	Irf1/H2-Aa/Cd74,10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002922	positive regulation of humoral immune response	3/127	13/13307	0.0002264117	0.0027685000	0.0019597181	Il1b/Tnf/Acod1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	9/127	217/13307	0.0002319756	0.0028204433	0.0019964868	Irf1/Cd74/Icam1/9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002687	positive regulation of leukocyte migration	7/127	129/13307	0.0002329434	0.0028204433	0.0019964868	Cd74/Cxcl10/Il1b 7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0097237	cellular response to toxic substance	7/127	130/13307	0.0002442740	0.0029419964	0.0020825297	Tnf/Nfe2l2/Txn1,7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071417	cellular response to organonitrogen compound	12/127	375/13307	0.0002453648	0.0029419964	0.0020825297	Irf1/Il1b/Icam1/S 12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	4/127	33/13307	0.0002613025	0.0031176716	0.0022068836	H2-K1/H2-D1/Hs 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045428	regulation of nitric oxide biosynthetic process	5/127	60/13307	0.0002625407	0.0031176716	0.0022068836	Il1b/Icam1/Tnf/S 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1904950	negative regulation of establishment of protein localiz	8/127	175/13307	0.0002704814	0.0031965987	0.0022627532	Dnaja1/Rsad2/Il18	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002367	cytokine production involved in immune response	6/127	94/13307	0.0002752582	0.0032375615	0.0022917493	Cd74/Rsad2/Il1b,6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000377	regulation of reactive oxygen species metabolic proces	8/127	176/13307	0.0002811253	0.0032874479	0.0023270620	Il1b/Arg2/Icam1/8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042274	ribosomal small subunit biogenesis	5/127	61/13307	0.0002838162	0.0032874479	0.0023270620	Rps27/Rps21/Rpl5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060330	regulation of response to interferon-gamma	3/127	14/13307	0.0002861543	0.0032874479	0.0023270620	Irgm1/Socs1/Parj3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060334	regulation of interferon-gamma-mediated signaling pa	3/127	14/13307	0.0002861543	0.0032874479	0.0023270620	Irgm1/Socs1/Parj3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 product	3/127	14/13307	0.0002861543	0.0032874479	0.0023270620	Cd74/Tnf/Ccl5 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032768	regulation of monooxygenase activity	4/127	34/13307	0.0002939686	0.0033460953	0.0023685763	Il1b/Arg2/Tnf/Nf 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	4/127	34/13307	0.0002939686	0.0033460953	0.0023685763	Irf1/Socs1/Nlrp3,4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048872	homeostasis of number of cells	10/127	276/13307	0.0003102037	0.0035146938	0.0024879209	Cd74/Pde4b/B2m 10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002224	toll-like receptor signaling pathway	6/127	97/13307	0.0003263889	0.0036811903	0.0026057776	Irf1/Rsad2/Tnf/N 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070661	leukocyte proliferation	10/127	278/13307	0.0003285285	0.0036884794	0.0026109372	Irf1/H2-Aa/Cd74,10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	5/127	63/13307	0.0003302674	0.0036912242	0.0026128802	H2-K1/H2-D1/Hs 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001906	cell killing	7/127	137/13307	0.0003366293	0.0037453806	0.0026512155	H2-K1/H2-D1/Hs 7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035821	modification of morphology or physiology of other org	6/127	98/13307	0.0003449917	0.0038212087	0.0027048914	Ccl4/Hspa8/Ccl5/6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002685	regulation of leukocyte migration	8/127	182/13307	0.0003524299	0.0038861693	0.0027508746	Cd74/Cxcl10/Il1b 8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072567	chemokine (C-X-C motif) ligand 2 production	3/127	15/13307	0.0003552039	0.0038993498	0.0027602046	Cd74/Tnf/Ccl5 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046425	regulation of JAK-STAT cascade	6/127	99/13307	0.0003644150	0.0039827666	0.0028192522	Irf1/Socs1/Tnf/Cr6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046635	positive regulation of alpha-beta T cell activation	5/127	65/13307	0.0003822586	0.0041593785	0.0029442692	Irf1/H2-Ab1/Socs5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903707	negative regulation of hemopoiesis	7/127	141/13307	0.0004008273	0.0043393382	0.0030716560	Irf1/Cd74/Socs1/7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043410	positive regulation of MAPK cascade	12/127	396/13307	0.0004023111	0.0043393382	0.0030716560	Cd74/Il1b/Ccl4/Ic12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1901653	cellular response to peptide	9/127	234/13307	0.0004043632	0.0043425099	0.0030739011	Irf1/Il1b/Icam1/S9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046632	alpha-beta T cell differentiation	6/127	102/13307	0.0004278623	0.0045552584	0.0032244979	Irf1/Rsad2/Socs1 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903409	reactive oxygen species biosynthetic process	6/127	102/13307	0.0004278623	0.0045552584	0.0032244979	Il1b/Arg2/Icam1/6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002830	positive regulation of type 2 immune response	3/127	16/13307	0.0004341332	0.0045630175	0.0032299902	Cd74/Rsad2/Nlrp3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019430	removal of superoxide radicals	3/127	16/13307	0.0004341332	0.0045630175	0.0032299902	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051953	negative regulation of amine transport	3/127	16/13307	0.0004341332	0.0045630175	0.0032299902	Il1b/Tnf/Il1rn 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006809	nitric oxide biosynthetic process	5/127	67/13307	0.0004402085	0.0046072679	0.0032613134	Il1b/Icam1/Tnf/S 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1904892	regulation of STAT cascade	6/127	103/13307	0.0004508236	0.0046756886	0.0033097459	Irf1/Socs1/Tnf/Cr6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045637	regulation of myeloid cell differentiation	8/127	189/13307	0.0004535959	0.0046756886	0.0033097459	Cd74/Tnf/Nfkbia,8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001914	regulation of T cell mediated cytotoxicity	4/127	38/13307	0.0004543179	0.0046756886	0.0033097459	H2-K1/H2-D1/Hs 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0048246	macrophage chemotaxis	4/127	38/13307	0.0004543179	0.0046756886	0.0033097459	Cd5l/Ccl3/Ccl2/Sl 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051341	regulation of oxidoreductase activity	5/127	69/13307	0.0005045478	0.0051710923	0.0036604237	Il1b/Arg2/Tnf/Nf 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0090026	positive regulation of monocyte chemotaxis	3/127	17/13307	0.0005234965	0.0053211382	0.0037666356	Cxcl10/Ccl5/Ccl2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	3/127	17/13307	0.0005234965	0.0053211382	0.0037666356	Irf1/Cd274/Socs13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046209	nitric oxide metabolic process	5/127	70/13307	0.0005392512	0.0054588140	0.0038640912	Il1b/Icam1/Tnf/S 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002369	T cell cytokine production	4/127	40/13307	0.0005542718	0.0054427187	0.0039234842	Rsad2/Il1b/Nlrp3 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043331	response to dsRNA	4/127	40/13307	0.0005542718	0.0054427187	0.0039234842	Nfkbia/Stat1/Nfk 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046636	negative regulation of alpha-beta T cell activation	4/127	40/13307	0.0005542718	0.0054427187	0.0039234842	Irf1/Cd274/Arg2/4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	7/127	150/13307	0.0005813063	0.0057896236	0.0040982590	Cd74/Il1b/Tnf/St 7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0015800	acidic amino acid transport	4/127	41/13307	0.0006096923	0.0059723269	0.0042275879	Il1b/Tnf/Slc7a11,4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1900407	regulation of cellular response to oxidative stress	5/127	72/13307	0.0006140070	0.0059723269	0.0042275879	Tnf/Nfe2l2/Txn1,5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0000028	ribosomal small subunit assembly	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Rps27/Rpl38/Rps3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002523	leukocyte migration involved in inflammatory response	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	S100a8/Ccl2/Slar 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002577	regulation of antigen processing and presentation	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Cd74/H2-Ab1/Fgl 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:0009110	vitamin biosynthetic process	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Il1b/Tnf/Nfkb1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032891	negative regulation of organic acid transport	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Il1b/Tnf/Il1rn 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051770	positive regulation of nitric-oxide synthase biosynthetic	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Nampt/Stat1/Ccl 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071450	cellular response to oxygen radical	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071451	cellular response to superoxide	3/127	18/13307	0.0006238300	0.0059723269	0.0042275879	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050688	regulation of defense response to virus	5/127	73/13307	0.0006541739	0.0062386470	0.0044161059	Il1b/Gbp4/Ccl5/F 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050702	interleukin-1 beta secretion	4/127	42/13307	0.0006689336	0.0063305218	0.0044811407	Arg2/Nlrp3/Gbp5 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903202	negative regulation of oxidative stress-induced cell de	4/127	42/13307	0.0006689336	0.0063305218	0.0044811407	Nfe2l2/Txnl1/Slc7 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032611	interleukin-1 beta production	5/127	74/13307	0.0006962775	0.0065391849	0.0046288456	Il1b/Arg2/Nlrp3/S 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001057	reactive nitrogen species metabolic process	5/127	74/13307	0.0006962775	0.0065391849	0.0046288456	Il1b/Icam1/Tnf/S 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1901699	cellular response to nitrogen compound	12/127	422/13307	0.0007074805	0.0066192306	0.0046855069	Irf1/Il1b/Icam1/S 12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001961	positive regulation of cytokine-mediated signaling path	4/127	43/13307	0.0007321404	0.0067232749	0.0047591560	Cd74/Irgm1/Zbp: 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1900408	negative regulation of cellular response to oxidative st	4/127	43/13307	0.0007321404	0.0067232749	0.0047591560	Nfe2l2/Txnl1/Slc7 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002428	antigen processing and presentation of peptide antigen	3/127	19/13307	0.0007356520	0.0067232749	0.0047591560	H2-K1/H2-D1/B2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0098869	cellular oxidant detoxification	3/127	19/13307	0.0007356520	0.0067232749	0.0047591560	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1901623	regulation of lymphocyte chemotaxis	3/127	19/13307	0.0007356520	0.0067232749	0.0047591560	Cxcl10/Ccl4/Ccl5 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071236	cellular response to antibiotic	6/127	113/13307	0.0007373009	0.0067232749	0.0047591560	Crip1/Nfe2l2/Txn 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031343	positive regulation of cell killing	5/127	75/13307	0.0007403768	0.0067232749	0.0047591560	H2-K1/H2-D1/Hsj 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	5/127	75/13307	0.0007403768	0.0067232749	0.0047591560	Irf1/Rsad2/Socs1 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001234	negative regulation of apoptotic signaling pathway	8/127	205/13307	0.0007747884	0.0070099907	0.0049621115	Cd74/Dnaja1/Il1b/ 8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043506	regulation of JUN kinase activity	5/127	76/13307	0.0007865310	0.0070902615	0.0050189321	Dnaja1/Il1b/Tnf/: 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071675	regulation of mononuclear cell migration	4/127	44/13307	0.0007994577	0.0071805837	0.0050828679	Cxcl10/Ccl5/Ccl2, 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071407	cellular response to organic cyclic compound	10/127	312/13307	0.0008079330	0.0072304157	0.0051181421	Dnaja1/Il1b/Socs 10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002703	regulation of leukocyte mediated immunity	8/127	207/13307	0.0008253435	0.0073595615	0.0052095596	Rsad2/Il1b/H2-K1 8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032479	regulation of type I interferon production	5/127	77/13307	0.0008348001	0.0073905245	0.0052314772	Irf1/Gbp4/Rel/Ac 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032642	regulation of chemokine production	5/127	77/13307	0.0008348001	0.0073905245	0.0052314772	Cd74/Il1b/Arg2/15	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006775	fat-soluble vitamin metabolic process	3/127	20/13307	0.0008594632	0.0075279229	0.0053287364	Il1b/Tnf/Nfkb1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032897	negative regulation of viral transcription	3/127	20/13307	0.0008594632	0.0075279229	0.0053287364	Cd4/Ccl5/Ifitm3 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034114	regulation of heterotypic cell-cell adhesion	3/127	20/13307	0.0008594632	0.0075279229	0.0053287364	Il1b/Tnf/Il1rn 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	4/127	45/13307	0.0008710306	0.0076022812	0.0053813718	Irf1/Socs1/Nlrp3, 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902882	regulation of response to oxidative stress	5/127	79/13307	0.0009379254	0.0081573097	0.0057742558	Tnf/Nfe2l2/Txn1,5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071622	regulation of granulocyte chemotaxis	4/127	46/13307	0.0009470046	0.0081786762	0.0057893804	Cd74/Il1b/Ccl5/C 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902883	negative regulation of response to oxidative stress	4/127	46/13307	0.0009470046	0.0081786762	0.0057893804	Nfe2l2/Txn1/Slc7 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0018108	peptidyl-tyrosine phosphorylation	9/127	264/13307	0.0009600715	0.0082626369	0.0058488131	Irf1/Cd74/Icam1/9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050921	positive regulation of chemotaxis	6/127	119/13307	0.0009667558	0.0082912742	0.0058690844	Cd74/Cxcl10/Il1b 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042136	neurotransmitter biosynthetic process	5/127	80/13307	0.0009929042	0.0084810212	0.0060033992	Il1b/Icam1/Tnf/S 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0000303	response to superoxide	3/127	21/13307	0.0009957474	0.0084810212	0.0060033992	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentia	4/127	47/13307	0.0010275253	0.0087216065	0.0061737006	Irf1/Socs1/Nlrp3,4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0018212	peptidyl-tyrosine modification	9/127	267/13307	0.0010394054	0.0087922307	0.0062236928	Irf1/Cd74/Icam1/9	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032602	chemokine production	5/127	81/13307	0.0010502427	0.0088234681	0.0062458046	Cd74/Il1b/Arg2/15	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032606	type I interferon production	5/127	81/13307	0.0010502427	0.0088234681	0.0062458046	Irf1/Gbp4/Rel/Ac 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034101	erythrocyte homeostasis	6/127	121/13307	0.0010543156	0.0088276601	0.0062487719	B2m/Stat1/Klf2/I 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	5/127	82/13307	0.0011100035	0.0092540854	0.0065506225	H2-K1/H2-D1/Hsj 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050701	interleukin-1 secretion	4/127	48/13307	0.0011127382	0.0092540854	0.0065506225	Arg2/Nlrp3/Gbp5 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0000305	response to oxygen radical	3/127	22/13307	0.0011449714	0.0093880095	0.0066454224	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002475	antigen processing and presentation via MHC class Ib	3/127	22/13307	0.0011449714	0.0093880095	0.0066454224	H2-K1/H2-D1/B2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002827	positive regulation of T-helper 1 type immune respons	3/127	22/13307	0.0011449714	0.0093880095	0.0066454224	Irf1/H2-Ab1/Il1b 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071677	positive regulation of mononuclear cell migration	3/127	22/13307	0.0011449714	0.0093880095	0.0066454224	Cxcl10/Ccl5/Ccl2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050728	negative regulation of inflammatory response	6/127	123/13307	0.0011478457	0.0093880095	0.0066454224	Nlrp3/Acod1/Soc 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002673	regulation of acute inflammatory response	4/127	49/13307	0.0012027887	0.0098049117	0.0069405320	Il1b/Tnf/Nlrp3/Ci 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051224	negative regulation of protein transport	7/127	170/13307	0.0012140259	0.0098639604	0.0069823304	Rsad2/Il1b/Arg2/ 7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006835	dicarboxylic acid transport	4/127	50/13307	0.0012978222	0.0103850060	0.0073511591	Il1b/Tnf/Slc7a11, 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060760	positive regulation of response to cytokine stimulus	4/127	50/13307	0.0012978222	0.0103850060	0.0073511591	Cd74/Irgm1/Zbp: 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1905517	macrophage migration	4/127	50/13307	0.0012978222	0.0103850060	0.0073511591	Ccl5/Ccl3/Ccl2/Sl 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002675	positive regulation of acute inflammatory response	3/127	23/13307	0.0013075857	0.0103850060	0.0073511591	Il1b/Tnf/Ccl5 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035743	CD4-positive, alpha-beta T cell cytokine production	3/127	23/13307	0.0013075857	0.0103850060	0.0073511591	Rsad2/Il1b/Nlrp3 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051767	nitric-oxide synthase biosynthetic process	3/127	23/13307	0.0013075857	0.0103850060	0.0073511591	Nampt/Stat1/Ccl 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:0051769	regulation of nitric-oxide synthase biosynthetic proces	3/127	23/13307	0.00130758570.01038500600.00735115910	Nampt/Stat1/Ccl 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002792	negative regulation of peptide secretion	6/127	127/13307	0.00135388850.01071828470.00758707470	Cd74/Rsad2/Il1b,6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050920	regulation of chemotaxis	7/127	175/13307	0.00143528010.01132633190.00801748870	Cd74/Cxcl10/Il1b 7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002483	antigen processing and presentation of endogenous pe	3/127	24/13307	0.00148402460.01159981310.00821107590	H2-K1/H2-D1/B2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019885	antigen processing and presentation of endogenous pe	3/127	24/13307	0.00148402460.01159981310.00821107590	H2-K1/H2-D1/B2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1903792	negative regulation of anion transport	3/127	24/13307	0.00148402460.01159981310.00821107590	Il1b/Tnf/Il1rn 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032890	regulation of organic acid transport	4/127	52/13307	0.00150341780.01171432790.00829213660	Il1b/Arg2/Tnf/Il1 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002221	pattern recognition receptor signaling pathway	6/127	130/13307	0.00152611050.01181659250.00836452590	Irf1/Rsad2/Tnf/N6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002700	regulation of production of molecular mediator of imm	6/127	130/13307	0.00152611050.01181659250.00836452590	Cd74/Rsad2/Il1b,6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032612	interleukin-1 production	5/127	89/13307	0.00160144060.01232291940.00872293590	Il1b/Arg2/Nlrp3/5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000106	regulation of leukocyte apoptotic process	5/127	89/13307	0.00160144060.01232291940.00872293590	Cd74/Cd274/Arg 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002758	innate immune response-activating signal transductior	6/127	132/13307	0.00164987390.01265586540.00895861600	Irf1/Rsad2/Tnf/N6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032480	negative regulation of type I interferon production	3/127	25/13307	0.00167470660.01276705370.00903732200	Gbp4/Rel/Acod1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0036037	CD8-positive, alpha-beta T cell activation	3/127	25/13307	0.00167470660.01276705370.00903732200	Irf1/Cd274/Socs13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072678	T cell migration	4/127	54/13307	0.00173068030.01315317030.00931063960	Cxcl10/Icam1/Ccl 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	8/127	233/13307	0.00175888890.01332655140.00943336960	Cd74/Il1b/Ccl4/Ic8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002702	positive regulation of production of molecular mediate	5/127	91/13307	0.00176734810.01334969410.00944975150	Cd74/Rsad2/Il1b,5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001913	T cell mediated cytotoxicity	4/127	55/13307	0.00185279560.01384851580.00980284880	H2-K1/H2-D1/Hs	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902106	negative regulation of leukocyte differentiation	5/127	92/13307	0.00185484910.01384851580.00980284880	Irf1/Cd74/Socs1/ 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling patl	5/127	92/13307	0.00185484910.01384851580.00980284880	Cd74/Dnaja1/Nfe 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072593	reactive oxygen species metabolic process	8/127	235/13307	0.00185581320.01384851580.00980284880	Il1b/Arg2/Icam1/8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019883	antigen processing and presentation of endogenous ar	3/127	26/13307	0.00188003460.01398700470.00990088000	H2-K1/H2-D1/B2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050707	regulation of cytokine secretion	7/127	185/13307	0.00197156020.01462388520.01035170390	Cd274/Il1b/Arg2,7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002791	regulation of peptide secretion	11/127	413/13307	0.00199034380.01465816590.01037596990	Cd74/Rsad2/Cd2 11	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001659	temperature homeostasis	6/127	137/13307	0.00199269540.01465816590.01037596990	Il1b/Tnf/Ccl5/Kdr 6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0030099	myeloid cell differentiation	10/127	352/13307	0.00199398530.01465816590.01037596990	Cd74/Tnf/Nfkbia,10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0009306	protein secretion	12/127	479/13307	0.00208572880.01528709250.01082116370	Rsad2/Cd274/Il1l12	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032722	positive regulation of chemokine production	4/127	57/13307	0.00211470700.01540804240.01090677960	Cd74/Il1b/Tnf/Cc 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045123	cellular extravasation	4/127	57/13307	0.00211470700.01540804240.01090677960	Icam1/Tnf/Ccl5/C 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046677	response to antibiotic	7/127	188/13307	0.00215943660.01568767220.01110471910	Crip1/Nfe2l2/Txn 7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042035	regulation of cytokine biosynthetic process	5/127	96/13307	0.00223684450.01620236330.01146904990	Irf1/Il1b/Tnf/Rel/5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051048	negative regulation of secretion	7/127	190/13307	0.00229218640.01655467980.01171844160	Cd74/Rsad2/Il1b,7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0010758	regulation of macrophage chemotaxis	3/127	28/13307	0.00233616500.01656579880.01172631230	Ccl5/Ccl2/Slamf8 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031640	killing of cells of other organism	3/127	28/13307	0.00233616500.01656579880.01172631230	Rpl30/Ccl2/Rps13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044364	disruption of cells of other organism	3/127	28/13307	0.00233616500.01656579880.01172631230	Rpl30/Ccl2/Rps13	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045589	regulation of regulatory T cell differentiation	3/127	28/13307	0.00233616500.01656579880.01172631230	Irf1/Socs1/Ctla4 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046885	regulation of hormone biosynthetic process	3/127	28/13307	0.00233616500.01656579880.01172631230	Il1b/Tnf/Nfkb1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001024	negative regulation of response to drug	3/127	28/13307	0.00233616500.01656579880.01172631230	Tnf/Nfe2l2/Txn1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0003158	endothelium development	5/127	97/13307	0.00234067360.01656579880.01172631230	Cxcl10/Il1b/Icam 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0001933	negative regulation of protein phosphorylation	10/127	360/13307	0.00234879140.01657575640.01173336090	Irf1/Dnaja1/Il1b/ 10	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002763	positive regulation of myeloid leukocyte differentiatior	4/127	59/13307	0.00240113400.01689686900.01196066450	Cd74/Tnf/Ccl5/Ci 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043434	response to peptide hormone	8/127	246/13307	0.00246694620.01726163520.01221886900	Irf1/Il1b/Socs1/S 8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070371	ERK1 and ERK2 cascade	8/127	246/13307	0.00246694620.01726163520.01221886900	Cd74/Il1b/Ccl4/Ic8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071375	cellular response to peptide hormone stimulus	7/127	193/13307	0.00250303460.01746467700.01236259470	Irf1/Il1b/Socs1/N7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034121	regulation of toll-like receptor signaling pathway	4/127	60/13307	0.00255389060.01766977580.01250777650	Irf1/Rsad2/Acod1 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051952	regulation of amine transport	4/127	60/13307	0.00255389060.01766977580.01250777650	Il1b/Arg2/Tnf/Il1 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070228	regulation of lymphocyte apoptotic process	4/127	60/13307	0.00255389060.01766977580.01250777650	Cd74/Cd274/Arg 4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002825	regulation of T-helper 1 type immune response	3/127	29/13307	0.00258769870.01775448850.01256774150	Irf1/Il2-Ab1/Il1b 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060142	regulation of syncytium formation by plasma membrar	3/127	29/13307	0.00258769870.01775448850.01256774150	Cxcl10/Cxcl9/Sta 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1990748	cellular detoxification	3/127	29/13307	0.00258769870.01775448850.01256774150	Tnf/Nfe2l2/Sod2 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032649	regulation of interferon-gamma production	5/127	100/13307	0.00267322250.01823994390.01291137730	Cd274/Il1b/Tnf/F 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signa	5/127	100/13307	0.00267322250.01823994390.01291137730	Cd74/Il1b/Tnf/Pe 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043405	regulation of MAP kinase activity	8/127	250/13307	0.00272467060.01853976970.01312361280	Cd74/Dnaja1/Il1l8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0006865	amino acid transport	5/127	101/13307	0.00279131610.01888918080.01337094790	Il1b/Arg2/Tnf/Slc 5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0031341	regulation of cell killing	5/127	101/13307	0.00279131610.01888918080.01337094790	H2-K1/H2-D1/Hs	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002920	regulation of humoral immune response	3/127	30/13307	0.00285534150.01921714850.01360310410	Il1b/Tnf/Acod1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045672	positive regulation of osteoclast differentiation	3/127	30/13307	0.00285534150.01921714850.01360310410	Tnf/Ccl5/Ccl3 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+

BP	GO:0046427	positive regulation of JAK-STAT cascade	4/127	62/13307	0.0028791816	0.0192204831	0.0136054644	Socs1/Tnf/Ccl5/P	4
BP	GO:0046637	regulation of alpha-beta T cell differentiation	4/127	62/13307	0.0028791816	0.0192204831	0.0136054644	Irf1/Socs1/Nlrp3/	4
BP	GO:0050766	positive regulation of phagocytosis	4/127	62/13307	0.0028791816	0.0192204831	0.0136054644	Il1b/Tnf/Hspa8/C	4
BP	GO:0051262	protein tetramerization	6/127	149/13307	0.0030341382	0.0201561868	0.0142678143	Cd74/Samhd1/Cc	6
BP	GO:0015837	amine transport	4/127	63/13307	0.0030519894	0.0201561868	0.0142678143	Il1b/Arg2/Tnf/Il1	4
BP	GO:0042108	positive regulation of cytokine biosynthetic process	4/127	63/13307	0.0030519894	0.0201561868	0.0142678143	Irf1/Il1b/Tnf/Rel	4
BP	GO:1903201	regulation of oxidative stress-induced cell death	4/127	63/13307	0.0030519894	0.0201561868	0.0142678143	Nfe2l2/Txnl1/Slc7	4
BP	GO:0032743	positive regulation of interleukin-2 production	3/127	31/13307	0.0031394234	0.0205142219	0.0145212540	Il1b/Pde4b/Cd83	3
BP	GO:0045066	regulatory T cell differentiation	3/127	31/13307	0.0031394234	0.0205142219	0.0145212540	Irf1/Socs1/Ctla4	3
BP	GO:0051085	chaperone cofactor-dependent protein refolding	3/127	31/13307	0.0031394234	0.0205142219	0.0145212540	Cd74/Hspa8/H2-I	3
BP	GO:2000515	negative regulation of CD4-positive, alpha-beta T cell a	3/127	31/13307	0.0031394234	0.0205142219	0.0145212540	Irf1/Cd274/Arg2	3
BP	GO:0032102	negative regulation of response to external stimulus	8/127	258/13307	0.0033030812	0.0215266771	0.0152379334	Arg2/Nlrp3/Acod	8
BP	GO:0006919	activation of cysteine-type endopeptidase activity involv	4/127	65/13307	0.0034186044	0.0222209289	0.0157293684	Tnf/Nlrp3/S100a	4
BP	GO:0034142	toll-like receptor 4 signaling pathway	3/127	32/13307	0.0034402608	0.0223030034	0.0157874658	Nfkbia/Acod1/Pe	3
BP	GO:0046328	regulation of JNK cascade	6/127	153/13307	0.0034584113	0.0223619793	0.0158292127	Dnaja1/Il1b/Tnf/	6
BP	GO:0042089	cytokine biosynthetic process	5/127	107/13307	0.0035806405	0.0230918595	0.0163458677	Irf1/Il1b/Tnf/Rel	5
BP	GO:0043507	positive regulation of JUN kinase activity	4/127	66/13307	0.0036126781	0.0231774416	0.0164064481	Il1b/Tnf/Spag9/Il	4
BP	GO:1904894	positive regulation of STAT cascade	4/127	66/13307	0.0036126781	0.0231774416	0.0164064481	Socs1/Tnf/Ccl5/P	4
BP	GO:0002474	antigen processing and presentation of peptide antigen	3/127	33/13307	0.0037581566	0.0239243479	0.0169351553	H2-K1/H2-D1/B2	3
BP	GO:0042832	defense response to protozoan	3/127	33/13307	0.0037581566	0.0239243479	0.0169351553	Gbp2b/Gbp2/Gbj	3
BP	GO:1902930	regulation of alcohol biosynthetic process	3/127	33/13307	0.0037581566	0.0239243479	0.0169351553	Il1b/Tnf/Nfkb1	3
BP	GO:0002218	activation of innate immune response	6/127	156/13307	0.0038045096	0.0241571693	0.0170999609	Irf1/Rsad2/Tnf/N	6
BP	GO:0002468	dendritic cell antigen processing and presentation	2/127	10/13307	0.0038679955	0.0241768494	0.0171138917	Cd74/Ifgl2	2
BP	GO:0002579	positive regulation of antigen processing and presenta	2/127	10/13307	0.0038679955	0.0241768494	0.0171138917	Cd74/H2-Ab1	2
BP	GO:0002679	respiratory burst involved in defense response	2/127	10/13307	0.0038679955	0.0241768494	0.0171138917	Slamf8/Rps19	2
BP	GO:0032769	negative regulation of monooxygenase activity	2/127	10/13307	0.0038679955	0.0241768494	0.0171138917	Arg2/Nfkb1	2
BP	GO:0045080	positive regulation of chemokine biosynthetic process	2/127	10/13307	0.0038679955	0.0241768494	0.0171138917	Il1b/Tnf	2
BP	GO:2000551	regulation of T-helper 2 cell cytokine production	2/127	10/13307	0.0038679955	0.0241768494	0.0171138917	Rsad2/Nlrp3	2
BP	GO:0071887	leukocyte apoptotic process	5/127	109/13307	0.0038761264	0.0241768494	0.0171138917	Cd74/Cd274/Arg	5
BP	GO:0097193	intrinsic apoptotic signaling pathway	8/127	266/13307	0.0039728942	0.0247180069	0.0174969570	Cd74/Dnaja1/Cri	8
BP	GO:0001909	leukocyte mediated cytotoxicity	5/127	110/13307	0.0040302416	0.0250118014	0.0177049231	H2-K1/H2-D1/Hs	5
BP	GO:0046627	negative regulation of insulin receptor signaling pathw	3/127	34/13307	0.0040934006	0.0252767491	0.0178924698	Il1b/Socs1/Socs3	3
BP	GO:2000403	positive regulation of lymphocyte migration	3/127	34/13307	0.0040934006	0.0252767491	0.0178924698	Cxcl10/Ccl4/Ccl5	3
BP	GO:0030218	erythrocyte differentiation	5/127	111/13307	0.0041886941	0.0257365035	0.0182179128	B2m/Stat1/Klf2/I	5
BP	GO:0042107	cytokine metabolic process	5/127	111/13307	0.0041886941	0.0257365035	0.0182179128	Irf1/Il1b/Tnf/Rel	5
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	6/127	160/13307	0.0043051922	0.0263866619	0.0186781357	Cd74/Dnaja1/Nfe	6
BP	GO:0032609	interferon-gamma production	5/127	112/13307	0.0043515502	0.0266047751	0.0188325299	Cd274/Il1b/Tnf/F	5
BP	GO:0001562	response to protozoan	3/127	35/13307	0.0044462697	0.0269835043	0.0191006182	Gbp2b/Gbp2/Gbj	3
BP	GO:0050706	regulation of interleukin-1 beta secretion	3/127	35/13307	0.0044462697	0.0269835043	0.0191006182	Arg2/Nlrp3/Ccl3	3
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	3/127	35/13307	0.0044462697	0.0269835043	0.0191006182	Cd74/Arg2/Ccl5	3
BP	GO:0042133	neurotransmitter metabolic process	5/127	113/13307	0.0045188766	0.0273569246	0.0193649486	Il1b/Icam1/Tnf/S	5
BP	GO:0007254	JNK cascade	6/127	162/13307	0.0045730559	0.0276172326	0.0195492109	Dnaja1/Il1b/Tnf/	6
BP	GO:0031397	negative regulation of protein ubiquitination	4/127	71/13307	0.0046959189	0.0276811776	0.0195944751	Dnaja1/Gbp4/Rp	4
BP	GO:0032088	negative regulation of NF-kappaB transcription factor a	4/127	71/13307	0.0046959189	0.0276811776	0.0195944751	Nfkbia/Nlrp3/Acc	4
BP	GO:0006750	glutathione biosynthetic process	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Nfe2l2/Slc7a11	2
BP	GO:0034116	positive regulation of heterotypic cell-cell adhesion	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Il1b/Tnf	2
BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Cd274/Arg2	2
BP	GO:0060263	regulation of respiratory burst	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Slamf8/Rps19	2
BP	GO:0072608	interleukin-10 secretion	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Cd274/Isg15	2
BP	GO:1901550	regulation of endothelial cell development	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Il1b/Tnf	2
BP	GO:1903140	regulation of establishment of endothelial barrier	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Il1b/Tnf	2
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferati	2/127	11/13307	0.0046981142	0.0276811776	0.0195944751	Cd274/Arg2	2
BP	GO:0042326	negative regulation of phosphorylation	10/127	397/13307	0.0047069208	0.0276811776	0.0195944751	Irf1/Dnaja1/Il1b/	10
BP	GO:1901342	regulation of vasculature development	8/127	274/13307	0.0047433376	0.0278290831	0.0196991720	Cxcl10/Il1b/Nfe2	8
BP	GO:0051084	'de novo' posttranslational protein folding	3/127	36/13307	0.0048170281	0.0281278002	0.0199106227	Cd74/Hspa8/H2-I	3
BP	GO:1901031	regulation of response to reactive oxygen species	3/127	36/13307	0.0048170281	0.0281278002	0.0199106227	Tnf/Nfe2l2/Txn1	3
BP	GO:0030335	positive regulation of cell migration	11/127	466/13307	0.0049902930	0.0290708109	0.0205781448	Cd74/Cxcl10/Cd2	11

aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+							

BP	GO:0006458	'de novo' protein folding	3/127	37/13307	0.00520592780.0300043555	0.021266714	5	Cd74/Hspa8/H2-I	3
BP	GO:0032350	regulation of hormone metabolic process	3/127	37/13307	0.00520592780.0300043555	0.021266714	5	Il1b/Tnf/Nfkb1	3
BP	GO:0046640	regulation of alpha-beta T cell proliferation	3/127	37/13307	0.00520592780.0300043555	0.021266714	5	Irf1/Cd274/Arg2	3
BP	GO:0098754	detoxification	3/127	37/13307	0.00520592780.0300043555	0.021266714	5	Tnf/Nfe2l2/Sod2	3
BP	GO:0002253	activation of immune response	9/127	341/13307	0.00538049000.0309396224	0.021901006	9	Irf1/Rsad2/Il1b/C	9
BP	GO:0010563	negative regulation of phosphorus metabolic process	11/127	471/13307	0.00539877620.0309396224	0.021901006	9	Irf1/Dnaja1/Il1b/	11
BP	GO:0045936	negative regulation of phosphate metabolic process	11/127	471/13307	0.00539877620.0309396224	0.021901006	9	Irf1/Dnaja1/Il1b/	11
BP	GO:0014048	regulation of glutamate secretion	2/127	12/13307	0.00560266020.0314990509	0.022297005	6	Il1b/Il1rn	2
BP	GO:0031269	pseudopodium assembly	2/127	12/13307	0.00560266020.0314990509	0.022297005	6	Ccl5/Cdc42ep2	2
BP	GO:0042033	chemokine biosynthetic process	2/127	12/13307	0.00560266020.0314990509	0.022297005	6	Il1b/Tnf	2
BP	GO:0045073	regulation of chemokine biosynthetic process	2/127	12/13307	0.00560266020.0314990509	0.022297005	6	Il1b/Tnf	2
BP	GO:0098712	L-glutamate import across plasma membrane	2/127	12/13307	0.00560266020.0314990509	0.022297005	6	Tnf/Slc7a11	2
BP	GO:0002832	negative regulation of response to biotic stimulus	3/127	38/13307	0.00561320860.0314990509	0.022297005	6	Arg2/Acod1/Fgl2	3
BP	GO:1900077	negative regulation of cellular response to insulin stimi	3/127	38/13307	0.00561320860.0314990509	0.022297005	6	Il1b/Socs1/Socs3	3
BP	GO:1905521	regulation of macrophage migration	3/127	38/13307	0.00561320860.0314990509	0.022297005	6	Ccl5/Ccl2/Slamf8	3
BP	GO:0046330	positive regulation of JNK cascade	5/127	119/13307	0.00562040430.0314990509	0.022297005	6	Il1b/Tnf/Spag9/C	5
BP	GO:0002757	immune response-activating signal transduction	8/127	282/13307	0.00562391960.0314990509	0.022297005	6	Irf1/Rsad2/Ctla4	8
BP	GO:0043281	regulation of cysteine-type endopeptidase activity inve	6/127	170/13307	0.00576876800.0322372334	0.022819537	5	Tnf/Nlrp3/Plaur	6
BP	GO:0050671	positive regulation of lymphocyte proliferation	5/127	120/13307	0.00582086510.0324512711	0.022971046	8	Cd74/Cd274/Il1b	5
BP	GO:2000147	positive regulation of cell motility	11/127	476/13307	0.00583334590.0324512711	0.022971046	8	Cd74/Cxcl10/Cd21	1
BP	GO:2001023	regulation of response to drug	4/127	76/13307	0.00597879550.0330744431	0.023412167	1	Arg2/Tnf/Nfe2l2/	4
BP	GO:0002698	negative regulation of immune effector process	5/127	121/13307	0.00602631980.0330744431	0.023412167	1	Irf1/Tnf/Fgl2/Slar	5
BP	GO:0001960	negative regulation of cytokine-mediated signaling pat	3/127	39/13307	0.00603909870.0330744431	0.023412167	1	Samhd1/Parp14/	3
BP	GO:0046782	regulation of viral transcription	3/127	39/13307	0.00603909870.0330744431	0.023412167	1	Ccl4/Ccl5/Ifitm3	3
BP	GO:0061028	establishment of endothelial barrier	3/127	39/13307	0.00603909870.0330744431	0.023412167	1	Il1b/Icam1/Tnf	3
BP	GO:0070232	regulation of T cell apoptotic process	3/127	39/13307	0.00603909870.0330744431	0.023412167	1	Cd274/Arg2/Ccl5	3
BP	GO:1902622	regulation of neutrophil migration	3/127	39/13307	0.00603909870.0330744431	0.023412167	1	Cd74/Il1b/Slamf8	3
BP	GO:1903531	negative regulation of secretion by cell	6/127	172/13307	0.00610035670.0333360200	0.023597327	6	Rsad2/Il1b/Arg2/6	
BP	GO:0010035	response to inorganic substance	9/127	348/13307	0.00612509260.0333973044	0.023640708	6	Selenom/Crip1/T	9
BP	GO:0032946	positive regulation of mononuclear cell proliferation	5/127	122/13307	0.00623683270.0338570921	0.023966175	1	Cd74/Cd274/Il1b	5
BP	GO:0050709	negative regulation of protein secretion	5/127	122/13307	0.00623683270.0338570921	0.023966175	1	Rsad2/Il1b/Arg2/	5
BP	GO:0050864	regulation of B cell activation	5/127	123/13307	0.00645246780.0348911146	0.024698121	2	Cd74/Ctla4/Sams	5
BP	GO:0046633	alpha-beta T cell proliferation	3/127	40/13307	0.00648381440.0348911146	0.024698121	2	Irf1/Cd274/Arg2	3
BP	GO:0050691	regulation of defense response to virus by host	3/127	40/13307	0.00648381440.0348911146	0.024698121	2	Il1b/Ccl5/Stat1	3
BP	GO:0050704	regulation of interleukin-1 secretion	3/127	40/13307	0.00648381440.0348911146	0.024698121	2	Arg2/Nlrp3/Ccl3	3
BP	GO:0070227	lymphocyte apoptotic process	4/127	78/13307	0.00655122110.0349526777	0.024741699	4	Cd74/Cd274/Arg	4
BP	GO:0010819	regulation of T cell chemotaxis	2/127	13/13307	0.00658015990.0349526777	0.024741699	4	Cxcl10/Ccl5	2
BP	GO:0019184	nonribosomal peptide biosynthetic process	2/127	13/13307	0.00658015990.0349526777	0.024741699	4	Nfe2l2/Slc7a11	2
BP	GO:0030730	sequestering of triglyceride	2/127	13/13307	0.00658015990.0349526777	0.024741699	4	Il1b/Tnf	2
BP	GO:0045628	regulation of T-helper 2 cell differentiation	2/127	13/13307	0.00658015990.0349526777	0.024741699	4	Irf1/Nlrp3	2
BP	GO:0046642	negative regulation of alpha-beta T cell proliferation	2/127	13/13307	0.00658015990.0349526777	0.024741699	4	Cd274/Arg2	2
BP	GO:0051051	negative regulation of transport	10/127	417/13307	0.00659817720.0349731713	0.024756206	1	Cd74/Rsad2/Il1b,	10
BP	GO:0051272	positive regulation of cellular component movement	11/127	489/13307	0.00709348160.0375179864	0.026557585	9	Cd74/Cxcl10/Cd21	1
BP	GO:0036473	cell death in response to oxidative stress	4/127	80/13307	0.00715889650.0376945465	0.026682566	2	Nfe2l2/Txnl1/Slc7	4
BP	GO:1903321	negative regulation of protein modification by small pr	4/127	80/13307	0.00715889650.0376945465	0.026682566	2	Dnaja1/Gbp4/Rp	4
BP	GO:0002764	immune response-regulating signaling pathway	8/127	294/13307	0.00717264650.0376945465	0.026682566	2	Irf1/Rsad2/Ctla4,8	
BP	GO:0070665	positive regulation of leukocyte proliferation	5/127	127/13307	0.00736749630.0386363399	0.027349226	7	Cd74/Cd274/Il1b	5
BP	GO:0019083	viral transcription	3/127	42/13307	0.00743053220.0386941015	0.027390114	0	Ccl4/Ccl5/Ifitm3	3
BP	GO:0034113	heterotypic cell-cell adhesion	3/127	42/13307	0.00743053220.0386941015	0.027390114	0	Il1b/Tnf/Il1rn	3
BP	GO:0044070	regulation of anion transport	4/127	81/13307	0.00747622920.0386941015	0.027390114	0	Il1b/Arg2/Tnf/Il1	4
BP	GO:0009266	response to temperature stimulus	5/127	128/13307	0.00760968920.0386941015	0.027390114	0	Dnaja1/Hspa8/Pc	5
BP	GO:0002227	innate immune response in mucosa	2/127	14/13307	0.00762916090.0386941015	0.027390114	0	Rpl39/Fau	2
BP	GO:0002829	negative regulation of type 2 immune response	2/127	14/13307	0.00762916090.0386941015	0.027390114	0	Irf1/Arg2	2
BP	GO:0030213	hyaluronan biosynthetic process	2/127	14/13307	0.00762916090.0386941015	0.027390114	0	Il1b/Nfkb1	2
BP	GO:0031268	pseudopodium organization	2/127	14/13307	0.00762916090.0386941015	0.027390114	0	Ccl5/Cdc42ep2	2
BP	GO:0035745	T-helper 2 cell cytokine production	2/127	14/13307	0.00762916090.0386941015	0.027390114	0	Rsad2/Nlrp3	2
BP	GO:0043374	CD8-positive, alpha-beta T cell differentiation	2/127	14/13307	0.00762916090.0386941015	0.027390114	0	Irf1/Socs1	2

aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+							

BP	GO:0044546	NLRP3 inflammasome complex assembly	2/127	14/13307	0.0076291609	0.0386941015	0.0273901140	Nlrp3/Gbp5	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0046886	positive regulation of hormone biosynthetic process	2/127	14/13307	0.0076291609	0.0386941015	0.0273901140	Il1b/Tnf	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050755	chemokine metabolic process	2/127	14/13307	0.0076291609	0.0386941015	0.0273901140	Il1b/Tnf	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051938	L-glutamate import	2/127	14/13307	0.0076291609	0.0386941015	0.0273901140	Tnf/Slc7a11	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070234	positive regulation of T cell apoptotic process	2/127	14/13307	0.0076291609	0.0386941015	0.0273901140	Cd274/Ccl5	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070486	leukocyte aggregation	2/127	14/13307	0.0076291609	0.0386941015	0.0273901140	Il1b/S100a8	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0060761	negative regulation of response to cytokine stimulus	3/127	43/13307	0.0079329116	0.0401522370	0.0284222739	Samhd1/Parp14/3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0043406	positive regulation of MAP kinase activity	6/127	182/13307	0.0079701703	0.0402583246	0.0284973694	Cd74/Il1b/Tnf/Sp6		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0034614	cellular response to reactive oxygen species	5/127	130/13307	0.0081106311	0.0408009346	0.0288814628	Tnf/Nfe2l2/Txn1,5		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050715	positive regulation of cytokine secretion	5/127	130/13307	0.0081106311	0.0408009346	0.0288814628	Cd274/Il1b/Tnf/N5		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0015807	L-amino acid transport	3/127	44/13307	0.0084548716	0.0422743582	0.0299244445	Arg2/Tnf/Slc7a113		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0061900	glial cell activation	3/127	44/13307	0.0084548716	0.0422743582	0.0299244445	Il1b/Tnf/Nampt 3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000351	regulation of endothelial cell apoptotic process	3/127	44/13307	0.0084548716	0.0422743582	0.0299244445	Icam1/Tnf/Nfe2l2:3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051345	positive regulation of hydrolase activity	10/127	434/13307	0.0086315635	0.0430706303	0.0304880958	Ccl4/Icam1/Tnf/N10		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0035094	response to nicotine	2/127	15/13307	0.0087482312	0.0431300022	0.0305301230	Tnf/Nfkbi1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045410	positive regulation of interleukin-6 biosynthetic proces	2/127	15/13307	0.0087482312	0.0431300022	0.0305301230	Il1b/Tnf	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0051044	positive regulation of membrane protein ectodomain p	2/127	15/13307	0.0087482312	0.0431300022	0.0305301230	Il1b/Tnf	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0140131	positive regulation of lymphocyte chemotaxis	2/127	15/13307	0.0087482312	0.0431300022	0.0305301230	Ccl4/Ccl5	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1902176	negative regulation of oxidative stress-induced intrinsi	2/127	15/13307	0.0087482312	0.0431300022	0.0305301230	Nfe2l2/Sod2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:1904996	positive regulation of leukocyte adhesion to vascular e	2/127	15/13307	0.0087482312	0.0431300022	0.0305301230	Icam1/Tnf	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0009408	response to heat	4/127	85/13307	0.0088380108	0.0434853803	0.0307820005	Dnaja1/Hspa8/P4		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2001233	regulation of apoptotic signaling pathway	9/127	370/13307	0.0089919707	0.0441554032	0.0312559662	Cd74/Dnaja1/Il1b9		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0052548	regulation of endopeptidase activity	7/127	246/13307	0.0092757906	0.0454587356	0.0321785467	Tnf/Serpina3g/N7		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042088	T-helper 1 type immune response	3/127	46/13307	0.0095581724	0.0463769371	0.0328285073	Irf1/H2-Ab1/Il1b 3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042446	hormone biosynthetic process	3/127	46/13307	0.0095581724	0.0463769371	0.0328285073	Il1b/Tnf/Nfkb1	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045646	regulation of erythrocyte differentiation	3/127	46/13307	0.0095581724	0.0463769371	0.0328285073	B2m/Stat1/Isg15 3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0072577	endothelial cell apoptotic process	3/127	46/13307	0.0095581724	0.0463769371	0.0328285073	Icam1/Tnf/Nfe2l:3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0002286	T cell activation involved in immune response	4/127	87/13307	0.0095758048	0.0463769371	0.0328285073	Irf1/Icam1/Nlrp3 4		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0050764	regulation of phagocytosis	4/127	87/13307	0.0095758048	0.0463769371	0.0328285073	Il1b/Tnf/Hspa8/C4		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045765	regulation of angiogenesis	7/127	248/13307	0.0096723697	0.0467529420	0.0330946672	Cxcl10/Il1b/Nfe2 7		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	6/127	190/13307	0.0097391336	0.0469837110	0.0332580200	Tnf/Nlrp3/Plaur/:6		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0015813	L-glutamate transmembrane transport	2/127	16/13307	0.0099359595	0.0474888589	0.0336155954	Tnf/Slc7a11	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0044130	negative regulation of growth of symbiont in host	2/127	16/13307	0.0099359595	0.0474888589	0.0336155954	Tnf/Sqstm1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0071498	cellular response to fluid shear stress	2/127	16/13307	0.0099359595	0.0474888589	0.0336155954	Nfe2l2/Klf2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0000187	activation of MAPK activity	4/127	88/13307	0.0099592725	0.0474888589	0.0336155954	Cd74/Il1b/Tnf/Sp4		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0019233	sensory perception of pain	4/127	88/13307	0.0099592725	0.0474888589	0.0336155954	Tnf/Fcgr4/Ccl2/Il 4		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0045446	endothelial cell differentiation	4/127	88/13307	0.0099592725	0.0474888589	0.0336155954	Il1b/Icam1/Tnf/K4		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0032872	regulation of stress-activated MAPK cascade	6/127	191/13307	0.0099784282	0.0474888589	0.0336155954	Dnaja1/Il1b/Tnf/:6		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0042531	positive regulation of tyrosine phosphorylation of STA	3/127	47/13307	0.0101398075	0.0481640857	0.0340935633	Tnf/Ccl5/Parp14 3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0003018	vascular process in circulatory system	5/127	138/13307	0.0103439946	0.0490396677	0.0347133552	Ccl4/Icam1/Tnf/I5		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0070302	regulation of stress-activated protein kinase signaling c	6/127	193/13307	0.0104695523	0.0495398360	0.0350674057	Dnaja1/Il1b/Tnf/:6		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0022626	cytosolic ribosome	24/127	104/13541	2.7675699160	5.5074641329	4.4281118657	Rpl39/Rps27/Rpl 24		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044445	cytosolic part	27/127	233/13541	3.3261577642	3.3095269754	2.6609262113	Rpl39/Rps27/Rpl 27		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044391	ribosomal subunit	24/127	184/13541	5.0310783879	3.3372819973	2.6832418069	Rpl39/Rps27/Rpl 24		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0005840	ribosome	25/127	215/13541	1.2586088006	6.2615787832	5.0344352025	Rpl39/Rps27/Rpl 25		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0022625	cytosolic large ribosomal subunit	16/127	58/13541	7.7885700377	3.0998508750	2.4923424120	Rpl39/Rpl37/Rpl:16		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0015934	large ribosomal subunit	16/127	118/13541	1.4224574241	4.7178171233	3.7932197976	Rpl39/Rpl37/Rpl:16		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042611	MHC protein complex	8/127	21/13541	8.8039752834	2.5028444019	2.0123372076	H2-Eb1/H2-Aa/C8		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0022627	cytosolic small ribosomal subunit	9/127	42/13541	1.4484970235	3.6031363460	2.8969940470	Rps27/Rps21/Rp9		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0015935	small ribosomal subunit	9/127	72/13541	2.1832622941	4.8274355171	3.8813551896	Rps27/Rps21/Rp9		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0009897	external side of plasma membrane	16/127	313/13541	3.6537554301	7.2709733059	5.8460086882	H2-Aa/Cd74/H2-,16		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042788	polysomal ribosome	5/127	28/13541	5.5432644822	0.0001002826	8.0629301559	Rpl39/Rps21/Rpl 5		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0098552	side of membrane	16/127	460/13541	6.1791203121	0.0001024704	8.2388270829	H2-Aa/Cd74/H2-,16		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0043230	extracellular organelle	6/127	82/13541	0.0001182260	0.0016693922	0.0013422249	Cd274/Gbp2b/Gbp2 6		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0020005	symbiont-containing vacuole membrane	3/127	11/13541	0.0001258335	0.0016693922	0.0013422249	Gbp2b/Gbp2/Gbp3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0042612	MHC class I protein complex	3/127	11/13541	0.0001258335	0.0016693922	0.0013422249	H2-K1/H2-D1/B2 3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0020003	symbiont-containing vacuole	3/127	13/13541	0.0002151354	0.0026757470	0.0021513543	Gbp2b/Gbp2/Gbp3		aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+

CC	GO:0042824	MHC class I peptide loading complex	3/127	14/13541	0.0002719354	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0065010	extracellular membrane-bounded organelle	3/127	15/13541	0.0003375946	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0030430	host cell cytoplasm	3/127	16/13541	0.0004126607	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0033655	host cell cytoplasm part	3/127	16/13541	0.0004126607	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0005844	polysome	5/127	68/13541	0.0004357885	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0033646	host intracellular part	3/127	19/13541	0.0006995184	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0043656	intracellular region of host	3/127	19/13541	0.0006995184	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0033643	host cell part	3/127	21/13541	0.0009470658	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0018995	host	3/127	23/13541	0.0012439565	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0043657	host cell	3/127	23/13541	0.0012439565	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044215	other organism	3/127	25/13541	0.0015935937	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044216	other organism cell	3/127	25/13541	0.0015935937	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044217	other organism part	3/127	25/13541	0.0015935937	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0044754	autolysosome	2/127	11/13541	0.0045415605	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0098797	plasma membrane protein complex	9/127	344/13541	0.0050932272	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
CC	GO:0005767	secondary lysosome	2/127	12/13541	0.0054165467	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0003735	structural constituent of ribosome	22/121	147/13229	6.1931004009	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0005198	structural molecule activity	23/121	428/13229	5.3185159381	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0042379	chemokine receptor binding	9/121	45/13229	2.2285728529	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0048020	CCR chemokine receptor binding	7/121	29/13229	5.9397280339	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0008009	chemokine activity	7/121	35/13229	2.4455703711	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0005125	cytokine activity	11/121	129/13229	2.5377931981	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0005126	cytokine receptor binding	12/121	217/13229	6.8139510435	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0001664	G protein-coupled receptor binding	11/121	204/13229	2.6020683122	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0048018	receptor ligand activity	12/121	255/13229	3.6990686364	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0030545	receptor regulator activity	12/121	276/13229	8.3048314173	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0042605	peptide antigen binding	4/121	23/13229	5.1545442699	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0031386	protein tag	3/121	11/13229	0.0001167402	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0044389	ubiquitin-like protein ligase binding	10/121	298/13229	0.0004039509	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0003823	antigen binding	4/121	39/13229	0.0004276664	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0042277	peptide binding	8/121	209/13229	0.0006636144	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0031625	ubiquitin protein ligase binding	9/121	280/13229	0.0010715100	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0008201	heparin binding	5/121	101/13229	0.0023198563	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0003924	GTPase activity	8/121	263/13229	0.0028552083	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
MF	GO:0033218	amide binding	8/121	264/13229	0.0029223417	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45+
BP	GO:0009617	response to bacterium	10/35	430/13403	9.3075909495	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1990868	response to chemokine	5/35	55/13403	2.8559111241	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1990869	cellular response to chemokine	5/35	55/13403	2.8559111241	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0030593	neutrophil chemotaxis	5/35	68/13403	8.3523640144	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0019882	antigen processing and presentation	5/35	73/13403	1.1923152411	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0061844	antimicrobial humoral immune response mediated by	4/35	33/13403	1.5107941900	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1990266	neutrophil migration	5/35	83/13403	2.2620772976	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0030595	leukocyte chemotaxis	6/35	155/13403	2.6710789455	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0097529	myeloid leukocyte migration	6/35	155/13403	2.6710789455	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002824	positive regulation of adaptive immune response base	5/35	86/13403	2.6981545225	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071621	granulocyte chemotaxis	5/35	86/13403	2.6981545225	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002821	positive regulation of adaptive immune response	5/35	93/13403	3.9741161649	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0019221	cytokine-mediated signaling pathway	7/35	262/13403	4.2390874175	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0019730	antimicrobial humoral response	4/35	43/13403	4.4727907330	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002699	positive regulation of immune effector process	6/35	174/13403	5.2155653837	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	4/35	45/13403	5.3801179031	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0070098	chemokine-mediated signaling pathway	4/35	45/13403	5.3801179031	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0097530	granulocyte migration	5/35	103/13403	6.5700953419	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0031343	positive regulation of cell killing	4/35	52/13403	9.6498473858	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002428	antigen processing and presentation of peptide antigen	3/35	17/13403	1.0818466900	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071248	cellular response to metal ion	5/35	117/13403	1.2250004094	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	4/35	59/13403	1.6013873651	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-

BP	GO:0002475	antigen processing and presentation via MHC class Ib	3/35	20/13403	1.8039652063	0.0009008115	0.0006508152	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071276	cellular response to cadmium ion	3/35	20/13403	1.8039652063	0.0009008115	0.0006508152	Mt1/Mt2/Fos 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0060326	cell chemotaxis	6/35	218/13403	1.8914412554	0.0009008115	0.0006508152	Cxcl10/Cxcl9/Cxc6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002822	regulation of adaptive immune response based on son	5/35	128/13403	1.8949405680	0.0009008115	0.0006508152	B2m/Irf1/H2-D1/5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002237	response to molecule of bacterial origin	6/35	219/13403	1.9410942367	0.0009008115	0.0006508152	Cxcl10/Cxcl9/B2r6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002483	antigen processing and presentation of endogenous pe	3/35	22/13403	2.4282231875	0.0010491598	0.0007579934	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0019885	antigen processing and presentation of endogenous pe	3/35	22/13403	2.4282231875	0.0010491598	0.0007579934	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071241	cellular response to inorganic substance	5/35	137/13403	2.6310020347	0.0010988818	0.0007939164	Mt1/B2m/Mt2/F5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006954	inflammatory response	8/35	491/13403	3.0105040324	0.0011719128	0.0008466795	Cxcl10/Cxcl9/Cxc8	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002819	regulation of adaptive immune response	5/35	141/13403	3.0219334383	0.0011719128	0.0008466795	B2m/Irf1/H2-D1/5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071222	cellular response to lipopolysaccharide	5/35	142/13403	3.1263716683	0.0011719128	0.0008466795	Cxcl10/Cxcl9/Cxc5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0019883	antigen processing and presentation of endogenous ar	3/35	24/13403	3.1799709748	0.0011719128	0.0008466795	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0031341	regulation of cell killing	4/35	72/13403	3.5338050848	0.0012651022	0.0009140067	B2m/Cxcl1/H2-D4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071219	cellular response to molecule of bacterial origin	5/35	150/13403	4.0665297855	0.0014153782	0.0010225776	Cxcl10/Cxcl9/Cxc5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	3/35	27/13403	4.5709453368	0.0015298777	0.0011053008	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071396	cellular response to lipid	7/35	379/13403	4.6396930033	0.0015298777	0.0011053008	Cxcl10/Cxcl9/Cxc7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0050900	leukocyte migration	6/35	260/13403	5.0901472784	0.0016353729	0.0011815186	Cxcl10/Cxcl9/Cxc6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001909	leukocyte mediated cytotoxicity	4/35	81/13403	5.6204219662	0.0017388461	0.0012562756	B2m/Cxcl1/H2-D4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0046686	response to cadmium ion	3/35	29/13403	5.6897599879	0.0017388461	0.0012562756	Mt1/Mt2/Fos 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002474	antigen processing and presentation of peptide antige	3/35	30/13403	6.3106505654	0.0018826774	0.0013601903	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001914	regulation of T cell mediated cytotoxicity	3/35	31/13403	6.9742986298	0.0020322781	0.0014682733	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071216	cellular response to biotic stimulus	5/35	170/13403	7.3831363529	0.0021025158	0.0015190184	Cxcl10/Cxcl9/Cxc5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002697	regulation of immune effector process	6/35	297/13403	0.0001063054	0.0029600172	0.0021385431	B2m/Irf1/Cxcl1/6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006959	humoral immune response	4/35	101/13403	0.0001329190	0.0036206000	0.0026157987	Cxcl10/Cxcl9/Cxc4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001906	cell killing	4/35	103/13403	0.0001434026	0.0038230523	0.0027620657	B2m/Cxcl1/H2-D4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1903706	regulation of hemopoiesis	6/35	317/13403	0.0001518894	0.0038933138	0.0028128280	B2m/Irf1/Cxcl1/6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0055065	metal ion homeostasis	7/35	458/13403	0.0001522524	0.0038933138	0.0028128280	Cxcl10/Mt1/B2m7	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002705	positive regulation of leukocyte mediated immunity	4/35	107/13403	0.0001661490	0.0041636956	0.0030081726	B2m/Cxcl1/H2-D4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010038	response to metal ion	5/35	204/13403	0.0001741236	0.0041957113	0.0030313032	Mt1/B2m/Mt2/F5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0032496	response to lipopolysaccharide	5/35	204/13403	0.0001741236	0.0041957113	0.0030313032	Cxcl10/Cxcl9/Cxc5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002711	positive regulation of T cell mediated immunity	3/35	45/13403	0.0002147221	0.0050491590	0.0036478991	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002460	adaptive immune response based on somatic recombi	5/35	214/13403	0.0002176014	0.0050491590	0.0036478991	B2m/Irf1/H2-D1/5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0048002	antigen processing and presentation of peptide antige	3/35	46/13403	0.0002292923	0.0052236970	0.0037739388	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0001913	T cell mediated cytotoxicity	3/35	47/13403	0.0002444884	0.0054704285	0.0039522565	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0032103	positive regulation of response to external stimulus	5/35	234/13403	0.0003289897	0.0072320033	0.0052249530	Cxcl10/Cxcl1/Nfk5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006875	cellular metal ion homeostasis	6/35	390/13403	0.0004635504	0.0100142872	0.0072350879	Cxcl10/Mt1/Cxcl:6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0035914	skeletal muscle cell differentiation	3/35	60/13403	0.0005041173	0.0104243256	0.0075313311	Fos/Nupr1/Egr1 3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0045820	negative regulation of glycolytic process	2/35	13/13403	0.0005074891	0.0104243256	0.0075313311	Nupr1/Ier3 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071280	cellular response to copper ion	2/35	13/13403	0.0005074891	0.0104243256	0.0075313311	Mt1/Mt2 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002709	regulation of T cell mediated immunity	3/35	61/13403	0.0005292461	0.0106958948	0.0077275335	B2m/H2-D1/H2-K3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0030812	negative regulation of nucleotide catabolic process	2/35	14/13403	0.0005911002	0.0115726348	0.0083609576	Nupr1/Ier3 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0051198	negative regulation of coenzyme metabolic process	2/35	14/13403	0.0005911002	0.0115726348	0.0083609576	Nupr1/Ier3 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010977	negative regulation of neuron projection development	4/35	152/13403	0.0006332279	0.0122066870	0.0088190455	B2m/H2-D1/H2-K4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002486	antigen processing and presentation of endogenous pe	2/35	15/13403	0.0006809211	0.0126677019	0.0091521179	H2-D1/H2-K1 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0035994	response to muscle stretch	5/35	275/13403	0.0006809211	0.0126677019	0.0091521179	Nfkbia/Fos 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002250	adaptive immune response	6/35	422/13403	0.0006874730	0.0126677019	0.0091521179	B2m/Irf1/H2-D1/5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0050778	positive regulation of immune response	6/35	422/13403	0.0007027815	0.0127155265	0.0091866701	B2m/Irf1/H2-D1/6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0031349	positive regulation of defense response	5/35	277/13403	0.0007103646	0.0127155265	0.0091866701	Irf1/Cxcl1/Nfkbia5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1903708	positive regulation of hemopoiesis	4/35	160/13403	0.0007675693	0.0129797518	0.0093775667	Irf1/Cxcl1/Fos/Nf4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006935	chemotaxis	6/35	430/13403	0.0007754134	0.0129797518	0.0093775667	Cxcl10/Cxcl9/Cxc6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002476	antigen processing and presentation of endogenous pe	2/35	16/13403	0.0007769205	0.0129797518	0.0093775667	H2-D1/H2-K1 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002484	antigen processing and presentation of endogenous pe	2/35	16/13403	0.0007769205	0.0129797518	0.0093775667	H2-D1/H2-K1 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071498	cellular response to fluid shear stress	2/35	16/13403	0.0007769205	0.0129797518	0.0093775667	Klf2/Spp1 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0042330	taxis	6/35	433/13403	0.0008041060	0.0131127559	0.0094736591	Cxcl10/Cxcl9/Cxc6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0030003	cellular cation homeostasis	6/35	434/13403	0.0008138513	0.0131127559	0.0094736591	Cxcl10/Mt1/Cxcl:6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002703	regulation of leukocyte mediated immunity	4/35	163/13403	0.0008227837	0.0131127559	0.0094736591	B2m/Cxcl1/H2-D4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0007263	nitric oxide mediated signal transduction	2/35	17/13403	0.0008790674	0.0131127559	0.0094736591	Mt1/Mt2 2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-

BP	GO:0030809	negative regulation of nucleotide biosynthetic process	2/35	17/13403	0.0008790674	0.0131127559	0.0094736591	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0045624	positive regulation of T-helper cell differentiation	2/35	17/13403	0.0008790674	0.0131127559	0.0094736591	Irf1/Nfkbiz	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1900372	negative regulation of purine nucleotide biosynthetic p	2/35	17/13403	0.0008790674	0.0131127559	0.0094736591	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1901739	regulation of myoblast fusion	2/35	17/13403	0.0008790674	0.0131127559	0.0094736591	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:2001170	negative regulation of ATP biosynthetic process	2/35	17/13403	0.0008790674	0.0131127559	0.0094736591	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006873	cellular ion homeostasis	6/35	443/13403	0.0009057495	0.0133518144	0.0096463732	Cxcl10/Mt1/Cxcl	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006882	cellular zinc ion homeostasis	2/35	19/13403	0.0011016803	0.0160512271	0.0115966357	Mt1/Mt2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0031345	negative regulation of cell projection organization	4/35	177/13403	0.0011181038	0.0161032657	0.0116342323	B2m/H2-D1/H2-K	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010043	response to zinc ion	2/35	20/13403	0.0012220849	0.0166442652	0.0120250918	Mt1/Mt2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0046688	response to copper ion	2/35	20/13403	0.0012220849	0.0166442652	0.0120250918	Mt1/Mt2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0051195	negative regulation of cofactor metabolic process	2/35	20/13403	0.0012220849	0.0166442652	0.0120250918	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0055069	zinc ion homeostasis	2/35	20/13403	0.0012220849	0.0166442652	0.0120250918	Mt1/Mt2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0090025	regulation of monocyte chemotaxis	2/35	20/13403	0.0012220849	0.0166442652	0.0120250918	Cxcl10/Dusp1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	3/35	83/13403	0.0012991139	0.0175031153	0.0126455909	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010499	proteasomal ubiquitin-independent protein catabolic p	2/35	21/13403	0.0013485140	0.0177038652	0.0127906280	Psmb9/Psmb8	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di	2/35	21/13403	0.0013485140	0.0177038652	0.0127906280	Irf1/Nfkbiz	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0031347	regulation of defense response	6/35	479/13403	0.0013564014	0.0177038652	0.0127906280	Irf1/Cxcl1/Nfkbia	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0098542	defense response to other organism	5/35	325/13403	0.0014515663	0.0185561428	0.0134063787	Cxcl10/Cxcl9/Irf1	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0072503	cellular divalent inorganic cation homeostasis	5/35	326/13403	0.0014714208	0.0185561428	0.0134063787	Cxcl10/Mt1/Cxcl	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002478	antigen processing and presentation of exogenous pep	2/35	22/13403	0.0014809371	0.0185561428	0.0134063787	B2m/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0034405	response to fluid shear stress	2/35	22/13403	0.0014809371	0.0185561428	0.0134063787	Klf2/Spp1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0060142	regulation of syncytium formation by plasma membrar	2/35	23/13403	0.0016193240	0.0200892385	0.0145140043	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002456	T cell mediated immunity	3/35	90/13403	0.0016404547	0.0201518608	0.0145592475	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0016525	negative regulation of angiogenesis	3/35	92/13403	0.0017473196	0.0212485245	0.0153515613	Cxcl10/Klf2/Dcn	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	2/35	24/13403	0.0017636444	0.0212485245	0.0153515613	Irf1/Nfkbiz	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0030217	T cell differentiation	4/35	204/13403	0.0018855523	0.0224119336	0.0161920972	B2m/Irf1/Nfkbiz/	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1900543	negative regulation of purine nucleotide metabolic prc	2/35	25/13403	0.0019138682	0.0224119336	0.0161920972	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1903579	negative regulation of ATP metabolic process	2/35	25/13403	0.0019138682	0.0224119336	0.0161920972	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:2000181	negative regulation of blood vessel morphogenesis	3/35	96/13403	0.0019739086	0.0228295904	0.0164938445	Cxcl10/Klf2/Dcn	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0072507	divalent inorganic cation homeostasis	5/35	349/13403	0.0019859739	0.0228295904	0.0164938445	Cxcl10/Mt1/Cxcl	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0045980	negative regulation of nucleotide metabolic process	2/35	26/13403	0.0020699653	0.0235787866	0.0170351211	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0045665	negative regulation of neuron differentiation	4/35	211/13403	0.0021323933	0.0239363646	0.0172934629	B2m/H2-D1/H2-K	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010035	response to inorganic substance	5/35	355/13403	0.0021395633	0.0239363646	0.0172934629	Mt1/B2m/Mt2/F	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0055076	transition metal ion homeostasis	3/35	100/13403	0.0022180441	0.0245313854	0.0177233514	Mt1/B2m/Mt2	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0019884	antigen processing and presentation of exogenous ant	2/35	27/13403	0.0022319057	0.0245313854	0.0177233514	B2m/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0050729	positive regulation of inflammatory response	3/35	102/13403	0.0023468377	0.0255703273	0.0184739626	Nfkbia/Nupr1/Nf	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0045622	regulation of T-helper cell differentiation	2/35	28/13403	0.0023996598	0.0259204635	0.0187269279	Irf1/Nfkbiz	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0060537	muscle tissue development	5/35	368/13403	0.0025020473	0.0267954306	0.0193590711	Ifrd1/Zfand5/Fos	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1901343	negative regulation of vasculature development	3/35	107/13403	0.0026888889	0.0285523548	0.0206284077	Cxcl10/Klf2/Dcn	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0007616	long-term memory	2/35	31/13403	0.0029375070	0.0309302212	0.0223463605	Sgk1/Egr1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0007520	myoblast fusion	2/35	32/13403	0.0031282195	0.0326638253	0.0235988488	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002706	regulation of lymphocyte mediated immunity	3/35	120/13403	0.0037175313	0.0380406440	0.0274834744	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0006110	regulation of glycolytic process	2/35	35/13403	0.0037342372	0.0380406440	0.0274834744	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0030811	regulation of nucleotide catabolic process	2/35	35/13403	0.0037342372	0.0380406440	0.0274834744	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002443	leukocyte mediated immunity	4/35	248/13403	0.0038174661	0.0385748797	0.0278694472	B2m/Cxcl1/H2-D:	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010765	positive regulation of sodium ion transport	2/35	37/13403	0.0041661922	0.0408093377	0.0294837909	Cxcl1/Sgk1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentia	2/35	37/13403	0.0041661922	0.0408093377	0.0294837909	Irf1/Nfkbiz	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	2/35	37/13403	0.0041661922	0.0408093377	0.0294837909	Irf1/Nfkbiz	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:1902107	positive regulation of leukocyte differentiation	3/35	125/13403	0.0041688709	0.0408093377	0.0294837909	Irf1/Fos/Nfkbiz	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0009636	response to toxic substance	4/35	256/13403	0.0042742218	0.0412411943	0.0297957971	Mt1/Mt2/Nupr1/	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002521	leukocyte differentiation	5/35	417/13403	0.0042788150	0.0412411943	0.0297957971	B2m/Irf1/Fos/Nfl	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0002548	monocyte chemotaxis	2/35	39/13403	0.0046202328	0.0435274571	0.0314475684	Cxcl10/Dusp1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0010677	negative regulation of cellular carbohydrate metabolic	2/35	39/13403	0.0046202328	0.0435274571	0.0314475684	Nupr1/Ier3	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0071675	regulation of mononuclear cell migration	2/35	39/13403	0.0046202328	0.0435274571	0.0314475684	Cxcl10/Dusp1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0050727	regulation of inflammatory response	4/35	265/13403	0.0048309017	0.0451725365	0.0326360998	Nfkbia/Nupr1/Nf	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0050768	negative regulation of neurogenesis	4/35	269/13403	0.0050933245	0.0469518483	0.0339216109	B2m/H2-D1/H2-K	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0098754	detoxification	2/35	41/13403	0.0050961303	0.0469518483	0.0339216109	Mt1/Mt2	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-

BP	GO:0051147	regulation of muscle cell differentiation	3/35	137/13403	0.0053840580	0.0492425158	0.0355765645	Cxcl10/Cxcl9/Tm	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0042612	MHC class I protein complex	3/36	11/13620	2.7578997234	0.0001847792	0.0001393465	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0042824	MHC class I peptide loading complex	3/36	14/13620	6.0509979354	0.0002027084	0.0001528673	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0042611	MHC protein complex	3/36	19/13620	1.5962548355	0.0003564969	0.0002688429	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0009897	external side of plasma membrane	6/36	246/13620	4.0390726853	0.0006765446	0.0005101986	Cxcl10/Cxcl9/Ly6	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0098552	side of membrane	6/36	393/13620	0.0005194465	0.0069605843	0.0052491445	Cxcl10/Cxcl9/Ly6	6	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0005839	proteasome core complex	2/36	17/13620	0.0009010456	0.0100616761	0.0075877526	Psmb9/Psmb8	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0005797	Golgi medial cisterna	2/36	23/13620	0.0016595842	0.0158845923	0.0119789541	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0070971	endoplasmic reticulum exit site	2/36	26/13620	0.0021212855	0.0177657663	0.0133975928	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0030176	integral component of endoplasmic reticulum membra	3/36	128/13620	0.0046162593	0.0343654862	0.0259158419	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
CC	GO:0031227	intrinsic component of endoplasmic reticulum membra	3/36	135/13620	0.0053544337	0.0358747060	0.0270539810	B2m/H2-D1/H2-K	3	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0008009	chemokine activity	4/36	33/13297	1.7506859770	0.0001680658	0.0001197837	Cxcl10/Cxcl9/Cxc	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0042379	chemokine receptor binding	4/36	43/13297	5.1791248061	0.0002485979	0.0001771805	Cxcl10/Cxcl9/Cxc	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0005125	cytokine activity	5/36	117/13297	1.4673995327	0.0004695678	0.0003346700	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0030881	beta-2-microglobulin binding	2/36	11/13297	0.0003860052	0.0061760839	0.0044018142	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0042610	CD8 receptor binding	2/36	11/13297	0.0003860052	0.0061760839	0.0044018142	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0046977	TAP binding	2/36	11/13297	0.0003860052	0.0061760839	0.0044018142	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0042608	T cell receptor binding	2/36	15/13297	0.0007319147	0.0096036332	0.0068446947	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0048018	receptor ligand activity	5/36	274/13297	0.0008003027	0.0096036332	0.0068446947	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0004298	threonine-type endopeptidase activity	2/36	18/13297	0.0010610707	0.0101862794	0.0072599579	Psmb9/Psmb8	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0070003	threonine-type peptidase activity	2/36	18/13297	0.0010610707	0.0101862794	0.0072599579	Psmb9/Psmb8	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0030545	receptor regulator activity	5/36	301/13297	0.0012188023	0.0106368201	0.0075810669	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0042605	peptide antigen binding	2/36	21/13297	0.0014489553	0.0115916431	0.0082615877	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0005126	cytokine receptor binding	4/36	203/13297	0.0021191304	0.0155996833	0.0111181953	Cxcl10/Cxcl9/Cxc	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0001664	G protein-coupled receptor binding	4/36	207/13297	0.0022749538	0.0155996833	0.0111181953	Cxcl10/Cxcl9/Cxc	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0000979	RNA polymerase II core promoter sequence-specific DI	2/36	35/13297	0.0040088503	0.0240531019	0.0171431099	Fos/Egr1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0003823	antigen binding	2/36	35/13297	0.0040088503	0.0240531019	0.0171431099	H2-D1/H2-K1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0001046	core promoter sequence-specific DNA binding	2/36	46/13297	0.0068444881	0.0386512270	0.0275474753	Fos/Egr1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0050840	extracellular matrix binding	2/36	54/13297	0.0093359143	0.0465454556	0.0331738444	Spp1/Dcn	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0001047	core promoter binding	2/36	55/13297	0.0096718332	0.0465454556	0.0331738444	Fos/Egr1	2	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
MF	GO:0001228	DNA-binding transcription activator activity, RNA polyr	4/36	312/13297	0.0096969699	0.0465454556	0.0331738444	Irf1/Fosb/Fos/Egı	4	aPD-L1+aTGFb vs PBS	Up-regulated genes	CD45-
BP	GO:0044403	symbiont process	11/45	318/13307	6.0079046100	7.2629173357	4.9049430232	Gsn/P4hb/Fn1/C	11	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0044419	interspecies interaction between organisms	11/45	333/13307	9.7012650051	7.2629173357	4.9049430232	Gsn/P4hb/Fn1/C	11	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	9/45	188/13307	1.0582201072	7.2629173357	4.9049430232	Gsn/P4hb/Cxcr4/	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0050792	regulation of viral process	8/45	158/13307	4.9106311192	2.5277473686	1.7070904496	Gsn/P4hb/Cxcr4/	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071248	cellular response to metal ion	7/45	115/13307	1.0362280140	4.2671869618	2.8818046453	Fosb/Gsn/Fn1/Lg	7	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	10/45	339/13307	1.4563151917	4.9975882997	3.3750743304	Gsn/P4hb/Grn/C	10	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010038	response to metal ion	8/45	199/13307	2.9152248737	8.0138514521	5.4120793273	Fosb/Gsn/Fn1/G	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071241	cellular response to inorganic substance	7/45	135/13307	3.1136868196	8.0138514521	5.4120793273	Fosb/Gsn/Fn1/Lg	7	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071277	cellular response to calcium ion	5/45	55/13307	1.0790585061	0.0002468646	0.0001667176	Fosb/Lgmn/Junb,	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0060326	cell chemotaxis	8/45	244/13307	1.3669331824	0.0002814515	0.0001900756	Ccr2/Dusp1/Cxcr	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0016032	viral process	8/45	251/13307	1.6898451023	0.0003163082	0.0002136158	Gsn/P4hb/Cxcr4/	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0009611	response to wounding	9/45	356/13307	2.4011235432	0.0003836795	0.0002591143	Fn1/Ccr2/Grn/Cd	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0001933	negative regulation of protein phosphorylation	9/45	360/13307	2.6319836298	0.0003836795	0.0002591143	Dusp1/Cdkn1a/D	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0051702	interaction with symbiont	5/45	66/13307	2.6966725137	0.0003836795	0.0002591143	Fn1/Jun/Arg1/Pf	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0030595	leukocyte chemotaxis	7/45	187/13307	2.7951398290	0.0003836795	0.0002591143	Ccr2/Dusp1/Lgm	7	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0048514	blood vessel morphogenesis	10/45	498/13307	4.8260842755	0.0006210567	0.0004194248	Fn1/Ccr2/Grn/Cx	10	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0009991	response to extracellular stimulus	8/45	292/13307	5.1994817375	0.0006297489	0.0004252950	Cdkn1a/Gatm/Ld	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0042326	negative regulation of phosphorylation	9/45	397/13307	5.8476398419	0.0006689050	0.0004517387	Dusp1/Cdkn1a/D	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002683	negative regulation of immune system process	9/45	413/13307	8.0488465084	0.0008722407	0.0005890596	Il7r/Ccr2/Dusp1/	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0051348	negative regulation of transferase activity	7/45	222/13307	8.6617736748	0.0008917295	0.0006022212	Dusp1/Rpl5/Cdkr	7	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043902	positive regulation of multi-organism process	6/45	151/13307	1.0926784610	0.0010713452	0.0007235229	P4hb/Grn/Jun/Lg	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0006935	chemotaxis	9/45	433/13307	1.1770471235	0.0011016091	0.0007439613	Fn1/Ccr2/Dusp1/	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0042330	taxis	9/45	436/13307	1.2439375764	0.0011135945	0.0007520556	Fn1/Ccr2/Dusp1/	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0051592	response to calcium ion	5/45	92/13307	1.3902450812	0.0011927144	0.0008054884	Fosb/Lgmn/Junb,	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0070848	response to growth factor	9/45	445/13307	1.4645013239	0.0012061632	0.0008145710	Dab2/Lgmn/Pme	9	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002548	monocyte chemotaxis	4/45	45/13307	1.5364175773	0.0012167245	0.0008217034	Ccr2/Dusp1/Lgm	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+

BP	GO:0010035	response to inorganic substance	8/45	348/13307	1.8684384183e-07	0.00014129848	0.00095424601	Fosb/Gsn/Fn1/Gi	8
BP	GO:0030099	myeloid cell differentiation	8/45	352/13307	2.0287929961e-07	0.00014129848	0.00095424601	Dab2/Zfp36/Junt	8
BP	GO:0030335	positive regulation of cell migration	9/45	466/13307	2.1128457385e-07	0.00014129848	0.00095424601	Fn1/Ccr2/Grn/Cx	9
BP	GO:0010563	negative regulation of phosphorus metabolic process	9/45	471/13307	2.2990357767e-07	0.00014129848	0.00095424601	Dusp1/Cdkn1a/D	9
BP	GO:0045936	negative regulation of phosphate metabolic process	9/45	471/13307	2.2990357767e-07	0.00014129848	0.00095424601	Dusp1/Cdkn1a/D	9
BP	GO:0032370	positive regulation of lipid transport	4/45	50/13307	2.3457439565e-07	0.00014129848	0.00095424601	Dab2/Nfkbia/Spp	4
BP	GO:0035994	response to muscle stretch	3/45	17/13307	2.3773669653e-07	0.00014129848	0.00095424601	Jun/Nfkbia/Fos	3
BP	GO:0032103	positive regulation of response to external stimulus	7/45	260/13307	2.4127991113e-07	0.00014129848	0.00095424601	Fn1/Ccr2/Grn/Cx	7
BP	GO:1903706	regulation of hemopoiesis	8/45	362/13307	2.4811466853e-07	0.00014129848	0.00095424601	Il7r/Ccr2/Zfp36/J	8
BP	GO:2000147	positive regulation of cell motility	9/45	476/13307	2.4990476210e-07	0.00014129848	0.00095424601	Fn1/Ccr2/Grn/Cx	9
BP	GO:0002704	negative regulation of leukocyte mediated immunity	4/45	51/13307	2.5391180032e-07	0.00014129848	0.00095424601	Il7r/Ccr2/Smad7/	4
BP	GO:0097529	myeloid leukocyte migration	6/45	180/13307	2.9623063609e-07	0.00015032106	0.00101517921	Ccr2/Dusp1/Lgm	6
BP	GO:0009612	response to mechanical stimulus	5/45	108/13307	3.0273644877e-07	0.00015032106	0.00101517921	Ccr4/Junb/Jun/I	5
BP	GO:0002521	leukocyte differentiation	9/45	488/13307	3.0405145936e-07	0.00015032106	0.00101517921	Il7r/Ccr2/Junb/Ju	9
BP	GO:0051272	positive regulation of cellular component movement	9/45	489/13307	3.0898287099e-07	0.00015032106	0.00101517921	Fn1/Ccr2/Grn/Cx	9
BP	GO:0050865	regulation of cell activation	9/45	491/13307	3.1905027362e-07	0.00015032106	0.00101517921	Gsn/Il7r/Ccr2/Gri	9
BP	GO:0007611	learning or memory	6/45	183/13307	3.2510424383e-07	0.00015032106	0.00101517921	Btg2/Gatm/Lgmr	6
BP	GO:0002710	negative regulation of T cell mediated immunity	3/45	19/13307	3.3717474823e-07	0.00015032106	0.00101517921	Il7r/Smad7/Arg1	3
BP	GO:0019221	cytokine-mediated signaling pathway	7/45	274/13307	3.3765241391e-07	0.00015032106	0.00101517921	Ccr2/Cxcr4/Fgr1/	7
BP	GO:1990868	response to chemokine	4/45	55/13307	3.4313211400e-07	0.00015032106	0.00101517921	Dusp1/Cxcr4/Ccl	4
BP	GO:1990869	cellular response to chemokine	4/45	55/13307	3.4313211400e-07	0.00015032106	0.00101517921	Dusp1/Cxcr4/Ccl	4
BP	GO:0071276	cellular response to cadmium ion	3/45	20/13307	3.9573844929e-07	0.00169755301	0.00114642651	Gsn/Jun/Fos	3
BP	GO:0050900	positive regulation of proteolysis	7/45	288/13307	4.6375512023e-07	0.00194871791	0.00131604831	Gsn/Grn/Dab2/Lt	7
BP	GO:0051851	modification by host of symbiont morphology or physi	4/45	61/13307	5.1733123564e-07	0.00209786751	0.00141677511	Jun/Arg1/Pf4/Ap	4
BP	GO:0002698	negative regulation of immune effector process	5/45	121/13307	5.2258916974e-07	0.00209786751	0.00141677511	Il7r/Ccr2/Grn/Sm	5
BP	GO:0090025	regulation of monocyte chemotaxis	3/45	22/13307	5.3206989858e-07	0.00209786751	0.00141677511	Ccr2/Dusp1/Lgm	3
BP	GO:1901214	regulation of neuron death	7/45	295/13307	5.4000475368e-07	0.00209786751	0.00141677511	Btg2/Grn/Lgmn/J	7
BP	GO:0050900	leukocyte migration	7/45	297/13307	5.6358699263e-07	0.00211579931	0.00142888521	Ccr2/Dusp1/Lgm	7
BP	GO:0034341	response to interferon-gamma	5/45	123/13307	5.6517223476e-07	0.00211579931	0.00142888521	Gsn/Cxcl16/Bst2/	5
BP	GO:0050890	cognition	6/45	206/13307	6.3006915539e-07	0.00231662921	0.00156451381	Btg2/Gatm/Lgmr	6
BP	GO:0043523	regulation of neuron apoptotic process	6/45	211/13307	7.1972652996e-07	0.00259985421	0.00175578711	Btg2/Grn/Lgmn/J	6
BP	GO:1905954	positive regulation of lipid localization	4/45	67/13307	7.4869222465e-07	0.00265785731	0.00179495901	Dab2/Nfkbia/Spp	4
BP	GO:0042110	T cell activation	8/45	426/13307	7.8643191003e-07	0.00270768741	0.00182861131	Gsn/Il7r/Ccr2/Cx	8
BP	GO:0046596	regulation of viral entry into host cell	3/45	25/13307	7.8902986202e-07	0.00270768741	0.00182861131	Gsn/P4hb/Lgals1	3
BP	GO:0071674	mononuclear cell migration	4/45	69/13307	8.4029078195e-07	0.00283632571	0.00191548591	Ccr2/Dusp1/Lgm	4
BP	GO:0071363	cellular response to growth factor stimulus	8/45	433/13307	8.8129602839e-07	0.00292675561	0.00197655691	Dab2/Lgmn/Pme	8
BP	GO:0050777	negative regulation of immune response	5/45	136/13307	9.1129405891e-07	0.00297834041	0.00201139421	Il7r/Ccr2/Grn/Sm	5
BP	GO:0043524	negative regulation of neuron apoptotic process	5/45	137/13307	9.4344604417e-07	0.00303524281	0.00204982271	Btg2/Grn/Lgmn/J	5
BP	GO:0070997	neuron death	7/45	325/13307	9.9283813651e-07	0.00312450571	0.00212395001	Btg2/Grn/Lgmn/J	7
BP	GO:0007179	transforming growth factor beta receptor signaling pat	5/45	139/13307	0.00001010365	0.00315203301	0.00212869591	Dab2/Pmepa1/Ju	5
BP	GO:0032496	response to lipopolysaccharide	6/45	226/13307	0.00001051431	0.00323119751	0.00218215891	Zfp36/Junb/Jun/I	6
BP	GO:0034612	response to tumor necrosis factor	5/45	141/13307	0.00001080871	0.00327283531	0.00221027851	Pid1/Zfp36/Cxcl1	5
BP	GO:0009617	response to bacterium	8/45	453/13307	0.00001206261	0.00357286191	0.00241289871	Grn/Zfp36/Junb/J	8
BP	GO:0007178	transmembrane receptor protein serine/threonine kin	6/45	233/13307	0.00001243021	0.00357286191	0.00241289871	Fn1/Dusp1/Dab2	6
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	6/45	234/13307	0.00001272521	0.00357286191	0.00241289871	Btg2/Grn/Lgmn/J	6
BP	GO:0051402	neuron apoptotic process	6/45	234/13307	0.00001272521	0.00357286191	0.00241289871	Btg2/Grn/Lgmn/J	6
BP	GO:0002709	regulation of T cell mediated immunity	4/45	77/13307	0.00001289721	0.00357286191	0.00241289871	Il7r/Ccr2/Smad7/	4
BP	GO:0048524	positive regulation of viral process	4/45	77/13307	0.00001289721	0.00357286191	0.00241289871	P4hb/Jun/Lgals1/	4
BP	GO:0014070	response to organic cyclic compound	8/45	458/13307	0.00001301431	0.00357286191	0.00241289871	Grn/Dab2/Zfp36/J	8
BP	GO:0002694	regulation of leukocyte activation	8/45	459/13307	0.00001321921	0.00357938791	0.00241730601	Gsn/Il7r/Ccr2/Gri	8
BP	GO:0002724	regulation of T cell cytokine production	3/45	30/13307	0.00013764371	0.00363344161	0.00245381061	Ccr2/Smad7/Arg	3
BP	GO:0046686	response to cadmium ion	3/45	30/13307	0.00013764371	0.00363344161	0.00245381061	Gsn/Jun/Fos	3
BP	GO:0002237	response to molecule of bacterial origin	6/45	243/13307	0.00015638691	0.00399111861	0.00269536451	Zfp36/Junb/Jun/I	6
BP	GO:0032368	regulation of lipid transport	4/45	81/13307	0.00015700851	0.00399111861	0.00269536451	Dab2/Nfkbia/Spp	4
BP	GO:0051817	modification of morphology or physiology of other org	4/45	81/13307	0.00015700851	0.00399111861	0.00269536451	Jun/Arg1/Pf4/Ap	4
BP	GO:0070371	ERK1 and ERK2 cascade	6/45	246/13307	0.00016719361	0.00418337571	0.00282520351	Fn1/Dusp1/Dab2	6
BP	GO:1902107	positive regulation of leukocyte differentiation	5/45	155/13307	0.00016863531	0.00418337571	0.00282520351	Il7r/Ccr2/Jun/Fos	5
								aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+

BP	GO:0045785	positive regulation of cell adhesion	7/45	356/13307	0.0001747282	0.0042829227	0.0028924316	Il7r/Fn1/Ccr2/Da	7	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0048525	negative regulation of viral process	4/45	84/13307	0.0001807496	0.0043783940	0.0029569073	Gsn/Zfp36/Jun/B	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071396	cellular response to lipid	7/45	375/13307	0.0002403942	0.0057554859	0.0038869133	Dab2/Pid1/Zfp36	7	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1902105	regulation of leukocyte differentiation	6/45	264/13307	0.0002451040	0.0058007964	0.0039175133	Il7r/Ccr2/Jun/Sm	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051249	regulation of lymphocyte activation	7/45	377/13307	0.0002483322	0.0058104095	0.0039240055	Gsn/Il7r/Ccr2/Cd	7	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0042060	wound healing	6/45	266/13307	0.0002552785	0.0059058271	0.0039884449	Fn1/Ccr2/Cdkn1a	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0031667	response to nutrient levels	6/45	269/13307	0.0002711623	0.0061926780	0.0041821669	Cdkn1a/Gatm/Zfp	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071560	cellular response to transforming growth factor beta st	5/45	172/13307	0.0002736929	0.0061926780	0.0041821669	Dab2/Pmepa1/Ju	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0019058	viral life cycle	5/45	174/13307	0.0002887273	0.0064618438	0.0043639455	Gsn/P4hb/Bst2/Il	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050920	regulation of chemotaxis	5/45	175/13307	0.0002964760	0.0064797804	0.0043760589	Fn1/Ccr2/Dusp1/	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1901342	regulation of vasculature development	6/45	274/13307	0.0002993577	0.0064797804	0.0043760589	Ccr2/Grn/Cxcr4/I	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0042035	regulation of cytokine biosynthetic process	4/45	96/13307	0.0003021409	0.0064797804	0.0043760589	Ccr2/Ltb/Zfp36/E	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071559	response to transforming growth factor beta	5/45	176/13307	0.0003043818	0.0064797804	0.0043760589	Dab2/Pmepa1/Ju	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050863	regulation of T cell activation	6/45	275/13307	0.0003052640	0.0064797804	0.0043760589	Gsn/Il7r/Ccr2/Sm	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050866	negative regulation of cell activation	5/45	177/13307	0.0003124468	0.0065645716	0.0044333218	Ccr2/Grn/Smad7	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050678	regulation of epithelial cell proliferation	6/45	277/13307	0.0003173517	0.0066002747	0.0044574336	Grn/Dab2/Zfp36/	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0035821	modification of morphology or physiology of other org	4/45	98/13307	0.0003269347	0.0066036034	0.0044596815	Jun/Arg1/Pf4/Ap	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002369	T cell cytokine production	3/45	40/13307	0.0003271333	0.0066036034	0.0044596815	Ccr2/Smad7/Arg	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060393	regulation of pathway-restricted SMAD protein phospl	3/45	40/13307	0.0003271333	0.0066036034	0.0044596815	Dab2/Pmepa1/Sr	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071901	negative regulation of protein serine/threonine kinase	4/45	100/13307	0.0003531556	0.0070596848	0.0047676919	Dusp1/Cdkn1a/D	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002823	negative regulation of adaptive immune response base	3/45	42/13307	0.0003783193	0.0074899948	0.0050582976	Il7r/Smad7/Arg1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1901216	positive regulation of neuron death	4/45	103/13307	0.0003952659	0.0077509774	0.0052345498	Grn/Jun/Egr1/Fo	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002707	negative regulation of lymphocyte mediated immunity	3/45	43/13307	0.0004057341	0.0078075375	0.0052727471	Il7r/Smad7/Arg1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060389	pathway-restricted SMAD protein phosphorylation	3/45	43/13307	0.0004057341	0.0078075375	0.0052727471	Dab2/Pmepa1/Sr	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0045637	regulation of myeloid cell differentiation	5/45	189/13307	0.0004224303	0.0079796702	0.0053889954	Zfp36/Jun/Nfkbia	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1901215	negative regulation of neuron death	5/45	189/13307	0.0004224303	0.0079796702	0.0053889954	Btg2/Grn/Lgmn/	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1903708	positive regulation of hemopoiesis	5/45	190/13307	0.0004327626	0.0079858895	0.0053931955	Il7r/Ccr2/Jun/Fo	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0048247	lymphocyte chemotaxis	3/45	44/13307	0.0004343951	0.0079858895	0.0053931955	Ccr2/Cxcl16/Ccl6	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0071675	regulation of mononuclear cell migration	3/45	44/13307	0.0004343951	0.0079858895	0.0053931955	Ccr2/Dusp1/Lgm	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1905952	regulation of lipid localization	4/45	106/13307	0.0004408535	0.0080224497	0.0054178860	Dab2/Nfkbia/Spp	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0001525	angiogenesis	7/45	415/13307	0.0004441764	0.0080224497	0.0054178860	Fn1/Ccr2/Grn/Cx	7	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0042089	cytokine biosynthetic process	4/45	107/13307	0.0004568499	0.0081713428	0.0055184396	Ccr2/Ltb/Zfp36/E	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0046718	viral entry into host cell	3/45	45/13307	0.0004643259	0.0081713428	0.0055184396	Gsn/P4hb/Lgals1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0070098	chemokine-mediated signaling pathway	3/45	45/13307	0.0004643259	0.0081713428	0.0055184396	Cxcr4/Ccl6/Pf4	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060394	negative regulation of pathway-restricted SMAD prote	2/45	10/13307	0.0004946087	0.0086305035	0.0058285295	Pmepa1/Smad7	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:1903050	regulation of proteolysis involved in cellular protein ca	5/45	197/13307	0.0005105381	0.0088335976	0.0059656872	Rpl5/Dab2/Hspa	5	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0042107	cytokine metabolic process	4/45	111/13307	0.0005249993	0.0089125882	0.0060190327	Ccr2/Ltb/Zfp36/E	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002820	negative regulation of adaptive immune response	3/45	47/13307	0.0005280892	0.0089125882	0.0060190327	Il7r/Smad7/Arg1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0043618	regulation of transcription from RNA polymerase II pro	3/45	47/13307	0.0005280892	0.0089125882	0.0060190327	Jun/Egr1/Klf2	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0002456	T cell mediated immunity	4/45	113/13307	0.0005616568	0.0094020445	0.0063495825	Il7r/Ccr2/Smad7/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0030260	entry into host cell	3/45	49/13307	0.0005972065	0.0096822695	0.0065388298	Gsn/P4hb/Lgals1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0044409	entry into host	3/45	49/13307	0.0005972065	0.0096822695	0.0065388298	Gsn/P4hb/Lgals1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051806	entry into cell of other organism involved in symbiotic	3/45	49/13307	0.0005972065	0.0096822695	0.0065388298	Gsn/P4hb/Lgals1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051828	entry into other organism involved in symbiotic interac	3/45	49/13307	0.0005972065	0.0096822695	0.0065388298	Gsn/P4hb/Lgals1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0007610	behavior	7/45	441/13307	0.0006383753	0.0102688662	0.0069349823	Btg2/Grn/Gatm/I	7	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0034754	cellular hormone metabolic process	3/45	51/13307	0.0006718561	0.0106231052	0.0071742143	Dab2/Egr1/Spp1	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060395	SMAD protein signal transduction	3/45	51/13307	0.0006718561	0.0106231052	0.0071742143	Dab2/Jun/Fos	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050921	positive regulation of chemotaxis	4/45	119/13307	0.0006825449	0.0106231052	0.0071742143	Fn1/Ccr2/Cxcr4/I	4	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0031331	positive regulation of cellular catabolic process	6/45	321/13307	0.0006930433	0.0106231052	0.0071742143	Btg2/Dab2/Zfp36	6	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0043620	regulation of DNA-templated transcription in response	3/45	52/13307	0.0007113102	0.0106231052	0.0071742143	Jun/Egr1/Klf2	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0050810	regulation of steroid biosynthetic process	3/45	52/13307	0.0007113102	0.0106231052	0.0071742143	Dab2/Egr1/Apoe	3	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0006700	C21-steroid hormone biosynthetic process	2/45	12/13307	0.0007223092	0.0106231052	0.0071742143	Dab2/Egr1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0010566	regulation of ketone biosynthetic process	2/45	12/13307	0.0007223092	0.0106231052	0.0071742143	Dab2/Egr1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0010875	positive regulation of cholesterol efflux	2/45	12/13307	0.0007223092	0.0106231052	0.0071742143	Nfkbia/Apoe	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051852	disruption by host of symbiont cells	2/45	12/13307	0.0007223092	0.0106231052	0.0071742143	Arg1/Pf4	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0051873	killing by host of symbiont cells	2/45	12/13307	0.0007223092	0.0106231052	0.0071742143	Arg1/Pf4	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+
BP	GO:0060213	positive regulation of nuclear-transcribed mRNA poly(	2/45	12/13307	0.0007223092	0.0106231052	0.0071742143	Btg2/Zfp36	2	aPD-L1+aTGFb vs PBS	Down-regulated genes CD45+

BP	GO:0050673	epithelial cell proliferation	6/45	328/13307	0.0007757888	0.0113287177	0.0076507431	Grn/Dab2/Zfp36/6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071356	cellular response to tumor necrosis factor	4/45	124/13307	0.0007965227	0.0114688130	0.0077453552	Pid1/Zfp36/Nfkbi 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903364	positive regulation of cellular protein catabolic process	4/45	124/13307	0.0007965227	0.0114688130	0.0077453552	Dab2/Hspa1b/Sn 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903900	regulation of viral life cycle	4/45	125/13307	0.0008208362	0.0117368179	0.0079263498	Gsn/P4hb/Bst2/Il 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0048146	positive regulation of fibroblast proliferation	3/45	55/13307	0.0008384458	0.0118384236	0.0079949682	Fn1/Cdkn1a/Jun 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0001667	ameboidal-type cell migration	6/45	333/13307	0.0008394414	0.0118384236	0.0079949682	Fn1/Grn/Cxcr4/L 6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0006706	steroid catabolic process	2/45	13/13307	0.0008518029	0.0118504202	0.0080030700	Spp1/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0090594	inflammatory response to wounding	2/45	13/13307	0.0008518029	0.0118504202	0.0080030700	Ccr2/Grn 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0035914	skeletal muscle cell differentiation	3/45	56/13307	0.0008838184	0.0122133037	0.0082481399	Btg2/Egr1/Fos 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903362	regulation of cellular protein catabolic process	5/45	223/13307	0.0008944853	0.0122783016	0.0082920357	Rpl5/Dab2/Hspa: 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002829	negative regulation of type 2 immune response	2/45	14/13307	0.0009916339	0.0132582748	0.0089538514	Ccr2/Arg1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0046886	positive regulation of hormone biosynthetic process	2/45	14/13307	0.0009916339	0.0132582748	0.0089538514	Dab2/Egr1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0060211	regulation of nuclear-transcribed mRNA poly(A) tail shi	2/45	14/13307	0.0009916339	0.0132582748	0.0089538514	Btg2/Zfp36 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1990000	amyloid fibril formation	2/45	14/13307	0.0009916339	0.0132582748	0.0089538514	Gsn/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0001558	regulation of cell growth	6/45	345/13307	0.0010087476	0.0134000736	0.0090496139	Fn1/Cdkn1a/Cxcr 6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002763	positive regulation of myeloid leukocyte differentiation	3/45	59/13307	0.0010292050	0.0135841866	0.0091739529	Jun/Fos/Pf4 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0001818	negative regulation of cytokine production	5/45	234/13307	0.0011094448	0.0145499810	0.0098261930	Fn1/Zfp36/Smad 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903034	regulation of response to wounding	4/45	136/13307	0.0011239923	0.0146014320	0.0098609400	Grn/Cdkn1a/Cxcr 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043407	negative regulation of MAP kinase activity	3/45	61/13307	0.0011340519	0.0146014320	0.0098609400	Dusp1/Dusp2/Ap 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0051818	disruption of cells of other organism involved in symbi	2/45	15/13307	0.0011417341	0.0146014320	0.0098609400	Arg1/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0051883	killing of cells in other organism involved in symbiotic i	2/45	15/13307	0.0011417341	0.0146014320	0.0098609400	Arg1/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0001659	temperature homeostasis	4/45	137/13307	0.0011549591	0.0146793885	0.0099135872	Ccr2/Gatm/Cxcr4 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0015850	organic hydroxy compound transport	4/45	138/13307	0.0011865207	0.0149880136	0.0101220142	Dab2/Nfkbia/Spp 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0042108	positive regulation of cytokine biosynthetic process	3/45	63/13307	0.0012454181	0.0156360731	0.0105596751	Ccr2/Ltb/Egr1 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903707	negative regulation of hemopoiesis	4/45	141/13307	0.0012848357	0.0159366076	0.0107626383	Zfp36/Smad7/Nfi 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic pr	4/45	141/13307	0.0012848357	0.0159366076	0.0107626383	Rpl5/Dab2/Hspa: 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071498	cellular response to fluid shear stress	2/45	16/13307	0.0013020354	0.0160532396	0.0108414046	Klf2/Spp1	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0045765	regulation of angiogenesis	5/45	248/13307	0.0014359536	0.0174242327	0.0117672919	Ccr2/Grn/Cxcr4/I 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0000188	inactivation of MAPK activity	2/45	17/13307	0.0014724703	0.0174242327	0.0117672919	Dusp1/Dusp2 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010743	regulation of macrophage derived foam cell differentia	2/45	17/13307	0.0014724703	0.0174242327	0.0117672919	Nfkbia/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010818	T cell chemotaxis	2/45	17/13307	0.0014724703	0.0174242327	0.0117672919	Ccr2/Cxcl16 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010874	regulation of cholesterol efflux	2/45	17/13307	0.0014724703	0.0174242327	0.0117672919	Nfkbia/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0090026	positive regulation of monocyte chemotaxis	2/45	17/13307	0.0014724703	0.0174242327	0.0117672919	Ccr2/Lgmn 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1900153	positive regulation of nuclear-transcribed mRNA catab	2/45	17/13307	0.0014724703	0.0174242327	0.0117672919	Btg2/Zfp36 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043409	negative regulation of MAPK cascade	4/45	148/13307	0.0015362083	0.0180696155	0.0122031451	Dusp1/Dab2/Dus 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043525	positive regulation of neuron apoptotic process	3/45	68/13307	0.0015533375	0.0180696155	0.0122031451	Grn/Jun/Egr1 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071347	cellular response to interleukin-1	3/45	68/13307	0.0015533375	0.0180696155	0.0122031451	Fn1/Egr1/Ccl6 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0043901	negative regulation of multi-organism process	4/45	150/13307	0.0016139010	0.0186686647	0.0126077074	Gsn/Zfp36/Jun/B 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0051444	negative regulation of ubiquitin-protein transferase ac	2/45	18/13307	0.0016529715	0.0190137900	0.0128407845	Rpl5/Smad7 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0009896	positive regulation of catabolic process	6/45	381/13307	0.0016779770	0.0191941928	0.0129626178	Btg2/Dab2/Zfp36 6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032102	negative regulation of response to external stimulus	5/45	258/13307	0.0017092643	0.0194440624	0.0131313650	Dusp1/Grn/Cdkn 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0019218	regulation of steroid metabolic process	3/45	71/13307	0.0017590411	0.0198949268	0.0134358520	Dab2/Egr1/Apoe 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0046651	lymphocyte proliferation	5/45	260/13307	0.0017682232	0.0198949268	0.0134358520	Il7r/Ccr2/Cdkn1a 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	5/45	261/13307	0.0017982579	0.0200831159	0.0135629437	Il7r/Ccr2/Smad7/5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032870	cellular response to hormone stimulus	6/45	387/13307	0.0018163411	0.0200831159	0.0135629437	Dab2/Pid1/Zfp366	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032943	mononuclear cell proliferation	5/45	262/13307	0.0018286666	0.0200831159	0.0135629437	Il7r/Ccr2/Cdkn1a 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0008207	C21-steroid hormone metabolic process	2/45	19/13307	0.0018434720	0.0200831159	0.0135629437	Dab2/Egr1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032352	positive regulation of hormone metabolic process	2/45	19/13307	0.0018434720	0.0200831159	0.0135629437	Dab2/Egr1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1900151	regulation of nuclear-transcribed mRNA catabolic proc	2/45	19/13307	0.0018434720	0.0200831159	0.0135629437	Btg2/Zfp36 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0030307	positive regulation of cell growth	4/45	158/13307	0.0019521630	0.0211552828	0.0142870216	Fn1/Cxcr4/Cxcl1 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002706	regulation of lymphocyte mediated immunity	4/45	159/13307	0.0019976394	0.0214714323	0.0145005301	Il7r/Ccr2/Smad7/4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002822	regulation of adaptive immune response based on som	4/45	160/13307	0.0020438459	0.0214714323	0.0145005301	Il7r/Ccr2/Smad7/4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071222	cellular response to lipopolysaccharide	4/45	160/13307	0.0020438459	0.0214714323	0.0145005301	Zfp36/Cxcl16/Nfi 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032373	positive regulation of sterol transport	2/45	20/13307	0.0020439051	0.0214714323	0.0145005301	Nfkbia/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032376	positive regulation of cholesterol transport	2/45	20/13307	0.0020439051	0.0214714323	0.0145005301	Nfkbia/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032897	negative regulation of viral transcription	2/45	20/13307	0.0020439051	0.0214714323	0.0145005301	Zfp36/Jun 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002718	regulation of cytokine production involved in immune	3/45	75/13307	0.0020587219	0.0215173025	0.0145315082	Ccr2/Smad7/Arg 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+

BP	GO:0002695	negative regulation of leukocyte activation	4/45	162/13307	0.0021384730	0.0222379595	0.0150181971	Ccr2/Grn/Smad7, 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032436	positive regulation of proteasomal ubiquitin-depender	3/45	77/13307	0.0022197485	0.0227688063	0.0153766995	Dab2/Hspa1b/Sn 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0120162	positive regulation of cold-induced thermogenesis	3/45	77/13307	0.0022197485	0.0227688063	0.0153766995	Ccr2/Gatm/Cxcr43	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002719	negative regulation of cytokine production involved in	2/45	21/13307	0.0022542046	0.0227688063	0.0153766995	Smad7/Arg1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010742	macrophage derived foam cell differentiation	2/45	21/13307	0.0022542046	0.0227688063	0.0153766995	Nfkbia/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903077	negative regulation of protein localization to plasma m	2/45	21/13307	0.0022542046	0.0227688063	0.0153766995	Dab2/Pid1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0016049	cell growth	6/45	404/13307	0.0022558700	0.0227688063	0.0153766995	Fn1/Cdkn1a/Cxcr 6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0062012	regulation of small molecule metabolic process	5/45	278/13307	0.0023683736	0.0236722398	0.0159868249	Dab2/Pid1/Ppp1r5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0070661	leukocyte proliferation	5/45	278/13307	0.0023683736	0.0236722398	0.0159868249	Il7r/Ccr2/Cdkn1a 5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071219	cellular response to molecule of bacterial origin	4/45	167/13307	0.0023882392	0.0237554816	0.0160430414	Zfp36/Cxcl16/Nfk 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0034405	response to fluid shear stress	2/45	22/13307	0.0024743043	0.0241449891	0.0163060917	Klf2/Spp1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0045940	positive regulation of steroid metabolic process	2/45	22/13307	0.0024743043	0.0241449891	0.0163060917	Dab2/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071677	positive regulation of mononuclear cell migration	2/45	22/13307	0.0024743043	0.0241449891	0.0163060917	Ccr2/Lgmn 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0090077	foam cell differentiation	2/45	22/13307	0.0024743043	0.0241449891	0.0163060917	Nfkbia/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0061136	regulation of proteasomal protein catabolic process	4/45	170/13307	0.0025473896	0.0247409214	0.0167085489	Dab2/Hspa1b/Sn 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010810	regulation of cell-substrate adhesion	4/45	171/13307	0.0026020240	0.0251528994	0.0169867744	Fn1/Dab2/Lgals1 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	2/45	23/13307	0.0027041387	0.0258968451	0.0174891911	Btg2/Zfp36 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1904376	negative regulation of protein localization to cell perip	2/45	23/13307	0.0027041387	0.0258968451	0.0174891911	Dab2/Pid1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0060840	artery development	3/45	83/13307	0.0027490763	0.0261868158	0.0176850201	Cxcr4/Smad7/Ap 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0007159	leukocyte cell-cell adhesion	5/45	288/13307	0.0027598538	0.0261868158	0.0176850201	Il7r/Ccr2/Smad7/5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002819	regulation of adaptive immune response	4/45	176/13307	0.0028873450	0.0272708413	0.0184171066	Il7r/Ccr2/Smad7/4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0070555	response to interleukin-1	3/45	85/13307	0.0029413333	0.0274553232	0.0185416947	Fn1/Egr1/Ccl6 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032801	receptor catabolic process	2/45	24/13307	0.0029436423	0.0274553232	0.0185416947	Lgmn/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0006469	negative regulation of protein kinase activity	4/45	177/13307	0.0029468802	0.0274553232	0.0185416947	Dusp1/Cdkn1a/D 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0017015	regulation of transforming growth factor beta receptoi	3/45	86/13307	0.0030404916	0.0279480910	0.0188744808	Dab2/Pmepa1/Sr 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0045638	negative regulation of myeloid cell differentiation	3/45	86/13307	0.0030404916	0.0279480910	0.0188744808	Zfp36/Nfkbia/Pf43	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0072676	lymphocyte migration	3/45	86/13307	0.0030404916	0.0279480910	0.0188744808	Ccr2/Cxcl16/Ccl6 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0031348	negative regulation of defense response	4/45	179/13307	0.0030684685	0.0280031886	0.0189116904	Grn/Zfp36/Arg1/ 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0048638	regulation of developmental growth	5/45	296/13307	0.0031053829	0.0280031886	0.0189116904	Fn1/Cdkn1a/Cxcr5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0050727	regulation of inflammatory response	5/45	296/13307	0.0031053829	0.0280031886	0.0189116904	Ccr2/Grn/Zfp36/I5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0030593	neutrophil chemotaxis	3/45	87/13307	0.0031416884	0.0280031886	0.0189116904	Cd6/Pf4/Spp1 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0090090	negative regulation of canonical Wnt signaling pathwa	3/45	87/13307	0.0031416884	0.0280031886	0.0189116904	Dab2/Fgr1/Apoe 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1903844	regulation of cellular response to transforming growth	3/45	87/13307	0.0031416884	0.0280031886	0.0189116904	Dab2/Pmepa1/Sr 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:2000060	positive regulation of ubiquitin-dependent protein cat	3/45	87/13307	0.0031416884	0.0280031886	0.0189116904	Dab2/Hspa1b/Sn 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0045639	positive regulation of myeloid cell differentiation	3/45	89/13307	0.0033502515	0.0296058711	0.0199940470	Jun/Fos/Pf4 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0048145	regulation of fibroblast proliferation	3/45	89/13307	0.0033502515	0.0296058711	0.0199940470	Fn1/Cdkn1a/Jun 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1901652	response to peptide	5/45	302/13307	0.0033843695	0.0297795595	0.0201113458	Gatm/Pid1/Lgmn5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0033344	cholesterol efflux	2/45	26/13307	0.0034513973	0.0300391986	0.0202866907	Nfkbia/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071480	cellular response to gamma radiation	2/45	26/13307	0.0034513973	0.0300391986	0.0202866907	Cdkn1a/Egr1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0048144	fibroblast proliferation	3/45	90/13307	0.0034576445	0.0300391986	0.0202866907	Fn1/Cdkn1a/Jun 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0031668	cellular response to extracellular stimulus	4/45	186/13307	0.0035210749	0.0304617368	0.0205720479	Cdkn1a/Ldha/Jur 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071216	cellular response to biotic stimulus	4/45	188/13307	0.0036583086	0.0315164221	0.0212843197	Zfp36/Cxcl16/Nfk 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0016525	negative regulation of angiogenesis	3/45	92/13307	0.0036787184	0.0315164221	0.0212843197	Ccr2/Klf2/Pf4 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0007616	long-term memory	2/45	27/13307	0.0037195194	0.0315164221	0.0212843197	Egr1/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0048535	lymph node development	2/45	27/13307	0.0037195194	0.0315164221	0.0212843197	Il7r/Ltb 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:1905476	negative regulation of protein localization to membrar	2/45	27/13307	0.0037195194	0.0315164221	0.0212843197	Dab2/Pid1 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0007613	memory	3/45	93/13307	0.0037924249	0.0317985330	0.0214748407	Lgmn/Egr1/Apoe 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:2000379	positive regulation of reactive oxygen species metabol	3/45	93/13307	0.0037924249	0.0317985330	0.0214748407	Cdkn1a/Pid1/Klf2 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002440	production of molecular mediator of immune response	4/45	190/13307	0.0037991447	0.0317985330	0.0214748407	Il7r/Ccr2/Smad7/4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0008202	steroid metabolic process	4/45	191/13307	0.0038709278	0.0321380666	0.0217041415	Dab2/Egr1/Spp1, 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0010632	regulation of epithelial cell migration	4/45	191/13307	0.0038709278	0.0321380666	0.0217041415	Grn/Lgmn/Jun/A 4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0071407	cellular response to organic cyclic compound	5/45	312/13307	0.0038889914	0.0321583674	0.0217178514	Dab2/Zfp36/Egr15	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0002367	cytokine production involved in immune response	3/45	94/13307	0.0039082611	0.0321884389	0.0217381600	Ccr2/Smad7/Arg 3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0031640	killing of cells of other organism	2/45	28/13307	0.0039970524	0.0322742391	0.0217961043	Arg1/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032371	regulation of sterol transport	2/45	28/13307	0.0039970524	0.0322742391	0.0217961043	Nfkbia/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0032374	regulation of cholesterol transport	2/45	28/13307	0.0039970524	0.0322742391	0.0217961043	Nfkbia/Apoe 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0044364	disruption of cells of other organism	2/45	28/13307	0.0039970524	0.0322742391	0.0217961043	Arg1/Pf4 2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+

BP	GO:0046885	regulation of hormone biosynthetic process	2/45	28/13307	0.0039970524	0.0322742391	0.0217961043	Dab2/Egr1	2
BP	GO:0045732	positive regulation of protein catabolic process	4/45	193/13307	0.0040172521	0.0323106337	0.0218206831	Dab2/Hspa1b/Sn	4
BP	GO:0033673	negative regulation of kinase activity	4/45	194/13307	0.0040918045	0.0327822006	0.0221391513	Dusp1/Cdkn1a/D	4
BP	GO:1901800	positive regulation of proteasomal protein catabolic pr	3/45	96/13307	0.0041463715	0.0329628531	0.0222611533	Dab2/Hspa1b/Sn	3
BP	GO:2000181	negative regulation of blood vessel morphogenesis	3/45	96/13307	0.0041463715	0.0329628531	0.0222611533	Ccr2/Klf2/Pf4	3
BP	GO:0002573	myeloid leukocyte differentiation	4/45	196/13307	0.0042437174	0.0336069778	0.0226961569	Junb/Jun/Fos/Pf4	4
BP	GO:0002688	regulation of leukocyte chemotaxis	3/45	100/13307	0.0046486761	0.0366728899	0.0247666918	Ccr2/Dusp1/Lgm	3
BP	GO:0002701	negative regulation of production of molecular mediat	2/45	31/13307	0.0048854796	0.0381734997	0.0257801145	Smad7/Arg1	2
BP	GO:0002828	regulation of type 2 immune response	2/45	31/13307	0.0048854796	0.0381734997	0.0257801145	Ccr2/Arg1	2
BP	GO:0006694	steroid biosynthetic process	3/45	102/13307	0.0049130536	0.0381734997	0.0257801145	Dab2/Egr1/Apoe	3
BP	GO:0007612	learning	3/45	102/13307	0.0049130536	0.0381734997	0.0257801145	Btg2/Lgmn/Jun	3
BP	GO:0061041	regulation of wound healing	3/45	103/13307	0.0050485872	0.0390000626	0.0263383261	Cdkn1a/Cxcr4/Ap	3
BP	GO:0030098	lymphocyte differentiation	5/45	332/13307	0.0050573175	0.0390000626	0.0263383261	Il7r/Ccr2/Smad7/	5
BP	GO:0002703	regulation of leukocyte mediated immunity	4/45	207/13307	0.0051479926	0.0393633927	0.0265836976	Il7r/Ccr2/Smad7/	4
BP	GO:0010975	regulation of neuron projection development	6/45	478/13307	0.0051649981	0.0393633927	0.0265836976	Fn1/Grn/Cxcr4/D	6
BP	GO:0071346	cellular response to interferon-gamma	3/45	104/13307	0.0051863650	0.0393633927	0.0265836976	Gsn/Ccl6/Arg1	3
BP	GO:1990266	neutrophil migration	3/45	104/13307	0.0051863650	0.0393633927	0.0265836976	Ccl6/Pf4/Spp1	3
BP	GO:1902895	positive regulation of pri-miRNA transcription by RNA	2/45	32/13307	0.0052000207	0.0393633927	0.0265836976	Jun/Fos	2
BP	GO:0010811	positive regulation of cell-substrate adhesion	3/45	105/13307	0.0053263975	0.0401723535	0.0271300217	Fn1/Dab2/Spp1	3
BP	GO:0001936	regulation of endothelial cell proliferation	3/45	106/13307	0.0054686949	0.0404740538	0.0273337722	Jun/Arg1/Apoe	3
BP	GO:0030178	negative regulation of Wnt signaling pathway	3/45	106/13307	0.0054686949	0.0404740538	0.0273337722	Dab2/Egr1/Apoe	3
BP	GO:1901343	negative regulation of vasculature development	3/45	106/13307	0.0054686949	0.0404740538	0.0273337722	Ccr2/Klf2/Pf4	3
BP	GO:0022407	regulation of cell-cell adhesion	5/45	339/13307	0.0055196982	0.0404740538	0.0273337722	Il7r/Ccr2/Smad7/	5
BP	GO:0036230	granulocyte activation	2/45	33/13307	0.0055236566	0.0404740538	0.0273337722	Ccr2/Grn	2
BP	GO:0042181	ketone biosynthetic process	2/45	33/13307	0.0055236566	0.0404740538	0.0273337722	Dab2/Egr1	2
BP	GO:0042832	defense response to protozoan	2/45	33/13307	0.0055236566	0.0404740538	0.0273337722	Arg1/Pf4	2
BP	GO:1902930	regulation of alcohol biosynthetic process	2/45	33/13307	0.0055236566	0.0404740538	0.0273337722	Dab2/Apoe	2
BP	GO:0051701	interaction with host	3/45	107/13307	0.0056132673	0.0406961885	0.0274837887	Gsn/P4hb/Lgals1	3
BP	GO:0071621	granulocyte chemotaxis	3/45	107/13307	0.0056132673	0.0406961885	0.0274837887	Ccl6/Pf4/Spp1	3
BP	GO:1903052	positive regulation of proteolysis involved in cellular pr	3/45	107/13307	0.0056132673	0.0406961885	0.0274837887	Dab2/Hspa1b/Sn	3
BP	GO:0031099	regeneration	3/45	108/13307	0.0057601248	0.0416143755	0.0281038777	Grn/Cdkn1a/Jun	3
BP	GO:0022409	positive regulation of cell-cell adhesion	4/45	215/13307	0.0058815779	0.0421957110	0.0284964772	Il7r/Ccr2/Smad7/	4
BP	GO:0071496	cellular response to external stimulus	4/45	215/13307	0.0058815779	0.0421957110	0.0284964772	Cdkn1a/Ldha/Jur	4
BP	GO:0042176	regulation of protein catabolic process	5/45	347/13307	0.0060840784	0.0434969358	0.0293752471	Rpl5/Dab2/Hspa:	5
BP	GO:0001562	response to protozoan	2/45	35/13307	0.0061979639	0.0438207664	0.0295939431	Arg1/Pf4	2
BP	GO:0045622	regulation of T-helper cell differentiation	2/45	35/13307	0.0061979639	0.0438207664	0.0295939431	Ccr2/Smad7	2
BP	GO:0061844	antimicrobial humoral immune response mediated by	2/45	35/13307	0.0061979639	0.0438207664	0.0295939431	Hist1h2bc/Pf4	2
BP	GO:0002761	regulation of myeloid leukocyte differentiation	3/45	111/13307	0.0062145040	0.0438207664	0.0295939431	Jun/Fos/Pf4	3
BP	GO:0006959	humoral immune response	3/45	113/13307	0.0065290231	0.0455703684	0.0307755203	Ccr2/Hist1h2bc/I	3
BP	GO:0106106	cold-induced thermogenesis	3/45	113/13307	0.0065290231	0.0455703684	0.0307755203	Ccr2/Gatm/Cxcr4	3
BP	GO:0120161	regulation of cold-induced thermogenesis	3/45	113/13307	0.0065290231	0.0455703684	0.0307755203	Ccr2/Gatm/Cxcr4	3
BP	GO:0002697	regulation of immune effector process	5/45	354/13307	0.0066104495	0.0456742134	0.0308456511	Il7r/Ccr2/Grn/Sn	5
BP	GO:0048871	multicellular organismal homeostasis	5/45	354/13307	0.0066104495	0.0456742134	0.0308456511	Ccr2/Gatm/Cxcr4	5
BP	GO:0061564	axon development	5/45	354/13307	0.0066104495	0.0456742134	0.0308456511	Fn1/Grn/Cxcr4/Is	5
BP	GO:0002366	leukocyte activation involved in immune response	4/45	223/13307	0.0066820974	0.0460148449	0.0310756934	Ccr2/Grn/Smad7,	4
BP	GO:0032350	regulation of hormone metabolic process	2/45	37/13307	0.0069079064	0.0470972829	0.0318067077	Dab2/Egr1	2
BP	GO:0042092	type 2 immune response	2/45	37/13307	0.0069079064	0.0470972829	0.0318067077	Ccr2/Arg1	2
BP	GO:1900271	regulation of long-term synaptic potentiation	2/45	37/13307	0.0069079064	0.0470972829	0.0318067077	Lgmn/Apoe	2
BP	GO:0002263	cell activation involved in immune response	4/45	227/13307	0.0071082597	0.0483033229	0.0326211955	Ccr2/Grn/Smad7,	4
BP	GO:0032434	regulation of proteasomal ubiquitin-dependent proteii	3/45	117/13307	0.0071862239	0.0485129016	0.0327627326	Dab2/Hspa1b/Sn	3
BP	GO:0042445	hormone metabolic process	3/45	117/13307	0.0071862239	0.0485129016	0.0327627326	Dab2/Egr1/Spp1	3
BP	GO:0001774	microglial cell activation	2/45	38/13307	0.0072760877	0.0487995589	0.0329563239	Grn/Jun	2
BP	GO:0002269	leukocyte activation involved in inflammatory respons	2/45	38/13307	0.0072760877	0.0487995589	0.0329563239	Grn/Jun	2
BP	GO:0001935	endothelial cell proliferation	3/45	118/13307	0.0073564412	0.0491782876	0.0332120947	Jun/Arg1/Apoe	3
BP	GO:0006869	lipid transport	4/45	230/13307	0.0074394697	0.0495723891	0.0334782474	Dab2/Nfkbia/Spp	4
MF	GO:0031625	ubiquitin protein ligase binding	8/45	280/13229	3.9816145582	0.0002764292	0.0001848756	Rpl5/Cdkn1a/Cxc	8
MF	GO:0005125	cytokine activity	6/45	129/13229	4.5626413579	0.0002764292	0.0001848756	Grn/Ltb/Cxcl16/C	6

aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+

MF	GO:0046332	SMAD binding	5/45	73/13229	4.5816998313	0.0002764292	0.0001848756	Dab2/Pmepa1/Ju	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0044389	ubiquitin-like protein ligase binding	8/45	298/13229	6.3028156897	0.0002852024	0.0001907431	Rpl5/Cdkn1a/Cxc	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0005178	integrin binding	5/45	104/13229	2.5942163299	0.0009391063	0.0006280734	P4hb/Fn1/Dab2/	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0019957	C-C chemokine binding	3/45	21/13229	4.6868174623	0.0012118770	0.0008105022	Ccr2/Cxcr4/Zfp36	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0070412	R-SMAD binding	3/45	21/13229	4.6868174623	0.0012118770	0.0008105022	Pmepa1/Jun/Fos	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0019956	chemokine binding	3/45	27/13229	0.0001016135	0.0022990060	0.0015375731	Ccr2/Cxcr4/Zfp36	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0048018	receptor ligand activity	6/45	255/13229	0.0002097263	0.0036944717	0.0024708592	Grn/Ltb/Cxcl16/C	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0008009	chemokine activity	3/45	35/13229	0.0002230866	0.0036944717	0.0024708592	Cxcl16/Ccl6/Pf4	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0000981	DNA-binding transcription factor activity, RNA polymer	8/45	493/13229	0.0002245259	0.0036944717	0.0024708592	Btg2/Fosb/Ier2/J	8	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0050839	cell adhesion molecule binding	5/45	175/13229	0.0003045548	0.0042331145	0.0028311030	P4hb/Fn1/Dab2/	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0030545	receptor regulator activity	6/45	276/13229	0.0003211447	0.0042331145	0.0028311030	Grn/Ltb/Cxcl16/C	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0001228	DNA-binding transcription activator activity, RNA polyr	6/45	277/13229	0.0003274232	0.0042331145	0.0028311030	Fosb/Ier2/Junb/J	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0050840	extracellular matrix binding	3/45	43/13229	0.0004127236	0.0049801983	0.0033307520	Tgfbi/Lgals1/Spp	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0042379	chemokine receptor binding	3/45	45/13229	0.0004723116	0.0053430260	0.0035734108	Cxcl16/Ccl6/Pf4	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase ac	2/45	12/13229	0.0007307594	0.0077804391	0.0052035504	Dusp1/Dusp2	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0005126	cytokine receptor binding	5/45	217/13229	0.0008123219	0.0081683480	0.0054629835	Ltb/Smad7/Cxcl1	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0033549	MAP kinase phosphatase activity	2/45	13/13229	0.0008617571	0.0082093707	0.0054904195	Dusp1/Dusp2	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0016493	C-C chemokine receptor activity	2/45	20/13229	0.0020676072	0.0187118454	0.0125144647	Ccr2/Cxcr4	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0001637	G protein-coupled chemoattractant receptor activity	2/45	21/13229	0.0022803166	0.0187607865	0.0125471966	Ccr2/Cxcr4	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0004950	chemokine receptor activity	2/45	21/13229	0.0022803166	0.0187607865	0.0125471966	Ccr2/Cxcr4	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0004896	cytokine receptor activity	3/45	82/13229	0.0027002468	0.0212497687	0.0142118255	Il7r/Ccr2/Cxcr4	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0043394	proteoglycan binding	2/45	27/13229	0.0037623204	0.0283741665	0.0189766161	Fn1/Apoe	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0008201	heparin binding	3/45	101/13229	0.0048582051	0.0351734049	0.0235239404	Fn1/Pf4/Apoe	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0001102	RNA polymerase II activating transcription factor bindi	2/45	32/13229	0.0052595271	0.0352583116	0.0235807260	Jun/Fos	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0008138	protein tyrosine/serine/threonine phosphatase activity	2/45	32/13229	0.0052595271	0.0352583116	0.0235807260	Dusp1/Dusp2	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0051019	mitogen-activated protein kinase binding	2/45	33/13229	0.0055867963	0.0361146479	0.0241534429	Dusp1/Dusp2	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0000979	RNA polymerase II core promoter sequence-specific DI	2/45	34/13229	0.0059231930	0.0369688942	0.0247247620	Egr1/Fos	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
MF	GO:0019955	cytokine binding	3/45	110/13229	0.0061594515	0.0371620240	0.0248539271	Ccr2/Cxcr4/Zfp36	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45+
BP	GO:0046034	ATP metabolic process	6/34	207/13403	1.1832976697	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0001503	ossification	7/34	323/13403	1.3593909705	0.0032721108	0.0024939693	Atp6v1b1/Ccn1/C	7	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009126	purine nucleoside monophosphate metabolic process	6/34	229/13403	2.0995880441	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009167	purine ribonucleoside monophosphate metabolic proc	6/34	229/13403	2.0995880441	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	6/34	231/13403	2.2053469104	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009161	ribonucleoside monophosphate metabolic process	6/34	233/13403	2.3153678362	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0030198	extracellular matrix organization	6/34	233/13403	2.3153678362	0.0032721108	0.0024939693	P3h4/Ccn1/Mmp	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009199	ribonucleoside triphosphate metabolic process	6/34	235/13403	2.4297790508	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009144	purine nucleoside triphosphate metabolic process	6/34	239/13403	2.6722977190	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009123	nucleoside monophosphate metabolic process	6/34	240/13403	2.7358785998	0.0032721108	0.0024939693	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009141	nucleoside triphosphate metabolic process	6/34	253/13403	3.6794459426	0.0040005612	0.0030491867	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0043062	extracellular structure organization	6/34	269/13403	5.1830532323	0.0051657763	0.0039373018	P3h4/Ccn1/Mmp	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0001649	osteoblast differentiation	5/34	169/13403	6.2167425784	0.0057194031	0.0043592705	Ccn1/Gja1/Cthrc	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0032963	collagen metabolic process	4/34	92/13403	8.2350521271	0.0070350873	0.0053620715	P3h4/Mmp23/Cc	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0006754	ATP biosynthetic process	4/34	105/13403	0.0001376438	0.0109748056	0.0083648843	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic proce	4/34	115/13403	0.0001955340	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	4/34	116/13403	0.0002021552	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009150	purine ribonucleotide metabolic process	6/34	348/13403	0.0002133667	0.0125424428	0.0095597214	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009201	ribonucleoside triphosphate biosynthetic process	4/34	118/13403	0.0002158813	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0045667	regulation of osteoblast differentiation	4/34	120/13403	0.0002302676	0.0125424428	0.0095597214	Ccn1/Gja1/Cthrc	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009259	ribonucleotide metabolic process	6/34	358/13403	0.0002486703	0.0125424428	0.0095597214	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009127	purine nucleoside monophosphate biosynthetic proce	4/34	125/13403	0.0002692449	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009168	purine ribonucleoside monophosphate biosynthetic pr	4/34	125/13403	0.0002692449	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0030199	collagen fibril organization	3/34	50/13403	0.0002694573	0.0125424428	0.0095597214	P3h4/Col1a2/Col	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0043589	skin morphogenesis	2/34	10/13403	0.0002775244	0.0125424428	0.0095597214	Col1a2/Col1a1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0006163	purine nucleotide metabolic process	6/34	367/13403	0.0002842517	0.0125424428	0.0095597214	Tpi1/Atp6v1b1/P	6	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009142	nucleoside triphosphate biosynthetic process	4/34	127/13403	0.0002860899	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0009156	ribonucleoside monophosphate biosynthetic process	4/34	129/13403	0.0003036801	0.0125424428	0.0095597214	Tpi1/Pgk1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0031214	biomineral tissue development	4/34	130/13403	0.0003127606	0.0125424428	0.0095597214	Ccn1/Gja1/Col1a	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-

BP	GO:0019693	ribose phosphate metabolic process	6/34	374/13403	0.00031460971	0.012542442	8 0.0095597214	Tpi1/Atp6v1b1/P	6
BP	GO:0009124	nucleoside monophosphate biosynthetic process	4/34	134/13403	0.00035104171	0.013543418	4 0.0103226547	Tpi1/Pgk1/COX2/	4
BP	GO:0071417	cellular response to organonitrogen compound	6/34	391/13403	0.00039903231	0.014913834	5 0.0113671719	Actb/Grb10/Prnp	6
BP	GO:0072521	purine-containing compound metabolic process	6/34	399/13403	0.00044446091	0.016108343	5 0.0122776144	Tpi1/Atp6v1b1/P	6
BP	GO:0033690	positive regulation of osteoblast proliferation	2/34	13/13403	0.00047875161	0.016840792	2 0.0128358792	Ccn1/Cthrc1	2
BP	GO:0045669	positive regulation of osteoblast differentiation	3/34	66/13403	0.00061191511	0.020910014	7 0.0159373989	Ccn1/Gja1/Cthrc	3
BP	GO:0048771	tissue remodeling	4/34	158/13403	0.00065452431	0.021744752	2 0.0165736273	P3h4/Gja1/Cthrc	4
BP	GO:1901699	cellular response to nitrogen compound	6/34	434/13403	0.00069300951	0.022401065	9 0.0170738630	Actb/Grb10/Prnp	6
BP	GO:0006006	glucose metabolic process	4/34	162/13403	0.00071889291	0.022626208	1 0.0172454640	Tpi1/Pgk1/Grb10	4
BP	GO:0062012	regulation of small molecule metabolic process	5/34	295/13403	0.00082295991	0.025237438	6 0.0192357172	Pgk1/Grb10/Fdp	5
BP	GO:0009117	nucleotide metabolic process	6/34	464/13403	0.00098238261	0.028858713	8 0.0219958160	Tpi1/Atp6v1b1/P	6
BP	GO:0120162	positive regulation of cold-induced thermogenesis	3/34	78/13403	0.00099641211	0.028858713	8 0.0219958160	Gadd45g/Gja1/G	3
BP	GO:0009152	purine ribonucleotide biosynthetic process	4/34	178/13403	0.00102177021	0.028858713	8 0.0219958160	Tpi1/Pgk1/COX2/	4
BP	GO:0070208	protein heterotrimerization	2/34	19/13403	0.00103960501	0.028858713	8 0.0219958160	Col1a2/Col1a1	2
BP	GO:0006753	nucleoside phosphate metabolic process	6/34	471/13403	0.00106169181	0.028858713	8 0.0219958160	Tpi1/Atp6v1b1/P	6
BP	GO:0006091	generation of precursor metabolites and energy	5/34	315/13403	0.00110419821	0.029347135	3 0.0223680858	Tpi1/Pgk1/Grb10	5
BP	GO:0022898	regulation of transmembrane transporter activity	4/34	184/13403	0.00115542971	0.029941613	3 0.0228211909	Actb/Gja1/Prnp/I	4
BP	GO:0046849	bone remodeling	3/34	83/13403	0.00119306261	0.029941613	3 0.0228211909	P3h4/Gja1/Cthrc	3
BP	GO:0042692	muscle cell differentiation	5/34	322/13403	0.00121779601	0.029941613	3 0.0228211909	Fdps/Actg1/Tmst	5
BP	GO:0009260	ribonucleotide biosynthetic process	4/34	187/13403	0.00122670481	0.029941613	3 0.0228211909	Tpi1/Pgk1/COX2/	4
BP	GO:0019318	hexose metabolic process	4/34	190/13403	0.00130101501	0.030508844	8 0.0232535290	Tpi1/Pgk1/Grb10	4
BP	GO:0006164	purine nucleotide biosynthetic process	4/34	191/13403	0.00132647151	0.030508844	8 0.0232535290	Tpi1/Pgk1/COX2/	4
BP	GO:0032409	regulation of transporter activity	4/34	191/13403	0.00132647151	0.030508844	8 0.0232535290	Actb/Gja1/Prnp/I	4
BP	GO:0030278	regulation of ossification	4/34	193/13403	0.00137842951	0.030529661	4 0.0232693951	Ccn1/Gja1/Cthrc	4
BP	GO:0046390	ribose phosphate biosynthetic process	4/34	193/13403	0.00137842951	0.030529661	4 0.0232693951	Tpi1/Pgk1/COX2/	4
BP	GO:0072522	purine-containing compound biosynthetic process	4/34	196/13403	0.00145901761	0.031727001	7 0.0241819957	Tpi1/Pgk1/COX2/	4
BP	GO:0006119	oxidative phosphorylation	3/34	90/13403	0.00150712091	0.032187797	4 0.0245332094	Pgk1/COX2/COX	3
BP	GO:0033688	regulation of osteoblast proliferation	2/34	24/13403	0.00166468191	0.034929115	6 0.0266226141	Ccn1/Cthrc1	2
BP	GO:0045778	positive regulation of ossification	3/34	95/13403	0.00176042011	0.036301078	5 0.0276683101	Ccn1/Gja1/Cthrc	3
BP	GO:0005996	monosaccharide metabolic process	4/34	208/13403	0.00181444811	0.036781828	5 0.0280347329	Tpi1/Pgk1/Grb10	4
BP	GO:0016055	Wnt signaling pathway	5/34	356/13403	0.00189723611	0.037658436	8 0.0287028747	Wls/Grb10/Celsr	5
BP	GO:0198738	cell-cell signaling by wnt	5/34	357/13403	0.00192070621	0.037658436	8 0.0287028747	Wls/Grb10/Celsr	5
BP	GO:0030282	bone mineralization	3/34	99/13403	0.00198113921	0.038216815	5 0.0291284652	Ccn1/Gja1/Col1a	3
BP	GO:0033687	osteoblast proliferation	2/34	27/13403	0.00210698021	0.039999181	0 0.0304869660	Ccn1/Cthrc1	2
BP	GO:0048009	insulin-like growth factor receptor signaling pathway	2/34	30/13403	0.00259881091	0.048565279	6 0.0370159586	Grb10/Igfbp5	2
BP	GO:0009165	nucleotide biosynthetic process	4/34	232/13403	0.00269865491	0.048906942	5 0.0372763705	Tpi1/Pgk1/COX2/	4
BP	GO:0034762	regulation of transmembrane transport	5/34	386/13403	0.00269887811	0.048906942	5 0.0372763705	Actb/Gja1/Grb10	5
CC	GO:0031012	extracellular matrix	8/35	353/13620	2.40063668731	0.000380170	1 0.0002804954	Ccn1/Mmp23/Cc	8
CC	GO:0043292	contractile fiber	5/35	164/13620	5.77186698631	0.004031664	9 0.0029626932	Myl9/Gja1/Actg1	5
CC	GO:0062023	collagen-containing extracellular matrix	6/35	284/13620	7.60691502111	0.004031664	9 0.0029626932	Ccn1/Ccdc80/Itb	6
CC	GO:0044420	extracellular matrix component	3/35	44/13620	0.00019154511	0.007613919	8 0.0055951347	Col1a2/Fbn1/Col	3
CC	GO:0098644	complex of collagen trimers	2/35	13/13620	0.00049158771	0.010582258	6 0.0077764363	Col1a2/Col1a1	2
CC	GO:0044449	contractile fiber part	4/35	147/13620	0.00052577711	0.010582258	6 0.0077764363	Myl9/Actg1/Acta	4
CC	GO:0098871	postsynaptic actin cytoskeleton	2/35	14/13620	0.00057259391	0.010582258	6 0.0077764363	Actb/Actg1	2
CC	GO:0005581	collagen trimer	3/35	64/13620	0.00058175171	0.010582258	6 0.0077764363	Col1a2/Cthrc1/Co	3
CC	GO:0099571	postsynaptic cytoskeleton	2/35	15/13620	0.00065961991	0.010582258	6 0.0077764363	Actb/Actg1	2
CC	GO:0045277	respiratory chain complex IV	2/35	16/13620	0.00075263581	0.010582258	6 0.0077764363	COX2/COX3	2
CC	GO:0045121	membrane raft	5/35	292/13620	0.00083842151	0.010582258	6 0.0077764363	Eno1/Actb/Pgk1/	5
CC	GO:0098857	membrane microdomain	5/35	293/13620	0.00085140851	0.010582258	6 0.0077764363	Eno1/Actb/Pgk1/	5
CC	GO:0098589	membrane region	5/35	302/13620	0.00097517991	0.010582258	6 0.0077764363	Eno1/Actb/Pgk1/	5
CC	GO:0001725	stress fiber	3/35	77/13620	0.00099832621	0.010582258	6 0.0077764363	Myl9/Actb/Acta2	3
CC	GO:0097517	contractile actin filament bundle	3/35	77/13620	0.00099832621	0.010582258	6 0.0077764363	Myl9/Actb/Acta2	3
CC	GO:0044305	calyx of Held	2/35	19/13620	0.00106732801	0.010606572	2 0.0077943033	Actb/Actg1	2
CC	GO:0032432	actin filament bundle	3/35	85/13620	0.00132917951	0.012431738	5 0.0091355377	Myl9/Actb/Acta2	3
CC	GO:0042641	actomyosin	3/35	87/13620	0.00142141071	0.012555794	9 0.0092267013	Myl9/Actb/Acta2	3
CC	GO:0070069	cytochrome complex	2/35	26/13620	0.00200578571	0.016785259	5 0.0123347488	COX2/COX3	2
CC	GO:0016469	proton-transporting two-sector ATPase complex	2/35	42/13620	0.00517871851	0.041170812	6 0.0302546190	Atp6v1b1/ATP6	2

aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-

CC	GO:0016328	lateral plasma membrane	2/35	47/13620	0.0064499456	0.0488353024	0.0358869153	Atp6v1b1/Gja1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
CC	GO:0030016	myofibril	3/35	152/13620	0.0068669439	0.0496292766	0.0364703721	Myl9/Actg1/Csrp	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0019838	growth factor binding	5/35	128/13297	1.9680797850	0.0024010573	0.0016158970	Ccn1/Ltbp4/Col1	5	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0015078	proton transmembrane transporter activity	4/35	90/13297	8.7522352480	0.0053388635	0.0035930228	Atp6v1b1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0005198	structural molecule activity	7/35	490/13297	0.0002423094	0.0086447539	0.0058178671	Actb/Actg1/Ltbp4	7	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0005201	extracellular matrix structural constituent	4/35	122/13297	0.0002834345	0.0086447539	0.0058178671	Ltbp4/Col1a2/Fb	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0048407	platelet-derived growth factor binding	2/35	11/13297	0.0003647251	0.0088992927	0.0059891702	Col1a2/Col1a1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0099186	structural constituent of postsynapse	2/35	16/13297	0.0007892125	0.0141024044	0.0094908330	Actb/Actg1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0005539	glycosaminoglycan binding	4/35	161/13297	0.0008091543	0.0141024044	0.0094908330	Ccn1/Ccdc80/Prn	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0004129	cytochrome-c oxidase activity	2/35	21/13297	0.0013697601	0.0152932091	0.0102922374	COX2/COX3	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0015002	heme-copper terminal oxidase activity	2/35	21/13297	0.0013697601	0.0152932091	0.0102922374	COX2/COX3	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0016676	oxidoreductase activity, acting on a heme group of dor	2/35	21/13297	0.0013697601	0.0152932091	0.0102922374	COX2/COX3	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0016675	oxidoreductase activity, acting on a heme group of dor	2/35	22/13297	0.0015042500	0.0152932091	0.0102922374	COX2/COX3	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0098918	structural constituent of synapse	2/35	22/13297	0.0015042500	0.0152932091	0.0102922374	Actb/Actg1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0015077	monovalent inorganic cation transmembrane transpor	4/35	202/13297	0.0018720899	0.0169398775	0.0114004352	Atp6v1b1/COX2/	4	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0005520	insulin-like growth factor binding	2/35	25/13297	0.0019439203	0.0169398775	0.0114004352	Ccn1/Igfbp5	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0001968	fibronectin binding	2/35	30/13297	0.0027955285	0.0227369656	0.0153018405	Ccdc80/Igfbp5	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0017147	Wnt-protein binding	2/35	32/13297	0.0031770504	0.0241966652	0.0162842095	Wls/Cthrc1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0002020	protease binding	3/35	115/13297	0.0033716664	0.0241966652	0.0162842095	Prnp/Col1a2/Col	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0030020	extracellular matrix structural constituent conferring t	2/35	34/13297	0.0035815704	0.0242750889	0.0163369882	Col1a2/Col1a1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0008201	heparin binding	3/35	124/13297	0.0041671639	0.0267575791	0.0180076891	Ccn1/Ccdc80/Fbr	3	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0005507	copper ion binding	2/35	42/13297	0.0054248916	0.0330918388	0.0222706076	Prnp/COX2	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
MF	GO:0005200	structural constituent of cytoskeleton	2/35	46/13297	0.0064784271	0.0376365769	0.0253291889	Actb/Actg1	2	aPD-L1+aTGFb vs PBS	Down-regulated genes	CD45-
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	8/46	188/13307	2.2546603474	0.0002453070	0.0002069540	Pfn1/Gapdh/Ifitm	8	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0050792	regulation of viral process	7/46	158/13307	1.0567133654	0.0005748520	0.0004849758	Pfn1/Ifitm2/Ppia,	7	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	9/46	339/13307	1.9498408228	0.0007071422	0.0005965828	Pfn1/Arhgdib/Ga	9	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0044403	symbiont process	8/46	318/13307	1.1520904611	0.0031336860	0.0026437444	Pfn1/Gapdh/Ifitm	8	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0044419	interspecies interaction between organisms	8/46	333/13307	1.6092817405	0.0035017970	0.0029543024	Pfn1/Gapdh/Ifitm	8	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0016032	viral process	7/46	251/13307	2.2320685904	0.0040474843	0.0034146733	Pfn1/Ifitm2/Ppia,	7	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0006958	complement activation, classical pathway	3/46	19/13307	3.6037323072	0.0056012296	0.0047254955	C1qa/C1qc/C1qb	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:1903900	regulation of viral life cycle	5/46	125/13307	6.7971288960	0.0092440952	0.0077988110	Ifitm2/Ppia/Lgals	5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0046596	regulation of viral entry into host cell	3/46	25/13307	8.4303264020	0.0101913279	0.0085979469	Ifitm2/Lgals1/Sn	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0002181	cytoplasmic translation	4/46	76/13307	0.0001336697	0.0139104895	0.0117356296	Rpl18/Rpl18a/Rp	4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0048524	positive regulation of viral process	4/46	77/13307	0.0001406391	0.0139104895	0.0117356296	Pfn1/Ppia/Cfl1/L	4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0043902	positive regulation of multi-organism process	5/46	151/13307	0.0001658770	0.0142903085	0.0120560652	Pfn1/Gapdh/Ppia	5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0002455	humoral immune response mediated by circulating imi	3/46	32/13307	0.0001787471	0.0142903085	0.0120560652	C1qa/C1qc/C1qb	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0052548	regulation of endopeptidase activity	6/46	246/13307	0.0001893317	0.0142903085	0.0120560652	Psme2/Gapdh/Ps	6	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0051651	maintenance of location in cell	4/46	84/13307	0.0001970171	0.0142903085	0.0120560652	Pfn1/Tmsb4x/Ftl	4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0006956	complement activation	3/46	37/13307	0.0002766464	0.0188119603	0.0158707714	C1qa/C1qc/C1qb	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0010810	regulation of cell-substrate adhesion	5/46	171/13307	0.0002958139	0.0189320952	0.0159721237	Spp1/Rac2/S100	5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0019058	viral life cycle	5/46	174/13307	0.0003205435	0.0193750758	0.0163458457	Ifitm2/Ppia/Lgals	5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0052547	regulation of peptidase activity	6/46	282/13307	0.0003945579	0.0225936352	0.0190611938	Psme2/Gapdh/Ps	6	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0072376	protein activation cascade	3/46	43/13307	0.0004330662	0.0235588016	0.0198754596	C1qa/C1qc/C1qb	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0046718	viral entry into host cell	3/46	45/13307	0.0004955496	0.0245930720	0.0207480251	Ifitm2/Lgals1/Sn	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0051701	interaction with host	4/46	107/13307	0.0004972863	0.0245930720	0.0207480251	Gapdh/Ifitm2/Lg	4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0006959	humoral immune response	4/46	113/13307	0.0006111524	0.0247606828	0.0208894305	C1qa/C1qc/Gapd	4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0042989	sequestering of actin monomers	2/46	11/13307	0.0006303563	0.0247606828	0.0208894305	Pfn1/Tmsb4x	2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0030260	entry into host cell	3/46	49/13307	0.0006372234	0.0247606828	0.0208894305	Ifitm2/Lgals1/Sn	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0044409	entry into host	3/46	49/13307	0.0006372234	0.0247606828	0.0208894305	Ifitm2/Lgals1/Sn	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0051806	entry into cell of other organism involved in symbiotic	3/46	49/13307	0.0006372234	0.0247606828	0.0208894305	Ifitm2/Lgals1/Sn	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0051828	entry into other organism involved in symbiotic intera	3/46	49/13307	0.0006372234	0.0247606828	0.0208894305	Ifitm2/Lgals1/Sn	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0030837	negative regulation of actin filament polymerization	3/46	50/13307	0.0006762619	0.0253714823	0.0214047335	Pfn1/Tmsb4x/Cfl	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0050808	synapse organization	6/46	315/13307	0.0007077378	0.0256672932	0.0216542953	Pfn1/C1qa/C1qc/	6	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0098885	modification of postsynaptic actin cytoskeleton	2/46	12/13307	0.0007547632	0.0264897541	0.0223481672	Pfn1/Cfl1	2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0032272	negative regulation of protein polymerization	3/46	63/13307	0.0013278337	0.0451463460	0.0380878616	Pfn1/Tmsb4x/Cfl	3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0022626	cytosolic ribosome	9/46	104/13541	5.6912741740	8.7076494863	6.4700801136	Rps5/Rps4x/Rpl1	9	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0005840	ribosome	10/46	215/13541	2.0449779068	1.5644080987	1.1624084944	Rps5/Rps4x/Rpl1	10	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+

CC	GO:0044391	ribosomal subunit	9/46	184/13541	9.27856327184	4.73206726863	5.51608713455	Rps5/Rps4x/Rpl19	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0044445	cytosolic part	9/46	233/13541	7.17526873572	2.74454029142	2.03928690382	Rps5/Rps4x/Rpl19	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0022625	cytosolic large ribosomal subunit	5/46	58/13541	1.44915875082	4.43442577763	3.29492937042	Rpl18/Rpl18a/Rp5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0042788	polysomal ribosome	4/46	28/13541	2.24809429825	5.73264046063	4.25954709155	Rpl18/Rpl18a/Eif4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0005844	polysome	5/46	68/13541	3.21455036057	7.02608864525	5.22062314199	Rps4x/Rpl18/Rpl5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0022627	cytosolic small ribosomal subunit	4/46	42/13541	2.18698977940	0.00022701170	0.00016867740	Rps5/Rps4x/Rps14	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0015934	large ribosomal subunit	5/46	118/13541	4.75556849730	0.00080844660	0.00060070330	Rpl18/Rpl18a/Rp5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0015935	small ribosomal subunit	4/46	72/13541	0.00010128000	0.00015495841	0.00115139370	Rps5/Rps4x/Rps14	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0043209	myelin sheath	5/46	188/13541	0.00044225636	0.00587747600	0.00436716480	Gapdh/Actg1/Ppi5	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0005581	collagen trimer	3/46	49/13541	0.00060591740	0.00772544730	0.00574027040	C1qa/C1qc/C1qb3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
CC	GO:0098685	Schaffer collateral - CA1 synapse	3/46	83/13541	0.00278786350	0.03281069200	0.02437946160	Pfn1/Actg1/Srgn3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
MF	GO:0003735	structural constituent of ribosome	9/45	147/13229	1.27302114910	1.92226193520	1.67502782780	Rps5/Rps4x/Rpl19	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
MF	GO:0005198	structural molecule activity	10/45	428/13229	1.30783281980	9.87413779000	8.60416323860	Rps5/Rps4x/Actg10	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
MF	GO:0061135	endopeptidase regulator activity	4/45	101/13229	0.00037501660	0.01887583560	0.01644809660	Psme2/Gapdh/Ps4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
MF	GO:0061134	peptidase regulator activity	4/45	129/13229	0.00094361750	0.03562156180	0.03104005040	Psme2/Gapdh/Ps4	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
MF	GO:0019843	rRNA binding	3/45	69/13229	0.00164744070	0.04975271130	0.04335370450	Rps5/Rps4x/Rps13	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45+
BP	GO:0061844	antimicrobial humoral immune response mediated by	4/29	33/13403	0.00038362920	0.00032436820	Cxcl2/Cxcl1/Rpl34	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-	
BP	GO:0019730	antimicrobial humoral response	4/29	43/13403	2.05745099200	0.00056991390	0.00048187660	Cxcl2/Cxcl1/Rpl34	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
BP	GO:0002181	cytoplasmic translation	4/29	76/13403	2.03605886380	0.00375992200	0.00317910940	Rpl30/Rpl36/Rpl34	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
BP	GO:0006959	humoral immune response	4/29	101/13403	6.24204948160	0.00864523850	0.00730976840	Cxcl2/Cxcl1/Rpl34	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
BP	GO:0009617	response to bacterium	6/29	430/13403	0.00026760370	0.02950840200	0.02501403960	Cxcl2/Cxcl1/Rpl36	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0022626	cytosolic ribosome	11/32	105/13620	3.76829736540	2.48707626120	1.66598409840	Rpl22/Rps15a/Rps11	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0022625	cytosolic large ribosomal subunit	9/32	58/13620	6.25326285350	2.06357674160	1.38230020970	Rpl22/Rpl30/Rpl29	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0005840	ribosome	12/32	215/13620	3.01142189990	6.62512817990	4.43788490520	Rpl22/Rps15a/Rps12	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0044391	ribosomal subunit	11/32	185/13620	2.16887310910	3.57864063000	2.39717554160	Rpl22/Rps15a/Rps11	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0044445	cytosolic part	11/32	232/13620	2.60357324250	3.43671668010	2.30210686700	Rpl22/Rps15a/Rps11	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0015934	large ribosomal subunit	9/32	118/13620	4.79028239330	5.26931063260	3.52968176350	Rpl22/Rpl30/Rpl29	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0070069	cytochrome complex	3/32	26/13620	2.95264758960	0.00027839240	0.00018648300	Cox8a/Uqcrb/Nd3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0045277	respiratory chain complex IV	2/32	16/13620	0.00062869780	0.00518675750	0.00347438300	Cox8a/Ndufa4 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0098803	respiratory chain complex	3/32	77/13620	0.00076582690	0.00561606440	0.00376195700	Cox8a/Uqcrb/Nd3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0070469	respiratory chain	3/32	84/13620	0.00098649630	0.00651087580	0.00436135220	Cox8a/Uqcrb/Nd3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0042788	polysomal ribosome	2/32	28/13620	0.00194586370	0.01167518240	0.00782069640	Rpl30/Rpl39 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
CC	GO:0022627	cytosolic small ribosomal subunit	2/32	43/13620	0.00454752610	0.02501139390	0.01675404370	Rps15a/Rps27l 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0003735	structural constituent of ribosome	11/30	147/13297	9.42124290070	6.31223274340	4.46269400560	Rpl22/Rps15a/Rps11	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0005198	structural molecule activity	12/30	490/13297	2.59276667690	8.68576836770	6.14076318220	Rpl22/Rps15a/Rps12	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0009055	electron transfer activity	3/30	62/13297	0.00035828090	0.00800161840	0.00565706800	Cox8a/Uqcrb/Nd3	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0004129	cytochrome-c oxidase activity	2/30	21/13297	0.00100619620	0.01057896920	0.00747923980	Cox8a/Ndufa4 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0015002	heme-copper terminal oxidase activity	2/30	21/13297	0.00100619620	0.01057896920	0.00747923980	Cox8a/Ndufa4 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0016676	oxidoreductase activity, acting on a heme group of dor	2/30	21/13297	0.00100619620	0.01057896920	0.00747923980	Cox8a/Ndufa4 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0016675	oxidoreductase activity, acting on a heme group of dor	2/30	22/13297	0.00110526540	0.01057896920	0.00747923980	Cox8a/Ndufa4 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0008009	chemokine activity	2/30	33/13297	0.00248769210	0.02083442160	0.01472975610	Cxcl2/Cxcl1 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0042379	chemokine receptor binding	2/30	43/13297	0.00419541320	0.03123252040	0.02208112210	Cxcl2/Cxcl1 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0045182	translation regulator activity	2/30	50/13297	0.00563604610	0.03776150900	0.02669706050	Rpl22/Rps27l 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
MF	GO:0048306	calcium-dependent protein binding	2/30	60/13297	0.00803061470	0.04891374450	0.03458159470	S100a6/S100a4 2	aPD-L1+aTGFb vs aPD-L1	Up-regulated genes	CD45-
BP	GO:0002181	cytoplasmic translation	13/52	76/13307	1.24655324630	1.08699443080	9.69687209520	Rpl30/Rpl35a/Rp13	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042274	ribosomal small subunit biogenesis	7/52	61/13307	3.39741664440	1.48127365690	1.32141626320	Rpsa/Rps19/Rps27	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0000028	ribosomal small subunit assembly	5/52	18/13307	6.16793421090	1.79281287730	1.59933451990	Rpsa/Rps19/Rps25	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0022613	ribonucleoprotein complex biogenesis	12/52	401/13307	3.30184380800	7.19801950140	6.42121730030	Rplp0/Rpl35a/Rp12	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042254	ribosome biogenesis	10/52	261/13307	5.43605019750	9.48047154450	8.45734967570	Rplp0/Rpl35a/Rp10	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042255	ribosome assembly	6/52	59/13307	1.01745618960	1.47870299560	1.31911230248	Rplp0/Rpsa/Rps16	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0022618	ribonucleoprotein complex assembly	8/52	206/13307	1.20777293070	0.00015045390	0.00013421710	Rplp0/Rpsa/Rpl18	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0071826	ribonucleoprotein complex subunit organization	8/52	217/13307	1.78500327890	0.00019456530	0.00017356800	Rplp0/Rpsa/Rpl18	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0061844	antimicrobial humoral immune response mediated by	4/52	35/13307	9.92500079480	0.00096162220	0.00085784500	Hist1h2bc/Rpl39	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0046034	ATP metabolic process	7/52	205/13307	1.38180622330	0.00120493500	0.00107489970	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0019730	antimicrobial humoral response	4/52	44/13307	2.50725642220	0.00171923900	0.00153370070	Hist1h2bc/Rpl39	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009126	purine nucleoside monophosphate metabolic process	7/52	228/13307	2.74522785120	0.00171923900	0.00153370070	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009167	purine ribonucleoside monophosphate metabolic proc	7/52	228/13307	2.74522785120	0.00171923900	0.00153370070	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+

BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	7/52	229/13307	2.8233760742E-3	0.0017192390	0.0015337007	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009161	ribonucleoside monophosphate metabolic process	7/52	232/13307	3.0689125866E-3	0.0017192390	0.0015337007	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009199	ribonucleoside triphosphate metabolic process	7/52	233/13307	3.1545670725E-3	0.0017192390	0.0015337007	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009144	purine nucleoside triphosphate metabolic process	7/52	237/13307	3.5171486597E-3	0.0017977320	0.0016037228	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009123	nucleoside monophosphate metabolic process	7/52	239/13307	3.7109148237E-3	0.0017977320	0.0016037228	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009141	nucleoside triphosphate metabolic process	7/52	253/13307	5.3283760693E-3	0.0024454441	0.0021815345	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0015985	energy coupled proton transport, down electrochemic	3/52	20/13307	6.1221481872E-3	0.0024717558	0.0022050067	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0015986	ATP synthesis coupled proton transport	3/52	20/13307	6.1221481872E-3	0.0024717558	0.0022050067	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0006364	rRNA processing	6/52	177/13307	6.2360813179E-3	0.0024717558	0.0022050067	Rpl35a/Rpl35/Rp	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042773	ATP synthesis coupled electron transport	4/52	59/13307	8.0502522794E-3	0.0030520956	0.0027227169	COX3/COX2/CYTI	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042273	ribosomal large subunit biogenesis	4/52	65/13307	0.0001177025	0.0042765277	0.0038150096	Rplp0/Rpl35a/Rp	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0016072	rRNA metabolic process	6/52	206/13307	0.0001439376	0.0050205442	0.0044787327	Rpl35a/Rpl35/Rp	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0022904	respiratory electron transport chain	4/52	78/13307	0.0002388732	0.0076852827	0.0068558956	COX3/COX2/CYTI	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:1902600	proton transmembrane transport	4/52	78/13307	0.0002388732	0.0076852827	0.0068558956	ATP8/Atp5k/CYTI	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0045333	cellular respiration	5/52	145/13307	0.0002467751	0.0076852827	0.0068558956	COX3/COX2/CYTI	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0022900	electron transport chain	4/52	81/13307	0.0002762200	0.0083056516	0.0074093149	COX3/COX2/CYTI	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009150	purine ribonucleotide metabolic process	7/52	341/13307	0.0003385987	0.0098419356	0.0087798049	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042742	defense response to bacterium	5/52	158/13307	0.0003670070	0.0103235543	0.0092094479	Hist1h2bc/Rpl39	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0006119	oxidative phosphorylation	4/52	88/13307	0.0003794317	0.0103395145	0.0092236857	COX3/COX2/CYTI	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009259	ribonucleotide metabolic process	7/52	351/13307	0.0004030790	0.0106510581	0.0095016078	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0006163	purine nucleotide metabolic process	7/52	362/13307	0.0004850306	0.0124396100	0.0110971412	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0019693	ribose phosphate metabolic process	7/52	368/13307	0.0005350534	0.0130866616	0.0116743638	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0030490	maturation of SSU-rRNA	3/52	41/13307	0.0005402750	0.0130866616	0.0116743638	Rps19/Rps21/Rp	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0006754	ATP biosynthetic process	4/52	103/13307	0.0006890481	0.0162391878	0.0144866728	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0050829	defense response to Gram-negative bacterium	3/52	45/13307	0.0007113102	0.0163226982	0.0145611709	Rps19/Hmgb2/Rp	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0072521	purine-containing compound metabolic process	7/52	389/13307	0.0007435194	0.0166243328	0.0148302534	ATP8/COX3/COX7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic proce	4/52	112/13307	0.0009432485	0.0202441010	0.0180593803	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0006959	humoral immune response	4/52	113/13307	0.0009750599	0.0202441010	0.0180593803	Hist1h2bc/Rpl39	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	4/52	113/13307	0.0009750599	0.0202441010	0.0180593803	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009201	ribonucleoside triphosphate biosynthetic process	4/52	115/13307	0.0010409384	0.0211092639	0.0188311757	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0034660	ncRNA metabolic process	7/52	425/13307	0.0012467819	0.0242535281	0.0216361145	Rpl35a/Rpl35/Rp	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0034101	erythrocyte homeostasis	4/52	121/13307	0.0012573141	0.0242535281	0.0216361145	Zfp36/Rps19/Hm	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0042775	mitochondrial ATP synthesis coupled electron transpor	3/52	55/13307	0.0012794292	0.0242535281	0.0216361145	COX3/CYTB/ND2	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0002227	innate immune response in mucosa	2/52	14/13307	0.0013226132	0.0244964396	0.0218528112	Hist1h2bc/Rpl39	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009127	purine nucleoside monophosphate biosynthetic proce	4/52	124/13307	0.0013765201	0.0244964396	0.0218528112	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009168	purine ribonucleoside monophosphate biosynthetic pr	4/52	124/13307	0.0013765201	0.0244964396	0.0218528112	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0015980	energy derivation by oxidation of organic compounds	5/52	214/13307	0.0014434499	0.0249673765	0.0222729252	COX3/COX2/CYTI	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009142	nucleoside triphosphate biosynthetic process	4/52	126/13307	0.0014602479	0.0249673765	0.0222729252	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0034470	ncRNA processing	6/52	322/13307	0.0015283361	0.0254602787	0.0227126339	Rpl35a/Rpl35/Rp	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009156	ribonucleoside monophosphate biosynthetic process	4/52	128/13307	0.0015474710	0.0254602787	0.0227126339	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009124	nucleoside monophosphate biosynthetic process	4/52	133/13307	0.0017813230	0.0285110151	0.0254341382	ATP8/COX2/Atp5	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009617	response to bacterium	7/52	453/13307	0.0017982865	0.0285110151	0.0254341382	Zfp36/Rpl13a/Hi	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0009117	nucleotide metabolic process	7/52	464/13307	0.0020608337	0.0320901257	0.0286269953	ATP8/COX3/COX7	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0019731	antibacterial humoral response	2/52	18/13307	0.0022016106	0.0327326144	0.0292185661	Hist1h2bc/Rpl39	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0051444	negative regulation of ubiquitin-protein transferase ac	2/52	18/13307	0.0022016106	0.0327326144	0.0292185661	Rpl23/Smad7	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0006753	nucleoside phosphate metabolic process	7/52	470/13307	0.0022161037	0.0327532614	0.0292185661	ATP8/COX3/COX7	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0050830	defense response to Gram-positive bacterium	3/52	67/13307	0.0022605150	0.0328528194	0.0293073799	Hist1h2bc/Rpl39	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0002262	myeloid cell homeostasis	4/52	152/13307	0.0028944315	0.0413761356	0.0369108694	Zfp36/Rps19/Hm	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0002385	mucosal immune response	2/52	22/13307	0.0032909648	0.0462858280	0.0412907133	Hist1h2bc/Rpl39	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0002251	organ or tissue specific immune response	2/52	23/13307	0.0035954068	0.0489874180	0.0437007508	Hist1h2bc/Rpl39	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0010837	regulation of keratinocyte proliferation	2/52	23/13307	0.0035954068	0.0489874180	0.0437007508	Zfp36/Ctsl	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0022626	cytosolic ribosome	28/53	104/13541	9.1254390535E-3	1.0037982958E-6	8.8200649768E-6	Rplp2/Rplp0/Rpl	28	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0044391	ribosomal subunit	28/53	184/13541	4.3139176664E-3	1.9640349639E-3	1.3344160999E-3	Rplp2/Rplp0/Rpl	28	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0005840	ribosome	29/53	215/13541	5.3564589926E-3	1.9640349639E-3	1.3344160999E-3	Rplp2/Rpl41/Rpl	29	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0044445	cytosolic part	28/53	233/13541	4.7169168280E-3	1.2971521277E-3	8.8131867050E-4	Rplp2/Rplp0/Rpl	28	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0022625	cytosolic large ribosomal subunit	17/53	58/13541	1.1953269742E-3	2.6297193433E-4	1.7866992667E-4	Rplp2/Rplp0/Rpl	17	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0015934	large ribosomal subunit	17/53	118/13541	7.2644527852E-3	1.3318163439E-3	9.0487043465E-4	Rplp2/Rplp0/Rpl	17	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+

CC	GO:0022627	cytosolic small ribosomal subunit	11/53	42/13541	4.2654121262	6.7027904841	4.5540490370	Rpsa/Rps3a1/Rp	11	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0015935	small ribosomal subunit	11/53	72/13541	2.7643152768	3.8009335057	2.5824524297	Rpsa/Rps3a1/Rp	11	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0042788	polysomal ribosome	7/53	28/13541	1.0367420686	1.2671291950	8.6092031431	Rpl39/Rps29/Rps	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0005844	polysome	7/53	68/13541	7.5344157907	8.2878573698	5.6309844331	Rpl39/Rps29/Rps	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0098803	respiratory chain complex	6/53	76/13541	4.7631845674	4.7631845674	3.2362306630	ND3/COX3/COX2	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0098800	inner mitochondrial membrane protein complex	7/53	125/13541	5.2283665210	4.7926693109	3.2562633596	ATP8/ND3/Atp5k	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0070469	respiratory chain	6/53	83/13541	8.0538467274	6.8147933847	4.6301467015	ND3/COX3/COX2	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0045263	proton-transporting ATP synthase complex, coupling fa	3/53	12/13541	1.2150094741	9.5465030115	6.4861408021	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0044455	mitochondrial membrane part	7/53	206/13541	1.4506007059	0.0001063773	7.2275543946	ATP8/ND3/Atp5k	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0005743	mitochondrial inner membrane	9/53	396/13541	2.0249491780	0.0001392152	9.4586441871	ATP8/ND3/COX3,	9	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0019866	organelle inner membrane	9/53	429/13541	3.7999149131	0.0002458768	0.0001670550	ATP8/ND3/COX3,	9	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0005753	mitochondrial proton-transporting ATP synthase comp	3/53	18/13541	4.4323063938	0.0002708631	0.0001840314	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0045259	proton-transporting ATP synthase complex	3/53	19/13541	5.2488122586	0.0003038786	0.0002064629	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0098798	mitochondrial protein complex	7/53	257/13541	5.9811216784	0.0003225620	0.0002191570	ATP8/ND3/Atp5k	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0033177	proton-transporting two-sector ATPase complex, protc	3/53	20/13541	6.1580032641	0.0003225620	0.0002191570	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0070069	cytochrome complex	3/53	26/13541	0.0001381333	0.0006906666	0.0004692567	COX3/COX2/CYTI	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0014069	postsynaptic density	7/53	296/13541	0.0001446812	0.0006913188	0.0004696999	Rplp0/Rpl23/Rps	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0032279	asymmetric synapse	7/53	298/13541	0.0001508332	0.0006913188	0.0004696999	Rplp0/Rpl23/Rps	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0098984	neuron to neuron synapse	7/53	311/13541	0.0001962107	0.0008633274	0.0005865669	Rplp0/Rpl23/Rps	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0005746	mitochondrial respiratory chain	4/53	75/13541	0.0002069759	0.0008645421	0.0005873922	ND3/CYTB/ND1/I	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0099572	postsynaptic specialization	7/53	315/13541	0.0002122057	0.0008645421	0.0005873922	Rplp0/Rpl23/Rps	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0016469	proton-transporting two-sector ATPase complex	3/53	41/13541	0.0005433532	0.0021346020	0.0014503038	ATP8/Atp5k/ATP	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:1990204	oxidoreductase complex	4/53	98/13541	0.0005756375	0.0021834525	0.0014834941	ND3/CYTB/ND1/I	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0000276	mitochondrial proton-transporting ATP synthase comp	2/53	10/13541	0.0006629706	0.0024308922	0.0016516110	ATP8/Atp5k	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0005747	mitochondrial respiratory chain complex I	3/53	48/13541	0.0008647348	0.0028824494	0.0019584106	ND3/ND1/ND2	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0030964	NADH dehydrogenase complex	3/53	48/13541	0.0008647348	0.0028824494	0.0019584106	ND3/ND1/ND2	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0045271	respiratory chain complex I	3/53	48/13541	0.0008647348	0.0028824494	0.0019584106	ND3/ND1/ND2	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
CC	GO:0045277	respiratory chain complex IV	2/53	16/13541	0.0017415219	0.0056343358	0.0038281133	COX3/COX2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0003735	structural constituent of ribosome	28/52	147/13229	4.3593661618	5.2748330557	4.1758139023	Rplp2/Rpl41/Rpl	28	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0005198	structural molecule activity	28/52	428/13229	1.6528071884	9.9994834904	7.9160765343	Rplp2/Rpl41/Rpl	28	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0015078	proton transmembrane transporter activity	5/52	96/13229	3.5956540248	0.0014502471	0.0011480860	ATP8/COX3/COX	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0019843	rRNA binding	4/52	69/13229	0.0001519386	0.0042369733	0.0033541937	Rplp0/Rpl37a/Rp	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0003954	NADH dehydrogenase activity	3/52	28/13229	0.0001750815	0.0042369733	0.0033541937	ND3/ND1/ND2	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0031369	translation initiation factor binding	3/52	36/13229	0.0003732179	0.0075265622	0.0059583920	Rps3a1/Rps19/R	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0015077	monovalent inorganic cation transmembrane transpor	5/52	208/13229	0.0013059797	0.0225747928	0.0178713018	ATP8/COX3/COX	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0003729	mRNA binding	5/52	220/13229	0.0016730925	0.0247340159	0.0195806476	Zfp36/Rpl13a/Rp	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0009055	electron transfer activity	3/52	62/13229	0.0018397201	0.0247340159	0.0195806476	COX3/COX2/CYTI	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0043021	ribonucleoprotein complex binding	4/52	140/13229	0.0021945568	0.0262214530	0.0207581750	Rpl35a/Rpsa/Rpl	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	3/52	71/13229	0.0027120532	0.0262214530	0.0207581750	ND3/ND1/ND2	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0004129	cytochrome-c oxidase activity	2/52	21/13229	0.0030338871	0.0262214530	0.0207581750	COX3/COX2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0015002	heme-copper terminal oxidase activity	2/52	21/13229	0.0030338871	0.0262214530	0.0207581750	COX3/COX2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0016676	oxidoreductase activity, acting on a heme group of dor	2/52	21/13229	0.0030338871	0.0262214530	0.0207581750	COX3/COX2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0016675	oxidoreductase activity, acting on a heme group of dor	2/52	22/13229	0.0033289073	0.0268531858	0.0212582854	COX3/COX2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0008137	NADH dehydrogenase (ubiquinone) activity	2/52	25/13229	0.0042908321	0.0305406286	0.0241774441	ND3/ND2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0050136	NADH dehydrogenase (quinone) activity	2/52	25/13229	0.0042908321	0.0305406286	0.0241774441	ND3/ND2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
MF	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone o	2/52	33/13229	0.0074019887	0.0497578131	0.0393907002	ND3/ND2	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45+
BP	GO:0043062	extracellular structure organization	10/70	269/13403	1.2329751267	0.0017316186	0.0015148279	Pdpn/Antxr1/Dd	10	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0001501	skeletal system development	12/70	433/13403	2.1601883506	0.0017316186	0.0015148279	Zfp385a/Osr1/Os	12	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0030198	extracellular matrix organization	9/70	233/13403	3.2146385264	0.0017316186	0.0015148279	Pdpn/Antxr1/Dd	9	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0002062	chondrocyte differentiation	6/70	101/13403	1.3997563917	0.0055215293	0.0048302591	Osr1/Osr2/Tgfbr	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0055021	regulation of cardiac muscle tissue growth	5/70	66/13403	2.3465604374	0.0055215293	0.0048302591	Fdps/Wnt2/Tgfbr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0061448	connective tissue development	8/70	228/13403	2.3626216279	0.0055215293	0.0048302591	Osr1/Osr2/Thbs3	8	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0051216	cartilage development	7/70	169/13403	2.7509914731	0.0055215293	0.0048302591	Osr1/Osr2/Thbs3	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0060420	regulation of heart growth	5/70	71/13403	3.3503155407	0.0055215293	0.0048302591	Fdps/Wnt2/Tgfbr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0003416	endochondral bone growth	4/70	36/13403	3.5423070736	0.0055215293	0.0048302591	Thbs3/Ddr2/Tgfb	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:0035265	organ growth	7/70	177/13403	3.7006805125	0.0055215293	0.0048302591	Fdps/Thbs3/Ddr2	7	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:1905048	regulation of metallopeptidase activity	3/70	13/13403	3.7584667277	0.0055215293	0.0048302591	Antxr1/Timp2/Ti	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-

BP	GO:0098868	bone growth	4/70	38/13403	4.40413832270.005930906	0.005188384	0Thbs3/Ddr2/Tgfb	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0055024	regulation of cardiac muscle tissue development	5/70	86/13403	8.435368465	5.009899371	7.0086600157	Fdps/Wnt2/Tgfbr	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0043502	regulation of muscle adaptation	5/70	87/13403	8.913705036	7.009899371	7.0086600157	Fdps/Klf4/Pi16/C	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:1901861	regulation of muscle tissue development	6/70	141/13403	9.188773274	9.009899371	7.0086600157	Fdps/Wnt2/Tgfbr	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0055017	cardiac muscle tissue growth	5/70	91/13403	0.000110391	0.011149560	9.0097536870	Fdps/Wnt2/Tgfbr	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0030199	collagen fibril organization	4/70	50/13403	0.000131074	0.012459832	0.0108999181	Ddr2/Tnxb/Dpt/C	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0046620	regulation of organ growth	5/70	97/13403	0.000149326	0.012700578	3.0111105241	Fdps/Wnt2/Tgfbr	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060419	heart growth	5/70	97/13403	0.000149326	0.012700578	3.0111105241	Fdps/Wnt2/Tgfbr	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0043500	muscle adaptation	5/70	101/13403	0.000180598	2.014592338	4.0127654446	Fdps/Klf4/Pi16/C	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:1905207	regulation of cardiocyte differentiation	4/70	55/13403	0.000190335	0.014646797	1 0.0128130853	Fdps/Pi16/Sema3	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0045995	regulation of embryonic development	5/70	112/13403	0.000292620	4 0.021494303	0 0.0188033149	Osr1/Lama4/Osr2	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0061050	regulation of cell growth involved in cardiac muscle cel	3/70	26/13403	0.000325440	9.022865762	6 0.0200030740	Fdps/Pi16/Col14	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0014743	regulation of muscle hypertrophy	4/70	64/13403	0.000342283	3 0.023047081	5 0.0201616926	Fdps/Pi16/Col14	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048762	mesenchymal cell differentiation	6/70	190/13403	0.000463153	37 0.028894334	2 0.0252768961	Pdpn/Osr1/Wnt26	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060348	bone development	6/70	192/13403	0.000489587	3 0.028894334	2 0.0252768961	Zfp385a/Osr2/Th	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0003417	growth plate cartilage development	3/70	30/13403	0.000500644	4 0.028894334	2 0.0252768961	Thbs3/Tgfbr2/Co	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048009	insulin-like growth factor receptor signaling pathway	3/70	30/13403	0.000500644	4 0.028894334	2 0.0252768961	Grb10/Igfbp6/Igf	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0010470	regulation of gastrulation	3/70	31/13403	0.000552217	2 0.030771830	1 0.0269193381	Osr1/Osr2/Klf4	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0001667	ameboidal-type cell migration	8/70	367/13403	0.000628543	0 0.032029744	6 0.0280197675	Myh9/Ddr2/Dcn/8	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060537	muscle tissue development	8/70	368/13403	0.000639861	0 0.032029744	6 0.0280197675	Fdps/Osr1/Wnt2,8	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0040019	positive regulation of embryonic development	3/70	33/13403	0.000665287	6 0.032029744	6 0.0280197675	Osr1/Osr2/Wnt2	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0007369	gastrulation	5/70	135/13403	0.000689408	0 0.032029744	6 0.0280197675	Osr1/Osr2/Tgfbr2	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0033002	muscle cell proliferation	6/70	207/13403	0.000727397	2 0.032029744	6 0.0280197675	Wnt2/Tgfbr2/Mn	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0016202	regulation of striated muscle tissue development	5/70	138/13403	0.000761520	9 0.032029744	6 0.0280197675	Fdps/Wnt2/Tgfbr	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0003298	physiological muscle hypertrophy	3/70	35/13403	0.000792138	1 0.032029744	6 0.0280197675	Fdps/Pi16/Col14	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0003301	physiological cardiac muscle hypertrophy	3/70	35/13403	0.000792138	1 0.032029744	6 0.0280197675	Fdps/Pi16/Col14	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0061049	cell growth involved in cardiac muscle cell developmer	3/70	35/13403	0.000792138	1 0.032029744	6 0.0280197675	Fdps/Pi16/Col14	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0110110	positive regulation of animal organ morphogenesis	4/70	80/13403	0.000800225	2 0.032029744	6 0.0280197675	Wnt2/Tgfbr2/Cdl	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048705	skeletal system morphogenesis	6/70	211/13403	0.000803834	7 0.032029744	6 0.0280197675	Wnt2/Tgfbr2/Cdl	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048634	regulation of muscle organ development	5/70	140/13403	0.000812635	8 0.032029744	6 0.0280197675	Osr1/Osr2/Thbs3	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048588	developmental cell growth	6/70	219/13403	0.000975254	5 0.037081151	8 0.0324387616	Fdps/Wnt2/Tgfbr	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0014897	striated muscle hypertrophy	4/70	85/13403	0.001004615	6 0.037081151	8 0.0324387616	Fdps/Tgfbr2/Pi16	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0006509	membrane protein ectodomain proteolysis	3/70	38/13403	0.001009635	3 0.037081151	8 0.0324387616	Fdps/Pi16/Col14	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0014896	muscle hypertrophy	4/70	86/13403	0.001049506	4 0.037688942	0 0.0329704593	Fdps/Pi16/Col14	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:1903053	regulation of extracellular matrix organization	3/70	39/13403	0.001089698	0 0.038062868	7 0.0332975721	Pdpn/Antxr1/Ddr	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048659	smooth muscle cell proliferation	5/70	152/13403	0.001175016	1 0.038062868	7 0.0332975721	Tgfbr2/Mmp2/Kl	5 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060346	bone trabecula formation	2/70	10/13403	0.001177687	7 0.038062868	7 0.0332975721	Thbs3/Mmp2	2 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0072498	embryonic skeletal joint development	2/70	10/13403	0.001177687	7 0.038062868	7 0.0332975721	Osr1/Osr2	2 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0090091	positive regulation of extracellular matrix disassembly	2/70	10/13403	0.001177687	7 0.038062868	7 0.0332975721	Pdpn/Ddr2	2 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060351	cartilage development involved in endochondral bone	3/70	41/13403	0.001261609	0 0.039975691	9 0.0349709186	Thbs3/Tgfbr2/Co	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060485	mesenchyme development	6/70	233/13403	0.001341609	7 0.041693103	5 0.0364733181	Pdpn/Osr1/Wnt26	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0001503	ossification	7/70	323/13403	0.001444292	4 0.043712936	7 0.0382402775	Osr1/Osr2/Thbs3	7 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0060349	bone morphogenesis	4/70	94/13403	0.001460704	5 0.043712936	7 0.0382402775	Osr2/Thbs3/Tgfb	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0048638	regulation of developmental growth	7/70	326/13403	0.001522891	5 0.044728333	0 0.0391285508	Fdps/Wnt2/Tgfbr	7 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:2000725	regulation of cardiac muscle cell differentiation	3/70	44/13403	0.001549991	7 0.044728333	0 0.0391285508	Fdps/Pi16/Col14	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0014745	negative regulation of muscle adaptation	2/70	12/13403	0.001715645	6 0.047468400	3 0.0415255742	Klf4/Igfbp5	2 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0016049	cell growth	8/70	430/13403	0.001740308	3 0.047468400	3 0.0415255742	Fdps/Tgfbr2/Ccn	8 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0033619	membrane protein proteolysis	3/70	46/13403	0.001763377	8 0.047468400	3 0.0415255742	Myh9/Timp2/Tim	3 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0030282	bone mineralization	4/70	99/13403	0.001768238	2 0.047468400	3 0.0415255742	Osr1/Osr2/Ddr2/	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0001525	angiogenesis	8/70	432/13403	0.001791814	6 0.047468400	3 0.0415255742	Myh9/Dcn/Tgfbr	8 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0051146	striated muscle cell differentiation	6/70	249/13403	0.001880225	6 0.048812059	1 0.0427010131	Myh9/Fdps/Ccn3	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
BP	GO:0051153	regulation of striated muscle cell differentiation	4/70	101/13403	0.001902945	3 0.048812059	1 0.0427010131	Fdps/Ccn3/Pi16/	4 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
CC	GO:0031012	extracellular matrix	22/69	353/13620	1.273777069	8 1.796025668	4 1.541940663	4Pcsk6/Prelp/Lam	22 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
CC	GO:0062023	collagen-containing extracellular matrix	19/69	284/13620	1.150798579	4 8.113129985	0 6.9653598229	Pcsk6/Prelp/Lam	19 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
CC	GO:0009897	external side of plasma membrane	9/69	246/13620	3.896818211	8 0.000183150	4 0.0001572400	Pdpn/Antxr2/B2r	9 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
CC	GO:0005604	basement membrane	6/69	91/13620	6.437875876	0 0.000226935	1 0.0001948304	Lama4/Timp2/Efe	6 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-
CC	GO:0098552	side of membrane	9/69	393/13620	0.000155094	1 0.004373653	8 0.0037549099	Pdpn/Antxr2/B2r	9 aPD-L1+aTGFb vs aPD-L1	Down-regulated genes CD45-

CC	GO:0005581	collagen trimer	4/69	64/13620	0.0003048493	0.0071639602	0.0061504698	Dcn/Scara3/Emili	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005201	extracellular matrix structural constituent	12/70	122/13297	1.3939296273	2.1048337373	1.7314073266	Prelp/Lama4/Dcr	12	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005539	glycosaminoglycan binding	12/70	161/13297	3.8133417536	2.8790730240	2.3682859312	Pcsk6/Prelp/Thbs	12	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0008201	heparin binding	10/70	124/13297	8.5265220162	4.2916827481	3.5302792909	Pcsk6/Prelp/Thbs	10	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005198	structural molecule activity	16/70	490/13297	3.5803412867	1.3515788357	1.1117901890	Rpl17/Rpl5/Cldn	16	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:1901681	sulfur compound binding	11/70	206/13297	9.1943826263	2.7767035531	2.2840782103	Pcsk6/Prelp/Thbs	11	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005520	insulin-like growth factor binding	4/70	25/13297	8.1948898513	0.0002062380	0.0001696485	Ccn3/Htra3/Igfbp	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0019838	growth factor binding	6/70	128/13297	5.6030959453	0.0012086678	0.0009942335	Pcsk6/Tgfbr2/Ccr	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0004252	serine-type endopeptidase activity	5/70	82/13297	6.9710532852	0.0013157863	0.0010823477	Pcsk6/Pamr1/Mr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0008236	serine-type peptidase activity	5/70	98/13297	0.0001625821	0.0027277665	0.0022438233	Pcsk6/Pamr1/Mr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0017171	serine hydrolase activity	5/70	102/13297	0.0001961917	0.0029624954	0.0024369080	Pcsk6/Pamr1/Mr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005518	collagen binding	4/70	60/13297	0.0002749783	0.0035117462	0.0028887142	Antxr1/Ddr2/Dcn	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005178	integrin binding	5/70	110/13297	0.0002790791	0.0035117462	0.0028887142	Myh9/Timp2/Ccr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0001968	fibronectin binding	3/70	30/13297	0.0005123008	0.0059505710	0.0048948580	Mmp2/Igfbp6/Igf	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0005509	calcium ion binding	8/70	405/13297	0.0012517169	0.0135006617	0.0111054589	Thbs3/Man1a/Pa	8	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0008191	metalloendopeptidase inhibitor activity	2/70	11/13297	0.0014571509	0.0137518625	0.0113120932	Timp2/Timp3	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0031994	insulin-like growth factor I binding	2/70	11/13297	0.0014571509	0.0137518625	0.0113120932	Igfbp6/Igfbp5	2	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0051015	actin filament binding	5/70	163/13297	0.0016580755	0.0147276119	0.0121147313	Myh9/Ablim1/Ar	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0004857	enzyme inhibitor activity	6/70	251/13297	0.0020368730	0.0170871020	0.0140556154	Rpl5/Cdkn1c/Tim	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0050840	extracellular matrix binding	3/70	54/13297	0.0028598937	0.0221801731	0.0182451058	Dcn/Cd248/Adan	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0004175	endopeptidase activity	6/70	272/13297	0.0030406288	0.0221801731	0.0182451058	Pcsk6/Pamr1/Mr	6	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0050839	cell adhesion molecule binding	5/70	188/13297	0.0030846598	0.0221801731	0.0182451058	Myh9/Timp2/Ccr	5	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0019199	transmembrane receptor protein kinase activity	3/70	65/13297	0.0048330667	0.0331724130	0.0272871713	Ddr2/Tgfbr2/Efer	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0019843	rRNA binding	3/70	68/13297	0.0054833411	0.0349423002	0.0287430563	Rpl17/Rpl5/Cavir	3	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
MF	GO:0061134	peptidase regulator activity	4/70	135/13297	0.0055537430	0.0349423002	0.0287430563	Timp2/Pi16/Fn1/	4	aPD-L1+aTGFb vs aPD-L1	Down-regulated genes	CD45-
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	12/62	186/13307	4.5767057691	7.5424111075	5.5305876031	H2-Aa/Irf1/H2-Ab	12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	13/62	261/13307	1.6664114380	1.3580616717	9.9581936584	H2-Aa/Irf1/H2-Ab	13	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0022409	positive regulation of cell-cell adhesion	12/62	215/13307	2.4721996451	1.3580616717	9.9581936584	H2-Aa/Irf1/H2-Ab	12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	9/62	93/13307	4.0111074005	1.6525762490	1.2117766567	Irf1/Cd274/Satb1	9	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0007159	leukocyte cell-cell adhesion	13/62	288/13307	5.6151473259	1.8507525586	1.3570924484	H2-Aa/Irf1/H2-Ab	13	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042110	T cell activation	15/62	426/13307	6.9840475169	1.9182850513	1.4066116753	H2-Aa/Irf1/H2-Ab	15	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046631	alpha-beta T cell activation	10/62	144/13307	1.0695008441	2.5179105587	1.8462961940	Irf1/H2-Ab1/Cd2	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0019886	antigen processing and presentation of exogenous pep	5/62	13/13307	2.3293237621	4.7984069500	3.5185048407	H2-Eb1/H2-Aa/H	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0022407	regulation of cell-cell adhesion	13/62	339/13307	4.0824282956	6.7792958152	4.9710217143	H2-Aa/Irf1/H2-Ab	13	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050863	regulation of T cell activation	12/62	275/13307	4.1136503733	6.7792958152	4.9710217143	H2-Aa/Irf1/H2-Ab	12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050870	positive regulation of T cell activation	10/62	171/13307	5.6998205460	8.5393675090	6.2616210401	H2-Aa/Irf1/H2-Ab	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	7/62	61/13307	1.2052152902	1.6551623319	1.2136729414	Irf1/Cd274/Arg2/	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002495	antigen processing and presentation of peptide antige	5/62	18/13307	1.5232310725	1.8583518950	1.3626647774	H2-Eb1/H2-Aa/H	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046634	regulation of alpha-beta T cell activation	8/62	98/13307	1.5786969982	1.8583518950	1.3626647774	Irf1/H2-Ab1/Cd2	8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002504	antigen processing and presentation of peptide or poly	5/62	19/13307	2.0598639759	2.2631038882	1.6594553294	H2-Eb1/H2-Aa/H	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050868	negative regulation of T cell activation	8/62	109/13307	3.6623370549	3.7722071666	2.7660282493	H2-Aa/Irf1/H2-Ab	8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045785	positive regulation of cell adhesion	12/62	356/13307	7.2417783888	6.4151052127	4.7039734186	H2-Aa/Irf1/H2-Ab	12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	8/62	119/13307	7.2910981575	6.4151052127	4.7039734186	H2-Aa/Irf1/H2-Ab	8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002478	antigen processing and presentation of exogenous pep	5/62	24/13307	7.3960557671	6.4151052127	4.7039734186	H2-Eb1/H2-Aa/H	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1903706	regulation of hemopoiesis	12/62	362/13307	8.6916136548	7.1618896515	5.2515644609	H2-Aa/Irf1/Cd74/	12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051251	positive regulation of lymphocyte activation	10/62	236/13307	1.2197631150	9.5722362551	7.0189877496	H2-Aa/Irf1/H2-Ab	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051249	regulation of lymphocyte activation	12/62	377/13307	1.3516734020	1.0087050346	7.3964830080	H2-Aa/Irf1/H2-Ab	12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0019882	antigen processing and presentation	7/62	87/13307	1.4689879144	1.0087050346	7.3964830080	H2-Eb1/H2-Aa/H	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045582	positive regulation of T cell differentiation	7/62	87/13307	1.4689879144	1.0087050346	7.3964830080	H2-Aa/Irf1/Cd74/	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0030217	T cell differentiation	10/62	245/13307	1.7294234502	1.1400359384	8.3594868249	H2-Aa/Irf1/Cd74/	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0019884	antigen processing and presentation of exogenous ant	5/62	29/13307	2.0298347433	1.2556297360	9.2070959180	H2-Eb1/H2-Aa/H	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045580	regulation of T cell differentiation	8/62	136/13307	2.0571603684	1.2556297360	9.2070959180	H2-Aa/Irf1/Cd74/	8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042098	T cell proliferation	9/62	190/13307	2.1560284115	1.2689767221	9.3049647233	H2-Aa/Irf1/H2-Ab	9	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051250	negative regulation of lymphocyte activation	8/62	139/13307	2.4341929728	1.3832931100	1.0143207015	H2-Aa/Irf1/H2-Ab	8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046651	lymphocyte proliferation	10/62	260/13307	3.0011379102	1.6486250920	1.2088794108	H2-Aa/Irf1/H2-Ab	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032943	mononuclear cell proliferation	10/62	262/13307	3.2213016136	1.6602189403	1.2173807763	H2-Aa/Irf1/H2-Ab	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0030098	lymphocyte differentiation	11/62	332/13307	3.2237260976	1.6602189403	1.2173807763	H2-Aa/Irf1/H2-Ab	11	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+

BP	GO:0050670	regulation of lymphocyte proliferation	9/62	202/13307	3.62441533911	1.81001105421	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045621	positive regulation of lymphocyte differentiation	7/62	100/13307	3.83886241961	1.85471803151	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0032944	regulation of mononuclear cell proliferation	9/62	204/13307	3.93902494561	1.85471803151	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070663	regulation of leukocyte proliferation	9/62	212/13307	5.44697424641	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070661	leukocyte proliferation	10/62	278/13307	5.55748922421	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042129	regulation of T cell proliferation	8/62	155/13307	5.61107835471	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:1902107	positive regulation of leukocyte differentiation	8/62	155/13307	5.61107835471	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002696	positive regulation of leukocyte activation	10/62	282/13307	6.33423014011	2.59227156741	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002250	adaptive immune response	11/62	356/13307	6.44921931221	2.59227156741	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0022408	negative regulation of cell-cell adhesion	8/62	159/13307	6.81253621341	2.67310944751	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002695	negative regulation of leukocyte activation	8/62	162/13307	7.85215461261	3.00938390731	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045619	regulation of lymphocyte differentiation	8/62	165/13307	9.02449560811	3.38000880951	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0009617	response to bacterium	12/62	453/13307	9.63790008721	3.52961345111	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050867	positive regulation of cell activation	10/62	296/13307	9.85362469581	3.53016851181	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046636	negative regulation of alpha-beta T cell activation	5/62	40/13307	1.08135922161	3.79165956861	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002694	regulation of leukocyte activation	12/62	459/13307	1.10699683711	3.80068914081	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	6/62	75/13307	1.25231474691	4.21186674071	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002821	positive regulation of adaptive immune response	7/62	120/13307	1.32677088991	4.37303685321	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002181	cytoplasmic translation	6/62	76/13307	1.35475344151	4.37771308171	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002819	regulation of adaptive immune response	8/62	176/13307	1.46916445961	4.65612121061	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050866	negative regulation of cell activation	8/62	177/13307	1.53313896691	4.76719437271	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0034341	response to interferon-gamma	7/62	123/13307	1.56696468461	4.78214407471	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002521	leukocyte differentiation	12/62	488/13307	2.10114609491	6.29579775351	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050865	regulation of cell activation	12/62	491/13307	2.23938402201	6.59018726491	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:1903708	positive regulation of hemopoiesis	8/62	190/13307	2.60719773091	7.53800326411	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002683	negative regulation of immune system process	11/62	413/13307	2.75341301981	7.82349078751	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:1902105	regulation of leukocyte differentiation	9/62	264/13307	3.36327881921	9.39437880341	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000106	regulation of leukocyte apoptotic process	6/62	89/13307	3.43586834761	9.43718506151	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0048002	antigen processing and presentation of peptide antigen	5/62	52/13307	4.09190496621	0.00010876541	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000107	negative regulation of leukocyte apoptotic process	5/62	52/13307	4.09190496621	0.00010876541	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0036037	CD8-positive, alpha-beta T cell activation	4/62	25/13307	5.02170480821	0.00013136141	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046632	alpha-beta T cell differentiation	6/62	102/13307	7.59651749691	0.00019561031	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di	4/62	28/13307	8.04342019801	0.00020084171	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045589	regulation of regulatory T cell differentiation	4/62	28/13307	8.04342019801	0.00020084171	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070228	regulation of lymphocyte apoptotic process	5/62	60/13307	8.35671423451	0.00020555021	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042130	negative regulation of T cell proliferation	5/62	62/13307	9.83091737541	0.00023825511	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0071887	leukocyte apoptotic process	6/62	109/13307	1.11390002871	0.00026585651	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002579	positive regulation of antigen processing and presenta	3/62	10/13307	1.12924484961	0.00026585651	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002828	regulation of type 2 immune response	4/62	31/13307	1.22321264371	0.00027614441	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045066	regulatory T cell differentiation	4/62	31/13307	1.22321264371	0.00027614441	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000515	negative regulation of CD4-positive, alpha-beta T cell a	4/62	31/13307	1.22321264371	0.00027614441	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046635	positive regulation of alpha-beta T cell activation	5/62	65/13307	1.24150067691	0.00027648551	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0007162	negative regulation of cell adhesion	8/62	236/13307	1.28738699301	0.00028288181	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0009615	response to virus	8/62	237/13307	1.32753236511	0.00028786491	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	3/62	11/13307	1.54755314021	0.00032697021	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferati	3/62	11/13307	1.54755314021	0.00032697021	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	4/62	34/13307	1.78412830551	0.00037218271	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	4/62	35/13307	2.00733053101	0.00041351001	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0032945	negative regulation of mononuclear cell proliferation	5/62	75/13307	2.50324692631	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050672	negative regulation of lymphocyte proliferation	5/62	75/13307	2.50324692631	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042092	type 2 immune response	4/62	37/13307	2.51438924071	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046640	regulation of alpha-beta T cell proliferation	4/62	37/13307	2.51438924071	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0010819	regulation of T cell chemotaxis	3/62	13/13307	2.66463594131	0.00050474941	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STA	3/62	13/13307	2.66463594131	0.00050474941	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046642	negative regulation of alpha-beta T cell proliferation	3/62	13/13307	2.66463594131	0.00050474941	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002687	positive regulation of leukocyte migration	6/62	129/13307	2.91095717881	0.00054514281	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070227	lymphocyte apoptotic process	5/62	78/13307	3.02929732751	0.00055469791	aPD-L1+aTGFb vs aTGFb	Up-regulated genes

BP	GO:0050670	regulation of lymphocyte proliferation	9/62	202/13307	3.62441533911	1.81001105421	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045621	positive regulation of lymphocyte differentiation	7/62	100/13307	3.83886241961	1.85471803151	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0032944	regulation of mononuclear cell proliferation	9/62	204/13307	3.93902494561	1.85471803151	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070663	regulation of leukocyte proliferation	9/62	212/13307	5.44697424641	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070661	leukocyte proliferation	10/62	278/13307	5.55748922421	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042129	regulation of T cell proliferation	8/62	155/13307	5.61107835471	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:1902107	positive regulation of leukocyte differentiation	8/62	155/13307	5.61107835471	2.37104028931	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002696	positive regulation of leukocyte activation	10/62	282/13307	6.33423014011	2.59227156741	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002250	adaptive immune response	11/62	356/13307	6.44921931221	2.59227156741	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0022408	negative regulation of cell-cell adhesion	8/62	159/13307	6.81253621341	2.67310944751	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002695	negative regulation of leukocyte activation	8/62	162/13307	7.85215461261	3.00938390731	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045619	regulation of lymphocyte differentiation	8/62	165/13307	9.02449560811	3.38000880951	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0009617	response to bacterium	12/62	453/13307	9.63790008721	3.52961345111	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050867	positive regulation of cell activation	10/62	296/13307	9.85362469581	3.53016851181	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046636	negative regulation of alpha-beta T cell activation	5/62	40/13307	1.08135922161	3.79165956861	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002694	regulation of leukocyte activation	12/62	459/13307	1.10699683711	3.80068914081	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	6/62	75/13307	1.25231474691	4.21186674071	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002821	positive regulation of adaptive immune response	7/62	120/13307	1.32677088991	4.37303685321	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002181	cytoplasmic translation	6/62	76/13307	1.35475344151	4.37771308171	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002819	regulation of adaptive immune response	8/62	176/13307	1.46916445961	4.65612121061	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050866	negative regulation of cell activation	8/62	177/13307	1.53313896691	4.76719437271	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0034341	response to interferon-gamma	7/62	123/13307	1.56696468461	4.78214407471	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002521	leukocyte differentiation	12/62	488/13307	2.10114609491	6.29579775351	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050865	regulation of cell activation	12/62	491/13307	2.23938402201	6.59018726491	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:1903708	positive regulation of hemopoiesis	8/62	190/13307	2.60719773091	7.53800326411	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002683	negative regulation of immune system process	11/62	413/13307	2.75341301981	7.82349078751	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:1902105	regulation of leukocyte differentiation	9/62	264/13307	3.36327881921	9.39437880341	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000106	regulation of leukocyte apoptotic process	6/62	89/13307	3.43586834761	9.43718506151	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0048002	antigen processing and presentation of peptide antigen	5/62	52/13307	4.09190496621	0.00010876541	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000107	negative regulation of leukocyte apoptotic process	5/62	52/13307	4.09190496621	0.00010876541	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0036037	CD8-positive, alpha-beta T cell activation	4/62	25/13307	5.02170480821	0.00013136141	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046632	alpha-beta T cell differentiation	6/62	102/13307	7.59651749691	0.00019561031	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di	4/62	28/13307	8.04342019801	0.00020084171	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045589	regulation of regulatory T cell differentiation	4/62	28/13307	8.04342019801	0.00020084171	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070228	regulation of lymphocyte apoptotic process	5/62	60/13307	8.35671423451	0.00020555021	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042130	negative regulation of T cell proliferation	5/62	62/13307	9.83091737541	0.00023825511	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0071887	leukocyte apoptotic process	6/62	109/13307	1.11390002871	0.00026585651	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002579	positive regulation of antigen processing and presenta	3/62	10/13307	1.12924484961	0.00026585651	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002828	regulation of type 2 immune response	4/62	31/13307	1.22321264371	0.00027614441	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0045066	regulatory T cell differentiation	4/62	31/13307	1.22321264371	0.00027614441	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000515	negative regulation of CD4-positive, alpha-beta T cell a	4/62	31/13307	1.22321264371	0.00027614441	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046635	positive regulation of alpha-beta T cell activation	5/62	65/13307	1.24150067691	0.00027648551	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0007162	negative regulation of cell adhesion	8/62	236/13307	1.28738699301	0.00028288181	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0009615	response to virus	8/62	237/13307	1.32753236511	0.00028786491	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	3/62	11/13307	1.54755314021	0.00032697021	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferati	3/62	11/13307	1.54755314021	0.00032697021	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	4/62	34/13307	1.78412830551	0.00037218271	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	4/62	35/13307	2.00733053101	0.00041351001	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0032945	negative regulation of mononuclear cell proliferation	5/62	75/13307	2.50324692631	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0050672	negative regulation of lymphocyte proliferation	5/62	75/13307	2.50324692631	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042092	type 2 immune response	4/62	37/13307	2.51438924071	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046640	regulation of alpha-beta T cell proliferation	4/62	37/13307	2.51438924071	0.00049329921	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0010819	regulation of T cell chemotaxis	3/62	13/13307	2.66463594131	0.00050474941	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STA	3/62	13/13307	2.66463594131	0.00050474941	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0046642	negative regulation of alpha-beta T cell proliferation	3/62	13/13307	2.66463594131	0.00050474941	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0002687	positive regulation of leukocyte migration	6/62	129/13307	2.91095717881	0.00054514281	aPD-L1+aTGFb vs aTGFb	Up-regulated genes
BP	GO:0070227	lymphocyte apoptotic process	5/62	78/13307	3.02929732751	0.00055469791	aPD-L1+aTGFb vs aTGFb	Up-regulated genes

BP	GO:0070664	negative regulation of leukocyte proliferation	5/62	78/13307	3.02929732759	0.00055469799	0.0004067407	H2-Aa/H2-Ab1/C	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043374	CD8-positive, alpha-beta T cell differentiation	3/62	14/13307	3.38009339319	0.00061213119	0.0004488545	Irf1/Satb1/Socs1	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046633	alpha-beta T cell proliferation	4/62	40/13307	3.4431204522	0.0006167676	0.0004522542	Irf1/Cd274/Arg2/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1903707	negative regulation of hemopoiesis	6/62	141/13307	4.8020218360	0.0008509389	0.0006239639	Irf1/Cd74/Socs1/	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0098542	defense response to other organism	9/62	370/13307	4.9726176272	0.0008717950	0.0006392570	Irf1/Cxcl10/Rpl39	9	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045581	negative regulation of T cell differentiation	4/62	44/13307	5.0436672382	0.0008741968	0.0006410181	Irf1/Cd74/Socs1/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902532	negative regulation of intracellular signal transduction	10/62	464/13307	5.0924088212	0.0008741968	0.0006410181	Irf1/Cd74/Dusp1	10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	4/62	45/13307	5.5164906103	0.0009372346	0.0006872415	Irf1/Socs1/Ccr7/(	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010818	T cell chemotaxis	3/62	17/13307	6.2517854699	0.0010407012	0.0007631100	Cxcl10/Ccl5/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	3/62	17/13307	6.2517854699	0.0010407012	0.0007631100	Irf1/Cd274/Socs1	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	7/62	217/13307	6.3954653963	0.0010539726	0.0007728415	Irf1/Cd74/Ccl5/S	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentia	4/62	47/13307	6.5580818881	0.0010700711	0.0007846459	Irf1/Socs1/Ccr7/(	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pat	5/62	92/13307	6.7130034179	0.0010815980	0.0007930982	Cd74/Dnaja1/Pla	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0001819	positive regulation of cytokine production	9/62	385/13307	6.7599878921	0.0010815980	0.0007930982	Irf1/Cd74/Ccl5/R	9	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0000028	ribosomal small subunit assembly	3/62	18/13307	7.4772471775	0.0011735717	0.0008605393	Rps27/Rpl38/Rps	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002577	regulation of antigen processing and presentation	3/62	18/13307	7.4772471775	0.0011735717	0.0008605393	H2-Ab1/Cd74/Cc	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032496	response to lipopolysaccharide	7/62	226/13307	8.2592451320	0.0012840788	0.0009415703	Cxcl10/Ccl5/Dusp	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1901623	regulation of lymphocyte chemotaxis	3/62	19/13307	8.8497707452	0.0013630301	0.0009994625	Cxcl10/Ccl5/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045620	negative regulation of lymphocyte differentiation	4/62	51/13307	9.0612289872	0.0013826764	0.0010138685	Irf1/Cd74/Socs1/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0072678	T cell migration	4/62	54/13307	0.0001134800	0.0017157347	0.0012580885	Cxcl10/Ccl5/Icam	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071346	cellular response to interferon-gamma	5/62	104/13307	0.0001202804	0.0017857860	0.0013094547	Irf1/H2-Ab1/Ccl5	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1990266	neutrophil migration	5/62	104/13307	0.0001202804	0.0017857860	0.0013094547	Cd74/Cxcl10/Ccl5	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002237	response to molecule of bacterial origin	7/62	243/13307	0.0001298728	0.0019109861	0.0014012596	Cxcl10/Ccl5/Dusp	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002827	positive regulation of T-helper 1 type immune respons	3/62	22/13307	0.0001392516	0.0020308561	0.0014891561	Irf1/H2-Ab1/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0019058	viral life cycle	6/62	174/13307	0.0001537037	0.0022219636	0.0016292885	Vps37b/Cd74/Ccl	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046426	negative regulation of JAK-STAT cascade	3/62	23/13307	0.0001596084	0.0022675406	0.0016627086	Irf1/Socs1/Socs3	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1904893	negative regulation of STAT cascade	3/62	23/13307	0.0001596084	0.0022675406	0.0016627086	Irf1/Socs1/Socs3	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002824	positive regulation of adaptive immune response base	5/62	113/13307	0.0001777959	0.0025043389	0.0018363446	Irf1/H2-Ab1/Cd2	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042274	ribosomal small subunit biogenesis	4/62	61/13307	0.0001827529	0.0025308983	0.0018558197	Rps21/Rps27/Rpl	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	4/62	61/13307	0.0001827529	0.0025308983	0.0018558197	Irf1/Ccl5/Socs1/S	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046637	regulation of alpha-beta T cell differentiation	4/62	62/13307	0.0001946786	0.0026631810	0.0019528180	Irf1/Socs1/Ccr7/(	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002685	regulation of leukocyte migration	6/62	182/13307	0.0001963230	0.0026631810	0.0019528180	Cd74/Cxcl10/Ccl5	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002460	adaptive immune response based on somatic recombi	7/62	260/13307	0.0001971529	0.0026631810	0.0019528180	Irf1/H2-Ab1/Cd7	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0018108	peptidyl-tyrosine phosphorylation	7/62	264/13307	0.0002164993	0.0029007387	0.0021270107	Irf1/Cd74/Ccl5/S	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0018212	peptidyl-tyrosine modification	7/62	267/13307	0.0002319939	0.0030827444	0.0022604692	Irf1/Cd74/Ccl5/S	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0007260	tyrosine phosphorylation of STAT protein	4/62	65/13307	0.0002338246	0.0030827444	0.0022604692	Irf1/Ccl5/Socs1/S	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0019221	cytokine-mediated signaling pathway	7/62	274/13307	0.0002716513	0.0035530265	0.0026053107	Irf1/Cd74/Cxcl10	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1903900	regulation of viral life cycle	5/62	125/13307	0.0002846524	0.0036937573	0.0027085037	Vps37b/Cd74/Ccl	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0097530	granulocyte migration	5/62	127/13307	0.0003063750	0.0039445781	0.0028924219	Cd74/Cxcl10/Ccl5	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051607	defense response to virus	6/62	199/13307	0.0003178106	0.0040600924	0.0029771245	Irf1/Cxcl10/Ccl5/	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002825	regulation of T-helper 1 type immune response	3/62	29/13307	0.0003228172	0.0040923291	0.0030007625	Irf1/H2-Ab1/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2001234	negative regulation of apoptotic signaling pathway	6/62	205/13307	0.0003725284	0.0046864650	0.0034364217	Cd74/Dnaja1/Pla	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902624	positive regulation of neutrophil migration	3/62	31/13307	0.0003944906	0.0048881251	0.0035842920	Cd74/Il1a/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000406	positive regulation of T cell migration	3/62	31/13307	0.0003944906	0.0048881251	0.0035842920	Cxcl10/Ccl5/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000108	positive regulation of leukocyte apoptotic process	3/62	32/13307	0.0004338589	0.0053358173	0.0039125691	Ccl5/Cd274/Cd44	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032642	regulation of chemokine production	4/62	77/13307	0.0004482907	0.0054724679	0.0040127703	Cd74/Ccl5/Il1a/A	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032735	positive regulation of interleukin-12 production	3/62	33/13307	0.0004756650	0.0057639417	0.0042264979	Irf1/Rel/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1901652	response to peptide	7/62	302/13307	0.0004884693	0.0058758943	0.0043085888	Irf1/Serpina3g/Sc	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002690	positive regulation of leukocyte chemotaxis	4/62	79/13307	0.0004942804	0.0059027116	0.0043282530	Cd74/Cxcl10/Ccl5	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000403	positive regulation of lymphocyte migration	3/62	34/13307	0.0005199706	0.0061648316	0.0045204565	Cxcl10/Ccl5/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032602	chemokine production	4/62	81/13307	0.0005435376	0.0063982150	0.0046915884	Cd74/Ccl5/Il1a/A	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002791	regulation of peptide secretion	8/62	413/13307	0.0006267543	0.0073254696	0.0053715119	Cd74/Ccl5/Cd274	8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002526	acute inflammatory response	4/62	85/13307	0.0006523728	0.0075712007	0.0055516980	Ccl5/Il1a/Icam1/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0044403	symbiont process	7/62	318/13307	0.0006639297	0.0076514418	0.0056105360	Vps37b/Cd74/Ccl	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0072676	lymphocyte migration	4/62	86/13307	0.0006818267	0.0078031286	0.0057217627	Cxcl10/Ccl5/Icam	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0030593	neutrophil chemotaxis	4/62	87/13307	0.0007122113	0.0080946508	0.0059355258	Cd74/Cxcl10/Ccl5	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046328	regulation of JNK cascade	5/62	153/13307	0.0007185930	0.0081112415	0.0059476911	Dusp10/Il1a/Dna	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+

BP	GO:0070372	regulation of ERK1 and ERK2 cascade	6/62	233/13307	0.0007325834	0.0082129088	0.0060222402	Cd74/Ccl5/Dusp16	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070232	regulation of T cell apoptotic process	3/62	39/13307	0.0007810720	0.0086389715	0.0063346572	Ccl5/Cd274/Arg2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902622	regulation of neutrophil migration	3/62	39/13307	0.0007810720	0.0086389715	0.0063346572	Cd74/Il1a/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050792	regulation of viral process	5/62	158/13307	0.0008308310	0.0091280636	0.0066932914	Vps37b/Cd74/Ccl 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0044419	interspecies interaction between organisms	7/62	333/13307	0.0008708265	0.0092880551	0.0068106076	Vps37b/Cd74/Ccl 7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902106	negative regulation of leukocyte differentiation	4/62	92/13307	0.0008786692	0.0092880551	0.0068106076	Irf1/Cd74/Socs1/ 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002822	regulation of adaptive immune response based on son	5/62	160/13307	0.0008792091	0.0092880551	0.0068106076	Irf1/H2-Ab1/Cd2 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	5/62	160/13307	0.0008792091	0.0092880551	0.0068106076	Cd74/Ccl5/Il1a/Ic 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071222	cellular response to lipopolysaccharide	5/62	160/13307	0.0008792091	0.0092880551	0.0068106076	Cxcl10/Ccl5/Cd27 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	5/62	160/13307	0.0008792091	0.0092880551	0.0068106076	Cd74/Dnaja1/Pla 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0007254	JNK cascade	5/62	162/13307	0.0009296595	0.0096648333	0.0070868860	Dusp10/Il1a/Dna 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002468	dendritic cell antigen processing and presentation	2/62	10/13307	0.0009383333	0.0096648333	0.0070868860	Cd74/Ccr7 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042090	interleukin-12 biosynthetic process	2/62	10/13307	0.0009383333	0.0096648333	0.0070868860	Irf1/Rel 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045075	regulation of interleukin-12 biosynthetic process	2/62	10/13307	0.0009383333	0.0096648333	0.0070868860	Irf1/Rel 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070371	ERK1 and ERK2 cascade	6/62	246/13307	0.0009716475	0.0099458081	0.0072929150	Cd74/Ccl5/Dusp16	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000404	regulation of T cell migration	3/62	43/13307	0.0010408577	0.0105884788	0.0077641630	Cxcl10/Ccl5/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043405	regulation of MAP kinase activity	6/62	250/13307	0.0010561270	0.0106778982	0.0078297311	Cd74/Dusp10/Du 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071219	cellular response to molecule of bacterial origin	5/62	167/13307	0.0010652169	0.0107041316	0.0078489672	Cxcl10/Ccl5/Cd27 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0016032	viral process	6/62	251/13307	0.0010781046	0.0107679783	0.0078957838	Vps37b/Cd74/Ccl 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0048247	lymphocyte chemotaxis	3/62	44/13307	0.0011133275	0.0109554905	0.0080332800	Cxcl10/Ccl5/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071675	regulation of mononuclear cell migration	3/62	44/13307	0.0011133275	0.0109554905	0.0080332800	Cxcl10/Ccl5/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0001660	fever generation	2/62	11/13307	0.0011434128	0.0109554905	0.0080332800	Ccl5/Il1a 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045625	regulation of T-helper 1 cell differentiation	2/62	11/13307	0.0011434128	0.0109554905	0.0080332800	Irf1/Ccr7 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0072683	T cell extravasation	2/62	11/13307	0.0011434128	0.0109554905	0.0080332800	Ccl5/Icam1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902166	negative regulation of intrinsic apoptotic signaling path	2/62	11/13307	0.0011434128	0.0109554905	0.0080332800	Cd74/Cd44 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2	2/62	11/13307	0.0011434128	0.0109554905	0.0080332800	Cd74/Ccl5 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046425	regulation of JAK-STAT cascade	4/62	99/13307	0.0011554019	0.0110063723	0.0080705898	Irf1/Ccl5/Socs1/S 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002688	regulation of leukocyte chemotaxis	4/62	100/13307	0.0011993818	0.0113596627	0.0083296454	Cd74/Cxcl10/Ccl5 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045088	regulation of innate immune response	6/62	259/13307	0.0012668610	0.0118028203	0.0086545974	Irf1/Cd74/Dusp10 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042088	T-helper 1 type immune response	3/62	46/13307	0.0012676572	0.0118028203	0.0086545974	Irf1/H2-Ab1/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071622	regulation of granulocyte chemotaxis	3/62	46/13307	0.0012676572	0.0118028203	0.0086545974	Cd74/Ccl5/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042254	ribosome biogenesis	6/62	261/13307	0.0013177832	0.0122006001	0.0089462755	Rps21/Rps27/Rpl 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1904892	regulation of STAT cascade	4/62	103/13307	0.0013383539	0.0123218284	0.0090351680	Irf1/Ccl5/Socs1/S 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002903	negative regulation of B cell apoptotic process	2/62	12/13307	0.0013679823	0.0123315927	0.0090423278	Cd74/Cd44 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010820	positive regulation of T cell chemotaxis	2/62	12/13307	0.0013679823	0.0123315927	0.0090423278	Ccl5/Ccr7 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0030335	positive regulation of cell migration	8/62	466/13307	0.0013685092	0.0123315927	0.0090423278	Cd74/Cxcl10/Ccl5 8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0001933	negative regulation of protein phosphorylation	7/62	360/13307	0.0013693455	0.0123315927	0.0090423278	Irf1/Dusp10/Dus 7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	5/62	177/13307	0.0013797566	0.0123578206	0.0090615598	Irf1/Cd74/Rel/Il1 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0097193	intrinsic apoptotic signaling pathway	6/62	266/13307	0.0014519612	0.0129342280	0.0094842193	Cd74/Crip1/Dnaj 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0097529	myeloid leukocyte migration	5/62	180/13307	0.0014862499	0.0131684944	0.0096559987	Cd74/Cxcl10/Ccl5 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071900	regulation of protein serine/threonine kinase activity	7/62	367/13307	0.0015294272	0.0134785887	0.0098833801	Cd74/Dusp10/Pir 7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071621	granulocyte chemotaxis	4/62	107/13307	0.0015406721	0.0135054666	0.0099030887	Cd74/Cxcl10/Ccl5 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000147	positive regulation of cell motility	8/62	476/13307	0.0015659272	0.0136542225	0.0100121662	Cd74/Cxcl10/Ccl5 8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0044406	adhesion of symbiont to host	2/62	13/13307	0.0016118615	0.0137924562	0.0101135282	Icam1/Gbp2b 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045060	negative thymic T cell selection	2/62	13/13307	0.0016118615	0.0137924562	0.0101135282	Cd74/Ccr7 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0090594	inflammatory response to wounding	2/62	13/13307	0.0016118615	0.0137924562	0.0101135282	Il1a/Cd44 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylatio	3/62	50/13307	0.0016152573	0.0137924562	0.0101135282	Irf1/Socs1/Socs3 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050707	regulation of cytokine secretion	5/62	185/13307	0.0016770581	0.0142463498	0.0104463526	Cd274/Il1a/Arg2/ 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045071	negative regulation of viral genome replication	3/62	51/13307	0.0017105476	0.0144563205	0.0106003167	Ccl5/Oasl1/Rsad2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071396	cellular response to lipid	7/62	375/13307	0.0017299379	0.0145456005	0.0106657827	Cxcl10/Ccl5/Cd27 7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	5/62	188/13307	0.0017998604	0.0149806564	0.0109847940	Vps37b/Cd74/Ccl 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071216	cellular response to biotic stimulus	5/62	188/13307	0.0017998604	0.0149806564	0.0109847940	Cxcl10/Ccl5/Cd27 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032655	regulation of interleukin-12 production	3/62	52/13307	0.0018092859	0.0149834331	0.0109868301	Irf1/Rel/Ccr7 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010951	negative regulation of endopeptidase activity	4/62	112/13307	0.0018224000	0.0149892562	0.0109911000	Serpina3g/Plaur/ 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051272	positive regulation of cellular component movement	8/62	489/13307	0.0018558145	0.0149892562	0.0109911000	Cd74/Cxcl10/Ccl5 8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002829	negative regulation of type 2 immune response	2/62	14/13307	0.0018748716	0.0149892562	0.0109911000	Irf1/Arg2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043383	negative T cell selection	2/62	14/13307	0.0018748716	0.0149892562	0.0109911000	Cd74/Ccr7 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+

BP	GO:0045591	positive regulation of regulatory T cell differentiation	2/62	14/13307	0.0018748716	0.0149892562	0.0109911000	Dusp10/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070234	positive regulation of T cell apoptotic process	2/62	14/13307	0.0018748716	0.0149892562	0.0109911000	Ccl5/Cd274	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 product	2/62	14/13307	0.0018748716	0.0149892562	0.0109911000	Cd74/Ccl5	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0006959	humoral immune response	4/62	113/13307	0.0018827524	0.0149892562	0.0109911000	H2-Ab1/Cxcl10/R	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032872	regulation of stress-activated MAPK cascade	5/62	191/13307	0.0019291467	0.0152847780	0.0112077958	Dusp10/Il1a/Dna	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032615	interleukin-12 production	3/62	54/13307	0.0020172835	0.0157695630	0.0115632717	Irf1/Rel/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070231	T cell apoptotic process	3/62	54/13307	0.0020172835	0.0157695630	0.0115632717	Ccl5/Cd274/Arg2	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070302	regulation of stress-activated protein kinase signaling c	5/62	193/13307	0.0020190399	0.0157695630	0.0115632717	Dusp10/Il1a/Dna	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050708	regulation of protein secretion	7/62	388/13307	0.0020989399	0.0163048803	0.0119558013	Ccl5/Cd274/Rsad	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000401	regulation of lymphocyte migration	3/62	55/13307	0.0021266293	0.0163048803	0.0119558013	Cxcl10/Ccl5/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0007259	JAK-STAT cascade	4/62	117/13307	0.0021380577	0.0163048803	0.0119558013	Irf1/Ccl5/Socs1/S	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043518	negative regulation of DNA damage response, signal tr	2/62	15/13307	0.0021568348	0.0163048803	0.0119558013	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0072567	chemokine (C-X-C motif) ligand 2 production	2/62	15/13307	0.0021568348	0.0163048803	0.0119558013	Cd74/Ccl5	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0140131	positive regulation of lymphocyte chemotaxis	2/62	15/13307	0.0021568348	0.0163048803	0.0119558013	Ccl5/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902165	regulation of intrinsic apoptotic signaling pathway in re	2/62	15/13307	0.0021568348	0.0163048803	0.0119558013	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050921	positive regulation of chemotaxis	4/62	119/13307	0.0022742725	0.0171141608	0.0125492186	Cd74/Cxcl10/Ccl5	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050671	positive regulation of lymphocyte proliferation	4/62	120/13307	0.0023445765	0.0173350878	0.0127112167	Cd74/Ccl5/Cd274	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0097696	STAT cascade	4/62	120/13307	0.0023445765	0.0173350878	0.0127112167	Irf1/Ccl5/Socs1/S	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043410	positive regulation of MAPK cascade	7/62	396/13307	0.0023547057	0.0173350878	0.0127112167	Cd74/Ccl5/Il1a/Ic	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032722	positive regulation of chemokine production	3/62	57/13307	0.0023562255	0.0173350878	0.0127112167	Cd74/Ccl5/Il1a	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045123	cellular extravasation	3/62	57/13307	0.0023562255	0.0173350878	0.0127112167	Ccl5/Il1a/Icam1	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042326	negative regulation of phosphorylation	7/62	397/13307	0.0023883015	0.0174929822	0.0128269951	Irf1/Dusp10/Dus	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002830	positive regulation of type 2 immune response	2/62	16/13307	0.0024575746	0.0177635219	0.0130253724	Cd74/Rsad2	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0031649	heat generation	2/62	16/13307	0.0024575746	0.0177635219	0.0130253724	Ccl5/Il1a	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0060009	Sertoli cell development	2/62	16/13307	0.0024575746	0.0177635219	0.0130253724	Il1a/Icam1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050727	regulation of inflammatory response	6/62	296/13307	0.0024893546	0.0178389319	0.0130806680	Ccl5/Dusp10/Soc	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032946	positive regulation of mononuclear cell proliferation	4/62	122/13307	0.0024896567	0.0178389319	0.0130806680	Cd74/Ccl5/Cd274	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050900	leukocyte migration	6/62	297/13307	0.0025315676	0.0180607080	0.0132432887	Cd74/Cxcl10/Ccl5	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042255	ribosome assembly	3/62	59/13307	0.0026006323	0.0184734572	0.0135459433	Rps27/Rpl38/Rps	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071356	cellular response to tumor necrosis factor	4/62	124/13307	0.0026408055	0.0186783153	0.0136961586	Irf1/Ccl5/Nfkbia/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0000188	inactivation of MAPK activity	2/62	17/13307	0.0027769155	0.0194738587	0.0142795029	Dusp10/Dusp2	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0090026	positive regulation of monocyte chemotaxis	2/62	17/13307	0.0027769155	0.0194738587	0.0142795029	Cxcl10/Ccl5	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051403	stress-activated MAPK cascade	5/62	209/13307	0.0028524386	0.0198884015	0.0145834727	Dusp10/Il1a/Dna	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043407	negative regulation of MAP kinase activity	3/62	61/13307	0.0028601645	0.0198884015	0.0145834727	Dusp10/Dusp2/D	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070665	positive regulation of leukocyte proliferation	4/62	127/13307	0.0028791816	0.0199365185	0.0146187552	Cd74/Ccl5/Cd274	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050663	cytokine secretion	5/62	212/13307	0.0030328327	0.0209125875	0.0153344727	Cd274/Il1a/Arg2/	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046688	response to copper ion	2/62	18/13307	0.0031146834	0.0212987480	0.0156176307	Il1a/Nfe2l2	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0060008	Sertoli cell differentiation	2/62	18/13307	0.0031146834	0.0212987480	0.0156176307	Il1a/Icam1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042108	positive regulation of cytokine biosynthetic process	3/62	63/13307	0.0031351248	0.0213499409	0.0156551687	Irf1/Rel/Il1a	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002438	acute inflammatory response to antigenic stimulus	2/62	19/13307	0.0034707052	0.0232509035	0.0170490785	Icam1/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002643	regulation of tolerance induction	2/62	19/13307	0.0034707052	0.0232509035	0.0170490785	Cd274/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002902	regulation of B cell apoptotic process	2/62	19/13307	0.0034707052	0.0232509035	0.0170490785	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010759	positive regulation of macrophage chemotaxis	2/62	19/13307	0.0034707052	0.0232509035	0.0170490785	Ccl5/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0001659	temperature homeostasis	4/62	137/13307	0.0037797833	0.0251438318	0.0184370969	Ccl5/Kdm6b/Il1a,	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045063	T-helper 1 cell differentiation	2/62	20/13307	0.0038448092	0.0251438318	0.0184370969	Irf1/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045624	positive regulation of T-helper cell differentiation	2/62	20/13307	0.0038448092	0.0251438318	0.0184370969	Irf1/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0060333	interferon-gamma-mediated signaling pathway	2/62	20/13307	0.0038448092	0.0251438318	0.0184370969	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070230	positive regulation of lymphocyte apoptotic process	2/62	20/13307	0.0038448092	0.0251438318	0.0184370969	Ccl5/Cd274	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902254	negative regulation of intrinsic apoptotic signaling path	2/62	20/13307	0.0038448092	0.0251438318	0.0184370969	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010466	negative regulation of peptidase activity	4/62	138/13307	0.0038792041	0.0252514005	0.0185159733	Serpina3g/Plaur/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071347	cellular response to interleukin-1	3/62	68/13307	0.0038919027	0.0252514005	0.0185159733	Irf1/Ccl5/Il1a	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0031349	positive regulation of defense response	6/62	325/13307	0.0039480768	0.0255154143	0.0187095654	Irf1/Cd74/Ccl5/R	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043154	negative regulation of cysteine-type endopeptidase ac	3/62	69/13307	0.0040554235	0.0260052061	0.0190687127	Plaur/Nr4a1/Cd4	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071674	mononuclear cell migration	3/62	69/13307	0.0040554235	0.0260052061	0.0190687127	Cxcl10/Ccl5/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0034612	response to tumor necrosis factor	4/62	141/13307	0.0041880958	0.0267518680	0.0196162139	Irf1/Ccl5/Nfkbia/	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002693	positive regulation of cellular extravasation	2/62	21/13307	0.0042368246	0.0269586370	0.0197678304	Il1a/Icam1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1903901	negative regulation of viral life cycle	3/62	71/13307	0.0043948881	0.0278568293	0.0204264436	Ccl5/Oasl1/Rsad	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+

BP	GO:1901653	cellular response to peptide	5/62	234/13307	0.0046173289	0.0291162244	0.0213499141	Irf1/Socs1/Icam1	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071677	positive regulation of mononuclear cell migration	2/62	22/13307	0.0046465819	0.0291162244	0.0213499141	Cxcl10/Ccl5	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0090025	regulation of monocyte chemotaxis	2/62	22/13307	0.0046465819	0.0291162244	0.0213499141	Cxcl10/Ccl5	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	6/62	339/13307	0.0048450463	0.0302448350	0.0221774851	Vps37b/Cd74/Ccl	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0031098	stress-activated protein kinase signaling cascade	5/62	238/13307	0.0049587253	0.0308376581	0.0226121816	Dusp10/Il1a/Dna	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002675	positive regulation of acute inflammatory response	2/62	23/13307	0.0050739127	0.0312007768	0.0228784439	Ccl5/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070233	negative regulation of T cell apoptotic process	2/62	23/13307	0.0050739127	0.0312007768	0.0228784439	Ccl5/Arg2	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0090023	positive regulation of neutrophil chemotaxis	2/62	23/13307	0.0050739127	0.0312007768	0.0228784439	Cd74/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000117	negative regulation of cysteine-type endopeptidase ac	3/62	75/13307	0.0051243542	0.0313938135	0.0230199910	Plaur/Nr4a1/Cd4	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043901	negative regulation of multi-organism process	4/62	150/13307	0.0052138264	0.0318236520	0.0233351766	Ccl5/Oasl1/Rsad2	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0014070	response to organic cyclic compound	7/62	458/13307	0.0052453546	0.0318979498	0.0233896566	Ccl5/Pim1/Dnaja	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043506	regulation of JUN kinase activity	3/62	76/13307	0.0053174175	0.0322172946	0.0236238210	Dusp10/Dnaja1/C	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010035	response to inorganic substance	6/62	348/13307	0.0054960997	0.0325976160	0.0239026975	Kdm6b/Crip1/Il1a	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0060326	cell chemotaxis	5/62	244/13307	0.0055040002	0.0325976160	0.0239026975	Cd74/Cxcl10/Ccl5	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0006925	inflammatory cell apoptotic process	2/62	24/13307	0.0055186498	0.0325976160	0.0239026975	Ccl5/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045061	thymic T cell selection	2/62	24/13307	0.0055186498	0.0325976160	0.0239026975	Cd74/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902230	negative regulation of intrinsic apoptotic signaling pat	2/62	24/13307	0.0055186498	0.0325976160	0.0239026975	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1905523	positive regulation of macrophage migration	2/62	24/13307	0.0055186498	0.0325976160	0.0239026975	Ccl5/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2000352	negative regulation of endothelial cell apoptotic proce	2/62	24/13307	0.0055186498	0.0325976160	0.0239026975	Icam1/Nfe2l2	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0043434	response to peptide hormone	5/62	246/13307	0.0056948468	0.0335182412	0.0245777599	Irf1/Serpina3g/Sc	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002697	regulation of immune effector process	6/62	354/13307	0.0059644906	0.0347044836	0.0254475901	Irf1/Cd74/Ccl5/D	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0006953	acute-phase response	2/62	25/13307	0.0059806270	0.0347044836	0.0254475901	Ccl5/Il1a	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046639	negative regulation of alpha-beta T cell differentiation	2/62	25/13307	0.0059806270	0.0347044836	0.0254475901	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0071624	positive regulation of granulocyte chemotaxis	2/62	25/13307	0.0059806270	0.0347044836	0.0254475901	Cd74/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010563	negative regulation of phosphorus metabolic process	7/62	471/13307	0.0060951792	0.0351218722	0.0257536467	Irf1/Dusp10/Dus	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045936	negative regulation of phosphate metabolic process	7/62	471/13307	0.0060951792	0.0351218722	0.0257536467	Irf1/Dusp10/Dus	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylatio	4/62	157/13307	0.0061193412	0.0351382382	0.0257656473	Cd74/Ccl5/Icam1	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042742	defense response to bacterium	4/62	158/13307	0.0062567051	0.0358022572	0.0262525494	Rpl39/Arg2/Plac8	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0045069	regulation of viral genome replication	3/62	81/13307	0.0063482586	0.0362004506	0.0265445307	Ccl5/Oasl1/Rsad2	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0001783	B cell apoptotic process	2/62	26/13307	0.0064596794	0.0367087989	0.0269172848	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0009306	protein secretion	7/62	479/13307	0.0066672174	0.0377579876	0.0276866184	Ccl5/Cd274/Rsad	7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0031295	T cell costimulation	2/62	27/13307	0.0069556431	0.0391225250	0.0286871862	Cd274/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042119	neutrophil activation	2/62	27/13307	0.0069556431	0.0391225250	0.0286871862	Ccl5/Fcgr4	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0048525	negative regulation of viral process	3/62	84/13307	0.0070200768	0.0393506349	0.0288544512	Ccl5/Oasl1/Rsad2	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032103	positive regulation of response to external stimulus	5/62	260/13307	0.0071640977	0.0400218073	0.0293465986	Cd74/Cxcl10/Ccl5	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0070555	response to interleukin-1	3/62	85/13307	0.0072530416	0.0403817994	0.0296105682	Irf1/Ccl5/Il1a	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:2001233	regulation of apoptotic signaling pathway	6/62	370/13307	0.0073562428	0.0408184786	0.0299307699	Cd74/Dnaja1/Pla	6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002507	tolerance induction	2/62	28/13307	0.0074683553	0.0410261652	0.0300830593	Cd274/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0010758	regulation of macrophage chemotaxis	2/62	28/13307	0.0074683553	0.0410261652	0.0300830593	Ccl5/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0046329	negative regulation of JNK cascade	2/62	28/13307	0.0074683553	0.0410261652	0.0300830593	Dusp10/Dnaja1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002286	T cell activation involved in immune response	3/62	87/13307	0.0077326391	0.0423368415	0.0310441326	Irf1/Icam1/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0002691	regulation of cellular extravasation	2/62	29/13307	0.0079976544	0.0430723350	0.0315834444	Il1a/Icam1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0031294	lymphocyte costimulation	2/62	29/13307	0.0079976544	0.0430723350	0.0315834444	Cd274/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0033032	regulation of myeloid cell apoptotic process	2/62	29/13307	0.0079976544	0.0430723350	0.0315834444	Ccl5/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0090022	regulation of neutrophil chemotaxis	2/62	29/13307	0.0079976544	0.0430723350	0.0315834444	Cd74/Ccr7	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1902253	regulation of intrinsic apoptotic signaling pathway by p	2/62	29/13307	0.0079976544	0.0430723350	0.0315834444	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0042102	positive regulation of T cell proliferation	3/62	89/13307	0.0082305971	0.0441824888	0.0323974815	Ccl5/Cd274/Ccr7	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051930	regulation of sensory perception of pain	2/62	30/13307	0.0085433799	0.0455646928	0.0334110037	Il1a/Fcgr4	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:1901797	negative regulation of signal transduction by p53 class	2/62	30/13307	0.0085433799	0.0455646928	0.0334110037	Cd74/Cd44	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0050920	regulation of chemotaxis	4/62	175/13307	0.0089145356	0.0473908219	0.0347500406	Cd74/Cxcl10/Ccl5	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0032743	positive regulation of interleukin-2 production	2/62	31/13307	0.0091053722	0.0479413850	0.0351537493	Il1a/Cd83	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051085	chaperone cofactor-dependent protein refolding	2/62	31/13307	0.0091053722	0.0479413850	0.0351537493	Cd74/H2-DMb1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0051931	regulation of sensory perception	2/62	31/13307	0.0091053722	0.0479413850	0.0351537493	Il1a/Fcgr4	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0006364	rRNA processing	4/62	177/13307	0.0092688431	0.0484922332	0.0355576671	Rps21/Rpl27/Rpl	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0006469	negative regulation of protein kinase activity	4/62	177/13307	0.0092688431	0.0484922332	0.0355576671	Dusp10/Dusp2/D	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0022626	cytosolic ribosome	14/64	104/13541	3.5091492922	3.7547897427	3.2505803970	Rpl37a/Rpl39/Rp	14	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0005840	ribosome	15/64	215/13541	5.0560868107	2.7050064437	2.3417665228	Rpl37a/Rpl39/Rp	15	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+

CC	GO:0044391	ribosomal subunit	14/64	184/13541	1.1766453549	4.1967017659	3.6331505696	Rpl37a/Rpl39/Rp 14	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0044445	cytosolic part	14/64	233/13541	3.0138473805	8.0620417430	6.9794360392	Rpl37a/Rpl39/Rp 14	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0022625	cytosolic large ribosomal subunit	9/64	58/13541	5.8250007264	1.2465501554	1.0791580293	Rpl37a/Rpl39/Rp 9	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0015934	large ribosomal subunit	9/64	118/13541	3.9233614222	6.9966612030	6.0571193888	Rpl37a/Rpl39/Rp 9	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0042611	MHC protein complex	5/64	21/13541	3.8612295128	5.3877523445	4.6642617444	H2-Eb1/H2-Aa/H 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0022627	cytosolic small ribosomal subunit	6/64	42/13541	4.0282260519	5.3877523445	4.6642617444	Rps21/Rps27/Rp 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0042788	polysomal ribosome	5/64	28/13541	1.8180005590	2.1614006646	1.8711584701	Rpl39/Rps21/Rpl 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0009897	external side of plasma membrane	11/64	313/13541	2.1085365892	2.2561341504	1.9531707352	H2-Aa/H2-Ab1/C 11	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0015935	small ribosomal subunit	6/64	72/13541	1.0744426325	1.0451396516	9.0479379585	Rps21/Rps27/Rp 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0098552	side of membrane	11/64	460/13541	9.0168983560	8.0400677008	6.9604127660	H2-Aa/H2-Ab1/C 11	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0005844	polysome	5/64	68/13541	1.6675184999	0.0001372495	0.0001188191	Rpl39/Rps21/Rpl 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0005942	phosphatidylinositol 3-kinase complex	2/64	25/13541	0.0061509454	0.0470107970	0.0406979846	Socs1/Socs3 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
CC	GO:0043230	extracellular organelle	3/64	82/13541	0.0068381455	0.0487787713	0.0422285477	Cd274/Icam1/Gb 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
MF	GO:0003735	structural constituent of ribosome	13/61	147/13229	9.5629544346	1.5587615728	1.2582834782	Rpl37a/Rpl39/Rp 13	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
MF	GO:0005198	structural molecule activity	13/61	428/13229	5.6670481889	4.6186442740	3.7283211769	Rpl37a/Rpl39/Rp 13	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
MF	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase ac	2/61	12/13229	0.0013399493	0.0428929700	0.0346246125	Dusp10/Dusp2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
MF	GO:0023023	MHC protein complex binding	2/61	12/13229	0.0013399493	0.0428929700	0.0346246125	Cd74/H2-DMb1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
MF	GO:0033549	MAP kinase phosphatase activity	2/61	13/13229	0.0015788823	0.0428929700	0.0346246125	Dusp10/Dusp2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
MF	GO:0046935	1-phosphatidylinositol-3-kinase regulator activity	2/61	13/13229	0.0015788823	0.0428929700	0.0346246125	Socs1/Socs3 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45+
BP	GO:0009617	response to bacterium	12/28	430/13403	1.9510581577	1.9295965180	1.1973335852	Cxcl10/Cxcl9/Cxc 12	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0019221	cytokine-mediated signaling pathway	10/28	262/13403	6.6098931608	3.2685921680	2.0281935330	Cxcl10/Cxcl9/Cxc 10	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071276	cellular response to cadmium ion	4/28	20/13403	7.2135804869	2.3780770338	1.4756201487	Mt1/Mt2/Jun/Fo 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1903706	regulation of hemopoiesis	8/28	317/13403	1.8449470578	4.2839915623	2.6582588269	Cxcl1/Irf1/Socs1/8	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002237	response to molecule of bacterial origin	7/28	219/13403	2.4986809448	4.2839915623	2.6582588269	Cxcl10/Cxcl9/Cxc 7	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0030593	neutrophil chemotaxis	5/28	68/13403	2.5989837587	4.2839915623	2.6582588269	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0046686	response to cadmium ion	4/28	29/13403	3.4908716074	4.9321028854	3.0604182664	Mt1/Mt2/Jun/Fo 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0061844	antimicrobial humoral immune response mediated by	4/28	33/13403	5.9799342263	7.3926936872	4.5872390183	Cxcl10/Cxcl9/Cxc 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1990266	neutrophil migration	5/28	83/13403	7.0849375481	7.6079160814	4.7207866271	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1903708	positive regulation of hemopoiesis	6/28	160/13403	7.9870069996	7.6079160814	4.7207866271	Cxcl1/Irf1/Socs1/6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071621	granulocyte chemotaxis	5/28	86/13403	8.4617873504	7.6079160814	4.7207866271	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0019730	antimicrobial humoral response	4/28	43/13403	1.7778007458	0.0001411119	8.7561359651	Cxcl10/Cxcl9/Cxc 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0097530	granulocyte migration	5/28	103/13403	2.0757598321	0.0001411119	8.7561359651	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	4/28	45/13403	2.1402219125	0.0001411119	8.7561359651	H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0070098	chemokine-mediated signaling pathway	4/28	45/13403	2.1402219125	0.0001411119	8.7561359651	Cxcl10/Cxcl9/Cxc 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0043618	regulation of transcription from RNA polymerase II pro	4/28	46/13403	2.3406934314	0.0001446841	8.9777912536	Klf2/Atf3/Dnajb1 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0032496	response to lipopolysaccharide	6/28	204/13403	3.2910065925	0.0001833837	0.0001137913	Cxcl10/Cxcl9/Cxc 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0043620	regulation of DNA-templated transcription in response	4/28	51/13403	3.5589057814	0.0001833837	0.0001137913	Klf2/Atf3/Dnajb1 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0035994	response to muscle stretch	3/28	15/13403	3.6534376383	0.0001833837	0.0001137913	Nfkbia/Jun/Fos 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0031343	positive regulation of cell killing	4/28	52/13403	3.8499561384	0.0001833837	0.0001137913	H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071248	cellular response to metal ion	5/28	117/13403	3.8938908393	0.0001833837	0.0001137913	Mt1/Mt2/B2m/Ji 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1990868	response to chemokine	4/28	55/13403	4.8292911723	0.0002076595	0.0001288547	Cxcl10/Cxcl9/Cxc 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1990869	cellular response to chemokine	4/28	55/13403	4.8292911723	0.0002076595	0.0001288547	Cxcl10/Cxcl9/Cxc 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1902107	positive regulation of leukocyte differentiation	5/28	125/13403	5.3883313952	0.0002153970	0.0001336559	Irf1/Socs1/Hsp90 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002428	antigen processing and presentation of peptide antigen	3/28	17/13403	5.4448197219	0.0002153970	0.0001336559	H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	4/28	59/13403	6.4076582882	0.0002437374	0.0001512414	H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071241	cellular response to inorganic substance	5/28	137/13403	8.4360795026	0.0003090104	0.0001917440	Mt1/Mt2/B2m/Ji 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002475	antigen processing and presentation via MHC class Ib	3/28	20/13403	9.0898357483	0.0003210659	0.0001992245	H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071222	cellular response to lipopolysaccharide	5/28	142/13403	1.0046218067	0.0003426106	0.0002125932	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002483	antigen processing and presentation of endogenous pe	3/28	22/13403	1.2244932769	0.0003906528	0.0002424039	H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0019885	antigen processing and presentation of endogenous pe	3/28	22/13403	1.2244932769	0.0003906528	0.0002424039	H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071219	cellular response to molecule of bacterial origin	5/28	150/13403	1.3112743778	0.0004052657	0.0002514713	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0031341	regulation of cell killing	4/28	72/13403	1.4216665585	0.0004223025	0.0002620428	H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0019882	antigen processing and presentation	4/28	73/13403	1.5019265454	0.0004223025	0.0002620428	H2-D1/H2-K1/B2 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0030595	leukocyte chemotaxis	5/28	155/13403	1.5371984525	0.0004223025	0.0002620428	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0097529	myeloid leukocyte migration	5/28	155/13403	1.5371984525	0.0004223025	0.0002620428	Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0019883	antigen processing and presentation of endogenous ar	3/28	24/13403	1.6048364378	0.0004289684	0.0002661791	H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0001909	leukocyte mediated cytotoxicity	4/28	81/13403	2.2696090285	0.0005856725	0.0003634155	H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-

BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	3/28	27/13403	2.3095276895:0.0005856725:0.0003634155:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0071216	cellular response to biotic stimulus	5/28	170/13403	2.4014710959:0.0005937637:0.0003684362:Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002699	positive regulation of immune effector process	5/28	174/13403	2.6858445695-0.0006478781:0.0004020147:H2-D1/Cxcl1/Irf1,5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002824	positive regulation of adaptive immune response base 4/28		86/13403	2.8761728359:0.0006772702:0.0004202528:H2-D1/Irf1/H2-K: 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002474	antigen processing and presentation of peptide antigen 3/28		30/13403	3.1922769528:0.0007342236:0.0004555930:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0001914	regulation of T cell mediated cytotoxicity	3/28	31/13403	3.5293658255:0.0007933051:0.0004922536:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002821	positive regulation of adaptive immune response	4/28	93/13403	3.9150303120.0.0008604366:0.0005339093:H2-D1/Irf1/H2-K: 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0098542	defense response to other organism	6/28	325/13403	4.6583596778:0.0010015473:0.0006214699:Cxcl10/Cxcl9/Cxc 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0006959	humoral immune response	4/28	101/13403	5.4122831363:0.0011388825:0.0007066878:Cxcl10/Cxcl9/Cxc 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0010038	response to metal ion	5/28	204/13403	5.7476526084:0.0011795360:0.0007319136:Mt1/Mt2/B2m/Ji 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0001906	cell killing	4/28	103/13403	5.8440105377-0.0011795360:0.0007319136:H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002705	positive regulation of leukocyte mediated immunity	4/28	107/13403	6.7822410067:0.0013415272:0.0008324308:H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0010035	response to inorganic substance	6/28	355/13403	7.6112128362:0.0014759783:0.0009158590:Mt1/Mt2/B2m/K 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0060326	cell chemotaxis	5/28	218/13403	7.8752971900:0.0014978209-0.0009294126:Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:1902105	regulation of leukocyte differentiation	5/28	222/13403	8.5825253054:0.0016015316:0.0009937660:Irf1/Socs1/Hsp90 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0071396	cellular response to lipid	6/28	379/13403	0.0001092020:0.0019646244:0.0012190687:Cxcl10/Cxcl9/Cxc 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002711	positive regulation of T cell mediated immunity	3/28	45/13403	0.0001092561:0.0019646244:0.0012190687:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0048002	antigen processing and presentation of peptide antigen 3/28		46/13403	0.0001167153:0.0020612770:0.0012790426:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0001913	T cell mediated cytotoxicity	3/28	47/13403	0.0001244990:0.0021601679:0.0013404054:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002822	regulation of adaptive immune response based on son 4/28		128/13403	0.0001360429:0.0023197671:0.0014394382:H2-D1/Irf1/H2-K: 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0050900	leukocyte migration	5/28	260/13403	0.0001802479:0.0030214447:0.0018748361:Cxcl10/Cxcl9/Cxc 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002521	leukocyte differentiation	6/28	417/13403	0.0001841782:0.0030358719:0.0018837883:Irf1/Socs1/B2m/I6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002819	regulation of adaptive immune response	4/28	141/13403	0.0001974815:0.0032017907:0.0019867425:H2-D1/Irf1/H2-K: 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002709	regulation of T cell mediated immunity	3/28	61/13403	0.0002709769:0.0043045878:0.0026710390:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0097201	negative regulation of transcription from RNA polymer 2/28		12/13403	0.0002742052:0.0043045878:0.0026710390:Dnajb1/Jun 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0055065	metal ion homeostasis	6/28	458/13403	0.0003059005:0.0047271192:0.0029332238:Cxcl10/Mt1/Cxcl: 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0042532	negative regulation of tyrosine phosphorylation of STA 2/28		13/13403	0.0003236420:0.0047773437:0.0029643886:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0043374	CD8-positive, alpha-beta T cell differentiation	2/28	13/13403	0.0003236420:0.0047773437:0.0029643886:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0071280	cellular response to copper ion	2/28	13/13403	0.0003236420:0.0047773437:0.0029643886:Mt1/Mt2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002697	regulation of immune effector process	5/28	297/13403	0.0003340077-0.0048578479:0.0030143423:H2-D1/Cxcl1/Irf1,5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002703	regulation of leukocyte mediated immunity	4/28	163/13403	0.0003437421-0.0049269707:0.0030572337:H2-D1/Cxcl1/H2- 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0045582	positive regulation of T cell differentiation	3/28	70/13403	0.0004069999:0.0057503274:0.0035681346:Irf1/Socs1/Hsp90 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0045637	regulation of myeloid cell differentiation	4/28	173/13403	0.0004308998-0.0058872206-0.0036530782:Nfkbia/B2m/Jun/ 4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002486	antigen processing and presentation of endogenous pe 2/28		15/13403	0.0004345471:0.0058872206:0.0036530782:H2-D1/H2-K1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation 2/28		15/13403	0.0004345471:0.0058872206-0.0036530782:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0006954	inflammatory response	6/28	491/13403	0.0004439525:0.0059333653:0.0036817114:Cxcl10/Cxcl9/Cxc 6	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002476	antigen processing and presentation of endogenous pe 2/28		16/13403	0.0004959838:0.0063704935:0.0039529537:H2-D1/H2-K1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002484	antigen processing and presentation of endogenous pe 2/28		16/13403	0.0004959838:0.0063704935:0.0039529537:H2-D1/H2-K1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0071498	cellular response to fluid shear stress	2/28	16/13403	0.0004959838:0.0063704935:0.0039529537:Klf2/Spp1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0072503	cellular divalent inorganic cation homeostasis	5/28	326/13403	0.0005119576:0.0064913602:0.0040279527:Cxcl10/Mt1/Cxcl: 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0030099	myeloid cell differentiation	5/28	332/13403	0.0005563202:0.0068544906:0.0042532787:Klf2/Nfkbia/B2m,5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0007263	nitric oxide mediated signal transduction	2/28	17/13403	0.0005613890:0.0068544906:0.0042532787:Mt1/Mt2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:1901739	regulation of myoblast fusion	2/28	17/13403	0.0005613890:0.0068544906:0.0042532787:Cxcl10/Cxcl9 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0045621	positive regulation of lymphocyte differentiation	3/28	81/13403	0.0006246953:0.0075344348:0.0046751908:Irf1/Socs1/Hsp90 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002708	positive regulation of lymphocyte mediated immunity 3/28		83/13403	0.0006708575:0.0079937119:0.0049601767:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0072507	divalent inorganic cation homeostasis	5/28	349/13403	0.0006978537:0.0081917398:0.0050830549:Cxcl10/Mt1/Cxcl: 5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0006882	cellular zinc ion homeostasis	2/28	19/13403	0.0007040423:0.0081917398:0.0050830549:Mt1/Mt2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0010043	response to zinc ion	2/28	20/13403	0.0007812592:0.0085851716:0.0053271832:Mt1/Mt2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0046639	negative regulation of alpha-beta T cell differentiation 2/28		20/13403	0.0007812592:0.0085851716:0.0053271832:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0046688	response to copper ion	2/28	20/13403	0.0007812592:0.0085851716:0.0053271832:Mt1/Mt2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0055069	zinc ion homeostasis	2/28	20/13403	0.0007812592:0.0085851716:0.0053271832:Mt1/Mt2 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0060333	interferon-gamma-mediated signaling pathway	2/28	20/13403	0.0007812592:0.0085851716:0.0053271832:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0030217	T cell differentiation	4/28	204/13403	0.0008011727:0.0087072514:0.0054029350:Irf1/Socs1/B2m/I4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0002456	T cell mediated immunity	3/28	90/13403	0.0008494237-0.0088843351:0.0055128172:H2-D1/H2-K1/B2 3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0036037	CD8-positive, alpha-beta T cell activation	2/28	21/13403	0.0008623823:0.0088843351:0.0055128172:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell di 2/28		21/13403	0.0008623823:0.0088843351:0.0055128172:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	
BP	GO:0046426	negative regulation of JAK-STAT cascade	2/28	21/13403	0.0008623823:0.0088843351:0.0055128172:Irf1/Socs1 2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-	

BP	GO:1904893	negative regulation of STAT cascade	2/28	21/13403	0.0008623823	0.0088843351	0.0055128172	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:2000379	positive regulation of reactive oxygen species metabol	3/28	92/13403	0.0009054584	0.0092319420	0.0057285107	Klf2/Cxcl1/Hsp90	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002478	antigen processing and presentation of exogenous pep	2/28	22/13403	0.0009473961	0.0093697476	0.0058140204	H2-K1/B2m	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0034405	response to fluid shear stress	2/28	22/13403	0.0009473961	0.0093697476	0.0058140204	Klf2/Spp1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045589	regulation of regulatory T cell differentiation	2/28	22/13403	0.0009473961	0.0093697476	0.0058140204	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002460	adaptive immune response based on somatic recombi	4/28	214/13403	0.0009577177	0.0093780483	0.0058191710	H2-D1/Irf1/H2-K	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045066	regulatory T cell differentiation	2/28	23/13403	0.0010362850	0.0099503491	0.0061742893	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0060142	regulation of syncytium formation by plasma membrar	2/28	23/13403	0.0010362850	0.0099503491	0.0061742893	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0036003	positive regulation of transcription from RNA polymer	2/28	24/13403	0.0011290338	0.0106344239	0.0065987644	Klf2/Atf3	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell ac	2/28	24/13403	0.0011290338	0.0106344239	0.0065987644	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0006875	cellular metal ion homeostasis	5/28	390/13403	0.0011497571	0.0106566790	0.0066125739	Cxcl10/Mt1/Cxcl	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0055076	transition metal ion homeostasis	3/28	100/13403	0.0011529470	0.0106566790	0.0066125739	Mt1/Mt2/B2m	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0009612	response to mechanical stimulus	3/28	102/13403	0.0012208370	0.0111797025	0.0069371151	Nfkbia/Jun/Fos	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0019884	antigen processing and presentation of exogenous ant	2/28	27/13403	0.0014302859	0.0129775486	0.0080526963	H2-K1/B2m	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0042026	protein refolding	2/28	28/13403	0.0015383209	0.0138309040	0.0085822117	B2m/Hsp90aa1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0050778	positive regulation of immune response	5/28	422/13403	0.0016317259	0.0144552244	0.0089696086	H2-D1/Irf1/H2-K	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045580	regulation of T cell differentiation	3/28	113/13403	0.0016394253	0.0144552244	0.0089696086	Irf1/Socs1/Hsp90	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002443	leukocyte mediated immunity	4/28	248/13403	0.0016516080	0.0144552244	0.0089696086	H2-D1/Cxcl1/H2-	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0051146	striated muscle cell differentiation	4/28	249/13403	0.0016761685	0.0145414977	0.0090231421	Cxcl10/Cxcl9/Krt	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0006935	chemotaxis	5/28	430/13403	0.0017725820	0.0152442060	0.0094591795	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0042330	taxis	5/28	433/13403	0.0018276529	0.0155823172	0.0096689808	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0030003	cellular cation homeostasis	5/28	434/13403	0.0018462877	0.0156066549	0.0096840826	Cxcl10/Mt1/Cxcl	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002706	regulation of lymphocyte mediated immunity	3/28	120/13403	0.0019473464	0.0163214036	0.0101275912	H2-D1/H2-K1/B2	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0007520	myoblast fusion	2/28	32/13403	0.0020081450	0.0163783110	0.0101629028	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0046636	negative regulation of alpha-beta T cell activation	2/28	32/13403	0.0020081450	0.0163783110	0.0101629028	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1902895	positive regulation of pri-miRNA transcription by RNA j	2/28	32/13403	0.0020081450	0.0163783110	0.0101629028	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0006873	cellular ion homeostasis	5/28	443/13403	0.0020203781	0.0163783110	0.0101629028	Cxcl10/Mt1/Cxcl	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071356	cellular response to tumor necrosis factor	3/28	126/13403	0.0022382190	0.0179967370	0.0111671520	Irf1/Nfkbia/Krt8	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0034105	positive regulation of tissue remodeling	2/28	34/13403	0.0022654565	0.0180688432	0.0112118946	Klf6/Spp1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1903707	negative regulation of hemopoiesis	3/28	128/13403	0.0023408516	0.0185208182	0.0114923495	Irf1/Socs1/Nfkbia	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002250	adaptive immune response	4/28	275/13403	0.0024080430	0.0189012266	0.0117283967	H2-D1/Irf1/H2-K	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0030098	lymphocyte differentiation	4/28	278/13403	0.0025046579	0.0195047770	0.0121029056	Irf1/Socs1/B2m/H	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0043370	regulation of CD4-positive, alpha-beta T cell differentia	2/28	37/13403	0.0026790868	0.0203816685	0.0126470254	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045581	negative regulation of T cell differentiation	2/28	37/13403	0.0026790868	0.0203816685	0.0126470254	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	2/28	37/13403	0.0026790868	0.0203816685	0.0126470254	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045619	regulation of lymphocyte differentiation	3/28	135/13403	0.0027229722	0.0205574008	0.0127560690	Irf1/Socs1/Hsp90	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0050870	positive regulation of T cell activation	3/28	136/13403	0.0027805156	0.0208328025	0.0129269585	Irf1/Socs1/Hsp90	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0006457	protein folding	3/28	140/13403	0.0030182101	0.0224436831	0.0139265257	Dnajb1/B2m/Hsp	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	2/28	40/13403	0.0031255568	0.0230152431	0.0142811843	Klf2/Hsp90aa1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0034612	response to tumor necrosis factor	3/28	142/13403	0.0031416155	0.0230152431	0.0142811843	Irf1/Nfkbia/Krt8	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0098754	detoxification	2/28	41/13403	0.0032816091	0.0235181987	0.0145932732	Mt1/Mt2	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymer	2/28	41/13403	0.0032816091	0.0235181987	0.0145932732	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1904407	positive regulation of nitric oxide metabolic process	2/28	41/13403	0.0032816091	0.0235181987	0.0145932732	Klf2/Hsp90aa1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045620	negative regulation of lymphocyte differentiation	2/28	42/13403	0.0034412514	0.0244848757	0.0151931057	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0009991	response to extracellular stimulus	4/28	308/13403	0.0036226045	0.0255911135	0.0158795372	Atf3/Spp1/Jun/Fo	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	3/28	151/13403	0.0037353236	0.0262002488	0.0162575116	Irf1/Socs1/Hsp90	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0035458	cellular response to interferon-beta	2/28	44/13403	0.0037712480	0.0262659462	0.0162982775	Irf1/Ifigp1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0010977	negative regulation of neuron projection development	3/28	152/13403	0.0038052291	0.0263172842	0.0163301332	H2-D1/H2-K1/B2	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0000768	syncytium formation by plasma membrane fusion	2/28	45/13403	0.0039415733	0.0268842482	0.0166819400	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0140253	cell-cell fusion	2/28	45/13403	0.0039415733	0.0268842482	0.0166819400	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045661	regulation of myoblast differentiation	2/28	46/13403	0.0041154304	0.0278778133	0.0172984568	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0042692	muscle cell differentiation	4/28	322/13403	0.0042452195	0.0283038957	0.0175628451	Cxcl10/Cxcl9/Krt	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0006949	syncytium formation	2/28	47/13403	0.0042928052	0.0283038957	0.0175628451	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0010830	regulation of myotube differentiation	2/28	47/13403	0.0042928052	0.0283038957	0.0175628451	Cxcl10/Cxcl9	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	2/28	47/13403	0.0042928052	0.0283038957	0.0175628451	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002763	positive regulation of myeloid leukocyte differentiatior	2/28	48/13403	0.0044736831	0.0289181215	0.0179439783	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0050732	negative regulation of peptidyl-tyrosine phosphorylatic	2/28	48/13403	0.0044736831	0.0289181215	0.0179439783	Irf1/Socs1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-

BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	2/28	48/13403	0.0044736831	0.0289181215	0.017943978	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0046635	positive regulation of alpha-beta T cell activation	2/28	49/13403	0.0046580498	0.0299143591	0.018562153	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0032370	positive regulation of lipid transport	2/28	50/13403	0.0048458911	0.0309199117	0.019186108	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0046637	regulation of alpha-beta T cell differentiation	2/28	51/13403	0.0050371926	0.0317311054	0.019689462	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1903428	positive regulation of reactive oxygen species biosynth	2/28	51/13403	0.0050371926	0.0317311054	0.019689462	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045785	positive regulation of cell adhesion	4/28	341/13403	0.0052014740	0.0325585939	0.020020927	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0035456	response to interferon-beta	2/28	53/13403	0.0054301197	0.0335649280	0.020827367	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	2/28	53/13403	0.0054301197	0.0335649280	0.020827367	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0070997	neuron death	4/28	346/13403	0.0054753741	0.0336344412	0.020870501	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0071277	cellular response to calcium ion	2/28	54/13403	0.0056317170	0.0342144123	0.021230378	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:2000377	regulation of reactive oxygen species metabolic proces	3/28	175/13403	0.0056389779	0.0342144123	0.021230378	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0042110	T cell activation	4/28	352/13403	0.0058166996	0.0346713660	0.021513923	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0031345	negative regulation of cell projection organization	3/28	177/13403	0.0058194608	0.0346713660	0.021513923	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0051607	defense response to virus	3/28	177/13403	0.0058194608	0.0346713660	0.021513923	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0007260	tyrosine phosphorylation of STAT protein	2/28	56/13403	0.0060451085	0.0358000737	0.022214297	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0001836	release of cytochrome c from mitochondria	2/28	57/13403	0.0062568746	0.0366144397	0.022719619	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0033209	tumor necrosis factor-mediated signaling pathway	2/28	57/13403	0.0062568746	0.0366144397	0.022719619	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0001933	negative regulation of protein phosphorylation	4/28	360/13403	0.0062936852	0.0366144397	0.022719619	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0051851	modification by host of symbiont morphology or physi	2/28	58/13403	0.0064720023	0.0374316393	0.023226699	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045428	regulation of nitric oxide biosynthetic process	2/28	59/13403	0.0066904777	0.0382478758	0.023733182	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0060395	SMAD protein signal transduction	2/28	59/13403	0.0066904777	0.0382478758	0.023733182	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0022409	positive regulation of cell-cell adhesion	3/28	187/13403	0.0067740040	0.0384059092	0.023831243	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0060537	muscle tissue development	4/28	368/13403	0.0067962363	0.0384059092	0.023831243	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0017038	protein import	3/28	188/13403	0.0068742885	0.0384059092	0.023831243	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0035914	skeletal muscle cell differentiation	2/28	60/13403	0.0069122870	0.0384059092	0.023831243	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	2/28	60/13403	0.0069122870	0.0384059092	0.023831243	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0002449	lymphocyte mediated immunity	3/28	190/13403	0.0070775193	0.0391042827	0.024264591	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0051251	positive regulation of lymphocyte activation	3/28	194/13403	0.0074946833	0.0411791214	0.025552049	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0051702	interaction with symbiont	2/28	63/13403	0.0075975790	0.0415138435	0.025759747	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0031668	cellular response to extracellular stimulus	3/28	196/13403	0.0077086477	0.0418893001	0.025992722	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:1905954	positive regulation of lipid localization	2/28	65/13403	0.0080708564	0.0436179073	0.027065339	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0006809	nitric oxide biosynthetic process	2/28	66/13403	0.0083123788	0.0445169594	0.027623210	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0007204	positive regulation of cytosolic calcium ion concentrati	3/28	202/13403	0.0083722492	0.0445169594	0.027623210	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0097191	extrinsic apoptotic signaling pathway	3/28	202/13403	0.0083722492	0.0445169594	0.027623210	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0001101	response to acid chemical	2/28	205/13403	0.0087163491	0.0460987664	0.028604737	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0034103	regulation of tissue remodeling	2/28	69/13403	0.0090563177	0.0469839159	0.029153981	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045445	myoblast differentiation	2/28	69/13403	0.0090563177	0.0469839159	0.029153981	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0046209	nitric oxide metabolic process	2/28	69/13403	0.0090563177	0.0469839159	0.029153981	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0042326	negative regulation of phosphorylation	4/28	400/13403	0.0090737390	0.0469839159	0.029153981	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0045665	negative regulation of neuron differentiation	3/28	211/13403	0.0094293763	0.0485711106	0.030138851	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0009615	response to virus	3/28	212/13403	0.0095514514	0.0489450024	0.030370854	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0032870	cellular response to hormone stimulus	4/28	408/13403	0.0097127293	0.0495148934	0.030724477	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0042612	MHC class I protein complex	3/28	11/13620	1.2698623857	0.0001511136	0.000102925	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0042824	MHC class I peptide loading complex	3/28	14/13620	2.7898405990	0.0001659955	0.000113061	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0042611	MHC protein complex	3/28	19/13620	7.3758318284	0.0002623028	0.000178658	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0009897	external side of plasma membrane	6/28	246/13620	8.8169041650	0.0002623028	0.000178658	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0098552	side of membrane	6/28	393/13620	0.0001220847	0.0029056160	0.001979057	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0005797	Golgi medial cisterna	2/28	23/13620	0.0010039599	0.0199118715	0.013562265	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0070971	endoplasmic reticulum exit site	2/28	26/13620	0.0012847648	0.0218410025	0.014876224	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0030176	integral component of endoplasmic reticulum membra	3/28	128/13620	0.0022369370	0.0332744385	0.022663704	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
CC	GO:0031227	intrinsic component of endoplasmic reticulum membra	3/28	135/13620	0.0026024973	0.0344107983	0.023437695	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0008009	chemokine activity	4/28	33/13297	6.1708817808	6.4177170520	3.702529068	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0042379	chemokine receptor binding	4/28	43/13297	1.8343584389	9.5386638823	5.503075316	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0005125	cytokine activity	5/28	117/13297	4.0464206180	0.0001402759	8.092841236	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0030881	beta-2-microglobulin binding	2/28	11/13297	0.0002324410	0.0035457322	0.002045614	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0042610	CD8 receptor binding	2/28	11/13297	0.0002324410	0.0035457322	0.002045614	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0046977	TAP binding	2/28	11/13297	0.0002324410	0.0035457322	0.002045614	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-

MF	GO:0048018	receptor ligand activity	5/28	274/13297	0.0002386550	0.0035457322	0.0020456147	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0030545	receptor regulator activity	5/28	301/13297	0.0003683563	0.0047886322	0.0027626724	Cxcl10/Cxcl9/Cxc	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0042608	T cell receptor binding	2/28	15/13297	0.0004414439	0.0051011306	0.0029429599	H2-D1/H2-K1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0005126	cytokine receptor binding	4/28	203/13297	0.0008101302	0.0075921343	0.0043800775	Cxcl10/Cxcl9/Cxc	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0001664	G protein-coupled receptor binding	4/28	207/13297	0.0008713495	0.0075921343	0.0043800775	Cxcl10/Cxcl9/Cxc	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0042605	peptide antigen binding	2/28	21/13297	0.0008760155	0.0075921343	0.0043800775	H2-D1/H2-K1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0070412	R-SMAD binding	2/28	22/13297	0.0009623633	0.0076989064	0.0044416767	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0000978	RNA polymerase II proximal promoter sequence-specif	5/28	427/13297	0.0017796962	0.0128068824	0.0073885860	Atf3/Irf1/Klf6/Jur	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0046982	protein heterodimerization activity	5/28	432/13297	0.0018732032	0.0128068824	0.0073885860	H2-D1/Atf3/H2-K	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0000987	proximal promoter sequence-specific DNA binding	5/28	437/13297	0.0019702896	0.0128068824	0.0073885860	Atf3/Irf1/Klf6/Jur	5	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0001102	RNA polymerase II activating transcription factor bindi	2/28	33/13297	0.0021684300	0.0132656898	0.0076532825	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0003823	antigen binding	2/28	35/13297	0.0024372448	0.0140818591	0.0081241494	H2-D1/H2-K1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0031625	ubiquitin protein ligase binding	4/28	278/13297	0.0025774035	0.0141078930	0.0081391690	Ubc/Nfkbia/Hsp9	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0044389	ubiquitin-like protein ligase binding	4/28	294/13297	0.0031540526	0.0164010735	0.0094621578	Ubc/Nfkbia/Hsp9	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0001228	DNA-binding transcription activator activity, RNA polyr	4/28	312/13297	0.0039023119	0.0193257353	0.0111494627	Irf1/Klf6/Jun/Fos	4	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0097110	scaffold protein binding	2/28	58/13297	0.0065718250	0.0310668094	0.0179231592	Krt8/Hsp90aa1	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0033613	activating transcription factor binding	2/28	66/13297	0.0084398990	0.0381630217	0.0220171279	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0042277	peptide binding	3/28	216/13297	0.0102670634	0.0444906084	0.0256676587	H2-D1/H2-K1/Nfl	3	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
MF	GO:0046332	SMAD binding	2/28	76/13297	0.0110695901	0.0460494951	0.0265670164	Jun/Fos	2	aPD-L1+aTGFb vs aTGFb	Up-regulated genes	CD45-
BP	GO:0051607	defense response to virus	13/35	199/13307	1.3961342787	1.7437717141	1.3873165885	Trim30a/Mx1/Oa	13	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0009615	response to virus	13/35	237/13307	1.3622361555	8.5071647915	6.7681627940	Trim30a/Mx1/Oa	13	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0098542	defense response to other organism	13/35	370/13307	4.0888585453	1.7023281077	1.3543447252	Trim30a/Mx1/Oa	13	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0050792	regulation of viral process	9/35	158/13307	2.0232410489	6.3175701753	5.0261567110	Trim30a/Pfn1/Jur	9	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0043903	regulation of symbiosis, encompassing mutualism thro	9/35	188/13307	9.5224886570	2.3787176665	1.8924693246	Trim30a/Pfn1/Jur	9	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0016032	viral process	9/35	251/13307	1.2054152381	2.2424514329	1.7840581118	Trim30a/Pfn1/Jur	9	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0009617	response to bacterium	11/35	453/13307	1.2567782250	2.2424514329	1.7840581118	Trim30a/Slfn4/U	11	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0048525	negative regulation of viral process	6/35	84/13307	7.4013983099	1.1555433111	9.1933157955	Jun/Oasl1/Isg20/	6	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0044403	symbiont process	9/35	318/13307	9.2759149755	1.2872908671	1.0241478054	Trim30a/Pfn1/Jur	9	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0044419	interspecies interaction between organisms	9/35	333/13307	1.3743884939	1.7166112289	1.3657081455	Trim30a/Pfn1/Jur	9	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0043900	regulation of multi-organism process	9/35	339/13307	1.5998875628	1.8165996054	1.4452572816	Trim30a/Pfn1/Jur	9	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0045071	negative regulation of viral genome replication	5/35	51/13307	2.0128074425	2.0949970798	1.6667458120	Oasl1/Isg20/Bst2	5	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0019058	viral life cycle	7/35	174/13307	2.8603195972	2.7481070591	2.1863495544	Trim30a/Oasl1/Is	7	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0035455	response to interferon-alpha	4/35	23/13307	3.4267267986	3.0571298367	2.4322030811	Ifit3/Ifit2/Bst2/Ifi	4	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:1903900	regulation of viral life cycle	6/35	125/13307	7.9088234672	6.5854136737	5.2392486688	Trim30a/Oasl1/Is	6	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:1903901	negative regulation of viral life cycle	5/35	71/13307	1.0744035277	8.3870625384	6.6726113828	Oasl1/Isg20/Bst2	5	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0045069	regulation of viral genome replication	5/35	81/13307	2.0748670025	0.0001524416	0.0001212801	Oasl1/Isg20/Bst2	5	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0043901	negative regulation of multi-organism process	6/35	150/13307	2.3001105145	0.0001596021	0.0001269768	Jun/Oasl1/Isg20/	6	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0035457	cellular response to interferon-alpha	3/35	12/13307	3.6081558472	0.0002371887	0.0001887035	Ifit3/Ifit2/Ifit1	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0019079	viral genome replication	5/35	97/13307	5.0640523330	0.0003162500	0.0002516034	Oasl1/Isg20/Bst2	5	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0048524	positive regulation of viral process	4/35	77/13307	4.7353151794	0.0028163850	0.0022406704	Trim30a/Pfn1/Jur	4	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0035456	response to interferon-beta	3/35	55/13307	0.0003981871	0.0226061693	0.0179851029	Ifit3/Bst2/Ifit1	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0034121	regulation of toll-like receptor signaling pathway	3/35	60/13307	0.0005147289	0.0279520190	0.0222381745	Trim30a/Irf7/Rsa	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0043902	positive regulation of multi-organism process	4/35	151/13307	0.0006344793	0.0330193619	0.0262696706	Trim30a/Pfn1/Jur	4	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0035994	response to muscle stretch	2/35	17/13307	0.0008916389	0.0445462808	0.0354403009	Fos/Jun	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0031625	ubiquitin protein ligase binding	5/34	280/13229	0.0006895774	0.0367810798	0.0281785912	Cdkn1a/Hspa1b/.	5	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0044389	ubiquitin-like protein ligase binding	5/34	298/13229	0.0009130375	0.0367810798	0.0281785912	Cdkn1a/Hspa1b/.	5	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0001158	enhancer sequence-specific DNA binding	3/34	81/13229	0.0011541041	0.0367810798	0.0281785912	H3f3b/Jun/Irf7	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0044183	protein binding involved in protein folding	2/34	21/13229	0.0013058371	0.0367810798	0.0281785912	Hspa1b/Hspa1a	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0051787	misfolded protein binding	2/34	21/13229	0.0013058371	0.0367810798	0.0281785912	Hspa1b/Hspa1a	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0070412	R-SMAD binding	2/34	21/13229	0.0013058371	0.0367810798	0.0281785912	Fos/Jun	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
MF	GO:0035326	enhancer binding	3/34	90/13229	0.0015642813	0.0377662207	0.0289333238	H3f3b/Jun/Irf7	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45+
BP	GO:0006457	protein folding	4/11	140/13403	3.5553111816	0.0027873639	0.0015718217	Cryab/Dnajb1/Hs	4	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45-
BP	GO:0061077	chaperone-mediated protein folding	3/11	50/13403	7.8928616580	0.0030940017	0.0017447378	Dnajb1/Hspa1b/I	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45-
BP	GO:1990000	amyloid fibril formation	2/11	14/13403	5.5427919343	0.0144851629	0.0081683249	Cryab/Apoe	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45-
BP	GO:0032462	regulation of protein homooligomerization	2/11	22/13403	0.0001401984	0.0248246883	0.0139988844	Cryab/Apoe	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45-
BP	GO:0060561	apoptotic process involved in morphogenesis	2/11	28/13403	0.0002288000	0.0248246883	0.0139988844	Cryab/Ccn1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45-
BP	GO:0051085	chaperone cofactor-dependent protein refolding	2/11	29/13403	0.0002456381	0.0248246883	0.0139988844	Dnajb1/Hspa1b	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes	CD45-

BP	GO:0043281	regulation of cysteine-type endopeptidase activity invc	3/11	172/13403	0.0003176843	0.0248246883	0.0139988844	Cryab/Hspa1b/Cc	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0051084	'de novo' posttranslational protein folding	2/11	34/13403	0.0003386571	0.0248246883	0.0139988844	Dnajb1/Hspa1b	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:1902742	apoptotic process involved in development	2/11	34/13403	0.0003386571	0.0248246883	0.0139988844	Cryab/Ccn1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0006469	negative regulation of protein kinase activity	3/11	177/13403	0.0003455961	0.0248246883	0.0139988844	Gadd45g/Hspb1/3		aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0006458	'de novo' protein folding	2/11	35/13403	0.0003590210	0.0248246883	0.0139988844	Dnajb1/Hspa1b	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0032459	regulation of protein oligomerization	2/11	36/13403	0.0003799697	0.0248246883	0.0139988844	Cryab/Apoe	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	3/11	191/13403	0.0004320720	0.0257102724	0.0144982739	Cryab/Hspa1b/Cc	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0033673	negative regulation of kinase activity	3/11	195/13403	0.0004591120	0.0257102724	0.0144982739	Gadd45g/Hspb1/3		aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0051348	negative regulation of transferase activity	3/11	223/13403	0.0006793540	0.0355075697	0.0200230656	Gadd45g/Hspb1/3		aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0042982	amyloid precursor protein metabolic process	2/11	51/13403	0.0007638381	0.0374024676	0.0210916170	Itm2b/Apoe	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0072593	reactive oxygen species metabolic process	3/11	237/13403	0.0008110228	0.0374024676	0.0210916170	Cryab/COX2/Ccn	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0052548	regulation of endopeptidase activity	3/11	256/13403	0.0010143711	0.0421451617	0.0237660686	Cryab/Hspa1b/Cc	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
BP	GO:0042773	ATP synthesis coupled electron transport	2/11	59/13403	0.0010213750	0.0421451617	0.0237660686	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0031430	M band	2/11	11/13620	3.2487069899	0.0020141983	0.0008207259	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0045277	respiratory chain complex IV	2/11	16/13620	7.0724869268	0.0021924709	0.0008933667	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0031672	A band	2/11	23/13620	0.0001486523	0.0029559159	0.0012044479	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0070069	cytochrome complex	2/11	26/13620	0.0001907042	0.0029559159	0.0012044479	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0014069	postsynaptic density	3/11	307/13620	0.0016359364	0.0120642785	0.0049158350	Cryab/Dnajb1/Hs	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0032279	asymmetric synapse	3/11	308/13620	0.0016512933	0.0120642785	0.0049158350	Cryab/Dnajb1/Hs	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0098803	respiratory chain complex	2/11	77/13620	0.0016787679	0.0120642785	0.0049158350	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0098984	neuron to neuron synapse	3/11	323/13620	0.0018926941	0.0120642785	0.0049158350	Cryab/Dnajb1/Hs	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0099572	postsynaptic specialization	3/11	323/13620	0.0018926941	0.0120642785	0.0049158350	Cryab/Dnajb1/Hs	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0070469	respiratory chain	2/11	84/13620	0.0019939031	0.0120642785	0.0049158350	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0030018	Z disc	2/11	89/13620	0.0022349224	0.0120642785	0.0049158350	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0043204	perikaryon	2/11	91/13620	0.0023350216	0.0120642785	0.0049158350	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0031674	I band	2/11	95/13620	0.0025415166	0.0121210793	0.0049389796	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0030017	sarcomere	2/11	133/13620	0.0049135444	0.0217599825	0.0088665463	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0043197	dendritic spine	2/11	146/13620	0.0058911818	0.0219418438	0.0089406494	Cryab/Dnajb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0044449	contractile fiber part	2/11	147/13620	0.0059698084	0.0219418438	0.0089406494	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0044309	neuron spine	2/11	149/13620	0.0061285180	0.0219418438	0.0089406494	Cryab/Dnajb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0030016	myofibril	2/11	152/13620	0.0063702127	0.0219418438	0.0089406494	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0043292	contractile fiber	2/11	164/13620	0.0073802071	0.0240827813	0.0098130178	Cryab/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0061827	sperm head	1/11	11/13620	0.0088514425	0.0274394718	0.0111807695	Dnajb1	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0034364	high-density lipoprotein particle	1/11	13/13620	0.0104531220	0.0294587984	0.0120035851	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0043083	synaptic cleft	1/11	13/13620	0.0104531220	0.0294587984	0.0120035851	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0034358	plasma lipoprotein particle	1/11	24/13620	0.0192203768	0.0476665345	0.0194226965	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0099524	postsynaptic cytosol	1/11	24/13620	0.0192203768	0.0476665345	0.0194226965	Dnajb1	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:1990777	lipoprotein particle	1/11	24/13620	0.0192203768	0.0476665345	0.0194226965	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
CC	GO:0032994	protein-lipid complex	1/11	26/13620	0.0208068151	0.0496162515	0.0202171483	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0001540	amyloid-beta binding	3/11	47/13297	6.6951011759	0.0004887423	0.0002114242	Cryab/Itm2b/Apc	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0051082	unfolded protein binding	3/11	87/13297	4.2980203444	0.0014853678	0.0006425527	Cryab/Dnajb1/Hs	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0044183	protein binding involved in protein folding	2/11	19/13297	0.0001055799	0.0014853678	0.0006425527	Hspa1b/Hspb1	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0004129	cytochrome-c oxidase activity	2/11	21/13297	0.0001295425	0.0014853678	0.0006425527	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0015002	heme-copper terminal oxidase activity	2/11	21/13297	0.0001295425	0.0014853678	0.0006425527	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0016676	oxidoreductase activity, acting on a heme group of dor	2/11	21/13297	0.0001295425	0.0014853678	0.0006425527	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0016675	oxidoreductase activity, acting on a heme group of dor	2/11	22/13297	0.0001424325	0.0014853678	0.0006425527	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0042277	peptide binding	3/11	216/13297	0.0006334838	0.0057805397	0.0025005939	Cryab/Itm2b/Apc	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0009055	electron transfer activity	2/11	62/13297	0.0011451100	0.0089326095	0.0038641425	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0033218	amide binding	3/11	271/13297	0.0012236451	0.0089326095	0.0038641425	Cryab/Itm2b/Apc	3	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0015078	proton transmembrane transporter activity	2/11	90/13297	0.0023948003	0.0158927658	0.0068750248	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0008201	heparin binding	2/11	124/13297	0.0044905418	0.0256145737	0.0110805654	Ccn1/Apoe	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0031072	heat shock protein binding	2/11	125/13297	0.0045614994	0.0256145737	0.0110805654	Dnajb1/Hspa1b	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0005539	glycosaminoglycan binding	2/11	161/13297	0.0074587376	0.0388919890	0.0168242202	Ccn1/Apoe	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0005212	structural constituent of eye lens	1/11	13/13297	0.0107058955	0.0459723747	0.0198871123	Cryab	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0017127	cholesterol transporter activity	1/11	13/13297	0.0107058955	0.0459723747	0.0198871123	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0043395	heparan sulfate proteoglycan binding	1/11	13/13297	0.0107058955	0.0459723747	0.0198871123	Apoe	1	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-
MF	GO:0015077	monovalent inorganic cation transmembrane transpor	2/11	202/13297	0.0115406714	0.0460352022	0.0199142907	COX2/COX3	2	aPD-L1+aTGFb vs aTGFb	Down-regulated genes CD45-

MF GO:1901681 sulfur compound binding 2/11 206/13297 0.0119817649 0.0460352022 0.0199142907 Ccn1/Apoe 2 aPD-L1+aTGFb vs aTGFb Down-regulated genes CD45-

Table 3

gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj	subcluster	comparison
Cxcl10	6.37E-19	1.60	0.673	0.062	1.14E-14	Fib_0	aPD-L1 + aTGF-β vs PBS
H2-K1	9.17E-13	0.69	1	0.876	1.63E-08	Fib_0	aPD-L1 + aTGF-β vs PBS
Igfbp5	1.25E-12	1.36	0.795	0.258	2.23E-08	Fib_0	aPD-L1 vs PBS
H2-D1	2.80E-11	0.68	0.99	0.928	4.99E-07	Fib_0	aPD-L1 + aTGF-β vs PBS
mt-Atp6	1.08E-10	-0.51	0.99	1	1.93E-06	Fib_0	aPD-L1 + aTGF-β vs PBS
Irf1	4.73E-10	0.73	0.654	0.278	8.43E-06	Fib_0	aPD-L1 + aTGF-β vs PBS
mt-Co2	4.99E-10	-0.48	0.99	1	8.90E-06	Fib_0	aPD-L1 + aTGF-β vs PBS
B2m	5.05E-10	0.59	1	0.928	9.01E-06	Fib_0	aPD-L1 + aTGF-β vs PBS
Col1a1	6.27E-10	-0.71	0.99	1	1.12E-05	Fib_0	aPD-L1 + aTGF-β vs PBS
Meg3	3.97E-09	-0.85	0.692	0.897	7.07E-05	Fib_0	aPD-L1 + aTGF-β vs PBS
Mt1	4.98E-09	0.60	0.99	0.866	8.88E-05	Fib_0	aPD-L1 + aTGF-β vs PBS
Col1a2	6.22E-09	-0.47	1	1	1.11E-04	Fib_0	aPD-L1 + aTGF-β vs PBS
mt-Co3	1.22E-08	-0.46	0.99	1	2.17E-04	Fib_0	aPD-L1 + aTGF-β vs PBS
Cxcl10	1.82E-08	0.82	0.425	0.062	3.24E-04	Fib_0	aPD-L1 vs PBS
Cd74	2.33E-08	0.57	0.327	0.021	4.15E-04	Fib_0	aPD-L1 + aTGF-β vs PBS
Col5a2	2.42E-08	-0.47	0.894	0.979	4.31E-04	Fib_0	aPD-L1 + aTGF-β vs PBS
Irf1	4.01E-08	0.61	0.671	0.278	7.15E-04	Fib_0	aPD-L1 vs PBS
Thy1	5.28E-08	-0.51	0.452	0.763	9.42E-04	Fib_0	aPD-L1 + aTGF-β vs PBS
mt-Cytb	7.25E-08	-0.49	0.971	0.979	1.29E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Sfrp2	8.04E-08	-0.82	0.596	0.835	1.43E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Gm42418	1.21E-07	0.46	1	1	2.15E-03	Fib_0	aPD-L1 vs PBS
Pcolce	1.58E-07	-0.64	0.795	0.938	2.82E-03	Fib_0	aPD-L1 vs PBS
Thbs2	1.93E-07	-0.57	0.519	0.835	3.44E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Fbln2	2.21E-07	-0.46	0.856	0.959	3.94E-03	Fib_0	aTGF-β vs PBS
Antxr1	2.80E-07	-0.36	0.308	0.67	5.00E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Cxcl9	3.55E-07	0.51	0.375	0.072	6.32E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Svep1	3.67E-07	-0.52	0.342	0.701	6.54E-03	Fib_0	aPD-L1 vs PBS
Lrp1	4.27E-07	-0.35	0.752	0.969	7.62E-03	Fib_0	aTGF-β vs PBS
Mmp2	5.16E-07	-0.41	0.875	0.99	9.20E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Cthrc1	5.23E-07	-0.73	0.394	0.68	9.33E-03	Fib_0	aPD-L1 + aTGF-β vs PBS
Phlda1	6.95E-07	0.66	0.683	0.33	1.24E-02	Fib_0	aPD-L1 + aTGF-β vs PBS
Rpl37a	8.80E-07	0.28	0.992	0.99	1.57E-02	Fib_0	aTGF-β vs PBS
P3h4	1.25E-06	-0.31	0.163	0.474	2.23E-02	Fib_0	aPD-L1 + aTGF-β vs PBS
Icam1	1.40E-06	0.48	0.538	0.216	2.50E-02	Fib_0	aPD-L1 + aTGF-β vs PBS
Rps15a	1.86E-06	0.28	1	0.979	3.32E-02	Fib_0	aTGF-β vs PBS
Malat1	1.92E-06	-0.39	1	0.99	3.43E-02	Fib_0	aTGF-β vs PBS
Svep1	2.06E-06	-0.47	0.472	0.701	3.66E-02	Fib_0	aTGF-β vs PBS
Tprgl	2.35E-06	-0.32	0.173	0.474	4.20E-02	Fib_0	aPD-L1 + aTGF-β vs PBS
mt-Nd1	2.73E-06	-0.39	0.933	1	4.87E-02	Fib_0	aPD-L1 + aTGF-β vs PBS

Table 4

gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj	subcluster	comparison
Gm10076	8.56E-75	0.53	0.908	0.546	1.53E-70	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl37a	2.23E-54	0.31	0.998	1	3.97E-50	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl39	3.32E-51	0.36	0.998	0.988	5.91E-47	Mac_0	aPD-L1 + aTGF-β vs PBS
Tmsb10	4.21E-45	0.59	0.976	0.908	7.50E-41	Mac_0	aPD-L1 + aTGF-β vs PBS
Irf1	2.21E-44	0.56	0.525	0.161	3.94E-40	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl37	5.56E-44	0.30	1	0.997	9.91E-40	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl37a	6.86E-43	0.53	1	1	1.22E-38	Mac_0	aPD-L1 vs PBS
Rps21	3.21E-39	0.31	0.996	0.987	5.72E-35	Mac_0	aPD-L1 + aTGF-β vs PBS
Rps29	2.22E-36	0.45	1	1	3.96E-32	Mac_0	aPD-L1 vs PBS
Rps27	2.29E-35	0.35	0.993	0.98	4.08E-31	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl38	6.26E-35	0.51	1	0.988	1.12E-30	Mac_0	aPD-L1 vs PBS
Rpl36	2.57E-34	0.27	0.996	0.999	4.58E-30	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl37	5.70E-33	0.45	1	0.997	1.02E-28	Mac_0	aPD-L1 vs PBS
Rps27	3.25E-32	0.60	0.992	0.98	5.79E-28	Mac_0	aPD-L1 vs PBS
Rps21	4.22E-32	0.52	1	0.987	7.53E-28	Mac_0	aPD-L1 vs PBS
Rpl39	1.20E-31	0.56	0.992	0.988	2.15E-27	Mac_0	aPD-L1 vs PBS
H2-Eb1	1.36E-31	1.22	0.88	0.478	2.43E-27	Mac_0	aPD-L1 vs PBS
Rpl35a	2.77E-31	0.26	0.998	0.99	4.93E-27	Mac_0	aPD-L1 + aTGF-β vs PBS
Crip1	6.29E-31	0.55	0.945	0.829	1.12E-26	Mac_0	aPD-L1 + aTGF-β vs PBS
Tmsb10	1.66E-30	0.76	0.968	0.908	2.95E-26	Mac_0	aPD-L1 vs PBS
AY036118	8.22E-30	-0.76	0.56	0.788	1.46E-25	Mac_0	aPD-L1 + aTGF-β vs PBS
H2-Aa	1.02E-28	1.13	0.864	0.497	1.81E-24	Mac_0	aPD-L1 vs PBS
Rpl35	1.22E-28	0.25	0.996	0.974	2.17E-24	Mac_0	aPD-L1 + aTGF-β vs PBS
Atp5e	1.29E-27	0.25	0.967	0.869	2.29E-23	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl41	1.35E-27	0.40	1	1	2.40E-23	Mac_0	aPD-L1 vs PBS
Cox7c	1.91E-27	0.44	0.968	0.787	3.40E-23	Mac_0	aPD-L1 vs PBS
Irf1	3.57E-27	0.77	0.696	0.271	6.36E-23	Mac_1	aPD-L1 + aTGF-β vs PBS
Tnf	3.62E-27	0.47	0.613	0.316	6.44E-23	Mac_0	aPD-L1 + aTGF-β vs PBS
Gm10076	1.49E-26	0.53	0.88	0.546	2.66E-22	Mac_0	aPD-L1 vs PBS
Serpina3g	2.08E-26	0.45	0.348	0.097	3.72E-22	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl36	2.76E-26	0.41	1	0.999	4.93E-22	Mac_0	aPD-L1 vs PBS
H2-Eb1	5.82E-26	0.92	0.696	0.478	1.04E-21	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl35	2.33E-25	0.43	1	0.974	4.16E-21	Mac_0	aPD-L1 vs PBS
Cd74	3.20E-25	0.99	0.92	0.795	5.71E-21	Mac_0	aPD-L1 vs PBS
H2-Ab1	3.44E-25	1.00	0.872	0.559	6.14E-21	Mac_0	aPD-L1 vs PBS
H2-DMb1	8.84E-25	0.71	0.808	0.403	1.58E-20	Mac_0	aPD-L1 vs PBS
Rps28	1.59E-24	0.43	0.984	0.968	2.83E-20	Mac_0	aPD-L1 vs PBS
Acod1	1.73E-24	0.42	0.416	0.151	3.08E-20	Mac_0	aPD-L1 + aTGF-β vs PBS
H2-Aa	4.23E-24	0.86	0.696	0.497	7.54E-20	Mac_0	aPD-L1 + aTGF-β vs PBS
mt-Atp8	1.02E-23	0.47	0.8	0.438	1.83E-19	Mac_0	aPD-L1 vs PBS
Rpl35a	1.92E-23	0.40	0.992	0.99	3.43E-19	Mac_0	aPD-L1 vs PBS
H2-T23	2.82E-23	0.54	0.792	0.415	5.04E-19	Mac_0	aPD-L1 vs PBS
Oasl1	3.30E-23	0.59	0.556	0.307	5.89E-19	Mac_0	aPD-L1 + aTGF-β vs PBS
Atp5k	5.04E-23	0.45	0.88	0.569	8.99E-19	Mac_0	aPD-L1 vs PBS
Atp5e	5.31E-23	0.42	0.944	0.869	9.47E-19	Mac_0	aPD-L1 vs PBS
Cd74	1.41E-22	0.82	0.856	0.795	2.51E-18	Mac_0	aPD-L1 + aTGF-β vs PBS
H2-Ab1	4.55E-22	0.85	0.713	0.559	8.12E-18	Mac_0	aPD-L1 + aTGF-β vs PBS
Tmsb10	9.67E-22	0.73	0.982	0.93	1.72E-17	Mac_1	aPD-L1 + aTGF-β vs PBS
Serpina3g	1.70E-21	0.59	0.416	0.097	3.03E-17	Mac_0	aPD-L1 vs PBS
Cxcl10	1.87E-21	0.63	0.731	0.484	3.34E-17	Mac_0	aPD-L1 + aTGF-β vs PBS
Txn1	2.99E-20	0.35	0.969	0.939	5.32E-16	Mac_0	aPD-L1 + aTGF-β vs PBS
Peli1	6.20E-20	0.34	0.521	0.277	1.11E-15	Mac_0	aPD-L1 + aTGF-β vs PBS
AY036118	6.35E-20	0.60	0.984	0.788	1.13E-15	Mac_0	aPD-L1 vs PBS
Tomm7	8.47E-20	0.39	0.76	0.401	1.51E-15	Mac_0	aPD-L1 vs PBS
Fam26f	9.59E-20	0.32	0.348	0.133	1.71E-15	Mac_0	aPD-L1 + aTGF-β vs PBS
Irf1	9.61E-20	0.49	0.504	0.161	1.71E-15	Mac_0	aPD-L1 vs PBS
Tnfaip2	1.13E-19	0.49	0.483	0.117	2.01E-15	Mac_1	aPD-L1 vs PBS
Dab2	1.27E-19	-0.30	0.766	0.914	2.26E-15	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl18	2.58E-19	-0.31	1	0.997	4.59E-15	Mac_0	aPD-L1 vs PBS
Gbp2b	2.78E-19	0.50	0.52	0.169	4.95E-15	Mac_0	aPD-L1 vs PBS
Igkc	8.14E-19	0.47	0.166	0.022	1.45E-14	Mac_0	aPD-L1 + aTGF-β vs PBS
Gbp4	9.65E-19	0.34	0.346	0.14	1.72E-14	Mac_0	aPD-L1 + aTGF-β vs PBS
mt-Nd3	1.64E-18	0.43	0.824	0.501	2.93E-14	Mac_0	aPD-L1 vs PBS
Ly6a	1.85E-18	0.70	0.578	0.365	3.30E-14	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl5	2.00E-18	-0.25	0.943	0.974	3.57E-14	Mac_0	aPD-L1 + aTGF-β vs PBS
Gbp2b	2.00E-18	0.37	0.392	0.169	3.57E-14	Mac_0	aPD-L1 + aTGF-β vs PBS
Ubc	3.41E-18	0.37	0.807	0.643	6.08E-14	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl13	3.42E-18	-0.31	1	1	6.09E-14	Mac_0	aPD-L1 vs PBS
Sem1	4.47E-18	0.36	0.952	0.84	7.98E-14	Mac_0	aPD-L1 vs PBS
Ccl4	1.25E-17	0.46	0.884	0.702	2.24E-13	Mac_0	aPD-L1 + aTGF-β vs PBS
Nfkbia	2.26E-17	0.35	0.825	0.641	4.03E-13	Mac_0	aPD-L1 + aTGF-β vs PBS
Fam26f	2.83E-17	0.47	0.432	0.133	5.04E-13	Mac_0	aPD-L1 vs PBS
Sec61g	2.85E-17	0.40	0.84	0.612	5.09E-13	Mac_0	aPD-L1 vs PBS
AY036118	2.88E-17	0.56	0.992	0.909	5.13E-13	Mac_1	aPD-L1 vs PBS
H2-DMb2	3.64E-17	0.26	0.455	0.231	6.49E-13	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl15	6.57E-17	-0.33	0.976	0.994	1.17E-12	Mac_0	aPD-L1 vs PBS

Rsad2	8.23E-17	0.59	0.47	0.252	1.47E-12	Mac_0	aPD-L1 + aTGF-β vs PBS
Acod1	9.69E-17	0.54	0.456	0.151	1.73E-12	Mac_0	aPD-L1 vs PBS
Ifi27l2a	1.32E-16	0.36	0.921	0.788	2.35E-12	Mac_0	aPD-L1 + aTGF-β vs PBS
H2-DMb2	1.45E-16	0.36	0.568	0.231	2.59E-12	Mac_0	aPD-L1 vs PBS
Pmepa1	1.60E-16	-0.32	0.667	0.841	2.85E-12	Mac_0	aPD-L1 + aTGF-β vs PBS
Irf1	1.75E-16	0.63	0.627	0.271	3.13E-12	Mac_1	aPD-L1 vs PBS
Cox17	1.88E-16	0.28	0.464	0.15	3.36E-12	Mac_0	aPD-L1 vs PBS
Spp1	2.25E-16	-1.08	0.492	0.836	4.01E-12	Mac_1	aPD-L1 vs PBS
Ndufa1	3.50E-16	0.33	0.656	0.317	6.24E-12	Mac_0	aPD-L1 vs PBS
Uba52	3.85E-16	0.34	0.576	0.242	6.86E-12	Mac_0	aPD-L1 vs PBS
Rpl8	4.25E-16	-0.35	0.992	1	7.57E-12	Mac_0	aPD-L1 vs PBS
Lst1	5.25E-16	0.60	0.864	0.697	9.36E-12	Mac_0	aPD-L1 vs PBS
Fcgr4	6.41E-16	0.62	0.792	0.556	1.14E-11	Mac_0	aPD-L1 vs PBS
Tnfaip2	8.42E-16	0.44	0.404	0.117	1.50E-11	Mac_1	aPD-L1 + aTGF-β vs PBS
Lgmn	1.67E-15	-0.27	0.974	0.983	2.98E-11	Mac_0	aPD-L1 + aTGF-β vs PBS
Fgl2	1.77E-15	0.38	0.512	0.314	3.16E-11	Mac_0	aPD-L1 + aTGF-β vs PBS
Arg1	1.92E-15	-0.58	0.181	0.367	3.42E-11	Mac_0	aTGF-β vs PBS
Rpl37a	2.03E-15	0.41	1	1	3.62E-11	Mac_1	aPD-L1 vs PBS
Rps27	4.75E-15	0.61	0.992	0.958	8.46E-11	Mac_1	aPD-L1 vs PBS
Tgfbi	5.45E-15	-0.35	0.884	0.945	9.71E-11	Mac_0	aPD-L1 + aTGF-β vs PBS
Hspa1a	7.48E-15	0.38	0.701	0.526	1.33E-10	Mac_0	aTGF-β vs PBS
Gm42418	8.24E-15	-0.44	1	1	1.47E-10	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl14	9.05E-15	-0.30	0.96	0.993	1.61E-10	Mac_0	aPD-L1 vs PBS
Ly6a	9.34E-15	0.70	0.68	0.365	1.66E-10	Mac_0	aPD-L1 vs PBS
Rps5	1.51E-14	-0.37	0.992	0.99	2.69E-10	Mac_0	aPD-L1 vs PBS
Tmsb10	1.75E-14	0.65	0.983	0.93	3.12E-10	Mac_1	aPD-L1 vs PBS
Rpl10a	2.81E-14	-0.36	0.96	0.988	5.00E-10	Mac_0	aPD-L1 vs PBS
Ifit1	3.16E-14	0.36	0.326	0.144	5.63E-10	Mac_0	aPD-L1 + aTGF-β vs PBS
Gbp4	3.17E-14	0.46	0.4	0.14	5.64E-10	Mac_0	aPD-L1 vs PBS
AY036118	3.60E-14	-0.41	0.676	0.788	6.42E-10	Mac_0	aTGF-β vs PBS
Rps4x	4.05E-14	-0.35	0.992	0.999	7.22E-10	Mac_0	aPD-L1 vs PBS
Pid1	4.89E-14	-0.29	0.7	0.834	8.71E-10	Mac_0	aPD-L1 + aTGF-β vs PBS
Ms4a7	5.46E-14	-0.39	0.632	0.8	9.73E-10	Mac_0	aPD-L1 + aTGF-β vs PBS
Slamf8	6.00E-14	0.33	0.386	0.126	1.07E-09	Mac_1	aPD-L1 + aTGF-β vs PBS
Stat1	6.00E-14	0.28	0.586	0.386	1.07E-09	Mac_0	aPD-L1 + aTGF-β vs PBS
Rpl3	6.44E-14	-0.37	0.976	0.997	1.15E-09	Mac_0	aPD-L1 vs PBS
Ifi27l2a	7.10E-14	0.30	0.898	0.788	1.27E-09	Mac_0	aTGF-β vs PBS
H2-DMb1	9.29E-14	0.36	0.573	0.403	1.66E-09	Mac_0	aPD-L1 + aTGF-β vs PBS
Gm10076	9.73E-14	0.40	0.778	0.54	1.73E-09	Mac_1	aPD-L1 + aTGF-β vs PBS
Lgals1	9.98E-14	-0.54	0.975	0.979	1.78E-09	Mac_1	aPD-L1 vs PBS
Rpl12	1.07E-13	-0.36	0.96	0.994	1.90E-09	Mac_0	aPD-L1 vs PBS
Tmsb10	1.15E-13	0.25	0.941	0.908	2.04E-09	Mac_0	aTGF-β vs PBS
Blvrb	1.33E-13	0.31	0.656	0.496	2.36E-09	Mac_0	aPD-L1 + aTGF-β vs PBS
Dab2	1.36E-13	-0.42	0.68	0.914	2.42E-09	Mac_0	aPD-L1 vs PBS
Rpl36al	1.38E-13	0.29	0.696	0.37	2.46E-09	Mac_0	aPD-L1 vs PBS
Uqcr11	1.39E-13	0.32	0.832	0.581	2.48E-09	Mac_0	aPD-L1 vs PBS
Il2rg	1.64E-13	0.29	0.44	0.163	2.93E-09	Mac_0	aPD-L1 vs PBS
AW112010	2.86E-13	0.53	0.777	0.673	5.10E-09	Mac_0	aPD-L1 + aTGF-β vs PBS
Klf2	3.97E-13	0.32	0.76	0.61	7.07E-09	Mac_0	aTGF-β vs PBS
Gbp2	5.33E-13	0.36	0.392	0.135	9.51E-09	Mac_0	aPD-L1 vs PBS
Ubc	5.59E-13	0.28	0.764	0.643	9.96E-09	Mac_0	aTGF-β vs PBS
Crip1	6.37E-13	0.70	0.912	0.829	1.14E-08	Mac_0	aPD-L1 vs PBS
Ifitm3	6.88E-13	0.30	0.958	0.938	1.23E-08	Mac_0	aPD-L1 + aTGF-β vs PBS
Pmepa1	7.62E-13	-0.53	0.193	0.514	1.36E-08	Mac_1	aPD-L1 + aTGF-β vs PBS
Cox6b1	1.15E-12	0.30	0.944	0.86	2.05E-08	Mac_0	aPD-L1 vs PBS
Ms4a7	1.61E-12	-0.64	0.203	0.586	2.87E-08	Mac_1	aPD-L1 vs PBS
Ccl2	1.62E-12	0.35	0.812	0.654	2.89E-08	Mac_0	aPD-L1 + aTGF-β vs PBS
Klf2	1.66E-12	0.34	0.783	0.61	2.95E-08	Mac_0	aPD-L1 + aTGF-β vs PBS
Itgb7	1.72E-12	0.34	0.496	0.213	3.07E-08	Mac_0	aPD-L1 vs PBS
Cd274	1.97E-12	0.43	0.602	0.322	3.52E-08	Mac_1	aPD-L1 + aTGF-β vs PBS
mt-Nd4l	2.27E-12	0.37	0.744	0.481	4.05E-08	Mac_0	aPD-L1 vs PBS
Rpl5	2.32E-12	-0.34	0.936	0.974	4.13E-08	Mac_0	aPD-L1 vs PBS
Cd74	2.33E-12	0.61	0.983	0.811	4.15E-08	Mac_1	aPD-L1 vs PBS
Cxcl9	2.36E-12	1.15	0.496	0.226	4.21E-08	Mac_0	aPD-L1 vs PBS
Rps3a1	2.45E-12	-0.33	0.976	0.993	4.36E-08	Mac_0	aPD-L1 vs PBS
Igkc	2.82E-12	1.63	0.212	0.028	5.02E-08	Mac_1	aPD-L1 vs PBS
Hk3	2.82E-12	0.44	0.6	0.337	5.03E-08	Mac_0	aPD-L1 vs PBS
Arpc1b	3.23E-12	-0.27	0.952	0.996	5.76E-08	Mac_0	aPD-L1 vs PBS
Cd83	3.65E-12	0.25	0.486	0.293	6.51E-08	Mac_0	aPD-L1 + aTGF-β vs PBS
Eef1g	3.68E-12	-0.35	0.528	0.778	6.57E-08	Mac_0	aPD-L1 vs PBS
H2-Eb1	4.17E-12	0.64	0.822	0.514	7.43E-08	Mac_1	aPD-L1 vs PBS
Cxcl9	4.66E-12	0.53	0.405	0.226	8.31E-08	Mac_0	aPD-L1 + aTGF-β vs PBS
Tnfaip3	5.16E-12	0.46	0.602	0.278	9.19E-08	Mac_1	aPD-L1 vs PBS
Iigp1	5.32E-12	0.25	0.315	0.147	9.48E-08	Mac_0	aPD-L1 + aTGF-β vs PBS
Gapdh	5.32E-12	-0.34	0.96	0.996	9.49E-08	Mac_0	aPD-L1 vs PBS
Samhd1	5.70E-12	0.43	0.608	0.329	1.02E-07	Mac_0	aPD-L1 vs PBS
Irgm1	6.11E-12	0.28	0.327	0.103	1.09E-07	Mac_1	aPD-L1 + aTGF-β vs PBS
Pmepa1	8.07E-12	-0.63	0.161	0.514	1.44E-07	Mac_1	aPD-L1 vs PBS
Gatm	9.20E-12	-0.30	0.875	0.944	1.64E-07	Mac_0	aPD-L1 + aTGF-β vs PBS
H2-Aa	1.03E-11	0.58	0.873	0.57	1.83E-07	Mac_1	aPD-L1 vs PBS
Rps2	1.20E-11	-0.30	0.984	0.991	2.13E-07	Mac_0	aPD-L1 vs PBS
Tpt1	1.56E-11	-0.29	1	1	2.78E-07	Mac_0	aPD-L1 vs PBS
Rpl18	2.24E-11	-0.35	0.966	0.988	3.99E-07	Mac_1	aPD-L1 vs PBS
Rpl27	2.58E-11	0.31	0.752	0.476	4.60E-07	Mac_0	aPD-L1 vs PBS
Samhd1	2.63E-11	0.26	0.508	0.329	4.69E-07	Mac_0	aPD-L1 + aTGF-β vs PBS
Psap	2.83E-11	0.33	1	0.994	5.05E-07	Mac_0	aPD-L1 vs PBS

Romo1	2.98E-11	0.30	0.584	0.32	5.32E-07	Mac_0	aPD-L1 vs PBS
Stat1	3.03E-11	0.46	0.632	0.386	5.39E-07	Mac_0	aPD-L1 vs PBS
Tnfaip2	4.00E-11	0.29	0.216	0.05	7.13E-07	Mac_0	aPD-L1 vs PBS
Iigp1	4.09E-11	0.30	0.4	0.147	7.28E-07	Mac_0	aPD-L1 vs PBS
Rps3	4.44E-11	-0.28	0.992	0.994	7.92E-07	Mac_0	aPD-L1 vs PBS
Ndufa2	5.46E-11	0.27	0.816	0.595	9.74E-07	Mac_0	aPD-L1 vs PBS
Rplp0	5.83E-11	-0.27	1	1	1.04E-06	Mac_0	aPD-L1 vs PBS
Rps21	8.20E-11	0.42	1	0.97	1.46E-06	Mac_1	aPD-L1 vs PBS
Pmepa1	1.07E-10	-0.43	0.616	0.841	1.91E-06	Mac_0	aPD-L1 vs PBS
Hspa1b	1.07E-10	0.37	0.525	0.363	1.91E-06	Mac_0	aTGF-β vs PBS
Gatm	1.15E-10	-0.69	0.363	0.61	2.05E-06	Mac_1	aPD-L1 + aTGF-β vs PBS
Aprt	1.15E-10	-0.30	0.792	0.961	2.05E-06	Mac_0	aPD-L1 vs PBS
Dusp1	1.18E-10	0.26	0.79	0.67	2.11E-06	Mac_0	aTGF-β vs PBS
Tpi1	1.32E-10	-0.28	0.759	0.843	2.36E-06	Mac_0	aPD-L1 + aTGF-β vs PBS
Ccl4	1.37E-10	0.36	0.824	0.702	2.45E-06	Mac_0	aTGF-β vs PBS
Ly6e	1.43E-10	0.41	0.896	0.713	2.55E-06	Mac_0	aPD-L1 vs PBS
Rnf19b	1.44E-10	0.27	0.528	0.254	2.56E-06	Mac_0	aPD-L1 vs PBS
Ighg1	1.59E-10	0.46	0.111	0.005	2.83E-06	Mac_1	aPD-L1 + aTGF-β vs PBS
Rpl13	1.85E-10	-0.35	0.992	1	3.30E-06	Mac_1	aPD-L1 vs PBS
Gm10076	2.11E-10	0.39	0.746	0.54	3.77E-06	Mac_1	aPD-L1 vs PBS
Cox6c	2.22E-10	0.30	0.816	0.71	3.96E-06	Mac_0	aPD-L1 vs PBS
Psmb9	2.60E-10	0.29	0.856	0.663	4.63E-06	Mac_0	aPD-L1 vs PBS
Fgl2	2.61E-10	0.41	0.568	0.314	4.65E-06	Mac_0	aPD-L1 vs PBS
H2-D1	2.77E-10	0.28	1	1	4.93E-06	Mac_0	aPD-L1 vs PBS
Atp5g2	2.82E-10	-0.27	0.712	0.901	5.03E-06	Mac_0	aPD-L1 vs PBS
Rpl37a	2.98E-10	0.27	0.994	1	5.32E-06	Mac_1	aPD-L1 + aTGF-β vs PBS
Eid1	3.28E-10	-0.28	0.384	0.696	5.85E-06	Mac_0	aPD-L1 vs PBS
Erp29	3.64E-10	-0.26	0.904	0.964	6.49E-06	Mac_0	aPD-L1 vs PBS
Txn1	5.05E-10	0.40	0.959	0.937	9.00E-06	Mac_1	aPD-L1 + aTGF-β vs PBS
Lgals3bp	5.82E-10	0.29	0.696	0.422	1.04E-05	Mac_0	aPD-L1 vs PBS
Fn1	6.49E-10	-0.56	0.359	0.579	1.16E-05	Mac_1	aTGF-β vs PBS
Rpl37a	6.79E-10	0.50	1	1	1.21E-05	Mac_2	aPD-L1 + aTGF-β vs PBS
Atp5j2	7.38E-10	0.25	0.904	0.744	1.32E-05	Mac_0	aPD-L1 vs PBS
Ppp1r15a	7.86E-10	0.27	0.521	0.353	1.40E-05	Mac_0	aPD-L1 + aTGF-β vs PBS
Rsad2	7.89E-10	0.66	0.496	0.252	1.41E-05	Mac_0	aPD-L1 vs PBS
Ccl5	8.37E-10	0.43	0.212	0.085	1.49E-05	Mac_0	aPD-L1 + aTGF-β vs PBS
Ms4a7	8.62E-10	-0.27	0.686	0.8	1.54E-05	Mac_0	aTGF-β vs PBS
Clec4a1	8.72E-10	0.32	0.488	0.246	1.56E-05	Mac_0	aPD-L1 vs PBS
Rpl36a	9.24E-10	0.28	0.936	0.922	1.65E-05	Mac_0	aPD-L1 vs PBS
Tap2	9.58E-10	0.25	0.392	0.169	1.71E-05	Mac_0	aPD-L1 vs PBS
Spp1	9.78E-10	-0.41	0.48	0.764	1.74E-05	Mac_0	aPD-L1 vs PBS
Rps6	1.03E-09	-0.27	0.944	0.988	1.83E-05	Mac_0	aPD-L1 vs PBS
AW112010	1.08E-09	0.57	0.848	0.673	1.93E-05	Mac_0	aPD-L1 vs PBS
Rack1	1.17E-09	-0.26	0.976	0.996	2.08E-05	Mac_0	aPD-L1 vs PBS
Fcgr4	1.30E-09	0.43	0.63	0.556	2.32E-05	Mac_0	aPD-L1 + aTGF-β vs PBS
Ldha	1.34E-09	-0.36	0.76	0.898	2.39E-05	Mac_0	aPD-L1 vs PBS
Apoe	1.57E-09	-0.56	0.749	0.867	2.79E-05	Mac_1	aPD-L1 + aTGF-β vs PBS
Rpl17	1.58E-09	-0.28	0.968	0.986	2.81E-05	Mac_0	aPD-L1 vs PBS
Atp5l	1.61E-09	0.25	0.928	0.821	2.87E-05	Mac_0	aPD-L1 vs PBS
Igkc	1.66E-09	0.33	0.136	0.022	2.96E-05	Mac_0	aPD-L1 vs PBS
Ccl3	1.77E-09	0.32	0.681	0.514	3.15E-05	Mac_0	aPD-L1 + aTGF-β vs PBS
Rps29	2.00E-09	0.30	1	1	3.56E-05	Mac_1	aPD-L1 vs PBS
Cd274	2.00E-09	0.52	0.576	0.322	3.57E-05	Mac_1	aPD-L1 vs PBS
Igkc	2.06E-09	0.52	0.164	0.028	3.67E-05	Mac_1	aPD-L1 + aTGF-β vs PBS
Atf3	2.19E-09	0.29	0.802	0.716	3.90E-05	Mac_0	aTGF-β vs PBS
Gm47283	2.28E-09	0.33	0.616	0.386	4.06E-05	Mac_0	aPD-L1 vs PBS
Fth1	2.29E-09	-0.41	1	1	4.09E-05	Mac_0	aPD-L1 vs PBS
Rps27	2.41E-09	0.81	1	1	4.30E-05	Mac_2	aPD-L1 vs PBS
H2-Eb1	2.45E-09	0.46	0.749	0.514	4.37E-05	Mac_1	aPD-L1 + aTGF-β vs PBS
Rgs10	2.54E-09	-0.30	0.616	0.856	4.52E-05	Mac_0	aPD-L1 vs PBS
2010107E04	2.59E-09	0.26	0.664	0.428	4.62E-05	Mac_0	aPD-L1 vs PBS
Bax	2.76E-09	-0.28	0.48	0.733	4.92E-05	Mac_0	aPD-L1 vs PBS
Rps27	2.83E-09	0.53	1	1	5.05E-05	Mac_2	aPD-L1 + aTGF-β vs PBS
Tmem256	2.84E-09	0.28	0.736	0.517	5.06E-05	Mac_0	aPD-L1 vs PBS
Nampt	2.94E-09	0.31	0.52	0.284	5.24E-05	Mac_0	aPD-L1 vs PBS
Ms4a7	3.03E-09	-0.58	0.322	0.586	5.40E-05	Mac_1	aPD-L1 + aTGF-β vs PBS
B2m	3.13E-09	0.26	1	1	5.59E-05	Mac_1	aPD-L1 vs PBS
Rpl7	3.38E-09	-0.30	0.968	0.968	6.02E-05	Mac_0	aPD-L1 vs PBS
Prelid1	3.58E-09	-0.27	0.36	0.643	6.38E-05	Mac_0	aPD-L1 vs PBS
Socs1	3.68E-09	0.27	0.31	0.114	6.56E-05	Mac_1	aPD-L1 + aTGF-β vs PBS
Ifrd1	3.74E-09	0.48	0.754	0.593	6.67E-05	Mac_1	aPD-L1 + aTGF-β vs PBS
Tap1	4.33E-09	0.26	0.656	0.389	7.73E-05	Mac_0	aPD-L1 vs PBS
H2-T23	4.36E-09	0.37	0.703	0.467	7.77E-05	Mac_1	aPD-L1 vs PBS
Rpl22l1	4.38E-09	0.36	0.746	0.484	7.81E-05	Mac_1	aPD-L1 vs PBS
Ccl7	5.75E-09	0.33	0.639	0.467	1.03E-04	Mac_0	aPD-L1 + aTGF-β vs PBS
Serpina3g	5.95E-09	0.25	0.246	0.072	1.06E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Rpl39	6.28E-09	0.42	0.992	0.96	1.12E-04	Mac_1	aPD-L1 vs PBS
Dab2	6.34E-09	-0.41	0.661	0.811	1.13E-04	Mac_1	aPD-L1 vs PBS
Sem1	6.35E-09	0.29	0.924	0.836	1.13E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Gnai2	6.51E-09	-0.27	0.915	0.949	1.16E-04	Mac_1	aPD-L1 vs PBS
Slamf8	7.89E-09	0.28	0.416	0.2	1.41E-04	Mac_0	aPD-L1 vs PBS
Pabpc1	8.11E-09	0.26	0.888	0.741	1.45E-04	Mac_0	aPD-L1 vs PBS
Pmepa1	8.57E-09	-0.34	0.281	0.514	1.53E-04	Mac_1	aTGF-β vs PBS
Rack1	9.90E-09	-0.30	0.906	0.986	1.77E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Ptpn18	1.07E-08	0.26	0.912	0.813	1.90E-04	Mac_0	aPD-L1 vs PBS
Eef1b2	1.08E-08	-0.26	0.904	0.951	1.93E-04	Mac_0	aPD-L1 vs PBS

Pde4d	1.13E-08	-0.33	0.14	0.371	2.01E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Cox7a2	1.32E-08	0.25	0.88	0.745	2.36E-04	Mac_0	aPD-L1 vs PBS
Tnfaip3	1.40E-08	0.27	0.344	0.14	2.49E-04	Mac_0	aPD-L1 vs PBS
H2-Ab1	1.54E-08	0.34	0.856	0.617	2.75E-04	Mac_1	aPD-L1 vs PBS
Irgm1	1.79E-08	0.26	0.305	0.103	3.19E-04	Mac_1	aPD-L1 vs PBS
Spp1	1.83E-08	-0.33	0.602	0.836	3.26E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Klf4	1.84E-08	0.42	0.695	0.439	3.28E-04	Mac_1	aPD-L1 vs PBS
H2-Aa	2.06E-08	0.39	0.789	0.57	3.68E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Rpl15	2.17E-08	-0.33	0.949	0.991	3.86E-04	Mac_1	aPD-L1 vs PBS
Unc93b1	2.20E-08	0.25	0.944	0.885	3.93E-04	Mac_0	aPD-L1 vs PBS
Gm47283	2.34E-08	0.49	0.619	0.369	4.17E-04	Mac_1	aPD-L1 vs PBS
Ubc	2.36E-08	0.45	0.808	0.643	4.20E-04	Mac_0	aPD-L1 vs PBS
Malt1	2.49E-08	0.42	0.508	0.252	4.44E-04	Mac_1	aPD-L1 vs PBS
H2-Ab1	2.57E-08	0.39	0.813	0.617	4.58E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Rgl1	2.67E-08	0.35	0.424	0.189	4.76E-04	Mac_1	aPD-L1 vs PBS
Rpl10a	2.71E-08	-0.34	0.856	0.953	4.84E-04	Mac_1	aPD-L1 vs PBS
Rpl22l1	2.95E-08	0.34	0.808	0.628	5.25E-04	Mac_0	aPD-L1 vs PBS
Hk3	3.07E-08	0.37	0.568	0.35	5.47E-04	Mac_1	aPD-L1 vs PBS
Tnf	3.10E-08	0.44	0.544	0.316	5.53E-04	Mac_0	aPD-L1 vs PBS
Eif4ebp1	3.12E-08	-0.30	0.288	0.543	5.56E-04	Mac_0	aPD-L1 vs PBS
Ccr2	3.31E-08	-0.28	0.357	0.497	5.89E-04	Mac_0	aPD-L1 + aTGF-β vs PBS
Fn1	3.31E-08	-0.69	0.351	0.579	5.90E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Tmsb10	4.10E-08	0.33	0.952	0.93	7.31E-04	Mac_1	aTGF-β vs PBS
Rpl37	4.27E-08	0.31	0.992	0.993	7.61E-04	Mac_1	aPD-L1 vs PBS
Ndufa1	4.44E-08	0.28	0.475	0.243	7.91E-04	Mac_1	aPD-L1 vs PBS
Rps14	4.72E-08	-0.29	0.992	0.995	8.41E-04	Mac_1	aPD-L1 vs PBS
Tln1	5.07E-08	-0.31	0.466	0.708	9.03E-04	Mac_1	aPD-L1 vs PBS
Cx3cr1	5.55E-08	-0.32	0.117	0.336	9.90E-04	Mac_1	aPD-L1 + aTGF-β vs PBS
Cotl1	5.64E-08	-0.30	0.626	0.759	1.00E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Cd36	5.72E-08	0.56	0.441	0.217	1.02E-03	Mac_1	aPD-L1 vs PBS
Ccl2	6.18E-08	0.26	0.776	0.654	1.10E-03	Mac_0	aTGF-β vs PBS
Gapdh	6.26E-08	-0.44	0.941	0.993	1.12E-03	Mac_1	aPD-L1 vs PBS
Rpl39	6.41E-08	0.28	0.971	0.96	1.14E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Blvrb	7.00E-08	0.35	0.712	0.496	1.25E-03	Mac_0	aPD-L1 vs PBS
Eid1	7.20E-08	-0.27	0.345	0.57	1.28E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Rps6	9.18E-08	-0.25	0.906	0.963	1.64E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Cd74	9.66E-08	0.38	0.901	0.811	1.72E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Srgn	9.99E-08	-0.45	0.857	0.932	1.78E-03	Mac_1	aTGF-β vs PBS
Upp1	1.10E-07	0.36	0.462	0.259	1.97E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Arg1	1.12E-07	-0.71	0.394	0.577	2.00E-03	Mac_1	aTGF-β vs PBS
Ccl4	1.14E-07	0.52	0.856	0.702	2.03E-03	Mac_0	aPD-L1 vs PBS
Ms4a6d	1.18E-07	-0.46	0.771	0.857	2.10E-03	Mac_1	aPD-L1 vs PBS
Sod2	1.30E-07	0.56	0.575	0.148	2.32E-03	Mac_2	aPD-L1 + aTGF-β vs PBS
Txn1	1.32E-07	0.31	0.952	0.939	2.35E-03	Mac_0	aPD-L1 vs PBS
Zfp36l2	1.36E-07	0.40	0.754	0.582	2.42E-03	Mac_1	aPD-L1 vs PBS
Rpl5	1.37E-07	-0.27	0.825	0.939	2.44E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Slc11a1	1.48E-07	0.35	0.576	0.392	2.65E-03	Mac_0	aPD-L1 vs PBS
mt-Atp8	1.55E-07	0.30	0.542	0.315	2.77E-03	Mac_1	aPD-L1 vs PBS
Pgam1	1.60E-07	-0.32	0.704	0.833	2.85E-03	Mac_0	aPD-L1 vs PBS
Cxcl14	1.62E-07	-0.38	0.234	0.456	2.88E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Selenom	1.65E-07	0.45	0.544	0.346	2.95E-03	Mac_0	aPD-L1 vs PBS
Pla2g16	1.83E-07	0.27	0.568	0.349	3.26E-03	Mac_0	aPD-L1 vs PBS
Cxcl14	1.89E-07	-0.43	0.203	0.456	3.37E-03	Mac_1	aPD-L1 vs PBS
Arpc1b	1.93E-07	-0.26	0.966	0.981	3.44E-03	Mac_1	aPD-L1 vs PBS
Isg15	1.95E-07	0.26	0.51	0.378	3.48E-03	Mac_0	aPD-L1 + aTGF-β vs PBS
Rps28	2.02E-07	0.31	0.975	0.9	3.60E-03	Mac_1	aPD-L1 vs PBS
Zfand5	2.02E-07	0.31	0.737	0.565	3.60E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Ccnl1	2.07E-07	0.33	0.836	0.643	3.69E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Lars2	2.09E-07	0.51	0.788	0.692	3.73E-03	Mac_1	aPD-L1 vs PBS
Tmed9	2.10E-07	-0.28	0.305	0.558	3.74E-03	Mac_1	aPD-L1 vs PBS
Pnrc1	2.19E-07	0.28	0.673	0.477	3.90E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Npm1	2.43E-07	-0.26	0.864	0.941	4.33E-03	Mac_0	aPD-L1 vs PBS
Rps29	2.44E-07	0.58	1	1	4.35E-03	Mac_2	aPD-L1 vs PBS
Rpl39	2.52E-07	0.53	1	1	4.49E-03	Mac_2	aPD-L1 + aTGF-β vs PBS
Tmx4	2.64E-07	-0.25	0.278	0.412	4.70E-03	Mac_0	aPD-L1 + aTGF-β vs PBS
H2-D1	2.74E-07	0.27	1	1	4.88E-03	Mac_1	aPD-L1 vs PBS
Sem1	2.98E-07	0.26	0.924	0.836	5.32E-03	Mac_1	aPD-L1 vs PBS
Lrp1	3.08E-07	-0.28	0.563	0.692	5.50E-03	Mac_1	aTGF-β vs PBS
Rap2a	3.10E-07	-0.25	0.272	0.517	5.53E-03	Mac_0	aPD-L1 vs PBS
Selenom	3.12E-07	0.82	0.468	0.313	5.56E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Itm2b	3.24E-07	0.29	1	0.977	5.77E-03	Mac_0	aPD-L1 vs PBS
Aif1	3.45E-07	0.32	0.96	0.944	6.15E-03	Mac_0	aPD-L1 vs PBS
Pf4	3.45E-07	-0.81	0.304	0.509	6.15E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Tomm7	3.71E-07	0.27	0.585	0.353	6.61E-03	Mac_1	aPD-L1 vs PBS
Itgb2	3.75E-07	0.29	0.744	0.617	6.69E-03	Mac_0	aPD-L1 vs PBS
Eno1	3.85E-07	-0.29	0.696	0.829	6.86E-03	Mac_0	aPD-L1 vs PBS
Ppp1r14b	3.95E-07	-0.29	0.424	0.624	7.03E-03	Mac_0	aPD-L1 vs PBS
Tgfbi	4.05E-07	-0.42	0.695	0.834	7.22E-03	Mac_1	aPD-L1 vs PBS
Csf1r	4.08E-07	-0.27	0.52	0.706	7.28E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Pid1	4.11E-07	-0.33	0.72	0.834	7.33E-03	Mac_0	aPD-L1 vs PBS
Ubc	4.14E-07	0.34	0.924	0.829	7.39E-03	Mac_1	aPD-L1 vs PBS
Mbnl2	4.16E-07	0.25	0.544	0.327	7.41E-03	Mac_0	aPD-L1 vs PBS
Rpl8	4.18E-07	-0.28	1	0.988	7.46E-03	Mac_1	aPD-L1 vs PBS
Spp1	4.21E-07	0.48	0.811	0.764	7.51E-03	Mac_0	aTGF-β vs PBS
Pf4	4.22E-07	-0.93	0.237	0.509	7.52E-03	Mac_1	aPD-L1 vs PBS
Gm10076	4.25E-07	0.60	0.875	0.716	7.57E-03	Mac_2	aPD-L1 + aTGF-β vs PBS

H2-K1	4.83E-07	0.29	1	0.995	8.62E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Tgfbi	5.03E-07	-0.37	0.725	0.834	8.96E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Aldoa	5.10E-07	-0.31	0.864	0.963	9.09E-03	Mac_0	aPD-L1 vs PBS
Psap	5.21E-07	0.35	0.975	0.965	9.28E-03	Mac_1	aPD-L1 vs PBS
Tmsb10	5.28E-07	0.65	1	0.989	9.41E-03	Mac_2	aPD-L1 + aTGF-β vs PBS
AY036118	5.38E-07	-0.51	0.865	0.909	9.58E-03	Mac_1	aPD-L1 + aTGF-β vs PBS
Gbp2b	5.83E-07	0.31	0.407	0.194	1.04E-02	Mac_1	aPD-L1 vs PBS
H2-T23	6.73E-07	0.32	0.626	0.467	1.20E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Man2b1	7.61E-07	-0.29	0.462	0.647	1.36E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Ubb	7.80E-07	0.28	0.994	0.988	1.39E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Rps27	7.89E-07	0.30	0.965	0.958	1.41E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Wfdc17	8.22E-07	0.99	0.508	0.322	1.47E-02	Mac_1	aPD-L1 vs PBS
Ifrd1	8.98E-07	0.39	0.788	0.593	1.60E-02	Mac_1	aPD-L1 vs PBS
Bola2	9.48E-07	0.56	0.675	0.239	1.69E-02	Mac_2	aPD-L1 + aTGF-β vs PBS
Wfdc17	9.79E-07	0.61	0.497	0.322	1.75E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Dusp2	9.95E-07	0.50	0.261	0	1.77E-02	Mac_2	aPD-L1 vs PBS
Trem2	1.16E-06	-0.31	0.596	0.743	2.07E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Rpl38	1.18E-06	0.27	0.992	0.981	2.11E-02	Mac_1	aPD-L1 vs PBS
Naaa	1.28E-06	0.31	0.624	0.447	2.28E-02	Mac_0	aPD-L1 vs PBS
Dynll1	1.29E-06	-0.29	0.559	0.748	2.31E-02	Mac_1	aPD-L1 vs PBS
Pf4	1.33E-06	-0.34	0.264	0.516	2.37E-02	Mac_0	aPD-L1 vs PBS
Gpi1	1.34E-06	-0.27	0.672	0.814	2.38E-02	Mac_0	aPD-L1 vs PBS
Cyth1	1.34E-06	0.27	0.475	0.257	2.39E-02	Mac_1	aPD-L1 vs PBS
Ugcg	1.35E-06	0.31	0.424	0.215	2.40E-02	Mac_1	aPD-L1 vs PBS
Atp5e	1.37E-06	0.27	0.877	0.792	2.44E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Rps12	1.38E-06	-0.27	0.958	0.998	2.47E-02	Mac_1	aPD-L1 vs PBS
Park7	1.41E-06	-0.31	0.331	0.547	2.51E-02	Mac_1	aPD-L1 vs PBS
Rpl5	1.42E-06	-0.27	0.881	0.939	2.53E-02	Mac_1	aPD-L1 vs PBS
Rps28	1.47E-06	0.64	1	1	2.62E-02	Mac_2	aPD-L1 vs PBS
Ccl12	1.55E-06	0.26	0.683	0.571	2.77E-02	Mac_0	aTGF-β vs PBS
Ccl5	1.62E-06	0.92	0.304	0.011	2.89E-02	Mac_2	aPD-L1 vs PBS
Rps2	1.64E-06	-0.28	0.915	0.967	2.92E-02	Mac_1	aPD-L1 vs PBS
Rack1	1.65E-06	-0.29	0.975	0.986	2.93E-02	Mac_1	aPD-L1 vs PBS
Itgb5	1.78E-06	-0.25	0.263	0.474	3.17E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Lars2	1.81E-06	0.37	0.72	0.563	3.23E-02	Mac_0	aPD-L1 vs PBS
Rpl14	1.90E-06	-0.27	0.932	0.965	3.40E-02	Mac_1	aPD-L1 vs PBS
Wfdc17	1.94E-06	0.64	0.359	0.245	3.46E-02	Mac_0	aPD-L1 + aTGF-β vs PBS
Adgre5	1.94E-06	0.36	0.398	0.206	3.47E-02	Mac_1	aPD-L1 vs PBS
Tmsb4x	2.04E-06	-0.31	1	1	3.64E-02	Mac_1	aPD-L1 vs PBS
Ppia	2.20E-06	-0.25	0.983	0.995	3.92E-02	Mac_1	aPD-L1 vs PBS
Sec61g	2.35E-06	0.28	0.729	0.582	4.19E-02	Mac_1	aPD-L1 vs PBS
Eif5a	2.40E-06	-0.27	0.703	0.829	4.28E-02	Mac_1	aPD-L1 vs PBS
Rps24	2.43E-06	0.35	1	1	4.34E-02	Mac_2	aPD-L1 + aTGF-β vs PBS
Rpl35a	2.45E-06	0.31	0.958	0.963	4.37E-02	Mac_1	aPD-L1 vs PBS
Rpl37a	2.47E-06	0.68	1	1	4.41E-02	Mac_2	aPD-L1 vs PBS
Gm10260	2.51E-06	0.44	1	0.943	4.47E-02	Mac_2	aPD-L1 + aTGF-β vs PBS
Marcks	2.53E-06	0.28	0.608	0.437	4.50E-02	Mac_0	aPD-L1 vs PBS
AW112010	2.74E-06	0.50	0.567	0.4	4.89E-02	Mac_1	aPD-L1 + aTGF-β vs PBS
Hk3	2.79E-06	0.27	0.515	0.35	4.98E-02	Mac_1	aPD-L1 + aTGF-β vs PBS

WHAT IS CLAIMED IS:

1. A pharmaceutical composition, comprising:
a CCL5 mimetic, or pharmaceutically acceptable salt thereof, and
a pharmaceutically acceptable carrier.
2. The pharmaceutical composition of claim 1, wherein the CCL5 mimetic is a human CCL5 peptide, wherein the CCL5 peptide has a sequence of SEQ ID NO: 1.
3. The pharmaceutical composition of claim 1, wherein the CCL5 mimetic is a CCL5 analog.
4. The pharmaceutical composition of claim 3, wherein the CCL5 analog is a polypeptide having the sequence of SEQ ID NO: 2.
5. The pharmaceutical composition of claim 3, wherein the CCL5 analog comprises an active fragment of a human CCL5 peptide.
6. The pharmaceutical composition of claim 5, wherein the active fragment of human CCL5 comprises amino acids 12-22 of SEQ ID NO: 1.
7. The pharmaceutical composition of claim 5, wherein the active fragment of human CCL5 comprises one or more of the following amino acid residues selected from the group consisting of: P2, Y3, D6, T7, F12, I15, and R17.
8. The pharmaceutical composition of any one of claims 1-7, wherein the CCL5 mimetic comprises a polypeptide having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99%sequence identity to SEQ ID NO: 1 or SEQ ID NO: 2.
9. The pharmaceutical composition of any one of claims 3-8, wherein the CCL5 mimetic is a CCL5 analog having a longer half-life *in vivo* as compared to CCL5.
10. The pharmaceutical composition of any one of claims 1-9, wherein the CCL5 mimetic is a conjugate of CCL5 or a CCL5 analog to a conjugate moiety.
11. The pharmaceutical composition of claim 10, wherein the conjugate moiety is selected from polyethylene glycol (PEG) and hyaluronic acid.
12. The pharmaceutical composition of claim 10, wherein the conjugate moiety is selected from the group consisting of HAS, human IgG, scFv, F(ab), $F(ab')_2$, transferrin, albumin, and an Fc domain of an immunoglobulin.
13. The pharmaceutical composition of claim 10, wherein the conjugate moiety is selected from the group consisting of: XTEN, a proline-alanine-serine polymer

(PAS), a homopolymer of glycine residues (HAP), a gelatin-like protein (GLP), a signal peptide and an elastin-like peptide (ELP).

14. The pharmaceutical composition of any one of claims 1-13, wherein the CCL5 mimetic comprises one or more modified or non-naturally occurring amino acids, selected from the group consisting of: a steric enantiomer (D isomer), a rare amino acid of plant origin, a non-naturally occurring amino acid or amino acid mimetic, or have been modified by any one or more modifications selected from acetylation, acylation, phosphorylation, dephosphorylation, glycosylation, myristollation, amidation, aspartic acid/asparagine hydroxylation, phosphopantethane attachment, methylation, methylthiolation, prensyl group attachment, intein N-/C-terminal splicing, ADP-ribosylation, bromination, citrullination, deamination, dihydroxylation, formylation, geranyl-geranilation, glycation, palmitoylation, α-methyl-amino acids, Cα-methyl amino acids, and Nα-methyl amino acids.

15. The pharmaceutical composition of any one of claims 1-14, wherein the CCL5 mimetic is chemically-synthesized and comprises one or more non-peptide bonds.

16. The pharmaceutical composition of any one of claims 1-15, comprising the pharmaceutically acceptable salt of a CCL5 mimetic, wherein the salt is hydrochloride, trihydrochloride, sulfate, mesylate, or tosylate.

17. The pharmaceutical composition of any one of claims 1-16, formulated for parenteral administration.

18. The pharmaceutical composition of any one of claims 1-16, formulated for intratumoral injection, intravenous injection or subcutaneous injection.

19. A kit for treatment of cancer, comprising:
the pharmaceutical composition of any one of claims 1-18, and
an additional therapeutic agent.

20. The kit of claim 19, wherein the additional therapeutic agent is an anti-PD-L1 antibody, an anti-PD-1 antibody, or a TGFβ inhibitor.

21. The kit of claim 19, wherein the additional therapeutic agent is a bispecific antibody against PD-L1 and TGFβ or against PD-1 and TGFβ.

22. The kit of claim 19, the additional therapeutic agent comprises an anti-PD-L1 antibody and an anti-TGFβ antibody.

23. The kit of claim 19, the additional therapeutic agent comprises an anti-PD-1 antibody and an anti-TGFβ antibody.

24. The kit of claim 19, the additional therapeutic agent comprises an anti-PD-L1 antibody, wherein the anti-PD-L1 antibody is atezolizumab.
25. The kit of claim 19, wherein the additional therapeutic agent is an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab.
26. The kit of claim 19, wherein the additional therapeutic agent comprises a T cell or an NK cell.
27. The kit of claim 26, wherein the T cell is a CAR-T, CAR-NK, CAR-macrophage,TCR-T cell.
28. The kit of claim 19, wherein the additional therapeutic agent is an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof.
29. The kit of claim 19, wherein the additional therapeutic agent is an agent activating NK cell,T cell activity, dendritic cell activity, or a combination thereof.
30. A method of treating cancer, comprising the step of:
administering to a subject with the cancer a therapeutically effective amount of an isolated chemokine mimetic, or pharmaceutically acceptable salt thereof.
31. The method of claim 30, wherein the isolated chemokine mimetic is selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.
32. The method of claim 31, wherein the isolated chemokine mimetic is two or more isolated chemokine mimetics selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.
33. The method of claim 30, wherein the isolated chemokine mimetic is a CCL5 mimetic or pharmaceutically acceptable salt thereof.
34. The method of any one of claims 30-33, wherein the isolated chemokine mimetic or pharmaceutically acceptable salt thereof is administered in a pharmaceutical composition further comprising a pharmaceutically acceptable carrier or excipient.
35. The method of any one of claims 30-34, wherein said administering is via intratumoral injection, intravenous injection or subcutaneous injection.
36. The method of claim 35, wherein said administering is via intratumoral injection.
37. The method of any one of claims 30-36, further comprising the step of administering to the subject an anti-PD-L1 antibody or an anti-PD-1 antibody.
38. The method of any one of claims 30-37, further comprising the step of administering to the subject a TGFβ inhibitor.
39. The method of any one of claims 30-36, further comprising the steps of

administering anti-PD-L1 antibody and an anti-TGFβ antibody.

40. The method of any one of claims 30-36, further comprising the step of administering a bi-specific antibody targeting both PD-L1 and TGFβ.

41. The method of any one of claims 30-36, further comprising the step of administering a bi-specific antibody targeting both PD-1 and TGFβ.

42. The method of any one of claims 30-36, further comprising the step of administering to the subject an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab.

43. The method of any one of claims 30-36, further comprising the step of administering to the subject a T cell, an NK cell, macrophage, or dendritic cell, optionally wherein the T cell is a CAR-T, CAR-NK, CAR-macrophage, or TCR-T cell.

44. The method of any one of claims 30-36, further comprising the step of administering to the subject an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof.

45. The method of any one of claims 30-36, further comprising the step of administering to the subject an agent activating NK cell, T cell activity, or dendritic cell activity.

46. The method of any one of claims 30-45, wherein the cancer is selected from the group consisting of: multiple myeloma, adrenocortical carcinoma, acute myeloid leukemia, Bladder Urothelial Carcinoma, glioma, breast invasive carcinoma, glioma, Cervical squamous cell carcinoma, endocervical adenocarcinoma, cholangiocarcinoma, chronic myelogenous leukemia, colon adenocarcinoma, esophageal carcinoma, glioblastoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell lymphoma, mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocyoma, paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma,sarcoma, skin cutaneous melanoma, stomach adenocarcinoma, testicular germ cell tumors, thyomas, thyroid carcinoma, uterine carcinosarcoma, uterine corps endometrial carcinoma, microsatellite instability-high cancer, basal cell carcinoma, Merkel cell carcinoma, uveal melanoma, and mucosal melanoma.

47. A method of treating cancer, comprising the steps of:

intratumorally administering a therapeutically effective amount of an isolated chemokine mimetic, or pharmaceutically acceptable salt thereof, to a subject who has been determined to have expression levels in a biological sample of one or more genes selected from the group consisting of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, CD8, CD3, TCRβ, TCR1, CD11c, WARS, NKp46 and NCR1, CD56, CD16, CD7 CD127, Tbet, Eomes, granzymes, and perforin that are lower than or higher than a predetermined threshold level.

48. The method of claim 47, wherein the biological sample is a tumor biopsy or a liquid biopsy.

49. The method of claim 47, wherein the biological sample is a blood sample.

50. The method of claim 47, wherein the biological sample comprises T-cells or NK cells isolated from the subject or a donor.

51. The method of any one of claims 47-49, further comprising the prior step of determining the expression levels of one or more genes selected from the group consisting of CCL5, CXCL9, CXCL13, CXCL10, CXCL11, CD8, CD3, TCRβ, TCR1, CD11c, WARS, NKp46, NCR1, CD11B, FcRs, collagen genes, CTLA4, CD56, CD16, CD7 CD127, Tbet, Eomes, granzymes, and perforin in the biological sample.

52. The method of any one of claims 47-51, further comprising the prior step of detecting CD8+ T cells, NK cells, mature NK cells, lymphocytes, fibroblasts, Tregs, or dendritic cells in the biological sample.

53. The method of claim 52, wherein the CD8+ T cells, NK cells, lymphocytes, or dendritic cells are detected by immune histochemistry.

54. The method of any one of claims 47-53, wherein the chemokine mimetic is selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.

55. The method of claim 54, wherein the chemokine mimetic is two or more chemokine mimetics selected from the group consisting of: CCL5, CXCL9, CXCL13, CXCL10, CXCL11, WARS, XCL-1, and an analog thereof.

56. The method of any one of claims 47-51, wherein the chemokine mimetic is a CCL5 mimetic or pharmaceutically acceptable salt thereof.

57. The method of claim 56, wherein the chemokine mimetic is CCL5 or a CCL5 analog.

58. The method of any one of claims 47-57, wherein the chemokine mimetic or

pharmaceutically acceptable salt thereof is administered in a pharmaceutical composition further comprising a pharmaceutically acceptable carrier or excipient.

59. The method of any one of claims 47-58, wherein said administering is via intratumoral injection, intravenous injection or subcutaneous injection.

60. The method of any one of claims 47-58, further comprising the step of administering to the subject an anti-PD-L1 antibody or an anti-PD-1 antibody.

61. The method of claim 47-60, furthercomprising the step of administering to the subject a TGFβ inhibitor.

62. The method of any one of claims 47-58, further comprising the step of administering an anti-PD-L1 antibody and a TGFβ antibody.

63. The method of any one of claims 47-58, further comprising the step of administering a bi-specific antibody targeting both PD-L1 and TGFβ.

64. The method of any one of claims 47-58, further comprising the step of administering a bi-specific antibody targeting both PD-1 and TGFβ.

65. The method of any one of claims 47-58, further comprising the step of administering to the subject an anti-CTLA4 antibody, optionally, wherein the anti-CTLA4 antibody is ipilimumab.

66. The method of any one of claims 47-58, further comprising the step of administering to the subject a T cell or an NK cell, optionally wherein the T cell is a CAR-T, CAR-NK cell, CAR-macrophage, or TCR-T cell.

67. The method of any one of claims 47-58, further comprising the step of administering to the subject an IL-15, IL-15 complex, IL-2, IL-7, or a variant thereof.

68. The method of any one of claims 47-58, further comprising the step of administering to the subject an agent activating NK cell or T cell activity.

69. The method of any one of claims 47-68, wherein the cancer is selected from the group consisting of: multiple myeloma, adrenocortical carcinoma, acute myeloid leukemia, Bladder Urothelial Carcinoma, glioma, breast invasive carcinoma, glioma, Cervical squamous cell carcinoma, endocervical adenocarcinoma, cholangiocarcinoma, chronic myelogenous leukemia, colon adenocarcinoma, esophageal carcinoma, glioblasoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, liver hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell

lymphoma, mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocyoma, paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma,sarcoma, skin cutaneous melanoma, stomach adenocarcinoma, testicular germ cell tumors, thyomas, thyroid carcinoma, uterine carcinosarcoma, uterine corps endometrial carcinoma, microsatellite instability-high cancer, basal cell carcinoma, Merkel cell carcinoma, uveal melanoma, and mucosal melanoma.

70. A method of treating cancer, comprising:

intratumorally administering to a subject with cancer a therapeutically effective amount of an TGFβ inhibitor; and

systemically administering to the subject a therapeutically effective amount of an anti-PD-L1 antibody.

71. The method of claim 70, wherein the TGFβ inhibitor is an anti-TGFβ antibody.

72. The method of any one of claims 70-71, wherein the anti-PD-L1 antibody is administered at least once a day, at least once a week, or at least once every two weeks; and the TGFβ inhibitor is administered at least once a day, at least once a week, or at least once every two weeks.

73. The method of any one of claims 70-71, wherein the anti-PD-L1 antibody is administered at least twice a day, at least twice a week, or at least twice every two weeks; and the TGFβ inhibitor is administered at least twice a day, at least twice a week, or at least twice every two weeks.

74. The method of any one of claims 70-71, wherein the anti-PD-L1 antibody is administered at least two times a week for at least 2 weeks or at least two times a week for at least 3 weeks; and the TGFβ inhibitor is administered at least two times a week for at least 2 weeks or at least two times a week for at least 3 weeks.

75. The method of any one of claims 70-74, wherein the cancer is selected from the group consisting of: multiple myeloma, adrenocortical carcinoma, acute myeloid leukemia, Bladder Urothelial Carcinoma, glioma, breast invasive carcinoma, glioma, Cervical squamous cell carcinoma, endocervical adenocarcinoma, cholangiocarcinoma, chronic myelogenous leukemia, colon adenocarcinoma, esophageal carcinoma, glioblastoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell lymphoma,

mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocyoma, paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma,sarcoma, skin cutaneous melanoma, stomach adenocarcinoma, testicular germ cell tumors, thyomas, thyroid carcinoma, uterine carcinosarcoma, uterine corps endometrial carcinoma, microsatellite instability-high cancer, basal cell carcinoma, Merkel cell carcinoma, uveal melanoma, and mucosal melanoma.

FIG. 1A

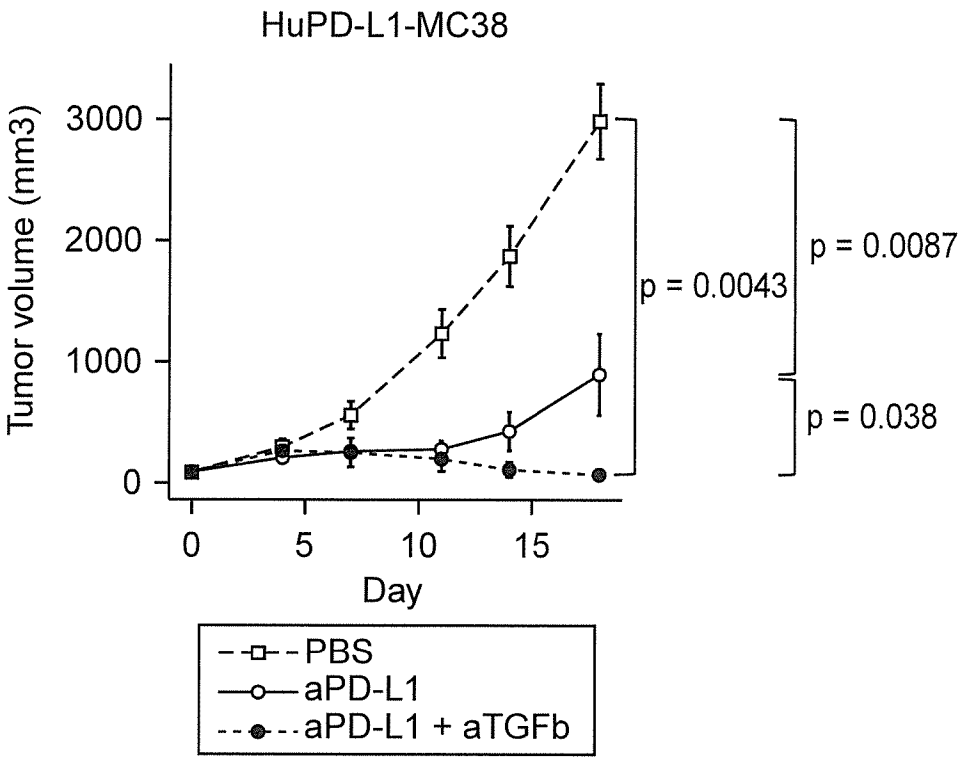

HuPD-L1-MC38
Tumor volume (mm3)
3000
2000
1000
0
0
5
10
15
Day
p = 0.0043
p = 0.0087
p = 0.038
PBS
aPD-L1
aPD-L1 + aTGFb

FIG. 1B

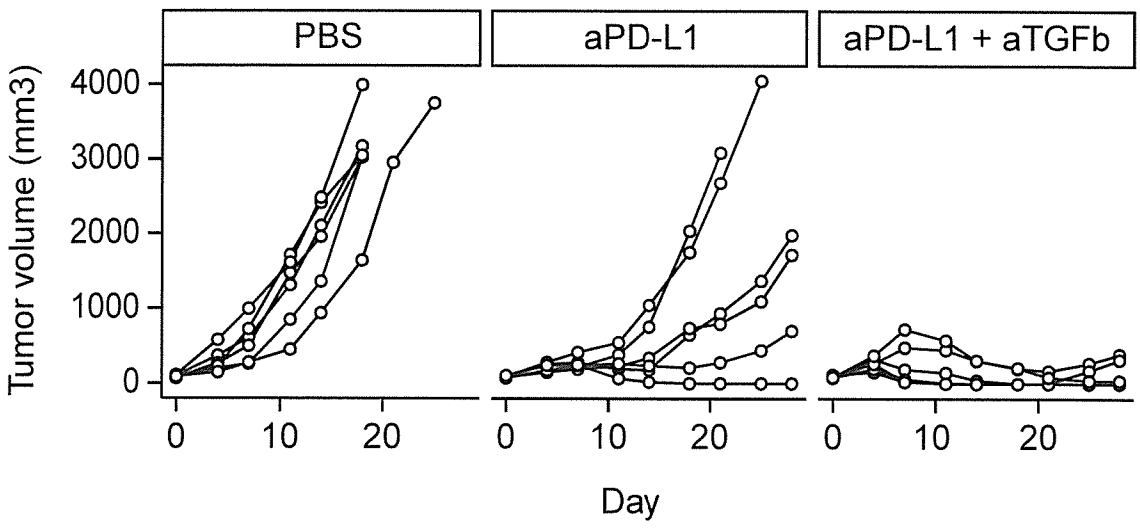

PBS
aPD-L1
aPD-L1 + aTGFb
Tumor volume (mm3)
4000
3000
2000
1000
0
0
10
20
Day

FIG. 1C

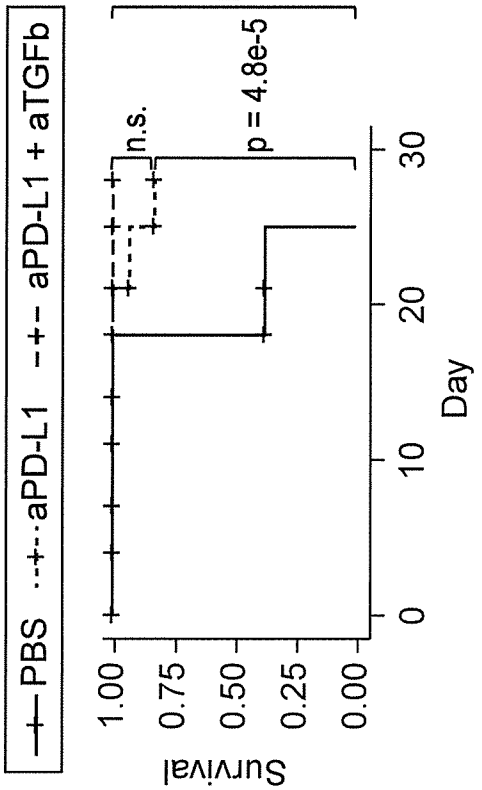


FIG. 1D

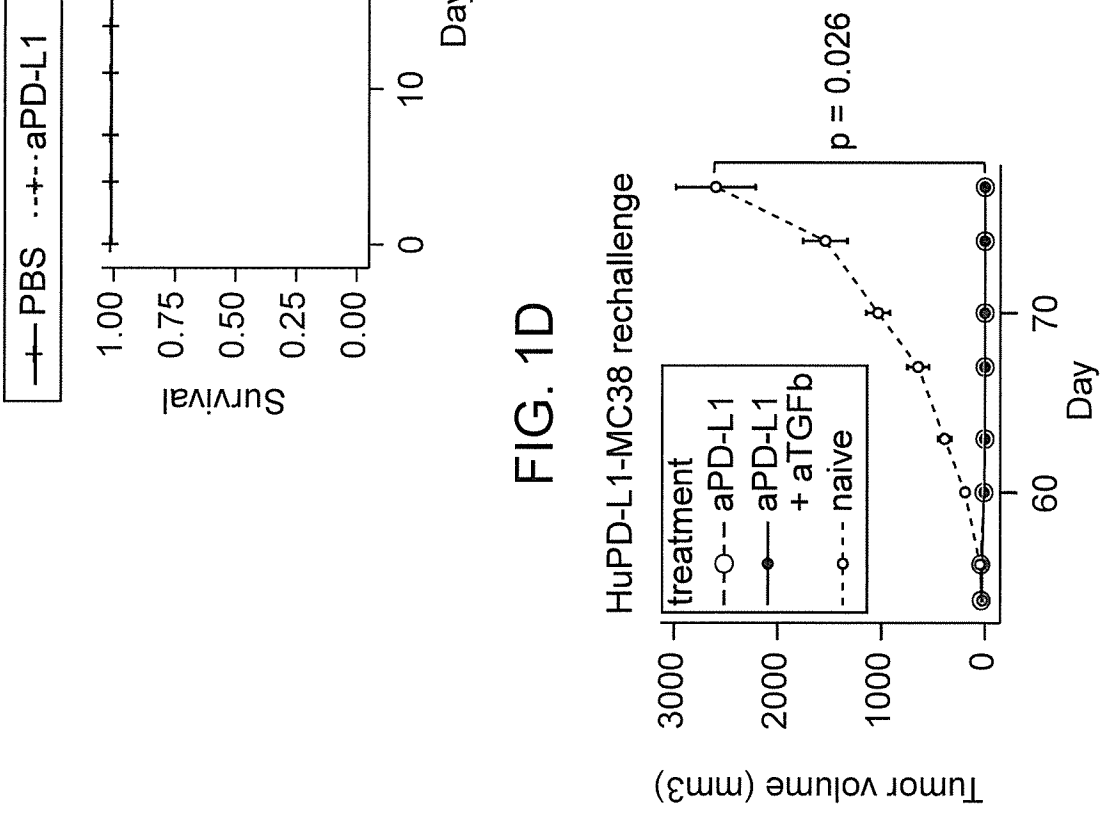


FIG. 1E

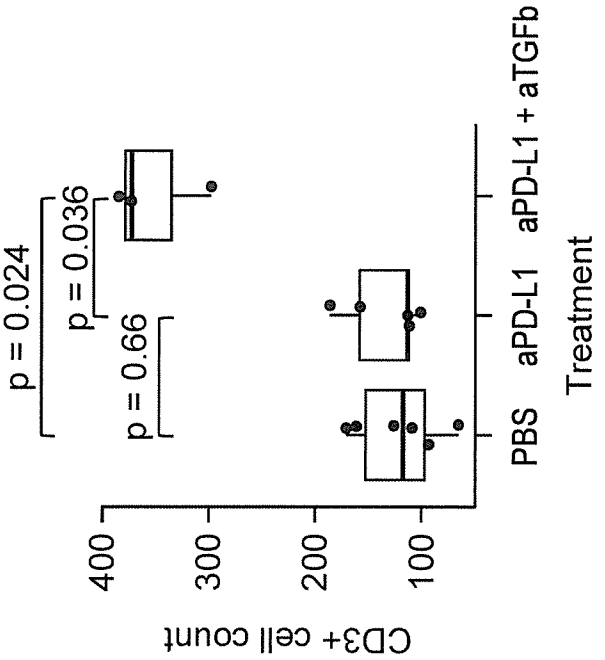


FIG. 1E (Continu...)

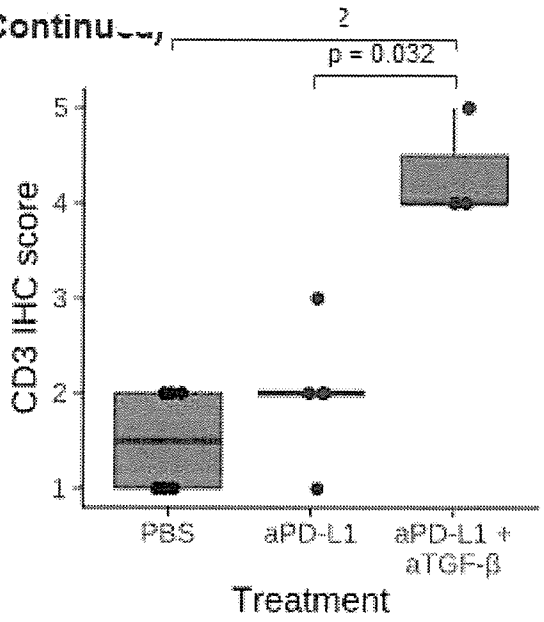


FIG. 1F
CD3 IHC

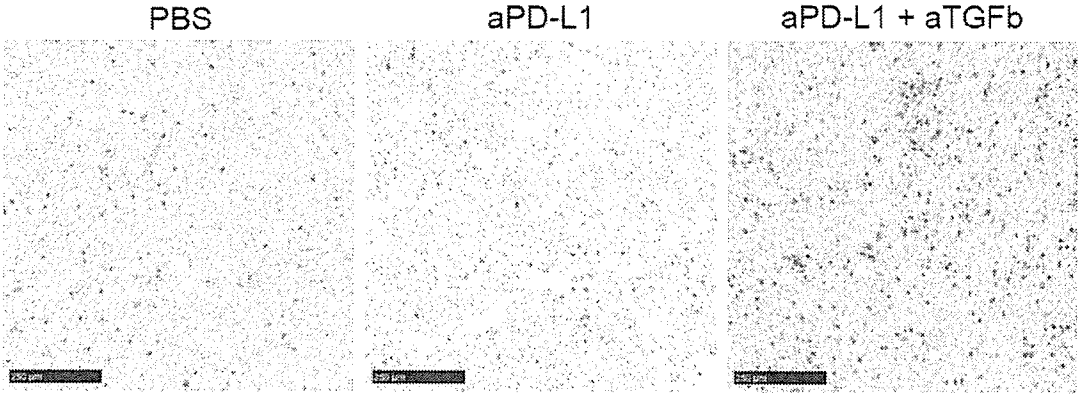


FIG. 2A

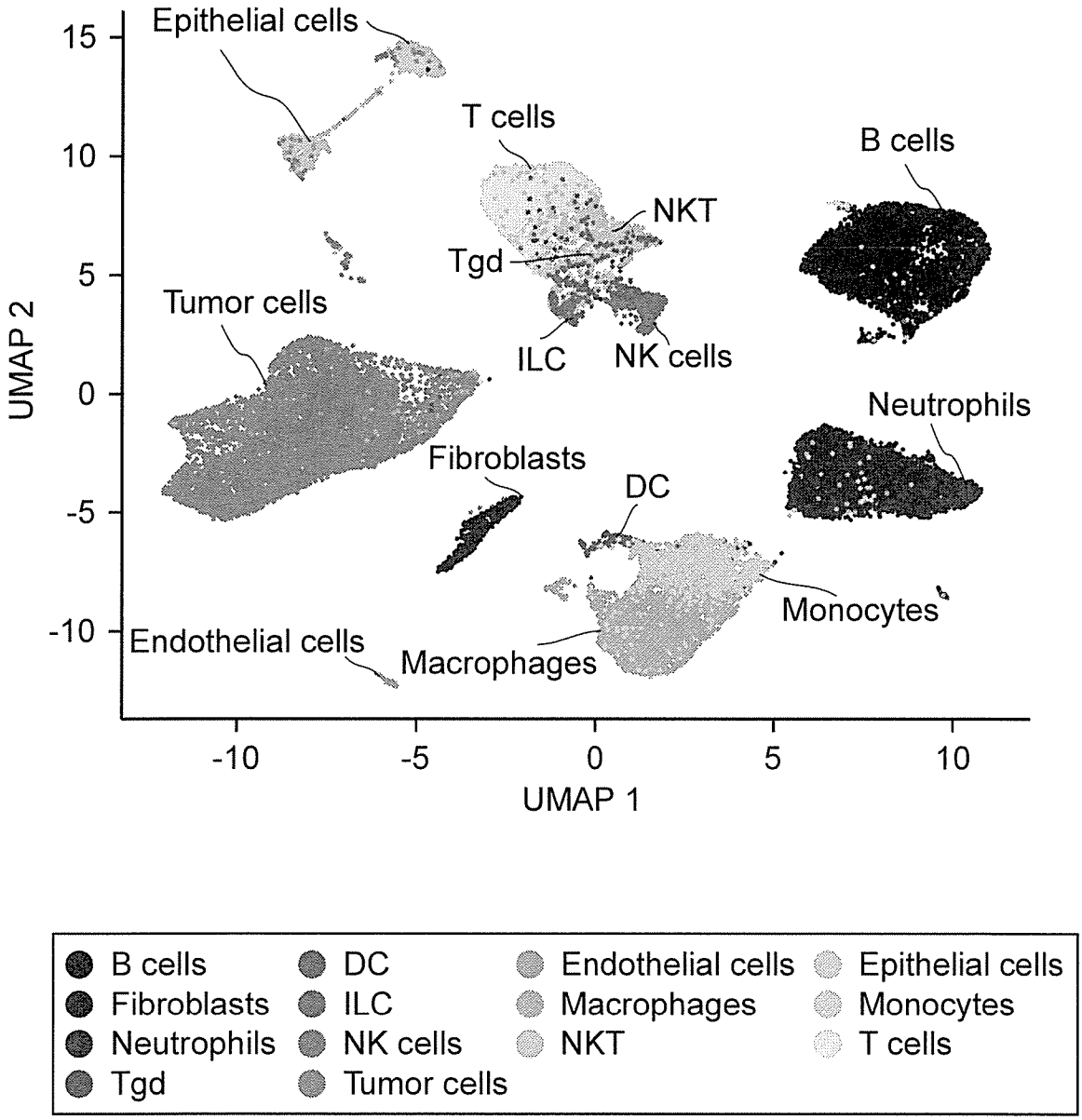

Epithelial cells
T cells
B cells
NKT
Tgd
Tumor cells
ILC
NK cells
Neutrophils
Fibroblasts
DC
Monocytes
Endothelial cells
Macrophages
UMAP 2
UMAP 1
15
10
5
0
-5
-10
-10
-5
0
5
10
B cells
DC
Endothelial cells
Epithelial cells
Fibroblasts
ILC
Macrophages
Monocytes
Neutrophils
NK cells
NKT
T cells
Tgd
Tumor cells

FIG. 2B

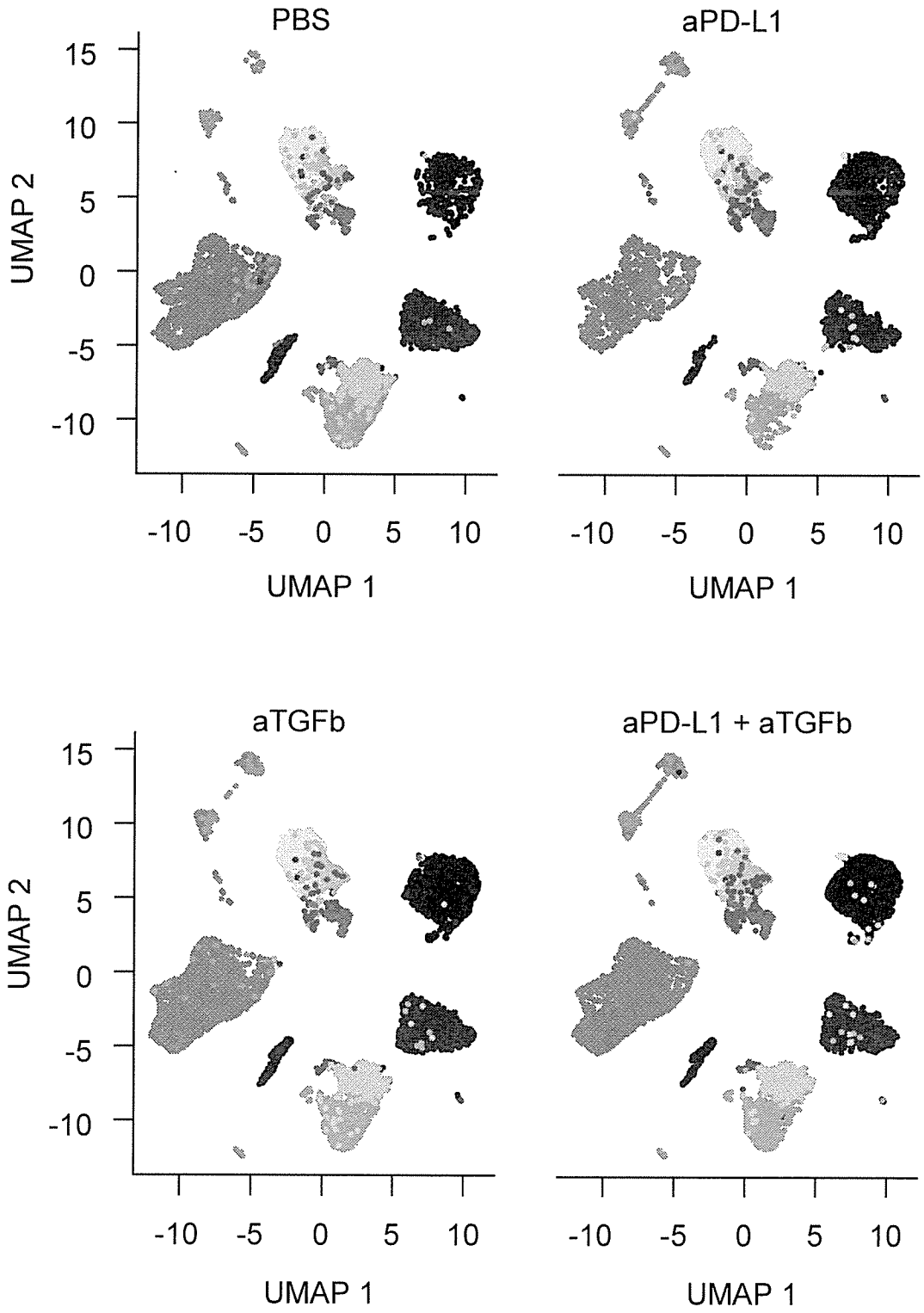


FIG. 2C

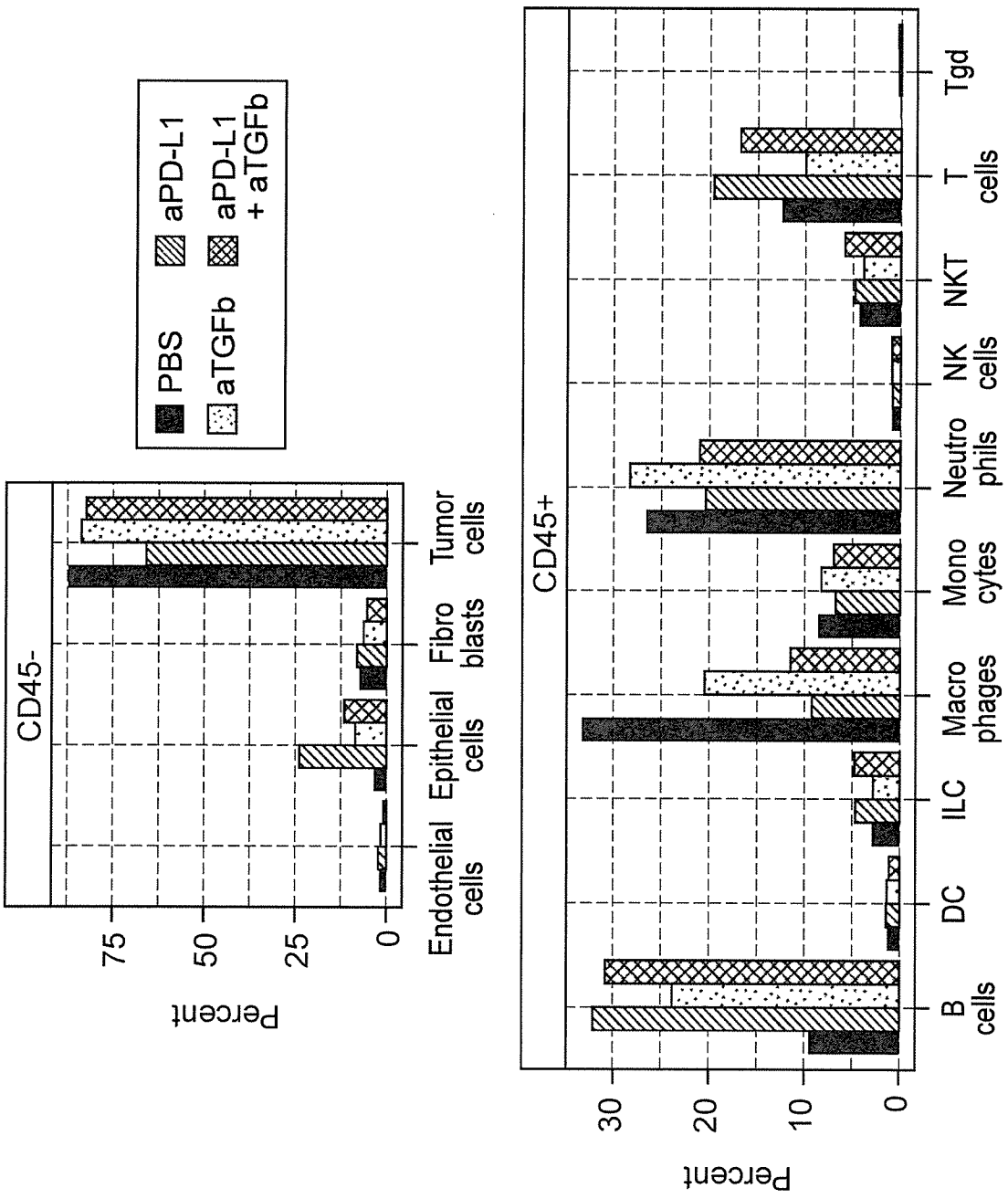

CD45-
Percent
75
50
25
0
PBS
aPD-L1
aTGFb
aPD-L1 + aTGFb
Endothelial cells
Epithelial cells
Fibro blasts
Tumor cells
CD45+
Percent
30
20
10
0
B cells
DC
ILC
Macro phages
Mono cytes
Neutro phils
NK cells
NKT
T cells
Tgd

FIG. 2D

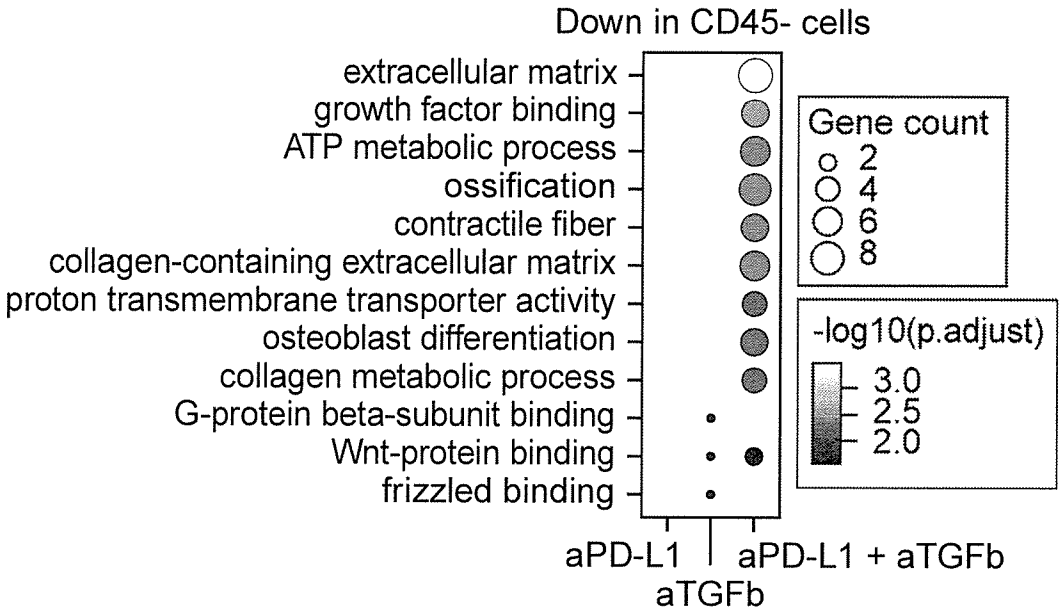

Down in CD45- cells
extracellular matrix
growth factor binding
ATP metabolic process
ossification
contractile fiber
collagen-containing extracellular matrix
proton transmembrane transporter activity
osteoblast differentiation
collagen metabolic process
G-protein beta-subunit binding
Wnt-protein binding
frizzled binding
Gene count
2
4
6
8
-log10(p.adjust)
3.0
2.5
2.0
aPD-L1
aTGFb
aPD-L1 + aTGFb

FIG. 2E

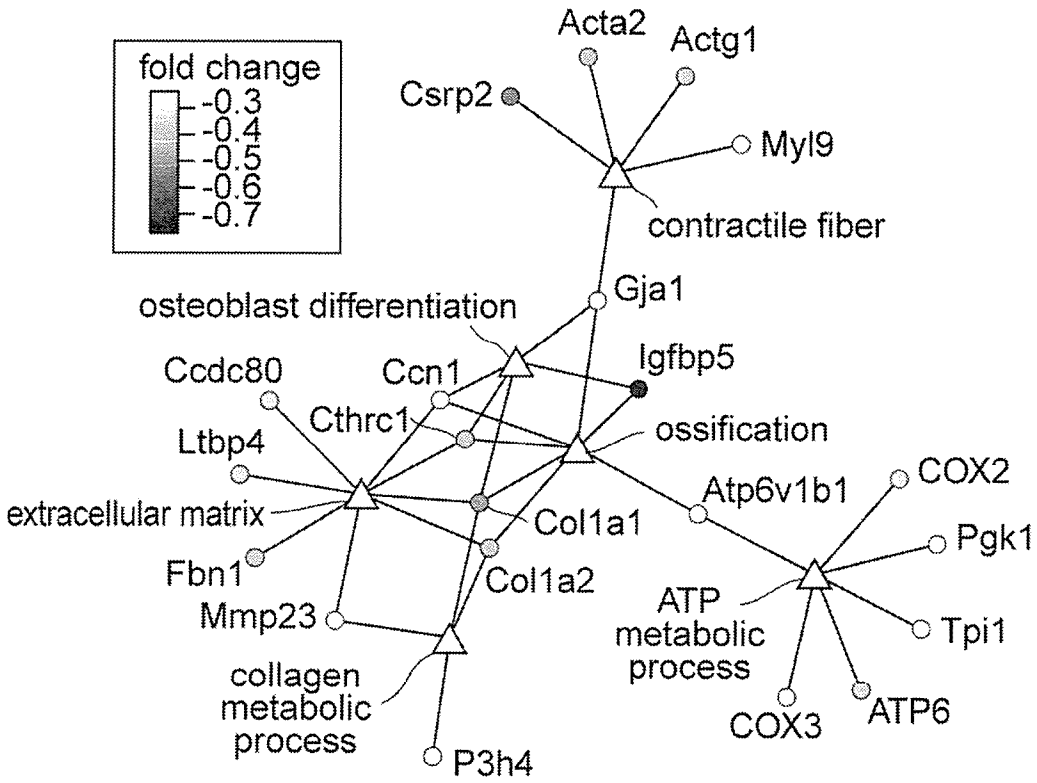

fold change
-0.3
-0.4
-0.5
-0.6
-0.7
Acta2
Actg1
Csrp2
Myl9
contractile fiber
Gja1
osteoblast differentiation
Igfbp5
Ccdc80
Ccn1
Cthrc1
ossification
Ltbp4
Atp6v1b1
COX2
extracellular matrix
Col1a1
Pgk1
Fbn1
Col1a2
ATP
metabolic
process
Tpi1
Mmp23
collagen
metabolic
process
COX3
ATP6
P3h4

FIG. 2F

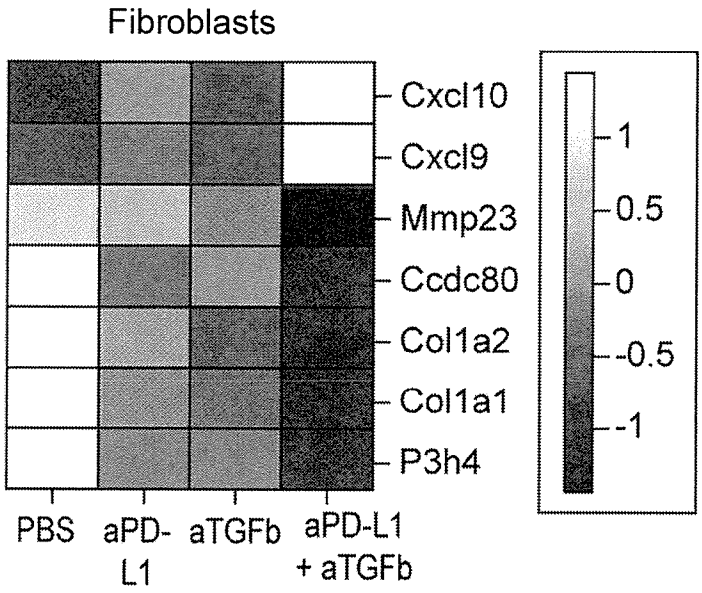

Fibroblasts
Cxcl10
Cxcl9
Mmp23
Ccdc80
Col1a2
Col1a1
P3h4
1
0.5
0
-0.5
-1
PBS
aPD-L1
aTGFb
aPD-L1 + aTGFb

FIG. 2G

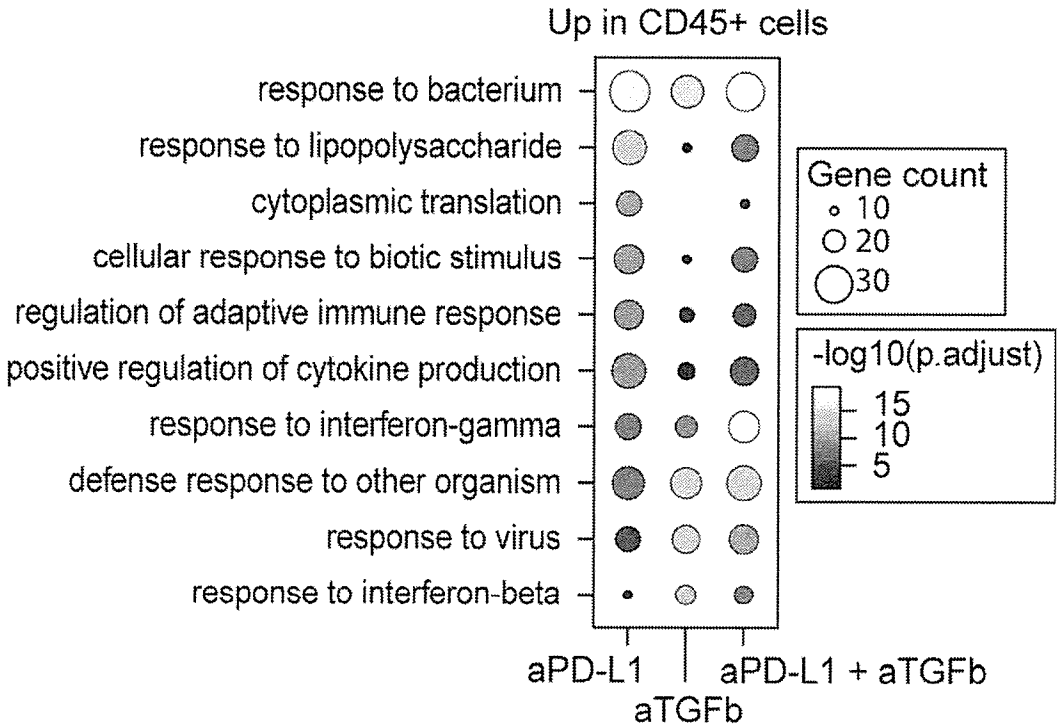

Up in CD45+ cells
response to bacterium
response to lipopolysaccharide
cytoplasmic translation
cellular response to biotic stimulus
regulation of adaptive immune response
positive regulation of cytokine production
response to interferon-gamma
defense response to other organism
response to virus
response to interferon-beta
Gene count
10
20
30
-log10(p.adjust)
15
10
5
aPD-L1
aTGFb
aPD-L1 + aTGFb

FIG. 2H

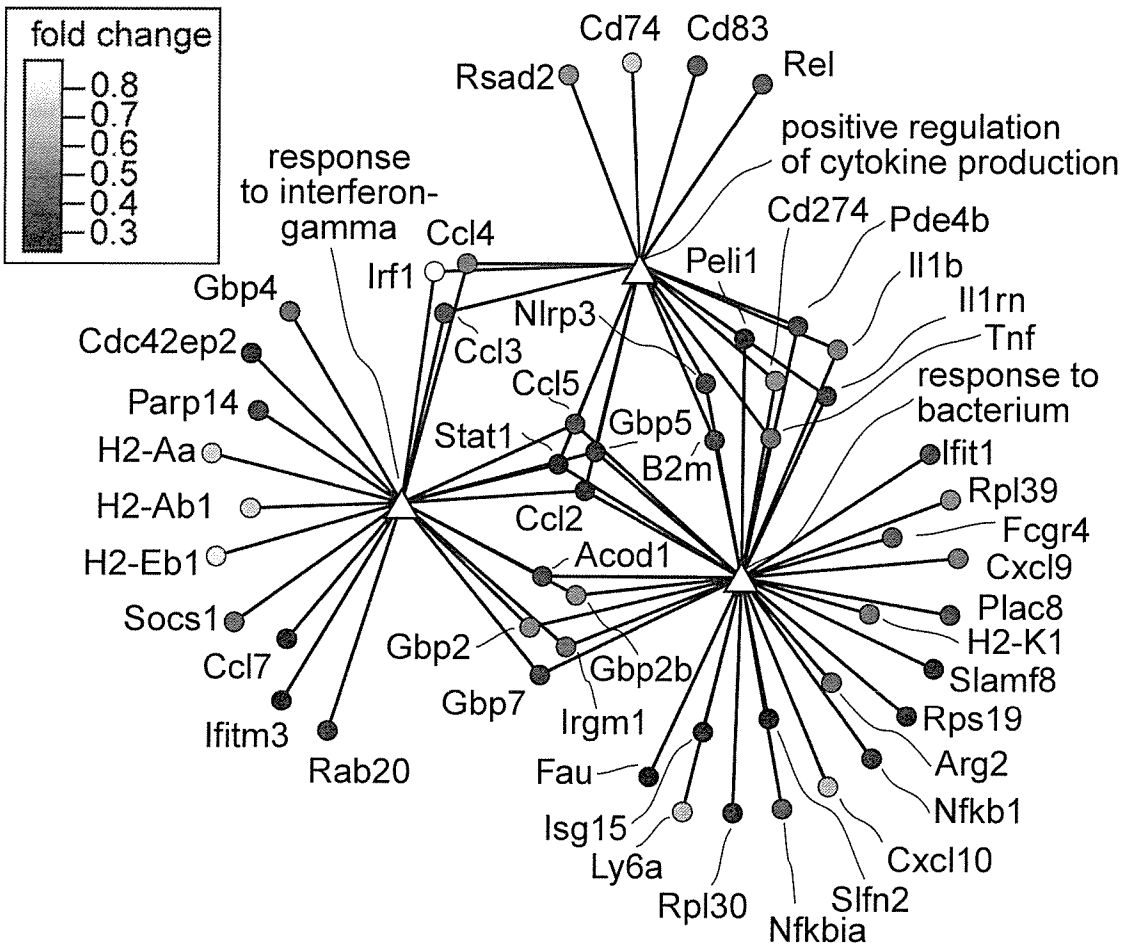

fold change
0.8
0.7
0.6
0.5
0.4
0.3
Cd74
Cd83
Rel
Rsad2
positive regulation
of cytokine production
response
to interferon-
gamma
Ccl4
Irf1
Cd274
Pde4b
Peli1
Il1b
Il1rn
Gbp4
Nlrp3
Tnf
Cdc42ep2
Ccl3
Ccl5
response to
bacterium
Parp14
Stat1
Gbp5
Ifit1
H2-Aa
B2m
Rpl39
H2-Ab1
Ccl2
Fcgr4
H2-Eb1
Acod1
Cxcl9
Socs1
Plac8
Gbp2
H2-K1
Ccl7
Gbp2b
Slamf8
Gbp7
Irgm1
Rps19
Ifitm3
Arg2
Rab20
Fau
Nfkb1
Isg15
Cxcl10
Ly6a
Slfn2
Rpl30
Nfkbia

FIG. 2I

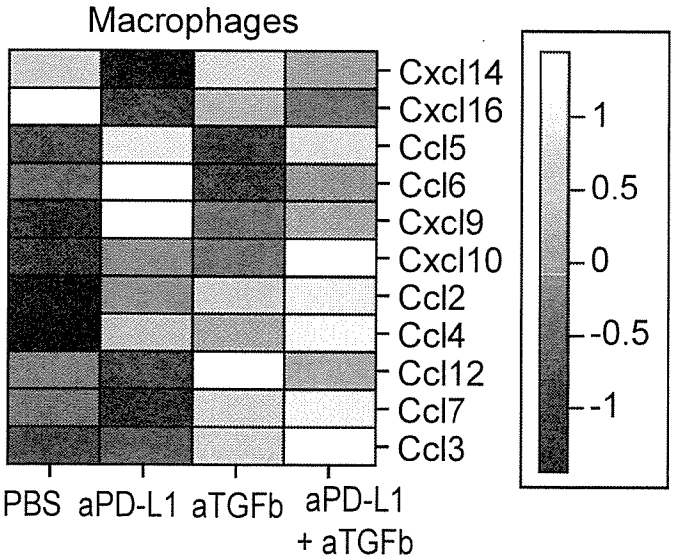

Macrophages
Cxcl14
Cxcl16
Ccl5
Ccl6
Cxcl9
Cxcl10
Ccl2
Ccl4
Ccl12
Ccl7
Ccl3
1
0.5
0
-0.5
-1
PBS
aPD-L1
aTGFb
aPD-L1
+ aTGFb

FIG. 3A

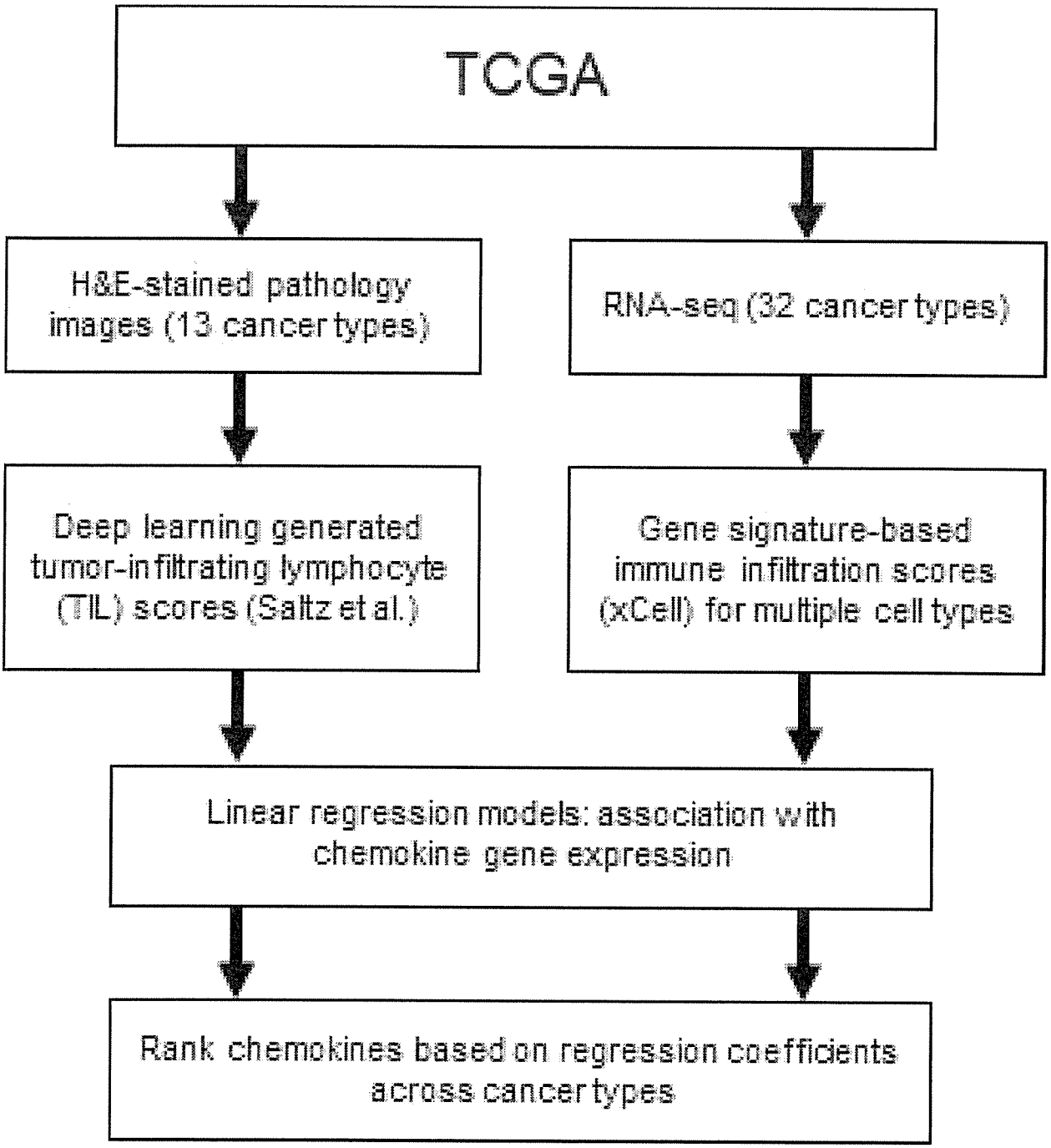

TCGA
H&E-stained pathology images (13 cancer types)
RNA-seq (32 cancer types)
Deep learning generated tumor-infiltrating lymphocyte (TIL) scores (Saltz et al.)
Gene signature-based immune infiltration scores (xCell) for multiple cell types
Linear regression models: association with chemokine gene expression
Rank chemokines based on regression coefficients across cancer types

FIG. 3B

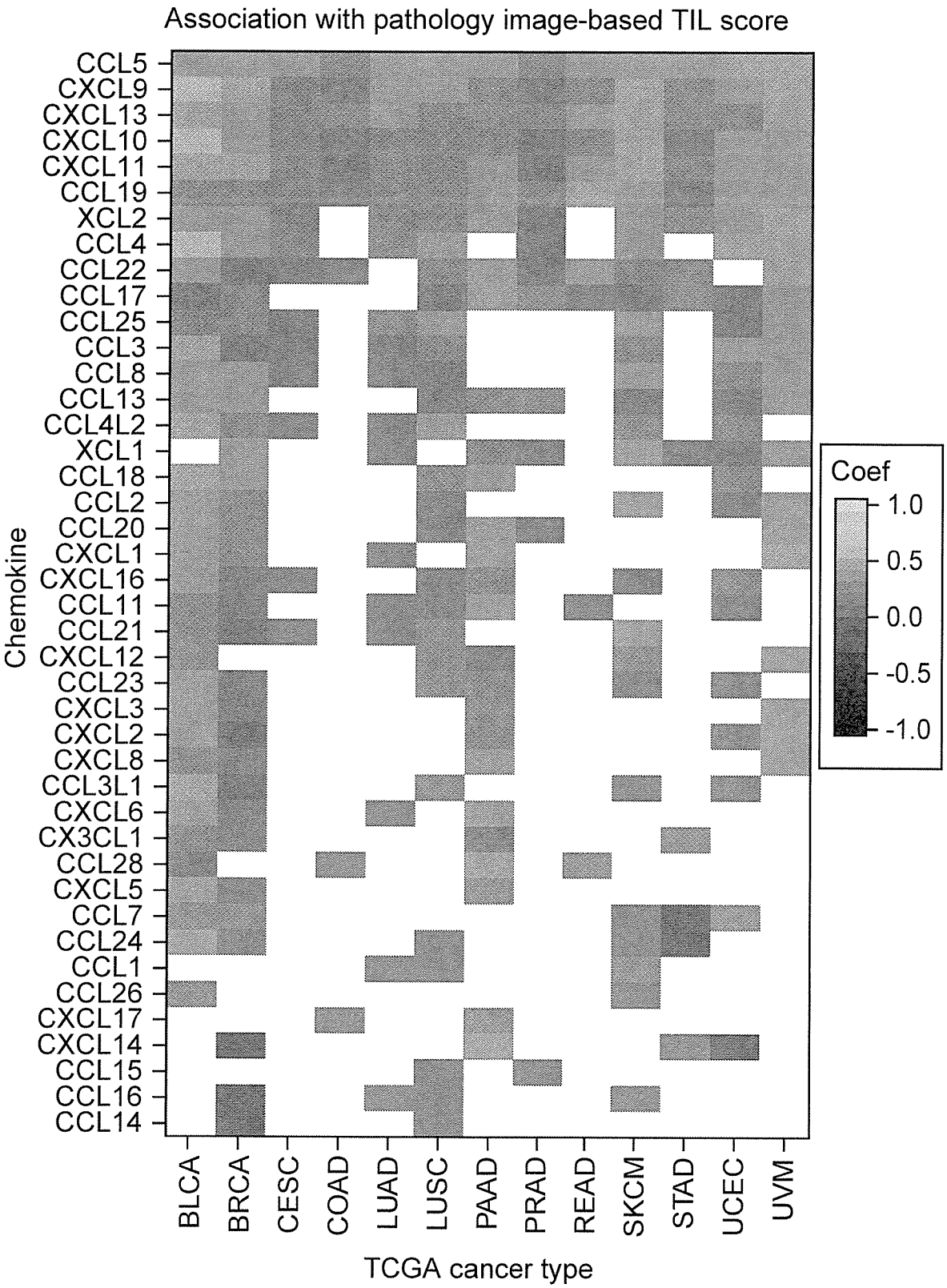

Association with pathology image-based TIL score
Chemokine
CCL5
CXCL9
CXCL13
CXCL10
CXCL11
CCL19
XCL2
CCL4
CCL22
CCL17
CCL25
CCL3
CCL8
CCL13
CCL4L2
XCL1
CCL18
CCL2
CCL20
CXCL1
CXCL16
CCL11
CCL21
CXCL12
CCL23
CXCL3
CXCL2
CXCL8
CCL3L1
CXCL6
CX3CL1
CCL28
CXCL5
CCL7
CCL24
CCL1
CCL26
CXCL17
CXCL14
CCL15
CCL16
CCL14
BLCA
BRCA
CESC
COAD
LUAD
LUSC
PAAD
PRAD
READ
SKCM
STAD
UCEC
UVM
TCGA cancer type
Coef
1.0
0.5
0.0
-0.5
-1.0

FIG. 3C

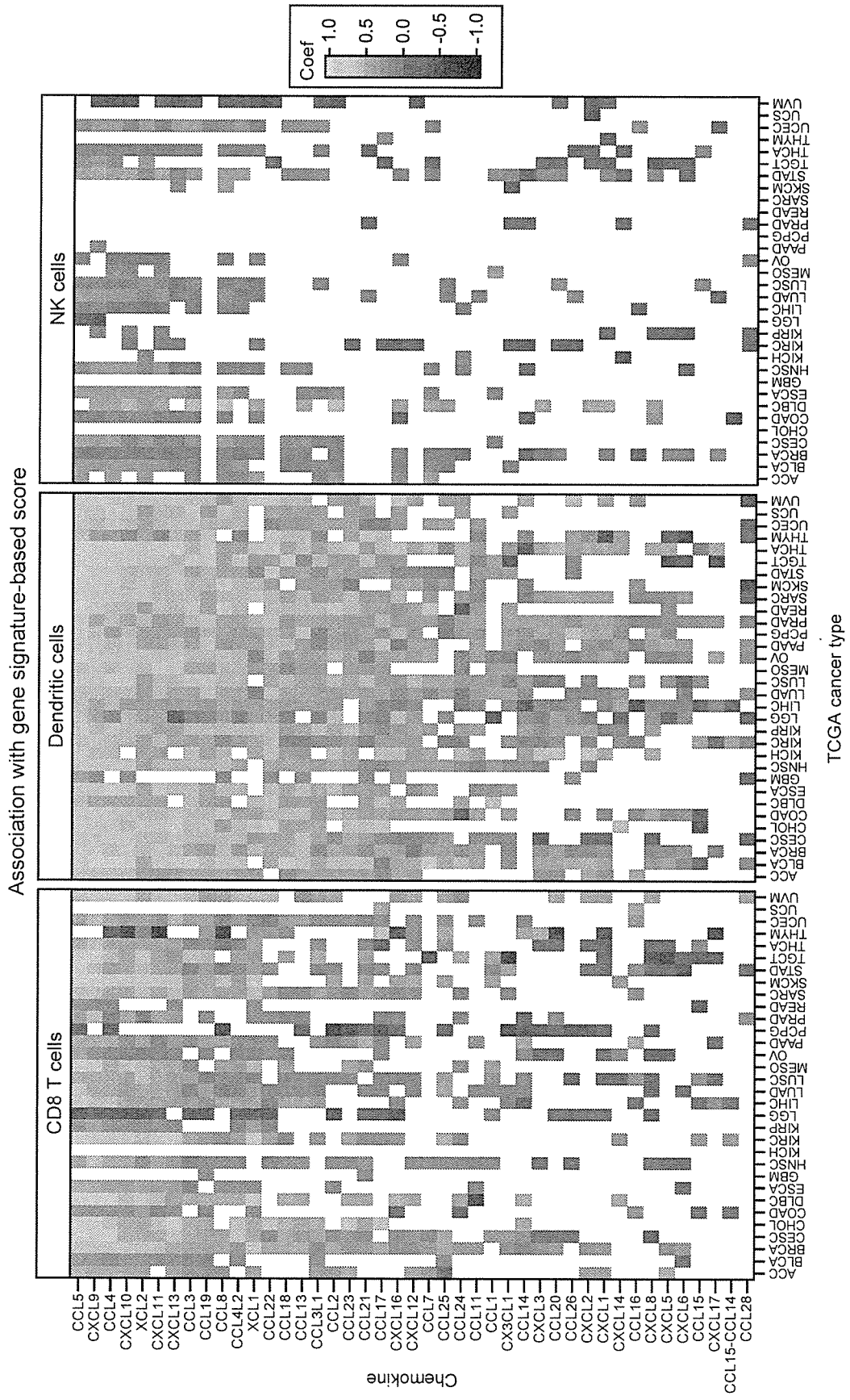

Association with gene signature-based score
CD8 T cells
Dendritic cells
NK cells
Coef
1.0
0.5
0.0
-0.5
-1.0
Chemokine
CCL5
CXCL9
CCL4
CXCL10
XCL2
CXCL11
CXCL13
CCL3
CCL19
CCL8
CCL4L2
XCL1
CCL22
CCL18
CCL13
CCL3L1
CCL2
CCL23
CCL21
CCL17
CXCL16
CXCL12
CCL7
CCL25
CCL24
CCL11
CCL1
CX3CL1
CCL14
CXCL3
CCL20
CCL26
CXCL2
CXCL1
CXCL14
CCL16
CXCL8
CXCL5
CXCL6
CCL15
CXCL17
CCL15-CCL14
CCL28
TCGA cancer type
ACC
BLCA
BRCA
CESC
CHOL
COAD
DLBC
ESCA
GBM
HNSC
KICH
KIRC
KIRP
LGG
LIHC
LUAD
LUSC
MESO
OV
PAAD
PCPG
PRAD
READ
SARC
SKCM
STAD
TGCT
THCA
THYM
UCEC
UCS
UVM

FIG. 4A

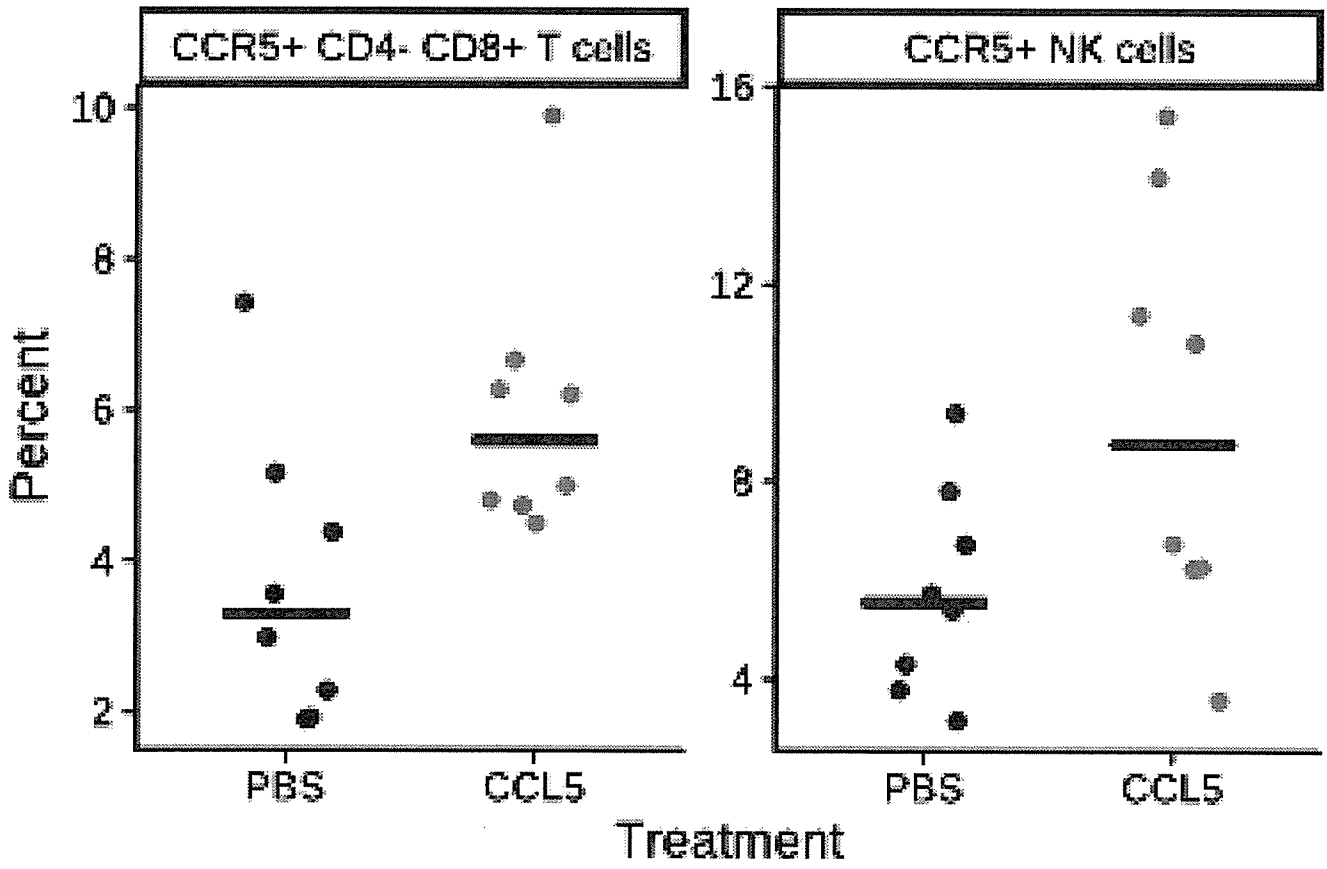

CCR5+ CD4- CD8+ T cells
CCR5+ NK cells
Percent
10
8
6
4
2
16
12
8
4
PBS
CCL5
PBS
CCL5
Treatment

FIG. 4B

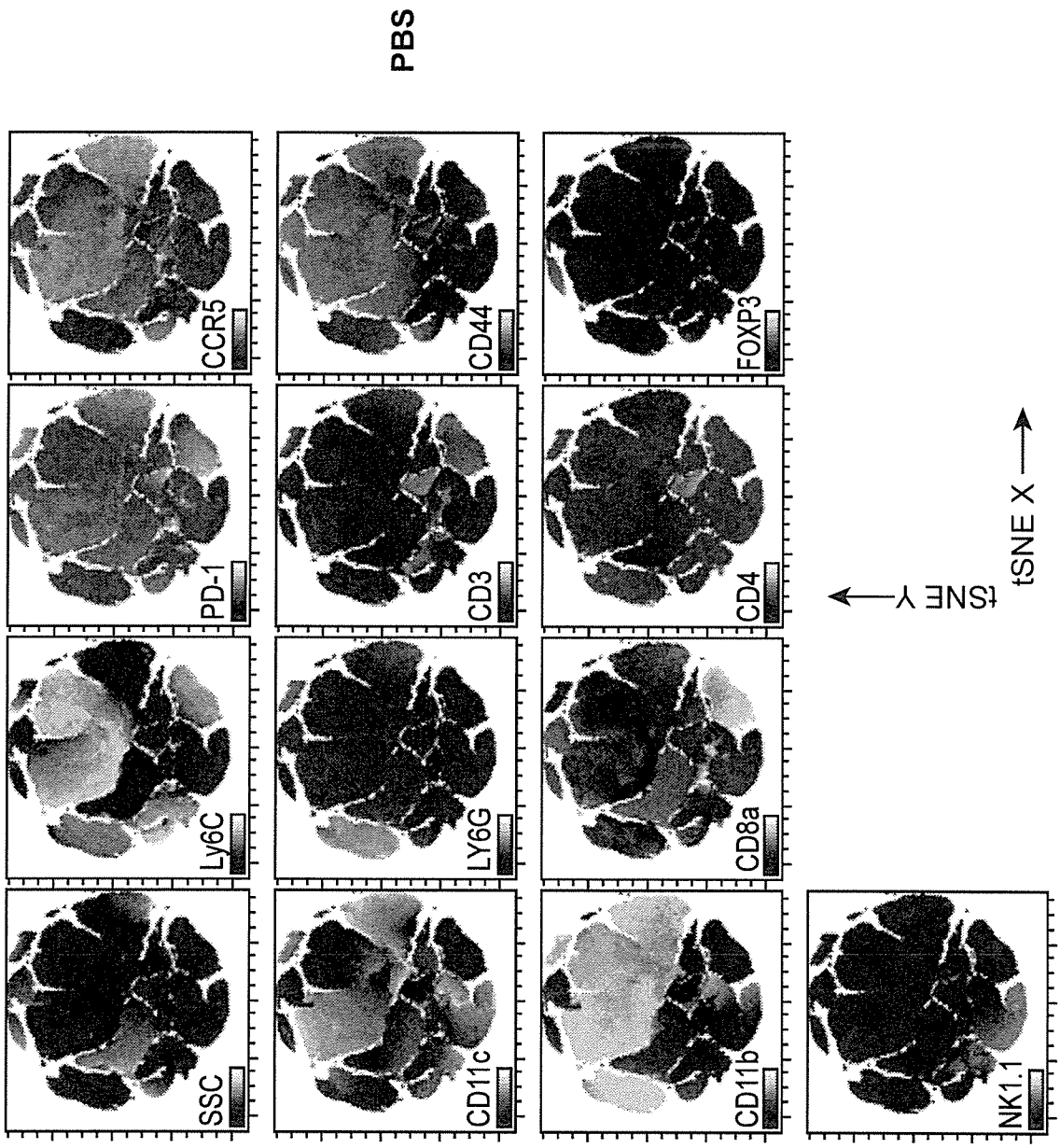

PBS
SSC
Ly6C
PD-1
CCR5
CD11c
LY6G
CD3
CD44
CD11b
CD8a
CD4
FOXP3
NK1.1
tSNE Y
tSNE X

FIG. 4C

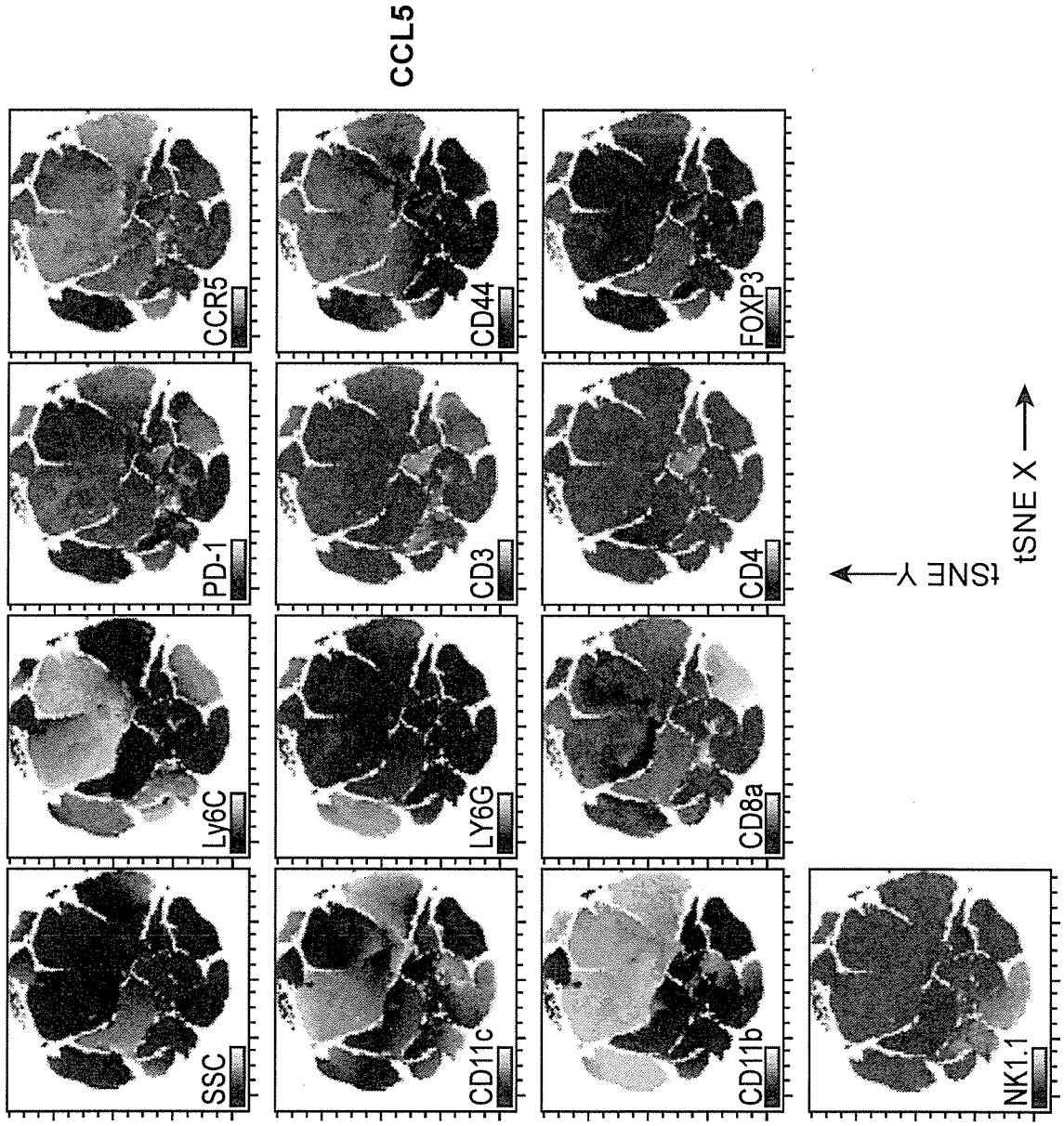

CCL5
SSC
Ly6C
PD-1
CCR5
CD11c
LY6G
CD3
CD44
CD11b
CD8a
CD4
FOXP3
NK1.1
tSNE Y
tSNE X

FIG. 4D

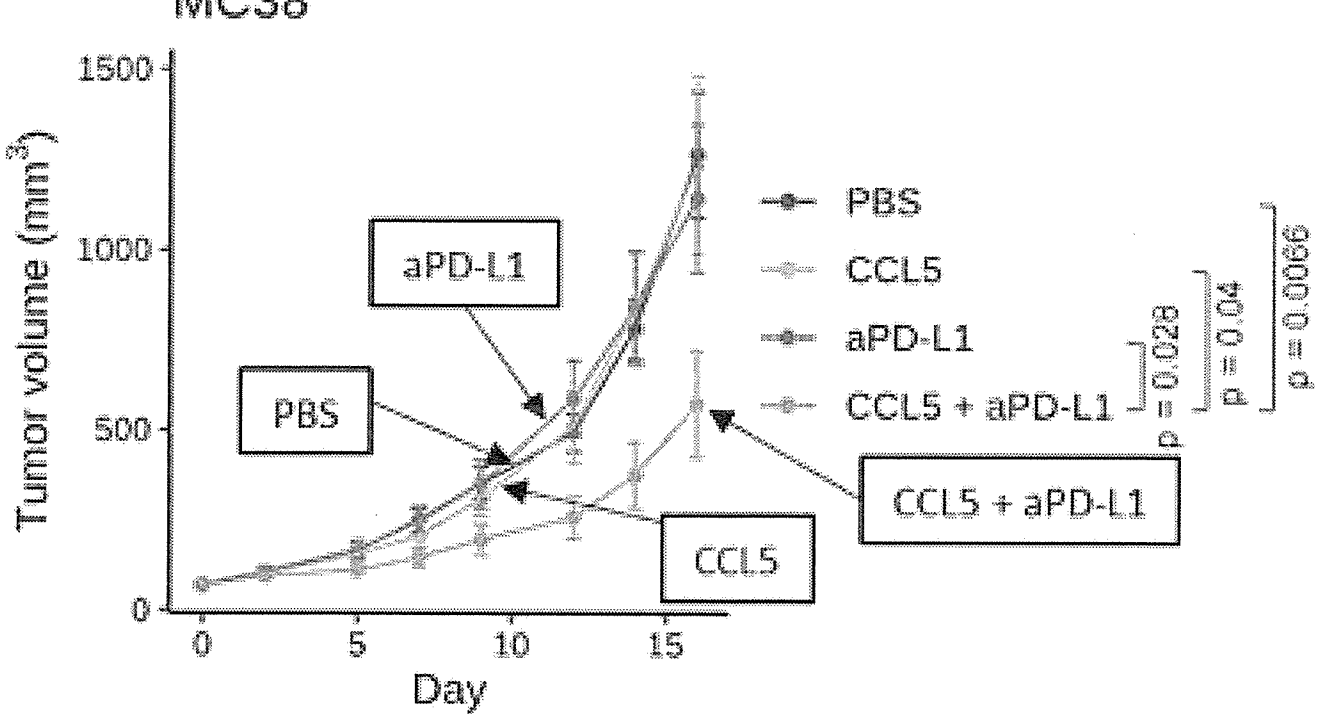

MC38
Tumor volume (mm3)
1500
1000
500
0
0
5
10
15
Day
PBS
aPD-L1
CCL5
CCL5 + aPD-L1
p = 0.028
p = 0.04
p = 0.0066

FIG. 4E

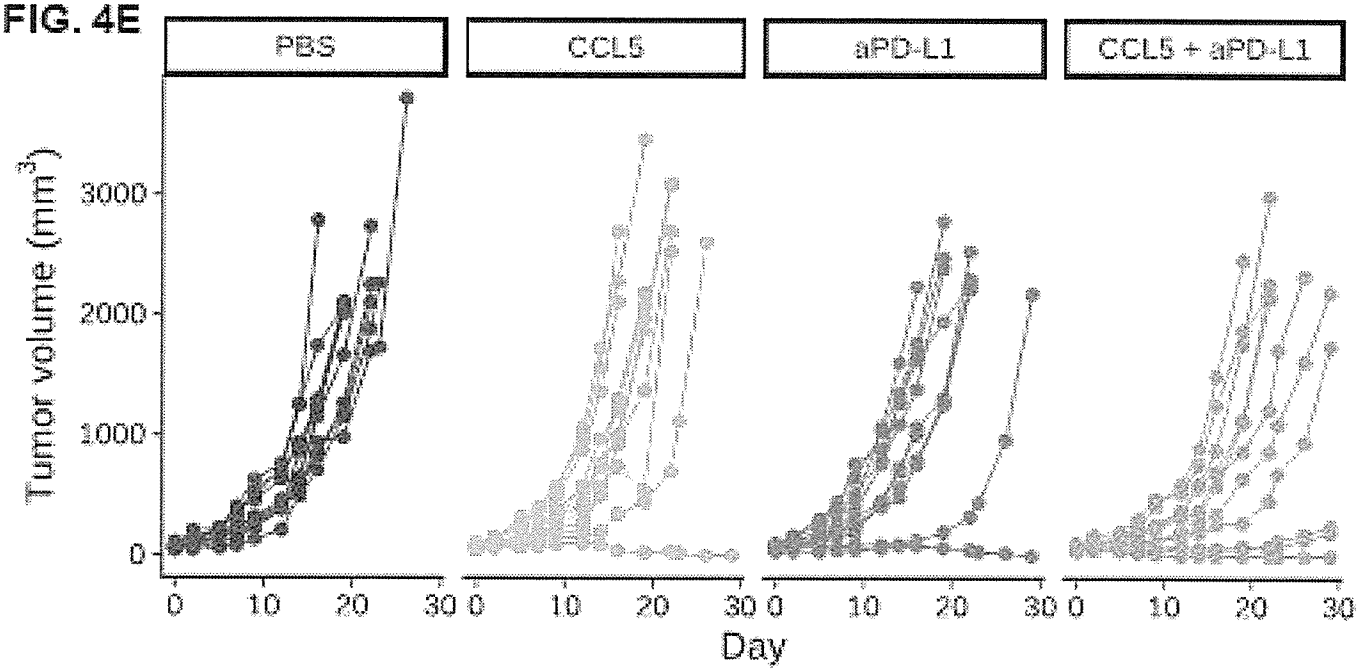

PBS
CCL5
aPD-L1
CCL5 + aPD-L1
Tumor volume (mm3)
3000
2000
1000
0
0
10
20
30
Day

FIG. 4F

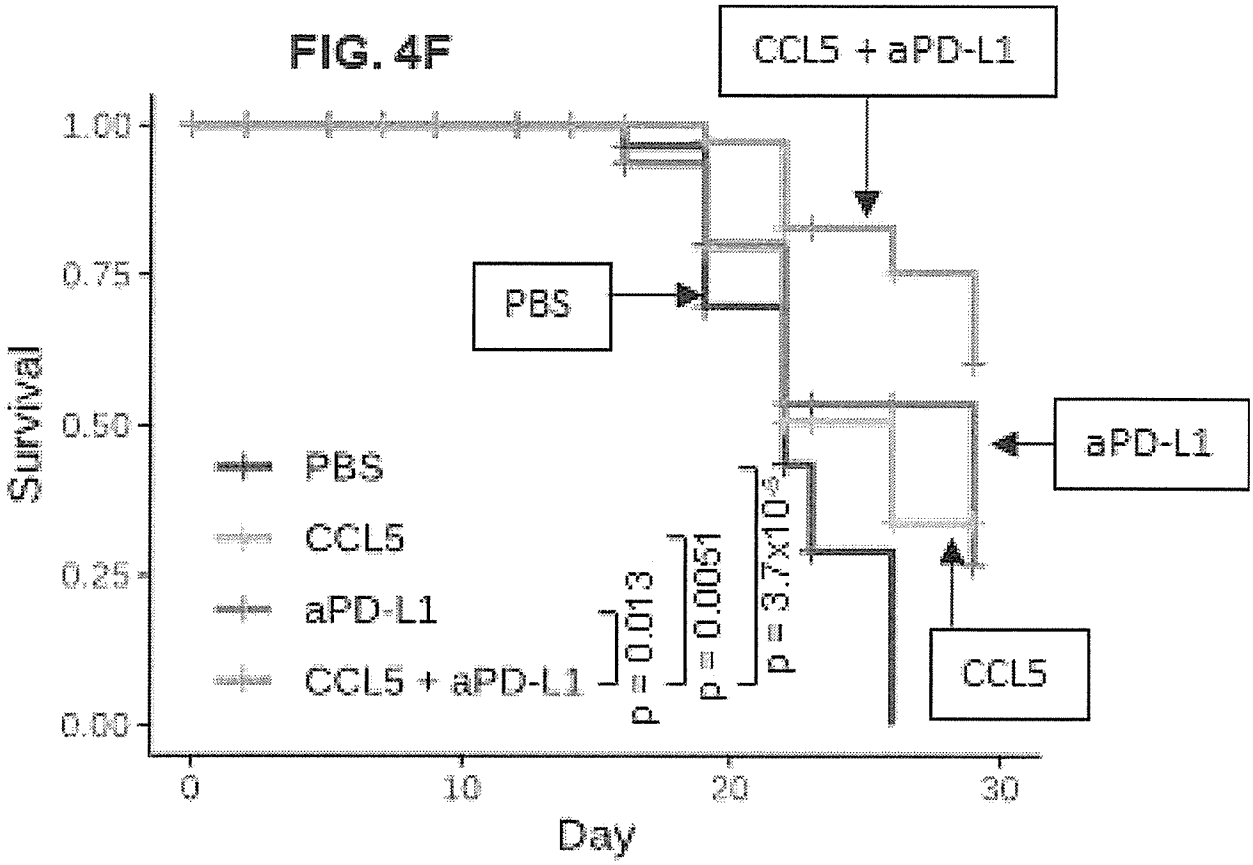

CCL5 + aPD-L1
PBS
aPD-L1
CCL5
1.00
0.75
0.50
0.25
0.00
Survival
PBS
CCL5
aPD-L1
CCL5 + aPD-L1
p = 0.013
p = 0.0051
p = 3.7x10-5
0
10
20
30
Day

FIG. 4G

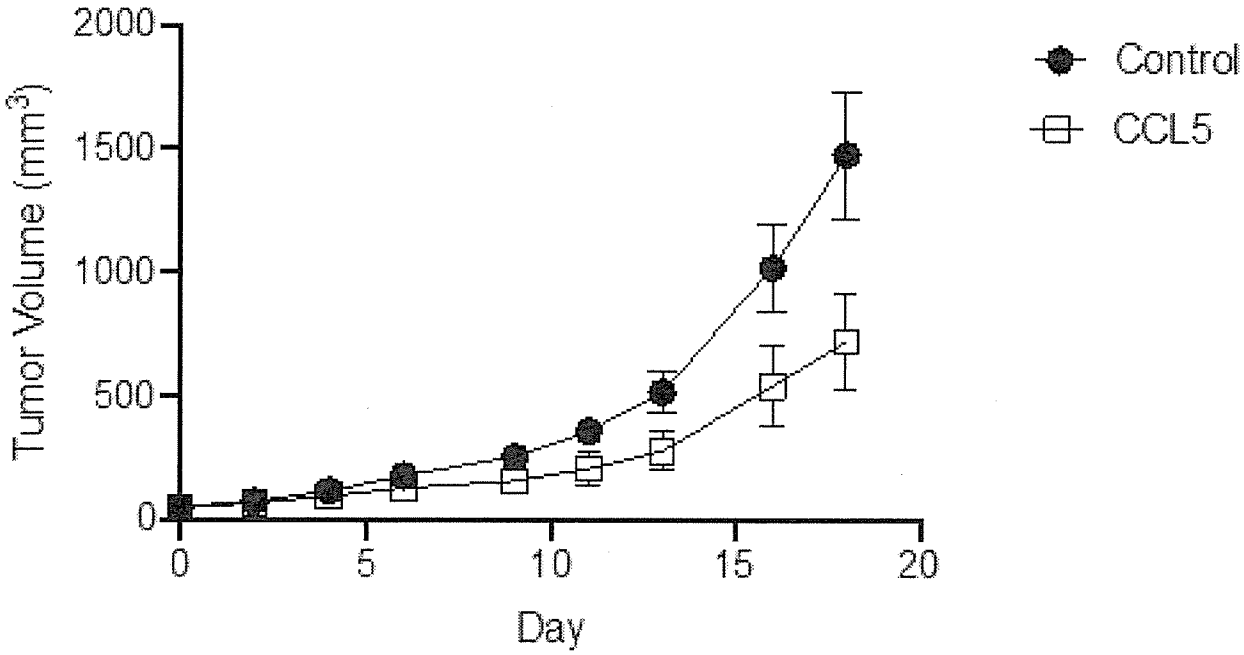

Control
CCL5
2000
1500
1000
500
0
Tumor Volume (mm3)
0
5
10
15
20
Day

FIG. 5A

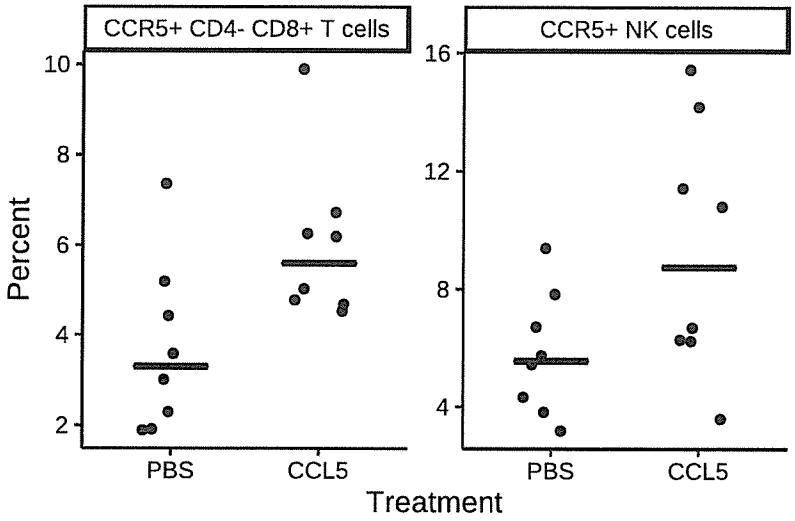


FIG. 5B

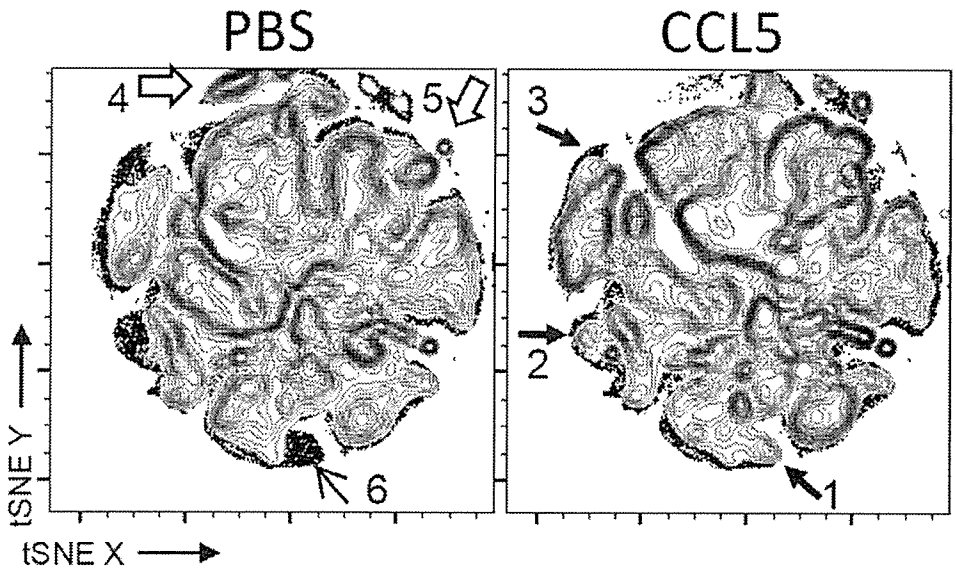


FIG. 5C

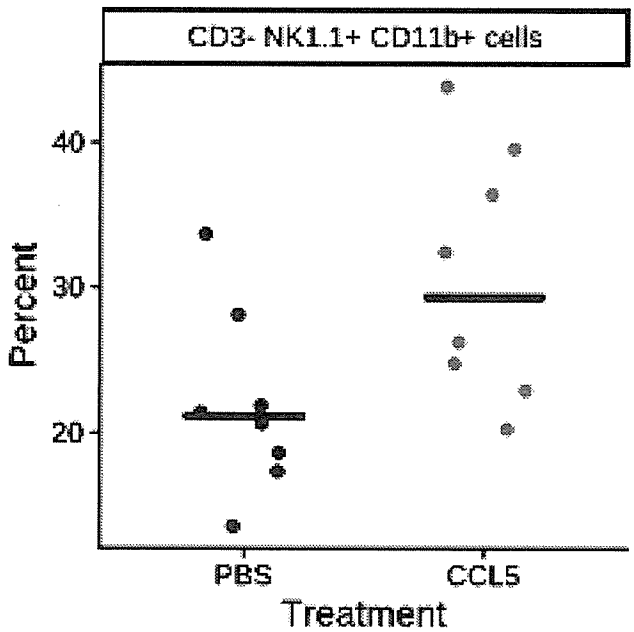


FIG. 5D

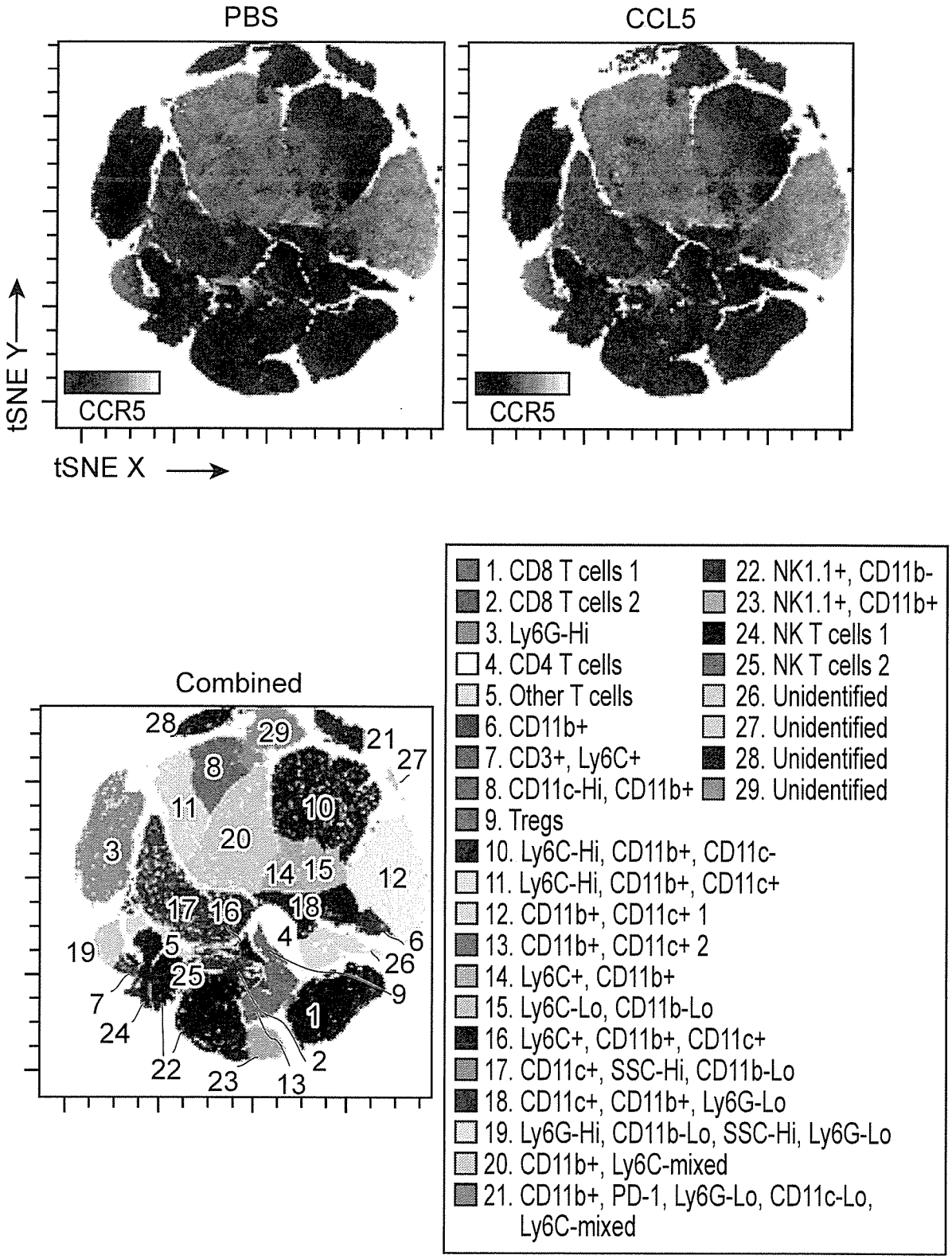

PBS
CCL5
tSNE Y
tSNE X
CCR5
CCR5
Combined
1. CD8 T cells 1
2. CD8 T cells 2
3. Ly6G-Hi
4. CD4 T cells
5. Other T cells
6. CD11b+
7. CD3+, Ly6C+
8. CD11c-Hi, CD11b+
9. Tregs
10. Ly6C-Hi, CD11b+, CD11c-
11. Ly6C-Hi, CD11b+, CD11c+
12. CD11b+, CD11c+ 1
13. CD11b+, CD11c+ 2
14. Ly6C+, CD11b+
15. Ly6C-Lo, CD11b-Lo
16. Ly6C+, CD11b+, CD11c+
17. CD11c+, SSC-Hi, CD11b-Lo
18. CD11c+, CD11b+, Ly6G-Lo
19. Ly6G-Hi, CD11b-Lo, SSC-Hi, Ly6G-Lo
20. CD11b+, Ly6C-mixed
21. CD11b+, PD-1, Ly6G-Lo, CD11c-Lo, Ly6C-mixed
22. NK1.1+, CD11b-
23. NK1.1+, CD11b+
24. NK T cells 1
25. NK T cells 2
26. Unidentified
27. Unidentified
28. Unidentified
29. Unidentified

FIG. 6A

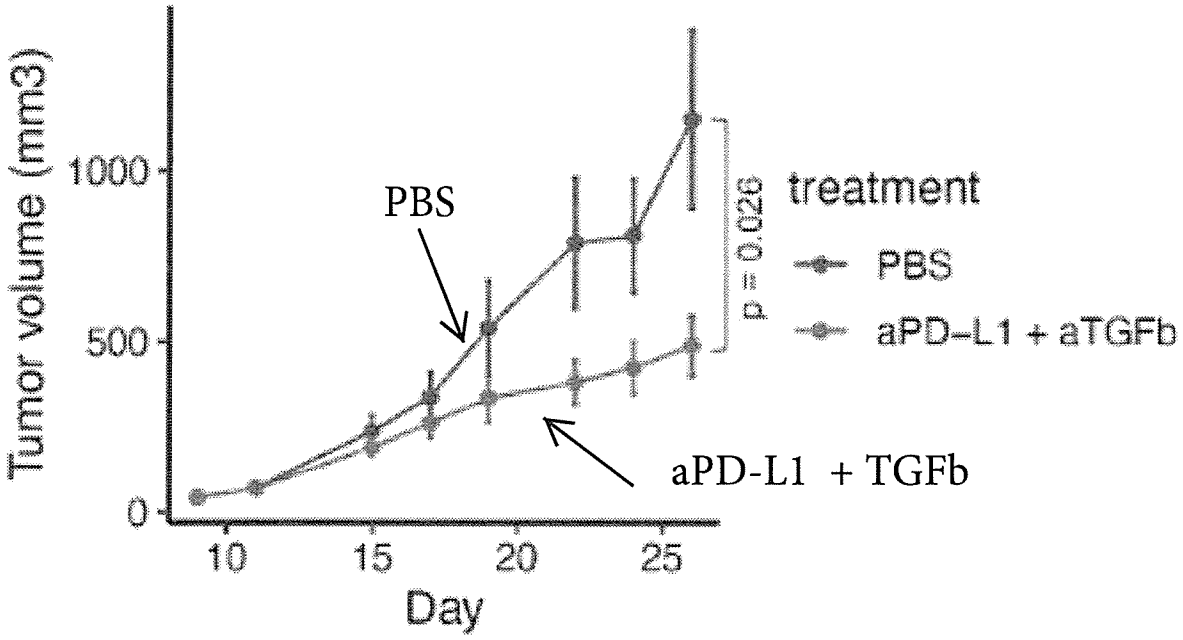

CT26
Tumor volume (mm3)
1000
500
0
PBS
p = 0.026
treatment
PBS
aPD–L1 + aTGFb
aPD-L1 + TGFb
10
15
20
25
Day

FIG. 6B

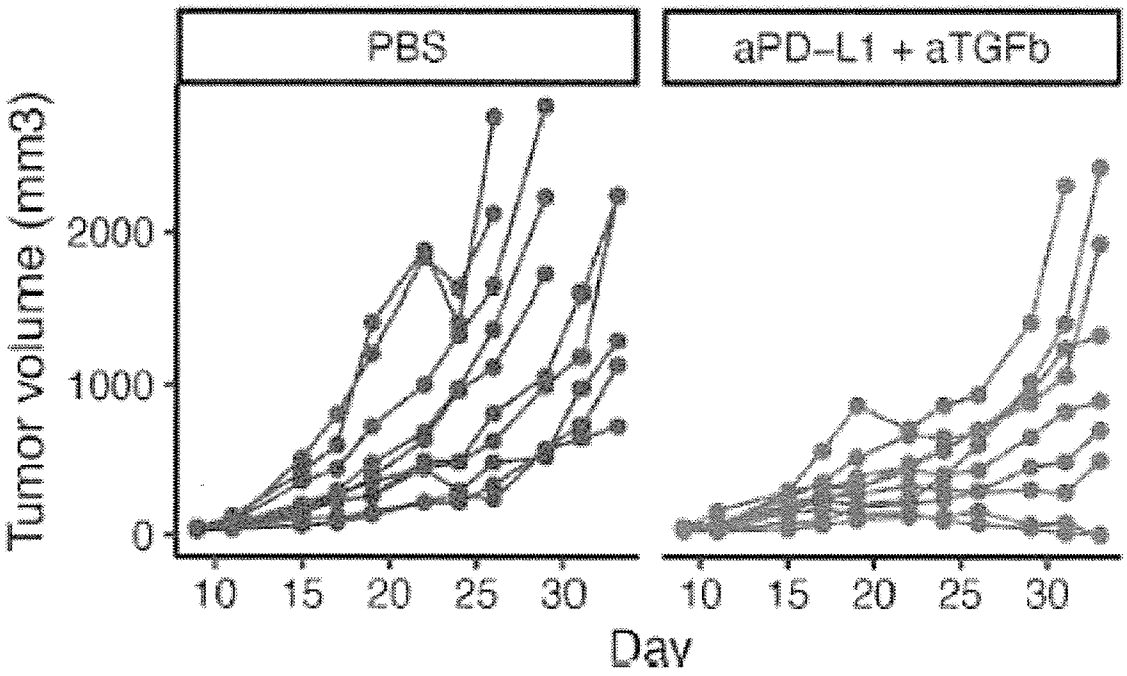

PBS
aPD–L1 + aTGFb
Tumor volume (mm3)
2000
1000
0
10
15
20
25
30
Day

FIG. 7A

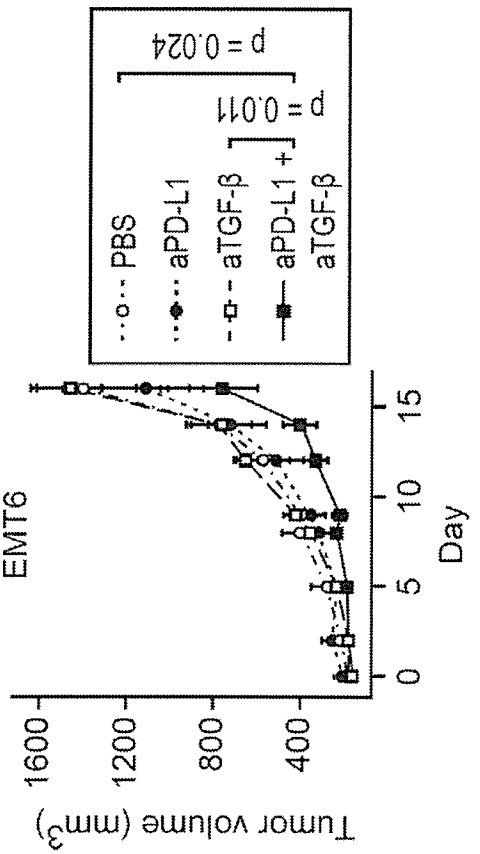


FIG. 7C

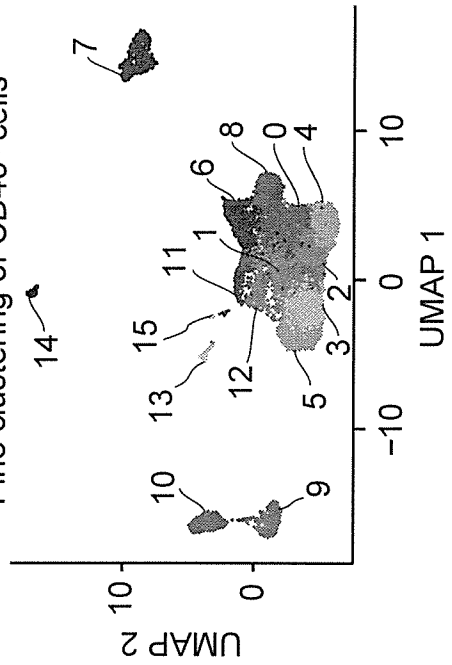


FIG. 7B

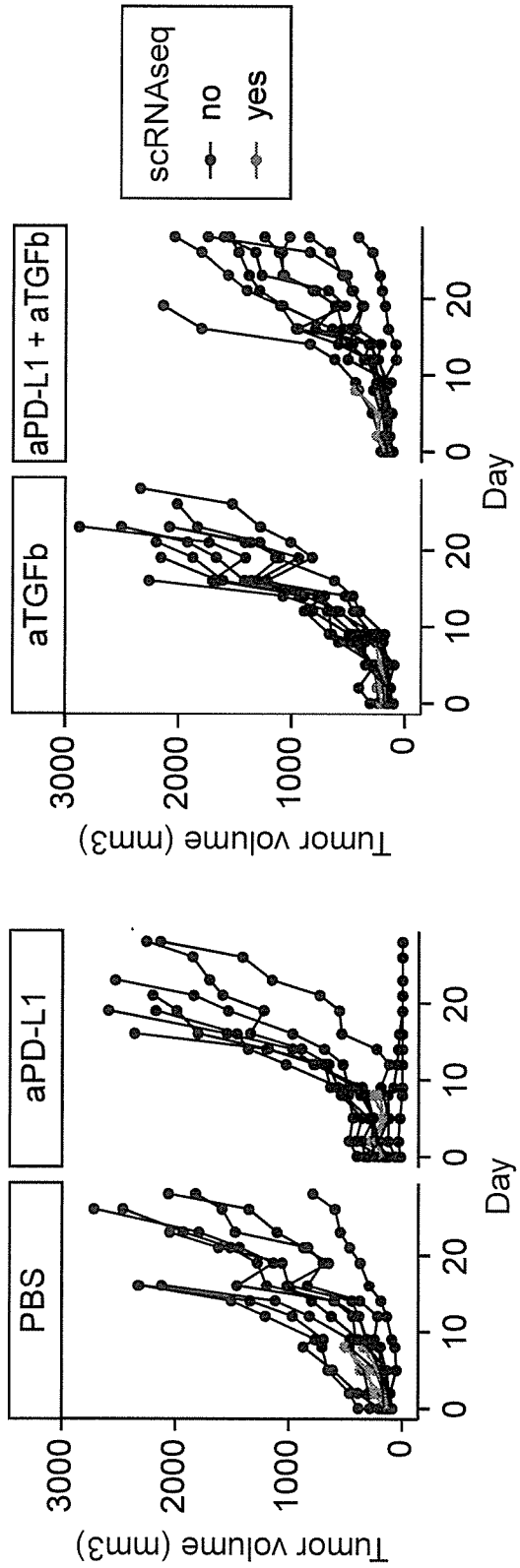


FIG. 7D

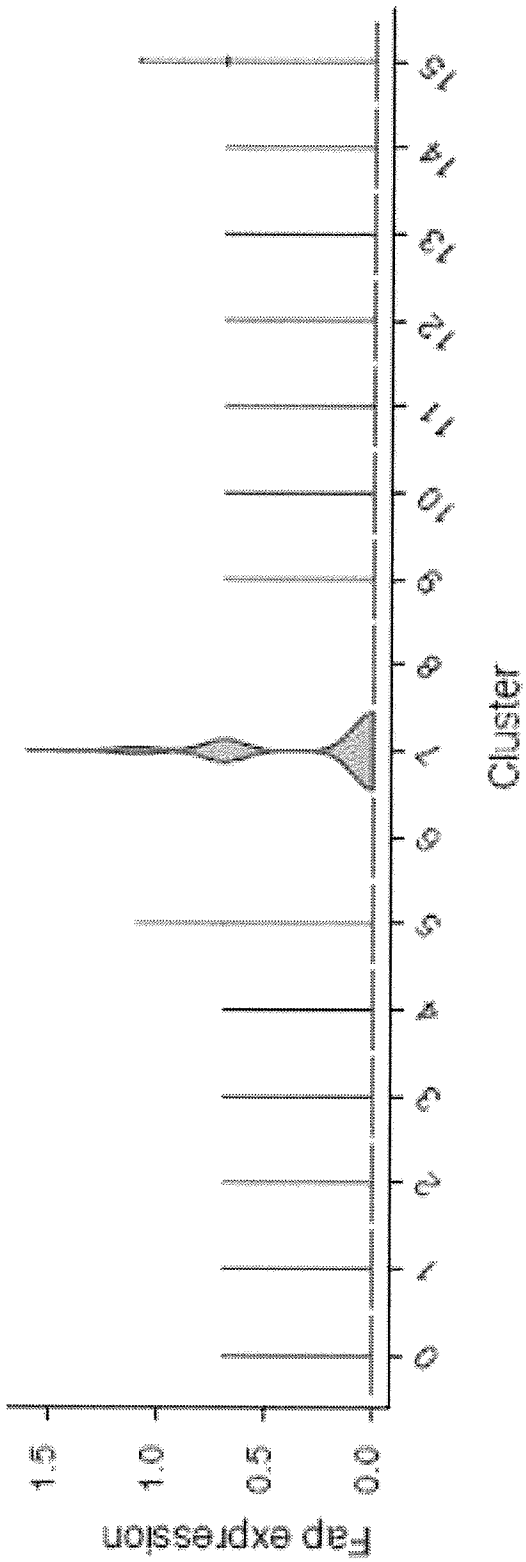

Fap expression
0.0
0.5
1.0
1.5
Cluster
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15

FIG. 7E

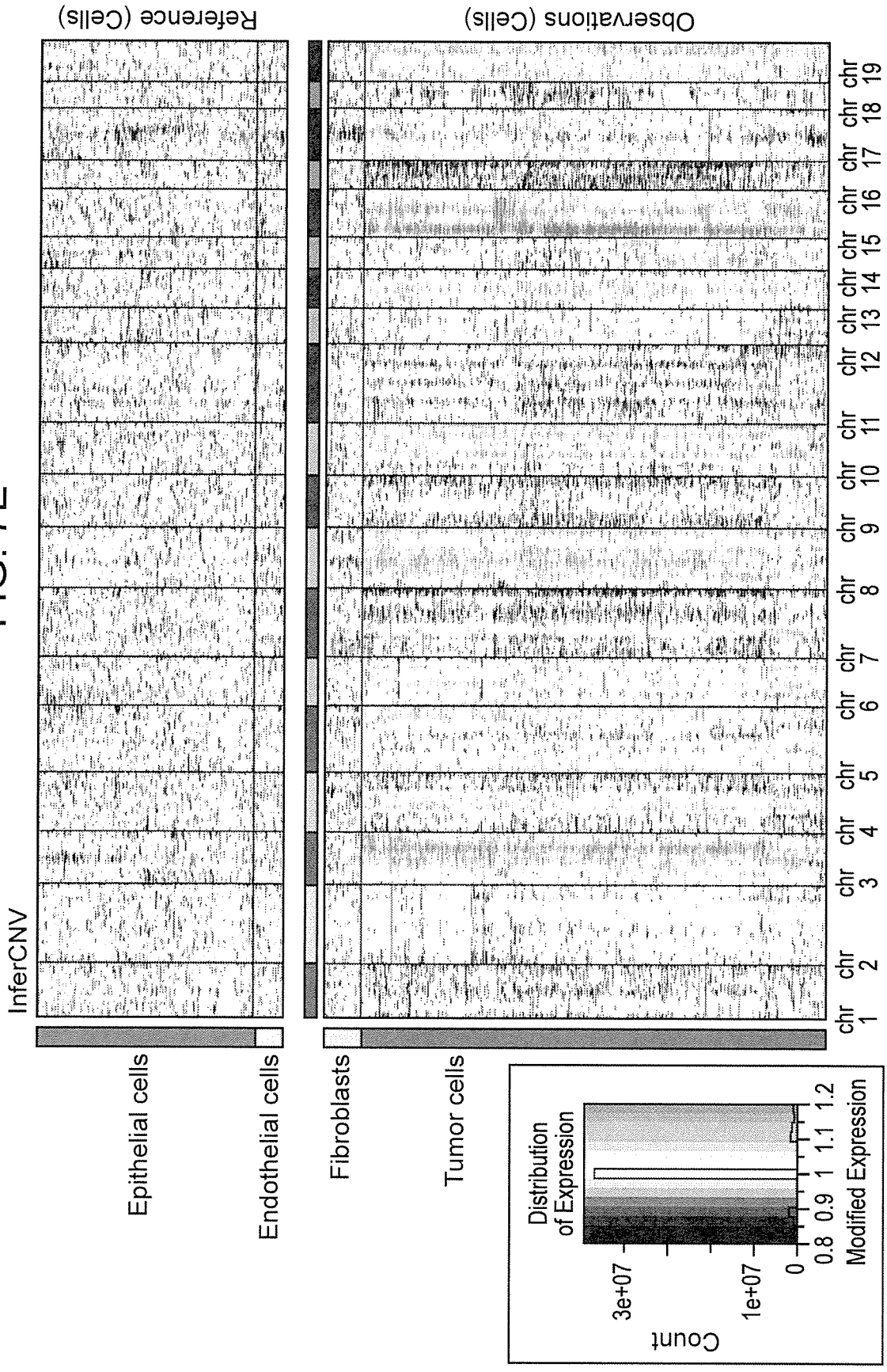

InferCNV
Reference (Cells)
Observations (Cells)
Epithelial cells
Endothelial cells
Fibroblasts
Tumor cells
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
chr 11
chr 12
chr 13
chr 14
chr 15
chr 16
chr 17
chr 18
chr 19
Genomic Region
Distribution of Expression
Count
3e+07
1e+07
0
0.8 0.9 1 1.1 1.2
Modified Expression

FIG. 7F

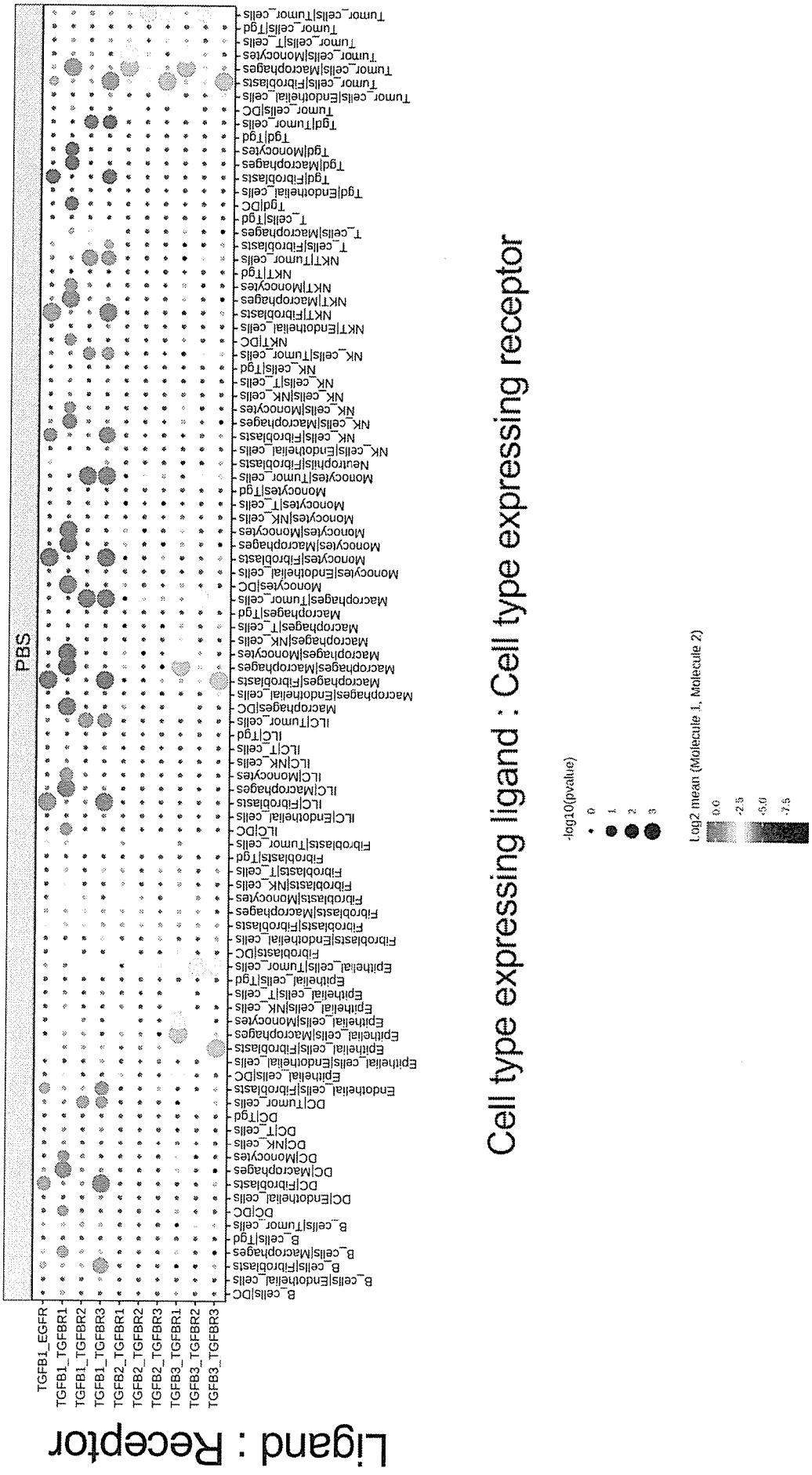

PBS
TGFB1_EGFR
TGFB1_TGFBR1
TGFB1_TGFBR2
TGFB1_TGFBR3
TGFB2_TGFBR1
TGFB2_TGFBR2
TGFB2_TGFBR3
TGFB3_TGFBR1
TGFB3_TGFBR2
TGFB3_TGFBR3
Ligand : Receptor
Cell type expressing ligand : Cell type expressing receptor
-log10(pvalue)
0
1
2
3
Log2 mean (Molecule 1, Molecule 2)
0.0
-2.5
-5.0
-7.5

FIG. 7F [ED) 24/41

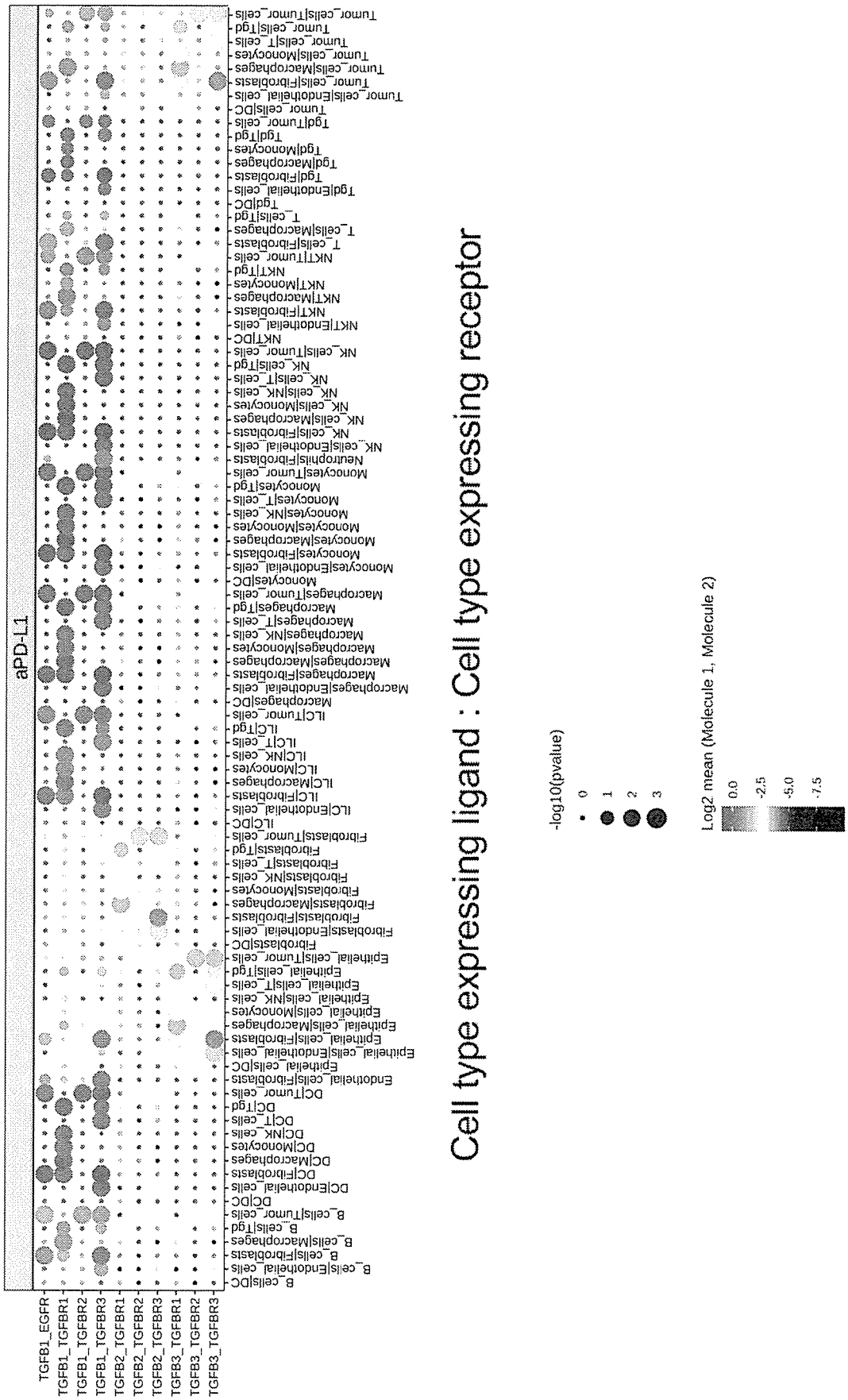


FIG. 7F (AMENDED) 24/41

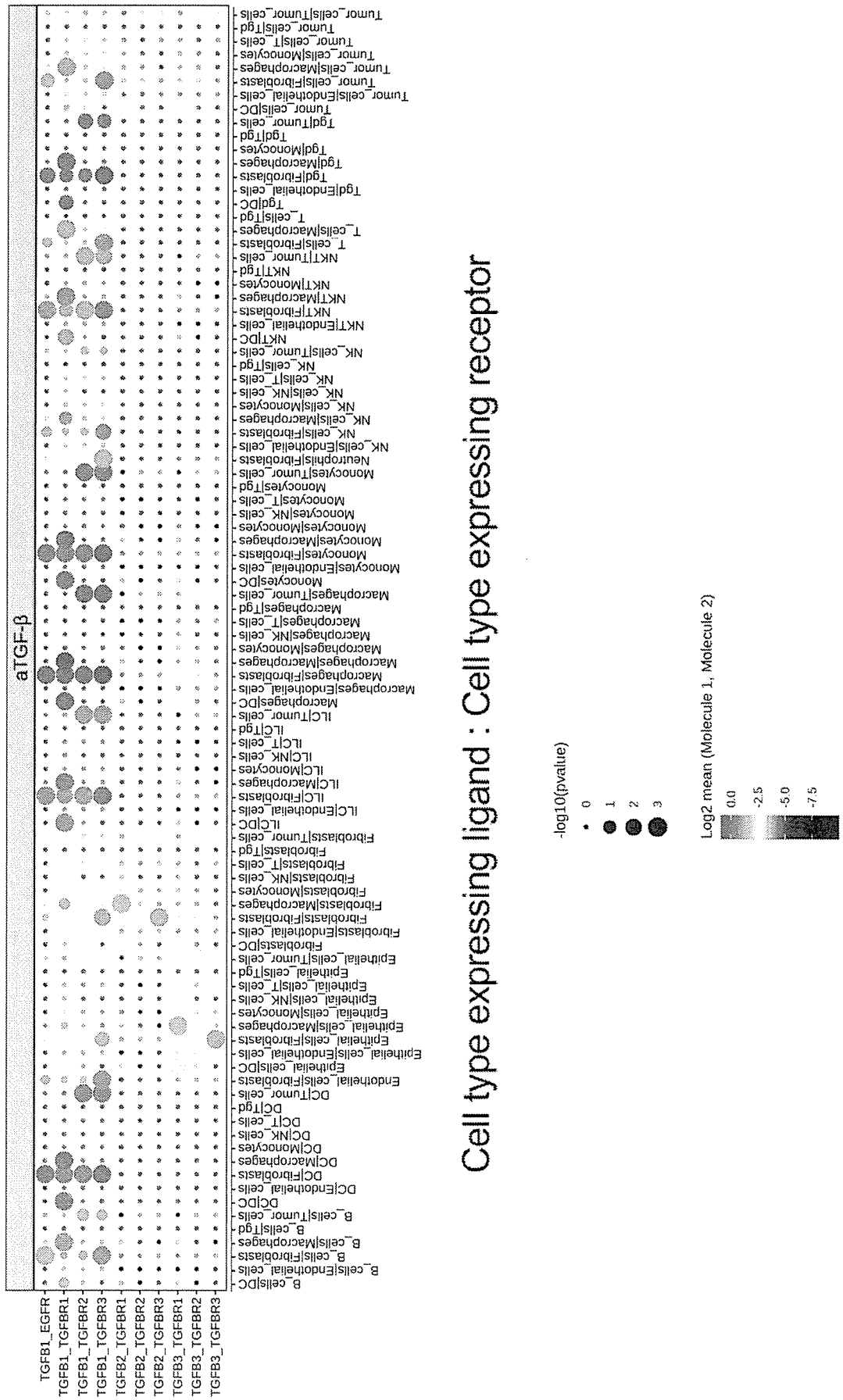


FIG. 7F ED) 24/41

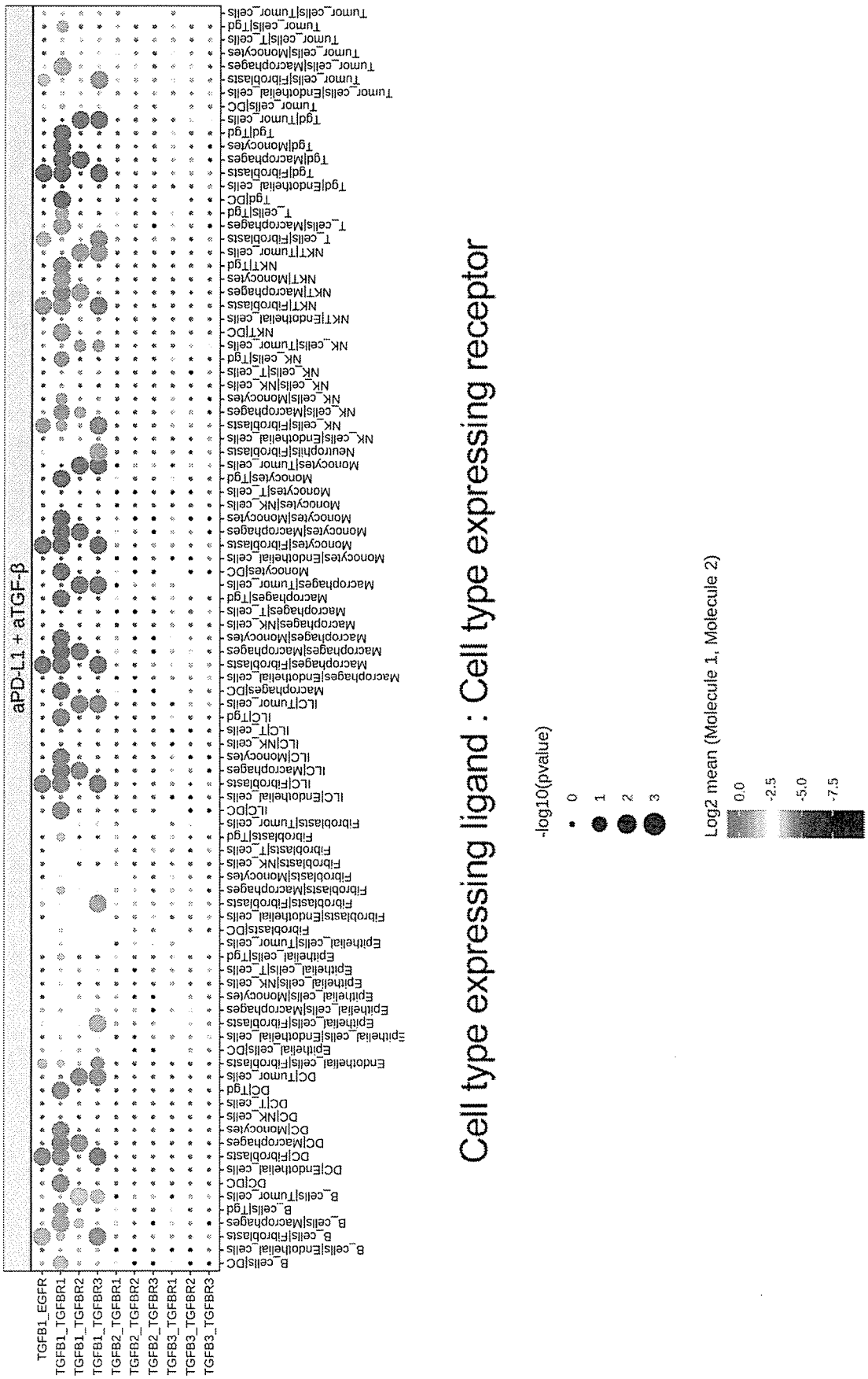


FIG. 7G

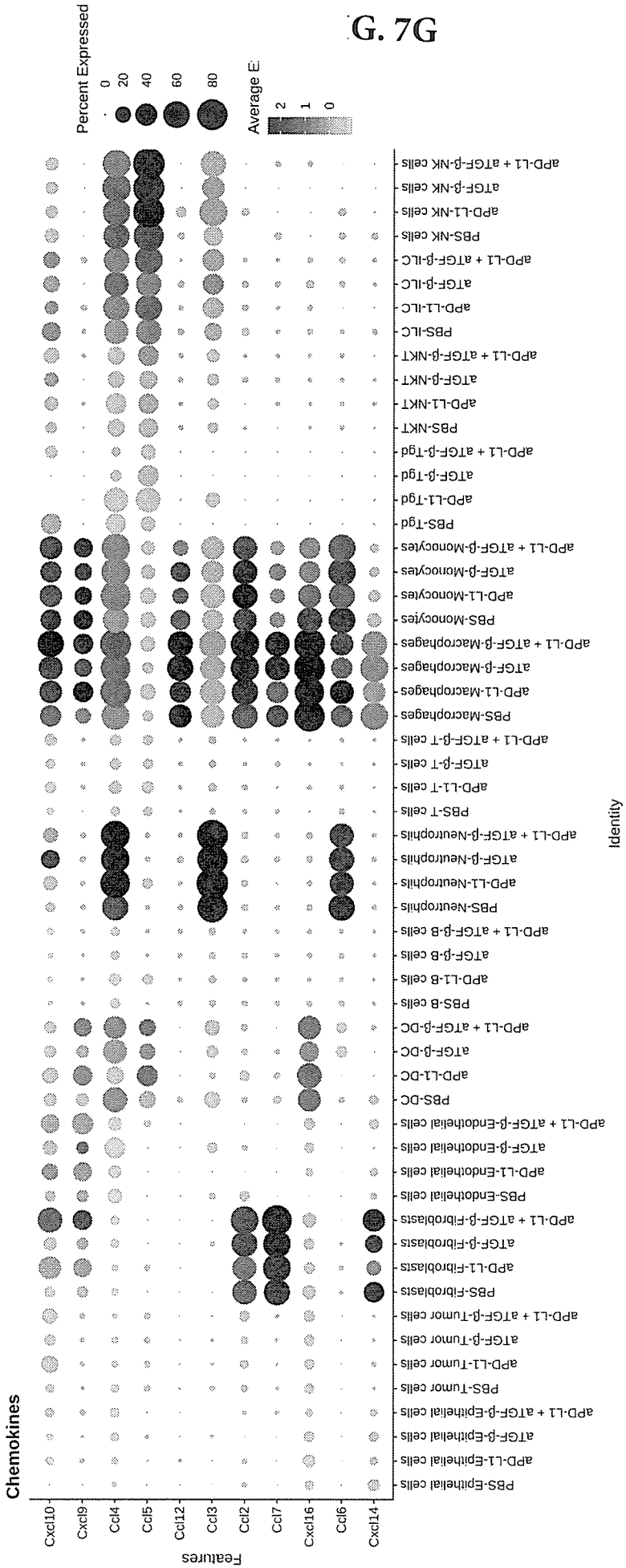

Chemokines
Features
Cxcl10
Cxcl9
Ccl4
Ccl5
Ccl12
Ccl3
Ccl2
Ccl7
Cxcl16
Ccl6
Cxcl14
Identity
PBS-Epithelial cells
aPD-L1-Epithelial cells
aTGF-β-Epithelial cells
aPD-L1 + aTGF-β-Epithelial cells
PBS-Tumor cells
aPD-L1-Tumor cells
aTGF-β-Tumor cells
aPD-L1 + aTGF-β-Tumor cells
PBS-Fibroblasts
aPD-L1-Fibroblasts
aTGF-β-Fibroblasts
aPD-L1 + aTGF-β-Fibroblasts
PBS-Endothelial cells
aPD-L1-Endothelial cells
aTGF-β-Endothelial cells
aPD-L1 + aTGF-β-Endothelial cells
PBS-DC
aPD-L1-DC
aTGF-β-DC
aPD-L1 + aTGF-β-DC
PBS-B cells
aPD-L1-B cells
aTGF-β-B cells
aPD-L1 + aTGF-β-B cells
PBS-Neutrophils
aPD-L1-Neutrophils
aTGF-β-Neutrophils
aPD-L1 + aTGF-β-Neutrophils
PBS-T cells
aPD-L1-T cells
aTGF-β-T cells
aPD-L1 + aTGF-β-T cells
PBS-Macrophages
aPD-L1-Macrophages
aTGF-β-Macrophages
aPD-L1 + aTGF-β-Macrophages
PBS-Monocytes
aPD-L1-Monocytes
aTGF-β-Monocytes
aPD-L1 + aTGF-β-Monocytes
PBS-Tgd
aPD-L1-Tgd
aTGF-β-Tgd
aPD-L1 + aTGF-β-Tgd
PBS-NKT
aPD-L1-NKT
aTGF-β-NKT
aPD-L1 + aTGF-β-NKT
PBS-ILC
aPD-L1-ILC
aTGF-β-ILC
aPD-L1 + aTGF-β-ILC
PBS-NK cells
aPD-L1-NK cells
aTGF-β-NK cells
aPD-L1 + aTGF-β-NK cells
Percent Expressed
0
20
40
60
80
Average E
2
1
0

FIG. 7H

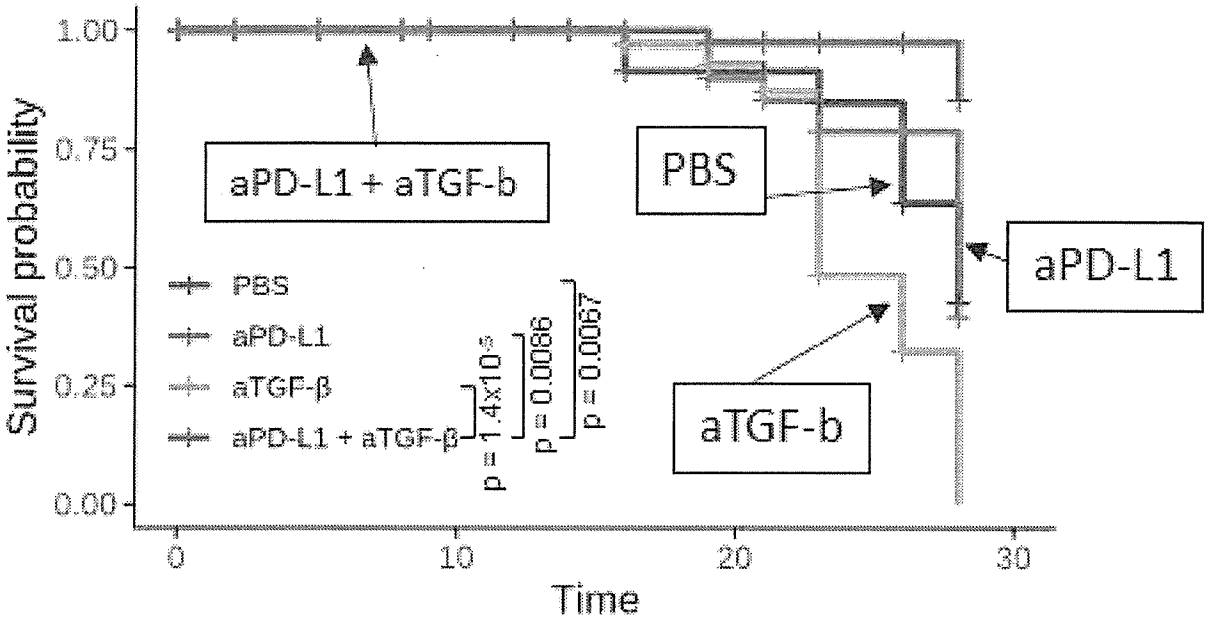

1.00
0.75
0.50
0.25
0.00
Survival probability
0
10
20
30
Time
PBS
aPD-L1
aTGF-β
aPD-L1 + aTGF-β
p = 1.4x10⁻⁵
p = 0.0086
p = 0.0067
aPD-L1 + aTGF-b
PBS
aPD-L1
aTGF-b

FIG. 7I

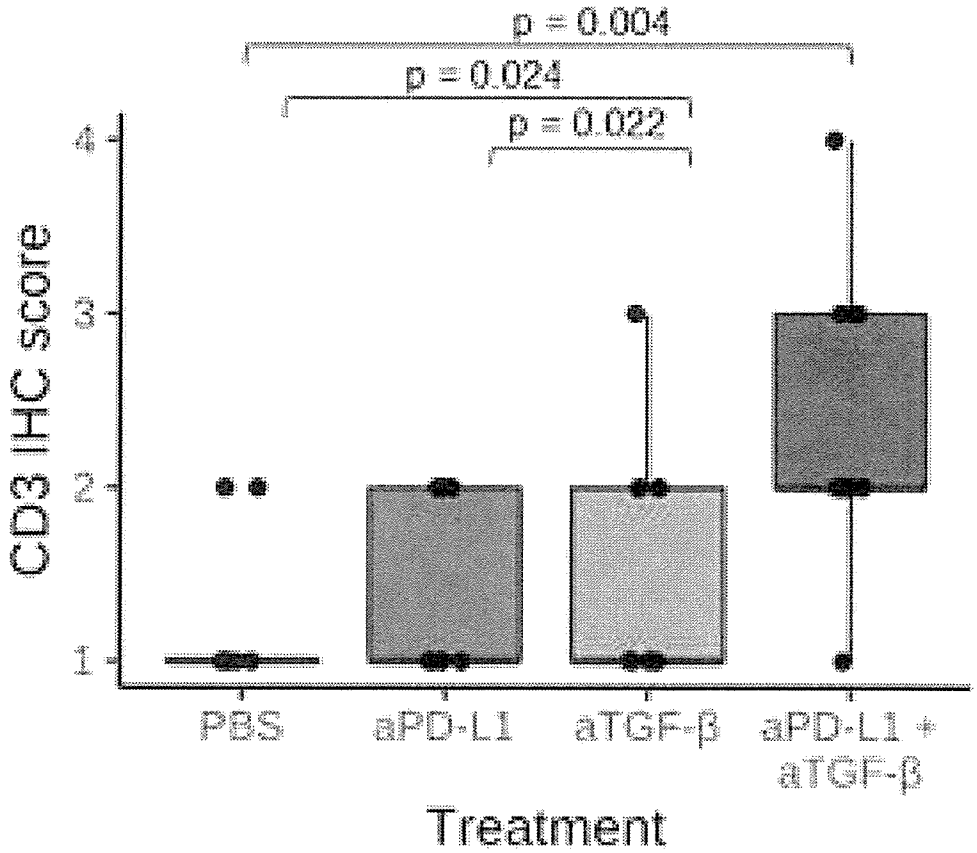

p = 0.004
p = 0.024
p = 0.022
CD3 IHC score
4
3
2
1
PBS
aPD-L1
aTGF-β
aPD-L1 + aTGF-β
Treatment

FIG. 8A

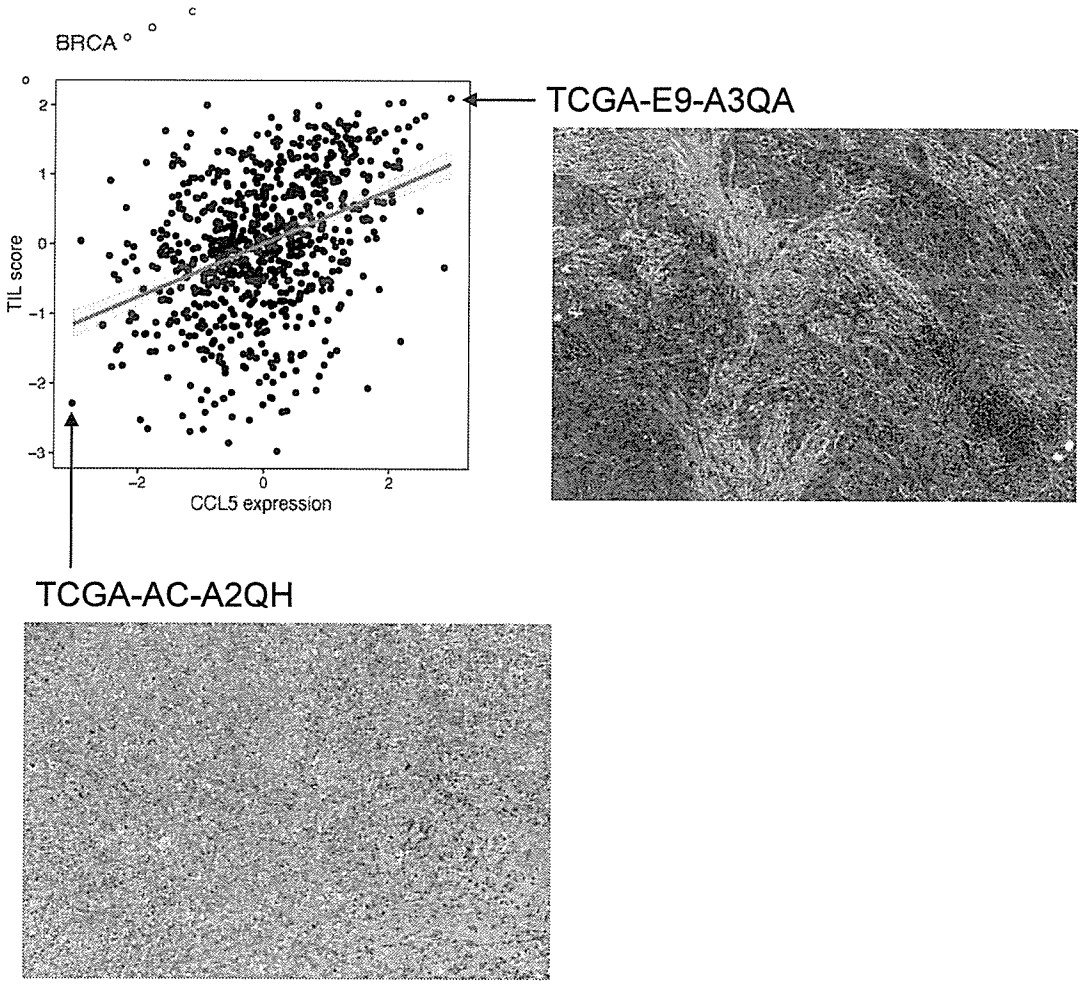


FIG. 8B

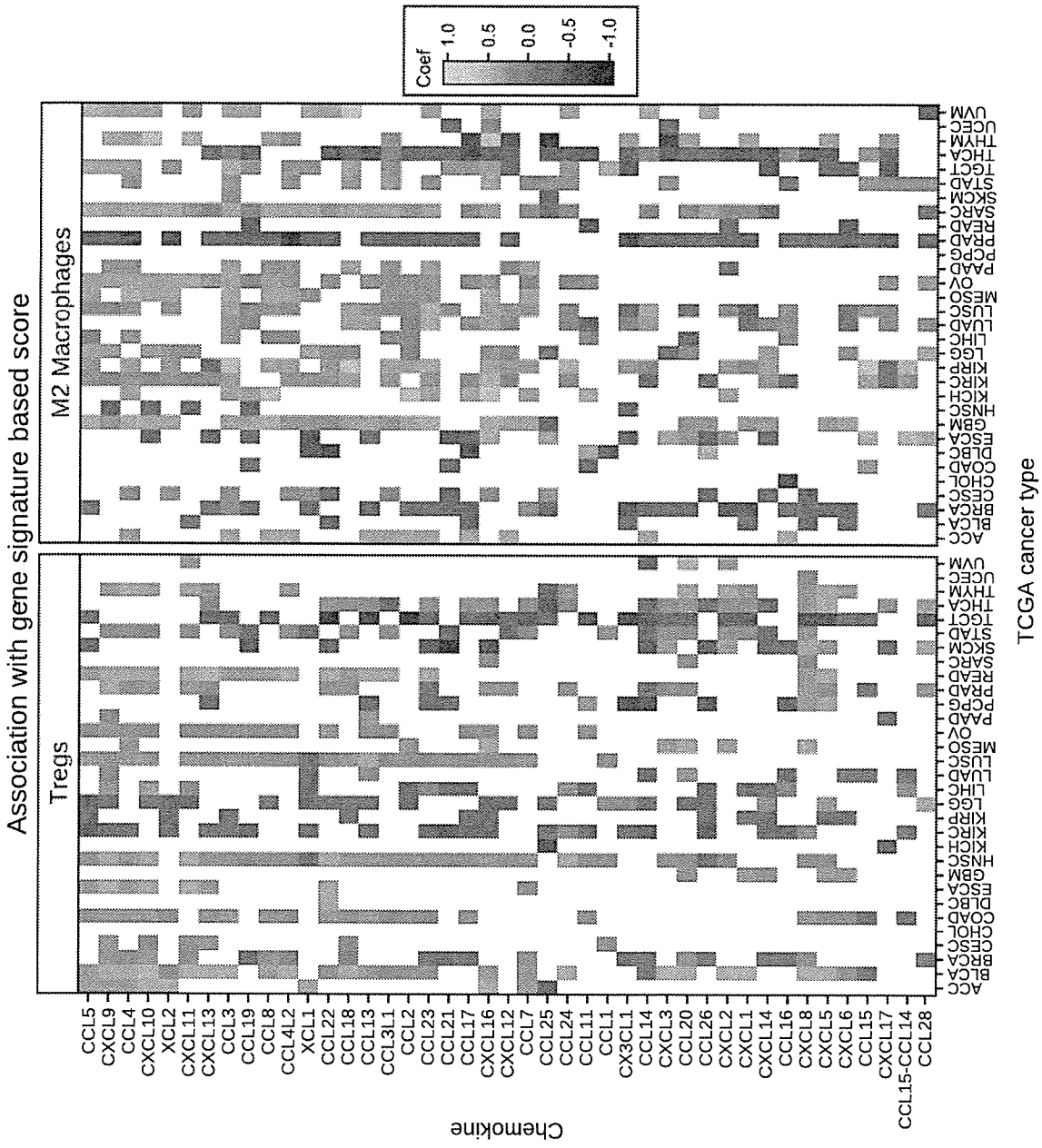

Association with gene signature based score
Tregs
M2 Macrophages
Coef
1.0
0.5
0.0
-0.5
-1.0
Chemokine
CCL5
CXCL9
CCL4
CXCL10
XCL2
CXCL11
CXCL13
CCL3
CCL19
CCL8
CCL4L2
XCL1
CCL22
CCL18
CCL13
CCL3L1
CCL2
CCL23
CCL21
CCL17
CXCL16
CXCL12
CCL7
CCL25
CCL24
CCL11
CCL1
CX3CL1
CCL14
CXCL3
CCL20
CCL26
CXCL2
CXCL1
CXCL14
CCL16
CXCL8
CXCL5
CXCL6
CCL15
CXCL17
CCL15-CCL14
CCL28
ACC
BLCA
BRCA
CESC
CHOL
COAD
DLBC
ESCA
GBM
HNSC
KICH
KIRC
KIRP
LGG
LIHC
LUAD
LUSC
MESO
OV
PAAD
PCPG
PRAD
READ
SARC
SKCM
STAD
TGCT
THCA
THYM
UCEC
UVM
TCGA cancer type

FIG. 9A

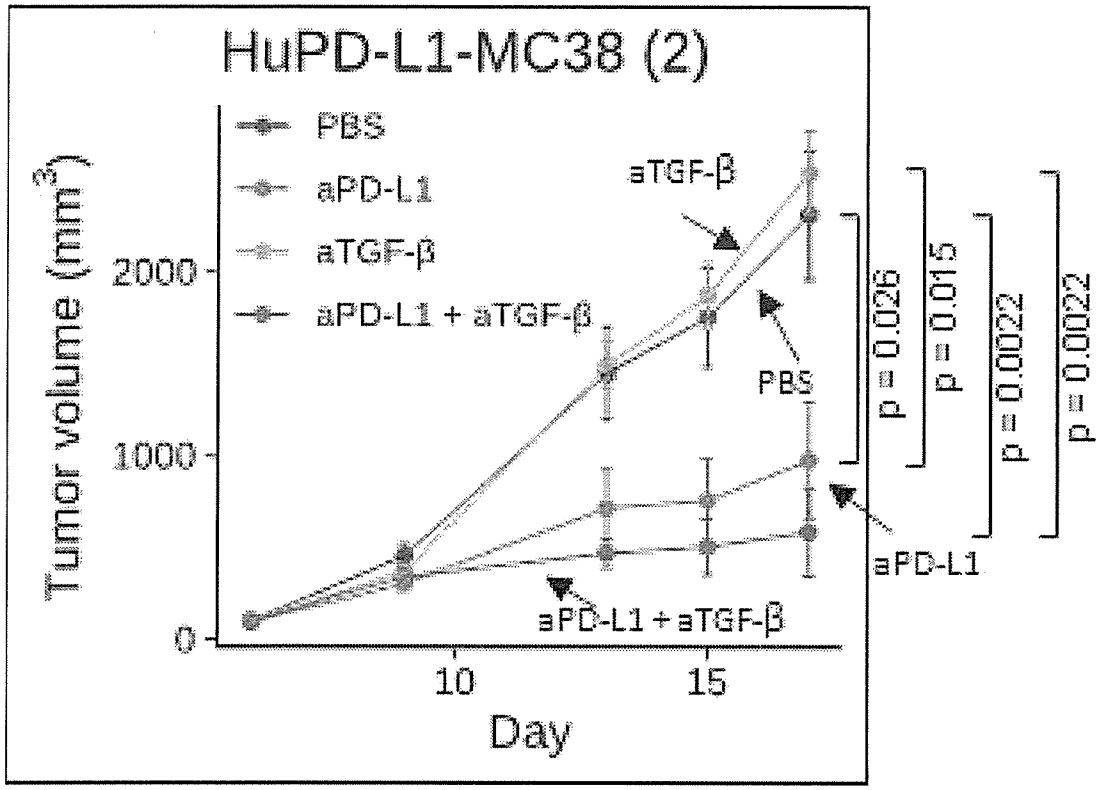
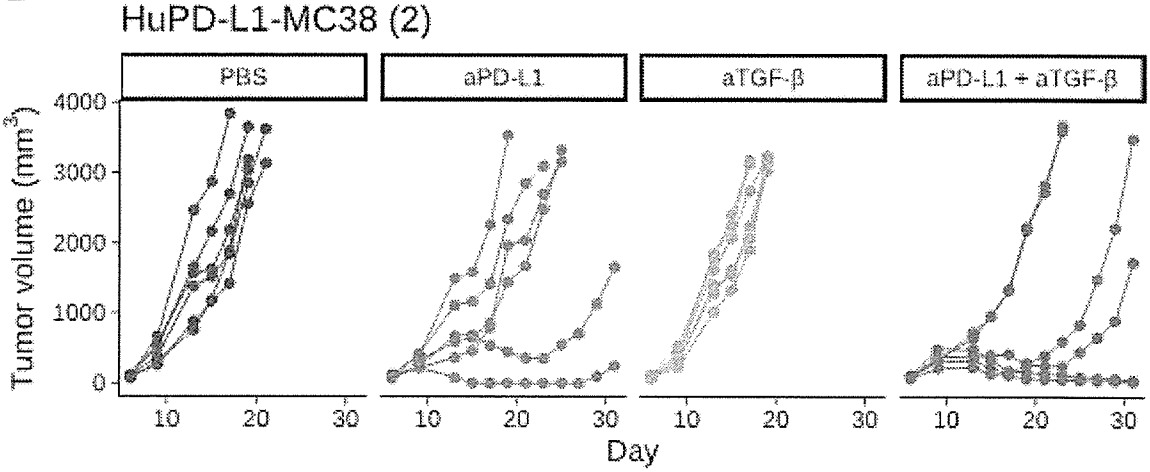

HuPD-L1-MC38 (2)
PBS
aPD-L1
aTGF-β
aPD-L1 + aTGF-β
Tumor volume (mm3)
2000
1000
0
10
15
Day
aTGF-β
PBS
aPD-L1
aPD-L1 + aTGF-β
p = 0.026
p = 0.015
p = 0.0022
p = 0.0022

FIG. 9B


HuPD-L1-MC38 (2)
PBS
aPD-L1
aTGF-β
aPD-L1 + aTGF-β
Tumor volume (mm3)
4000
3000
2000
1000
0
10
20
30
Day

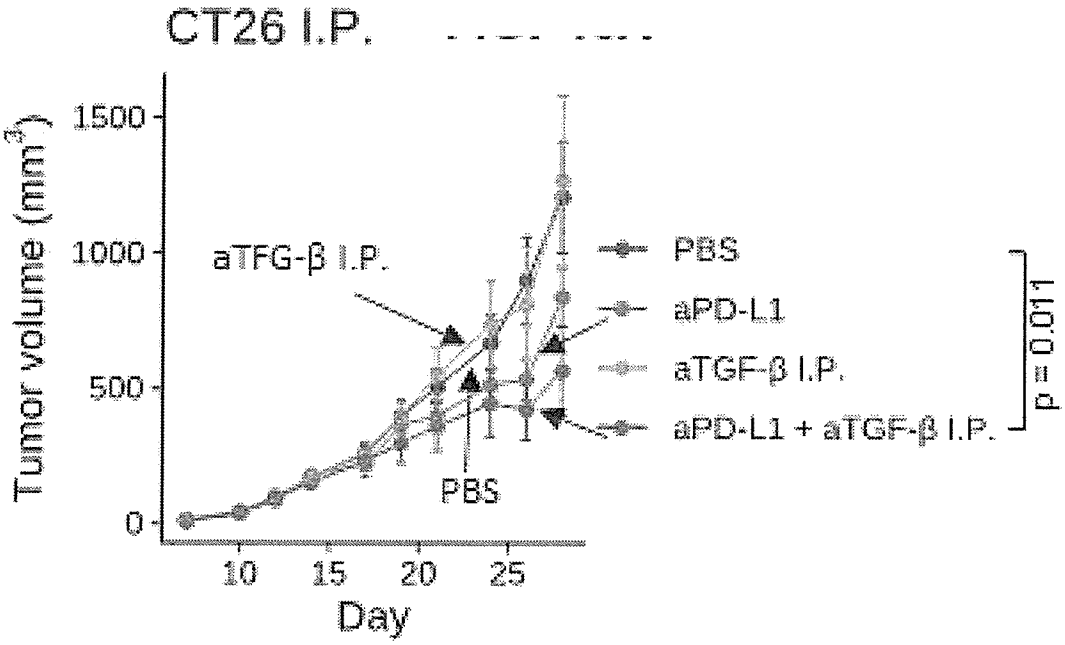

CT26 I.P.
Tumor volume (mm3)
1500
1000
500
0
aTFG-β I.P.
PBS
10
15
20
25
Day
PBS
aPD-L1
aTGF-β I.P.
aPD-L1 + aTGF-β I.P.
p = 0.011

FIG. 10B

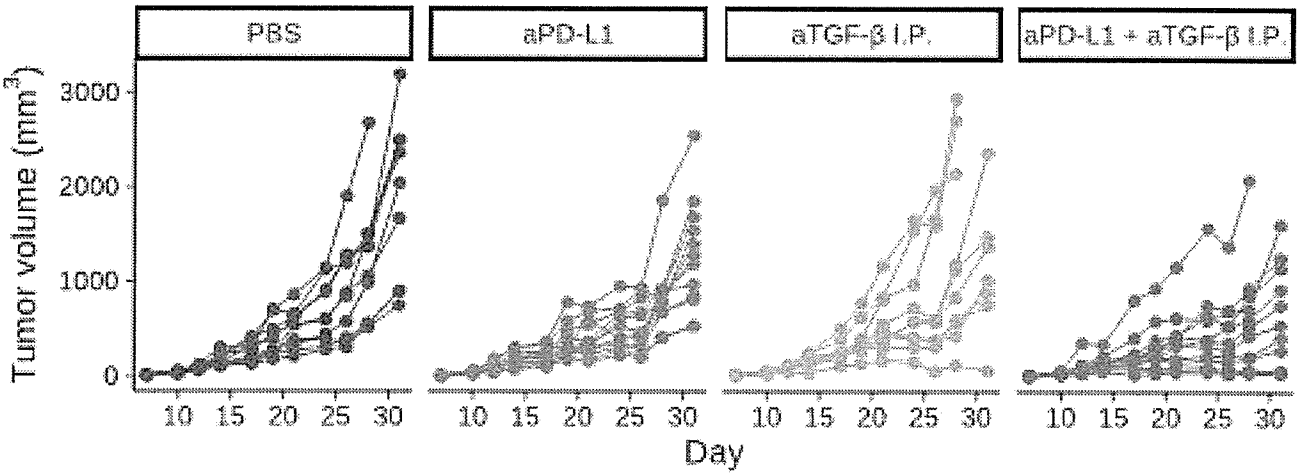

CT26 I.P.
PBS
aPD-L1
aTGF-β I.P.
aPD-L1 + aTGF-β I.P.
Tumor volume (mm3)
3000
2000
1000
0
10
15
20
25
30
Day

FIG. 10C

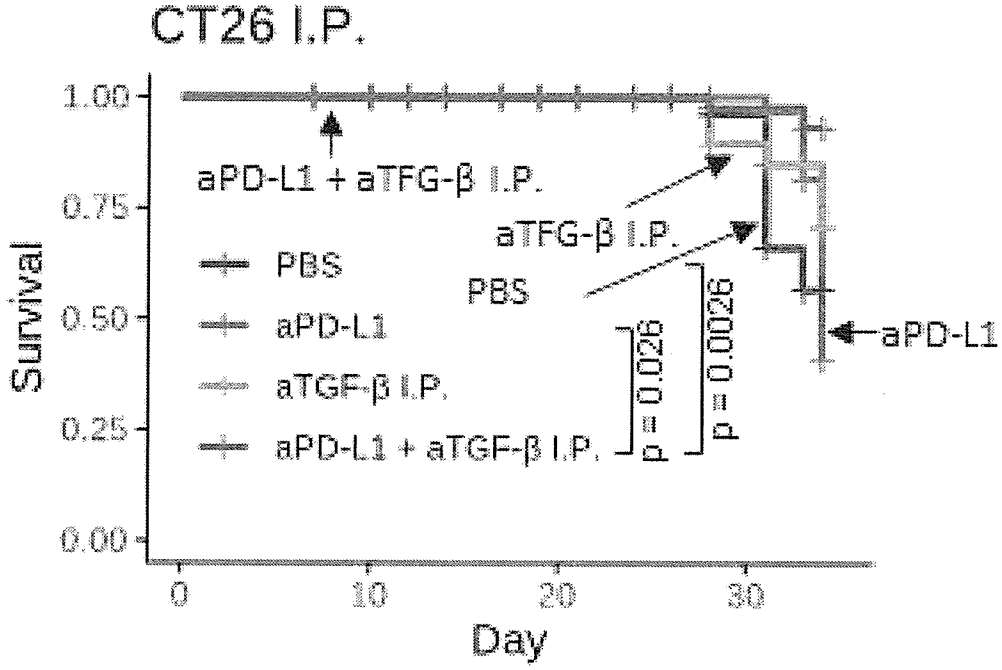

CT26 I.P.
1.00
0.75
0.50
0.25
0.00
Survival
0
10
20
30
Day
aPD-L1 + aTFG-β I.P.
aTFG-β I.P.
PBS
PBS
aPD-L1
aTGF-β I.P.
aPD-L1 + aTGF-β I.P.
p = 0.026
p = 0.0026
aPD-L1

FIG. 10D

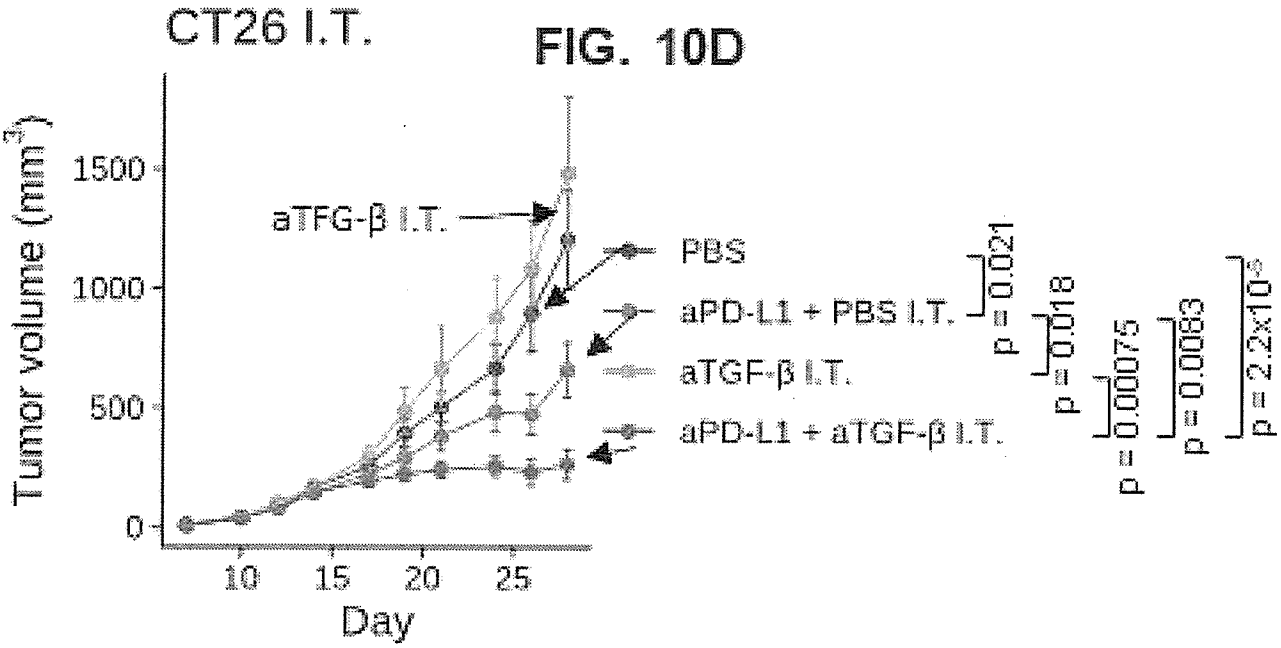


FIG. 10E

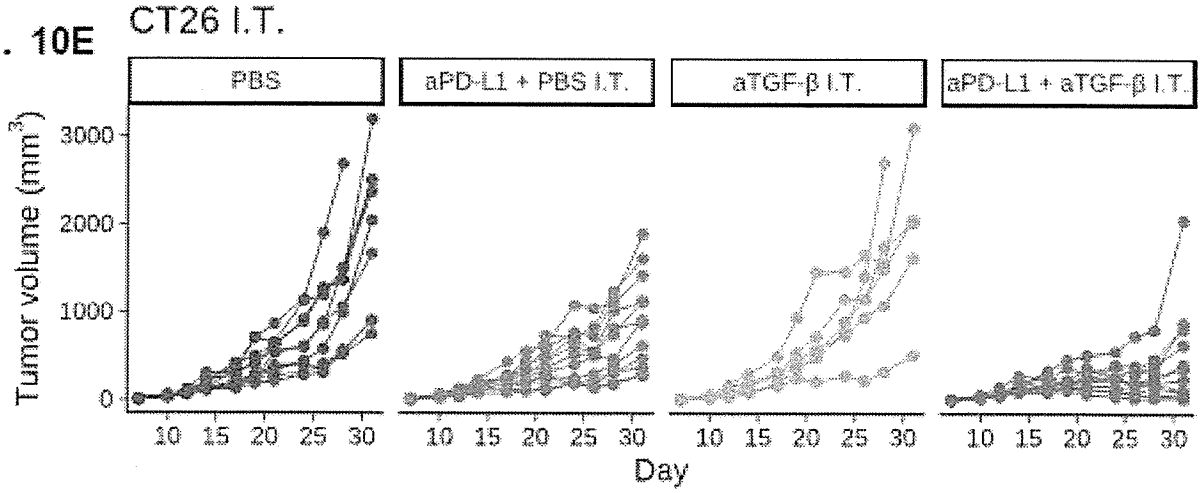


FIG. 10F

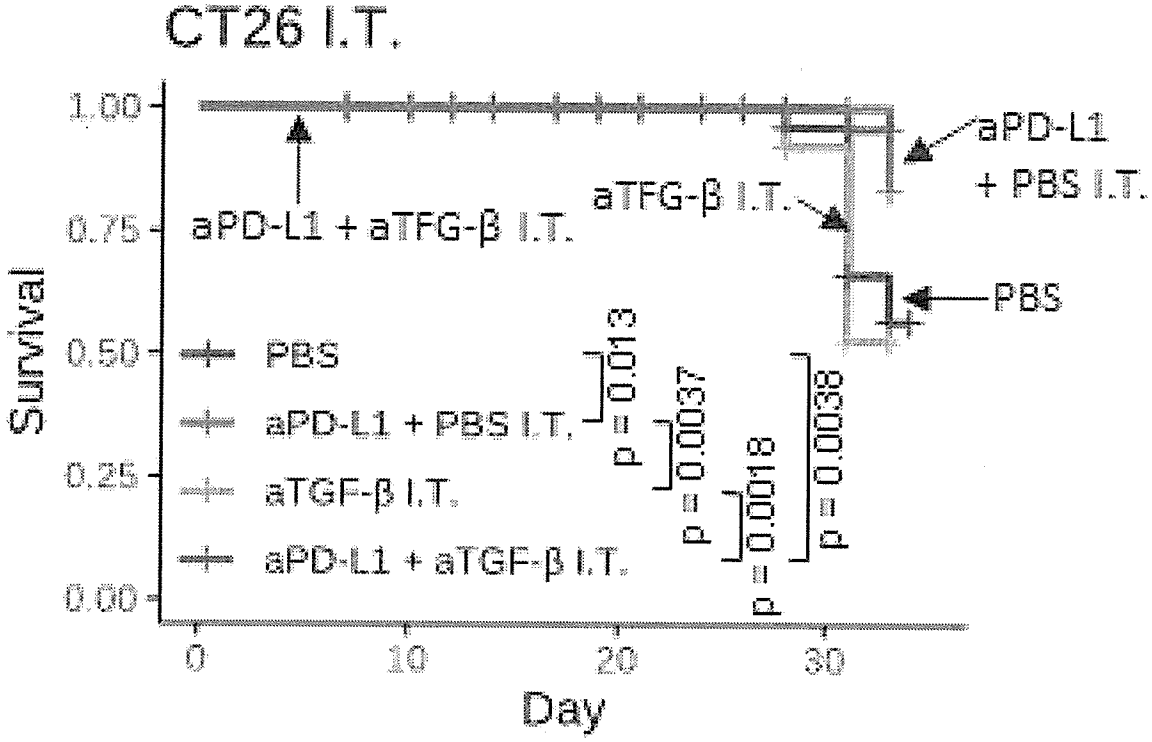

CT26 I.T.
Survival
1.00
0.75
0.50
0.25
0.00
0
10
20
30
Day
aPD-L1 + aTFG-β I.T.
aTFG-β I.T.
aPD-L1 + PBS I.T.
PBS
PBS
aPD-L1 + PBS I.T.
aTGF-β I.T.
aPD-L1 + aTGF-β I.T.
p = 0.013
p = 0.0037
p = 0.0018
p = 0.0038

FIG. 11A

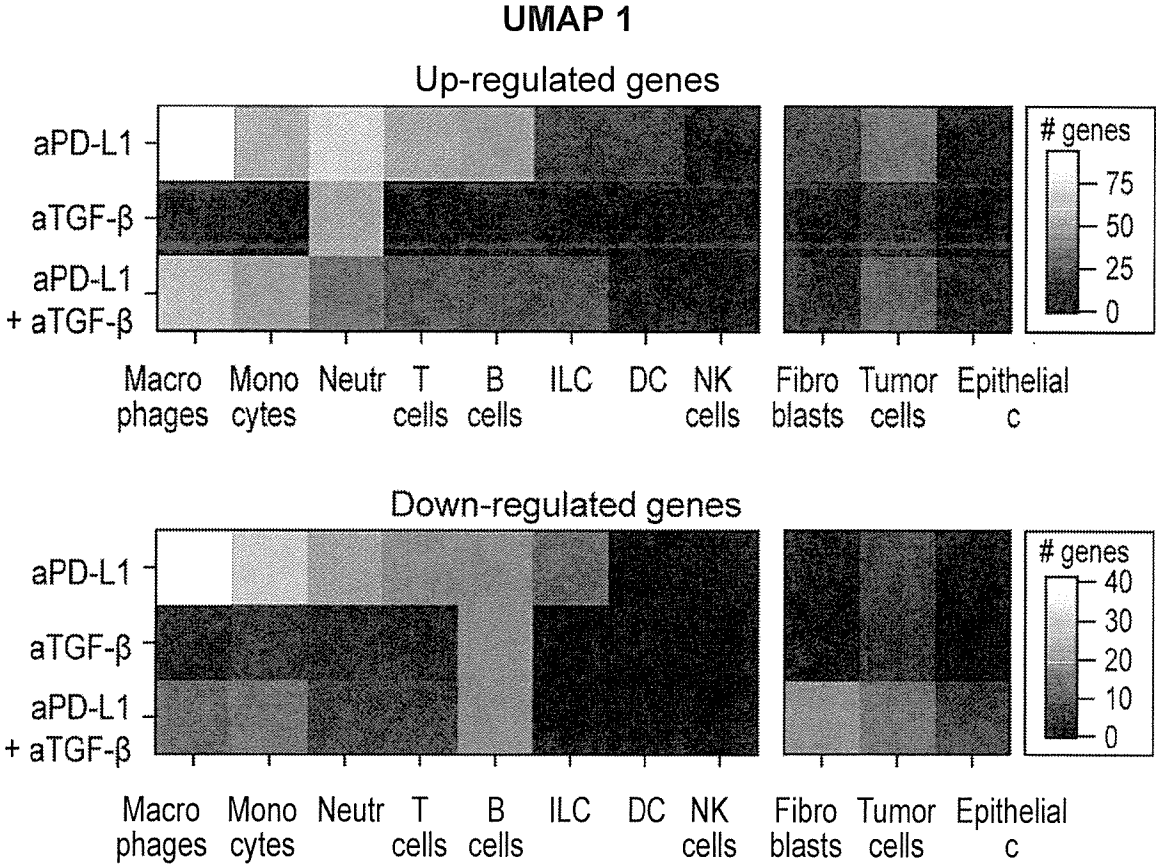


FIG. 11B

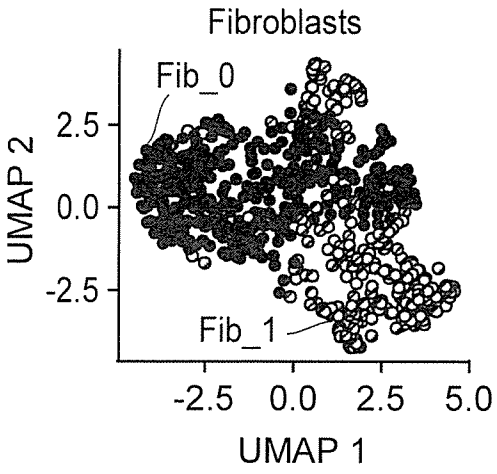


FIG. 11C

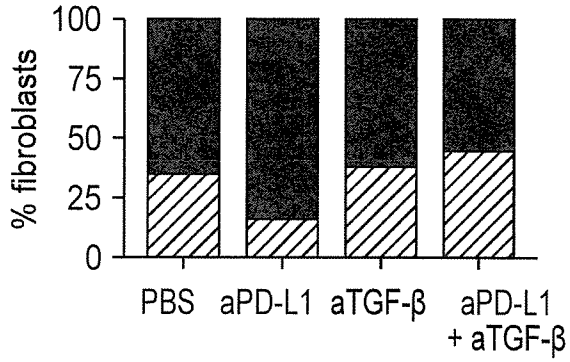


FIG. 11D

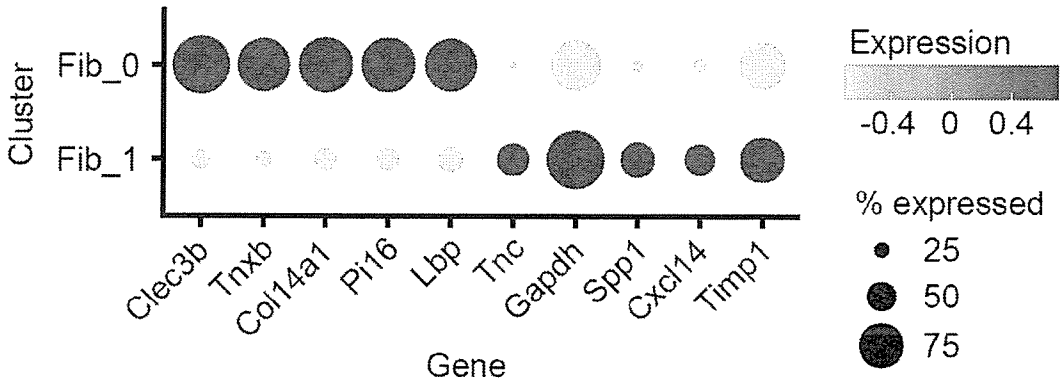


FIG. 11E

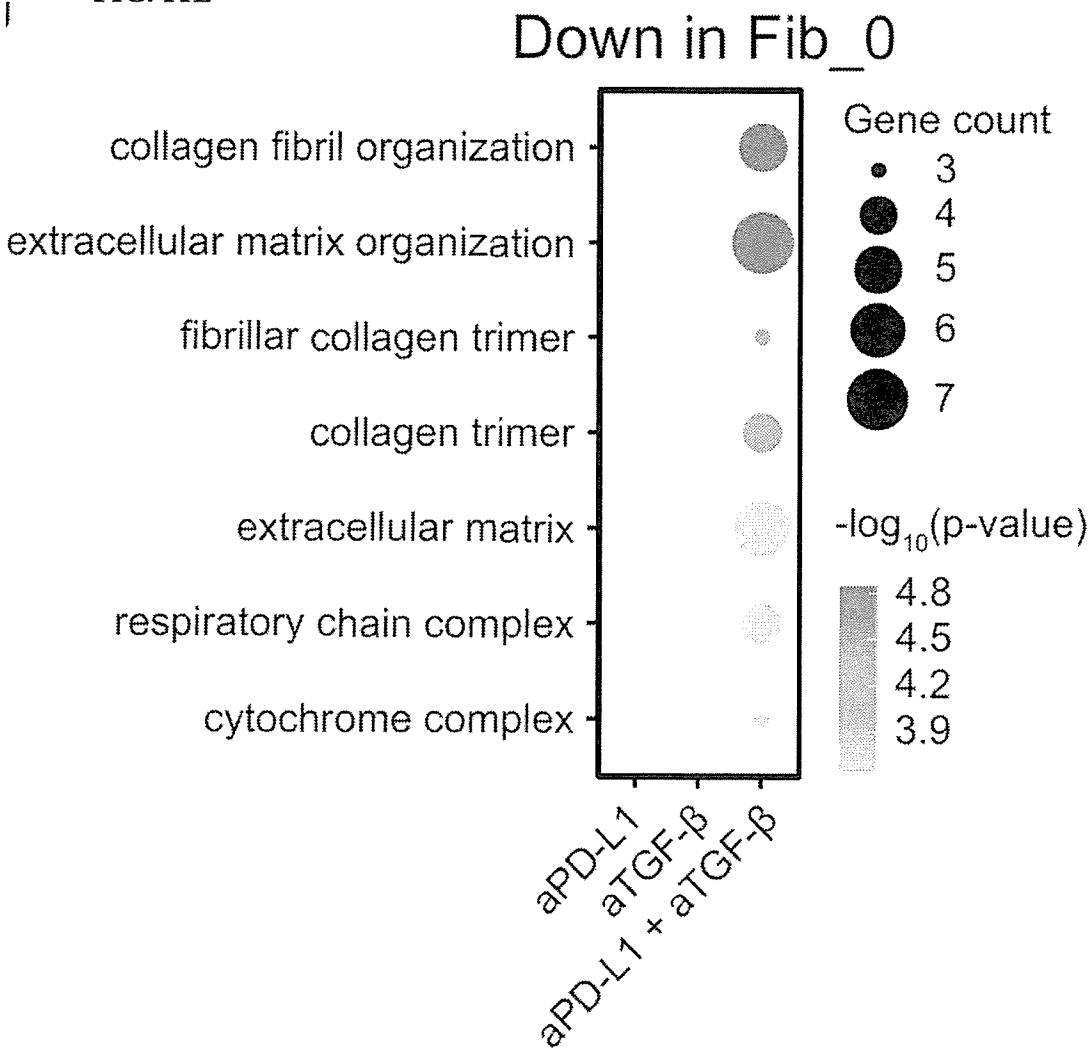


FIG. 11F

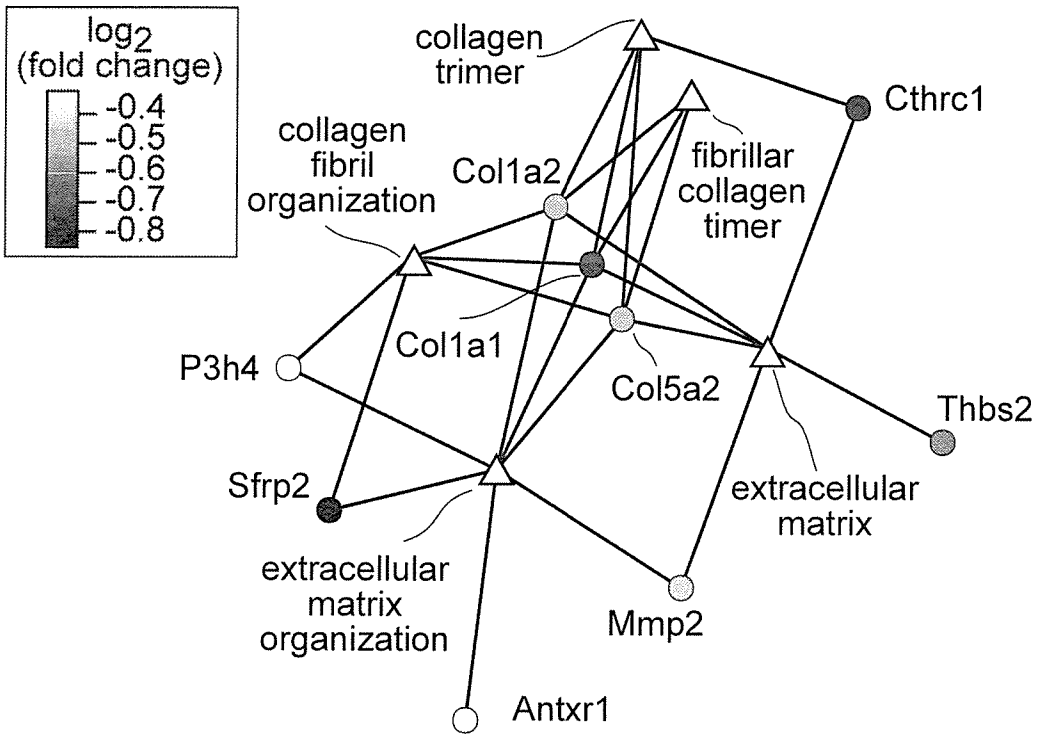


FIG. 11G

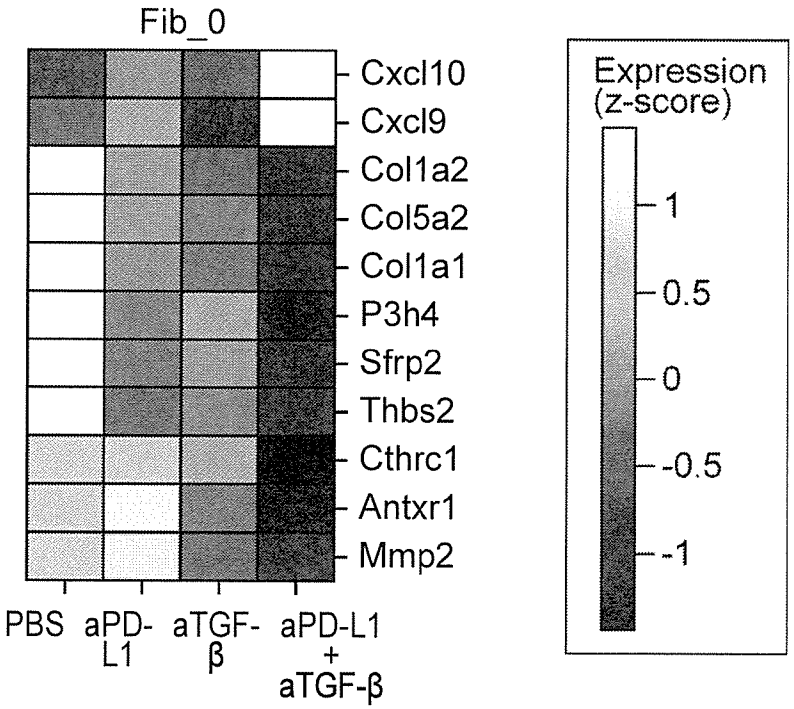


FIG. 12A

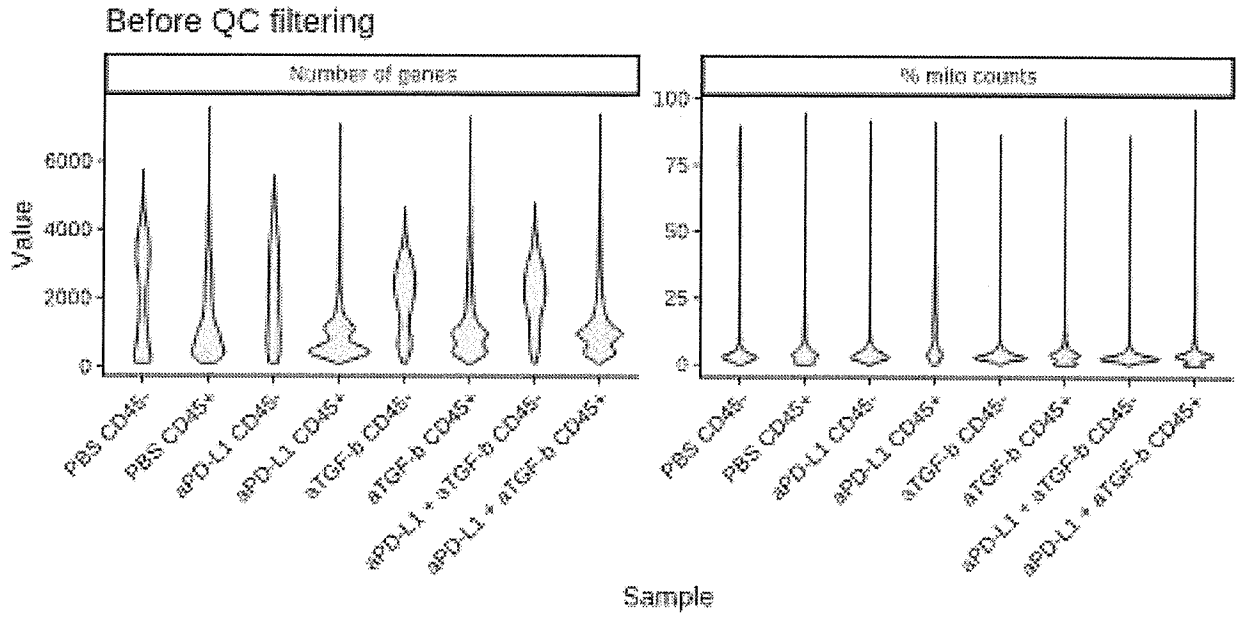


FIG. 12B

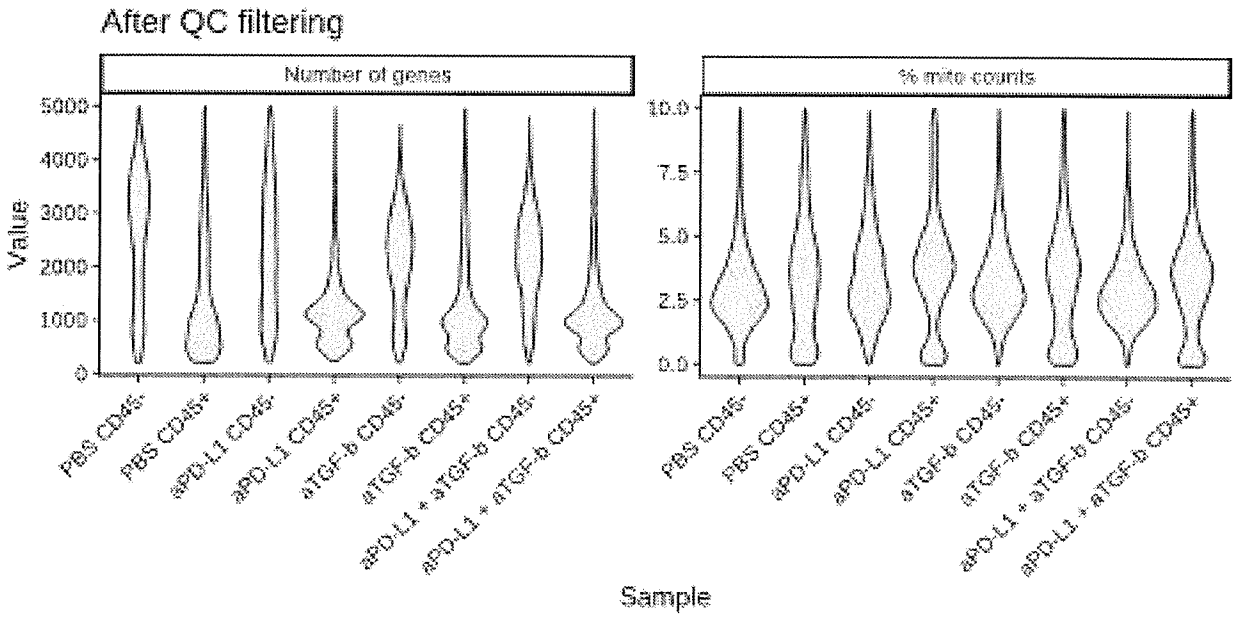


FIG. 13A

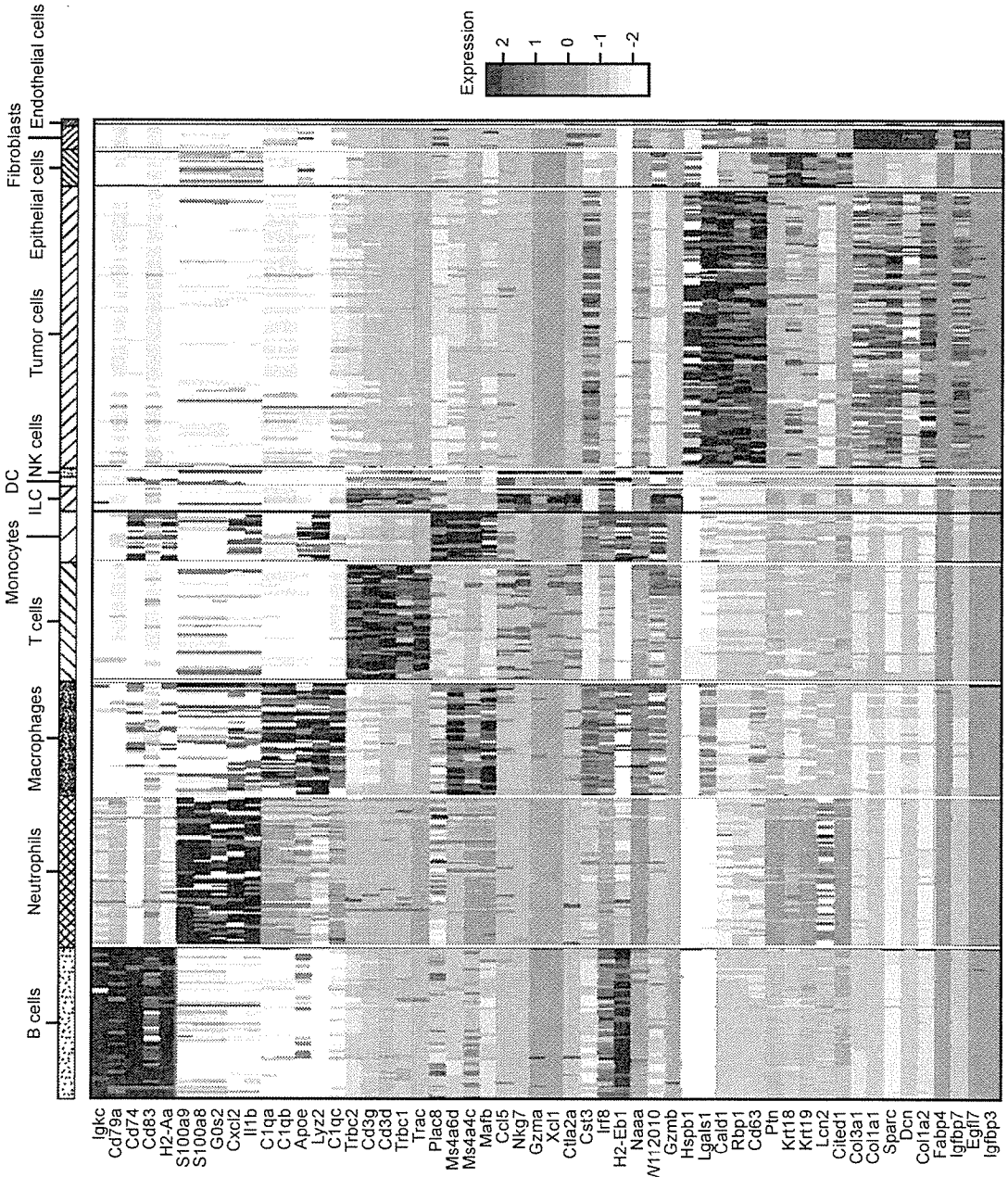

B cells
Neutrophils
Macrophages
T cells
Monocytes
ILC
DC
NK cells
Tumor cells
Epithelial cells
Fibroblasts
Endothelial cells
Expression
2
1
0
-1
-2
Igkc
Cd79a
Cd74
Cd83
H2-Aa
S100a9
S100a8
G0s2
Cxcl2
Il1b
C1qa
C1qb
Apoe
Lyz2
C1qc
Tnfrsf1b
Cd3g
Cd3d
Tnfrsf1b
Trac
Plac8
Ms4a6d
Ms4a4c
Maf
Ccl5
Nkg7
Gzma
Xcl1
Ctla2a
Cst3
Irf8
H2-Eb1
Naaa
AW112010
Gzmb
Hspb1
Lgals1
Cald1
Rbp1
Cd63
Ptn
Krt18
Krt19
Lcn2
Cited1
Col3a1
Col1a1
Sparc
Dcn
Col1a2
Fabp4
Igfbp7
Egfl7
Igfbp3

FIG. 13B

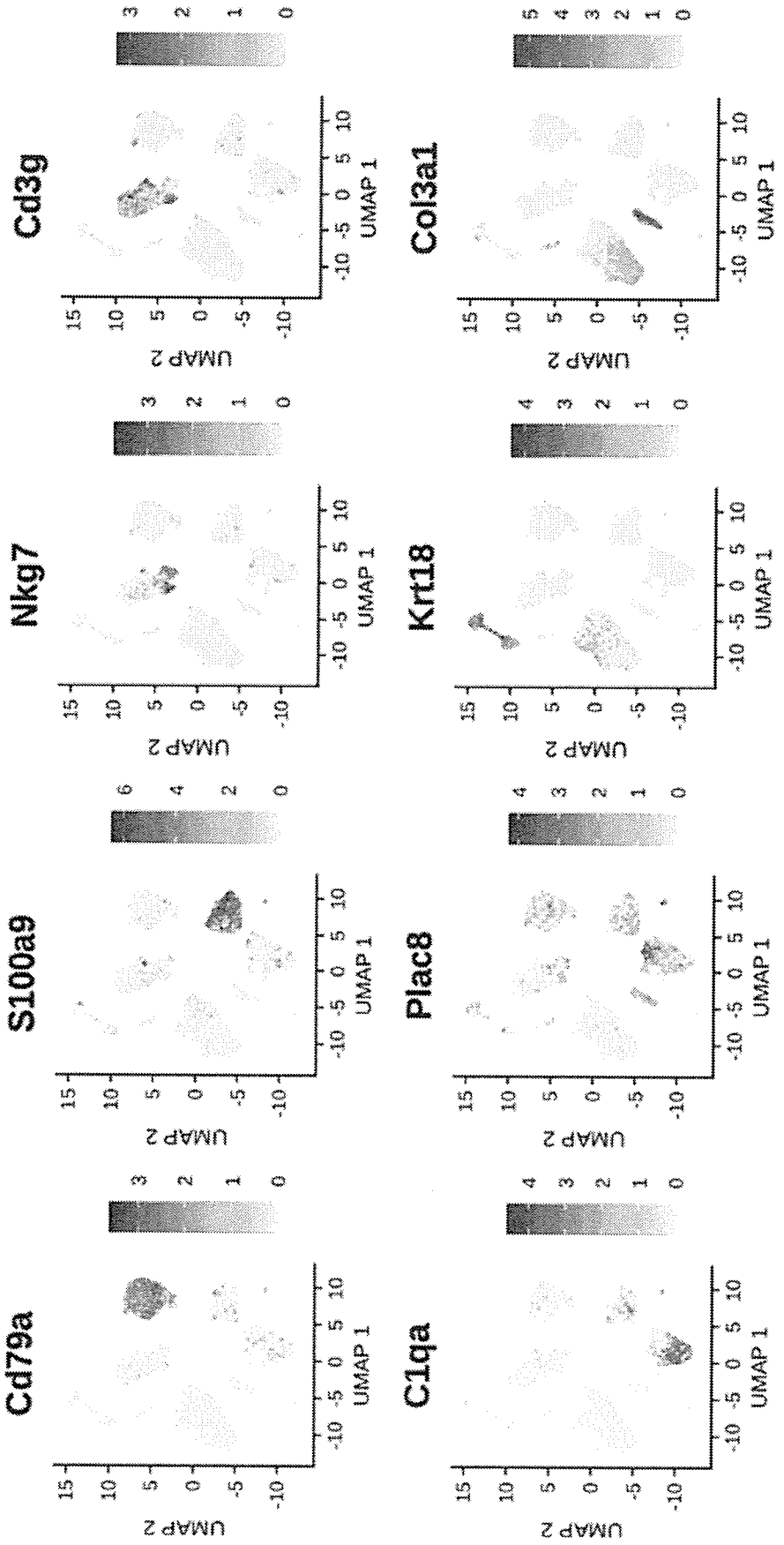


FIG. 13B (CONTINUED)

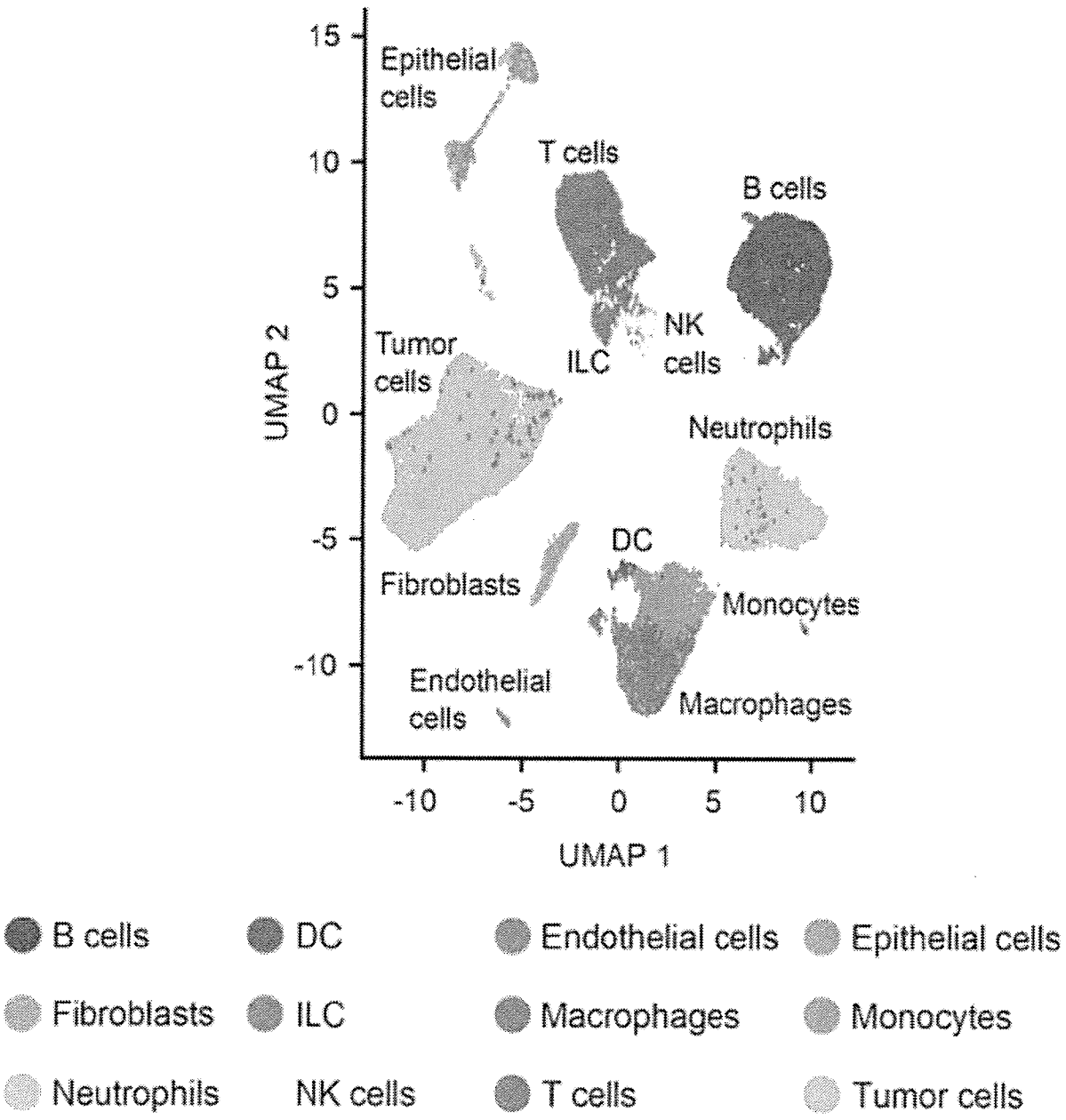


FIG. 14A

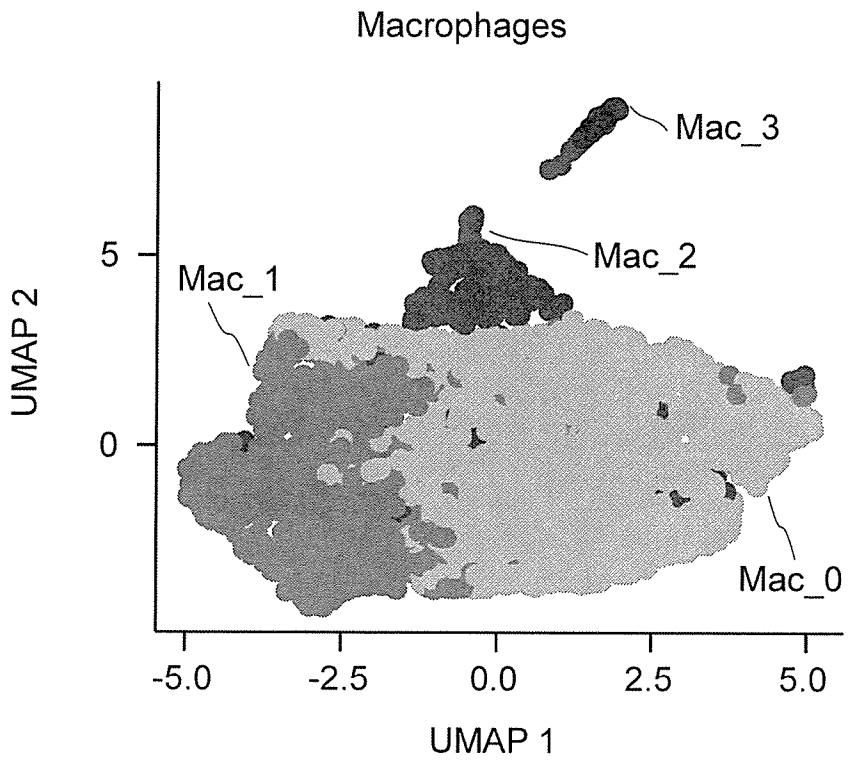


FIG. 14B

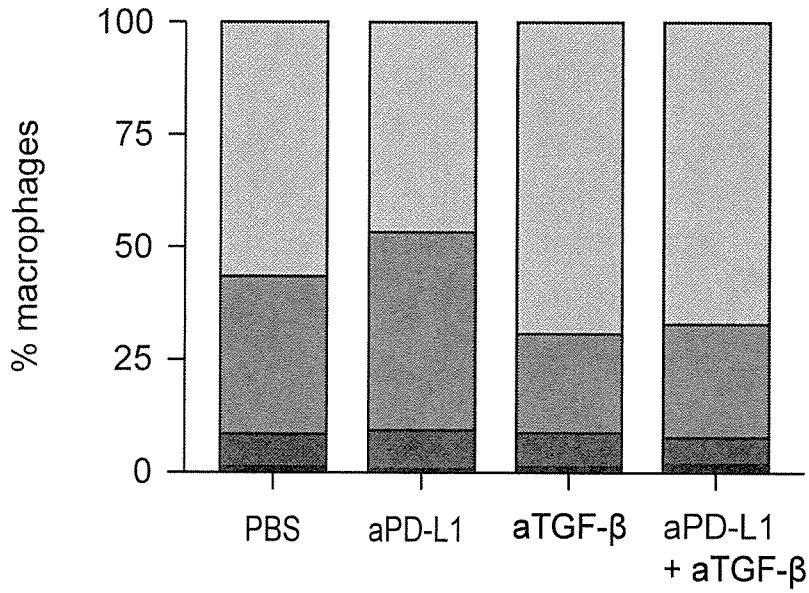


FIG. 14C

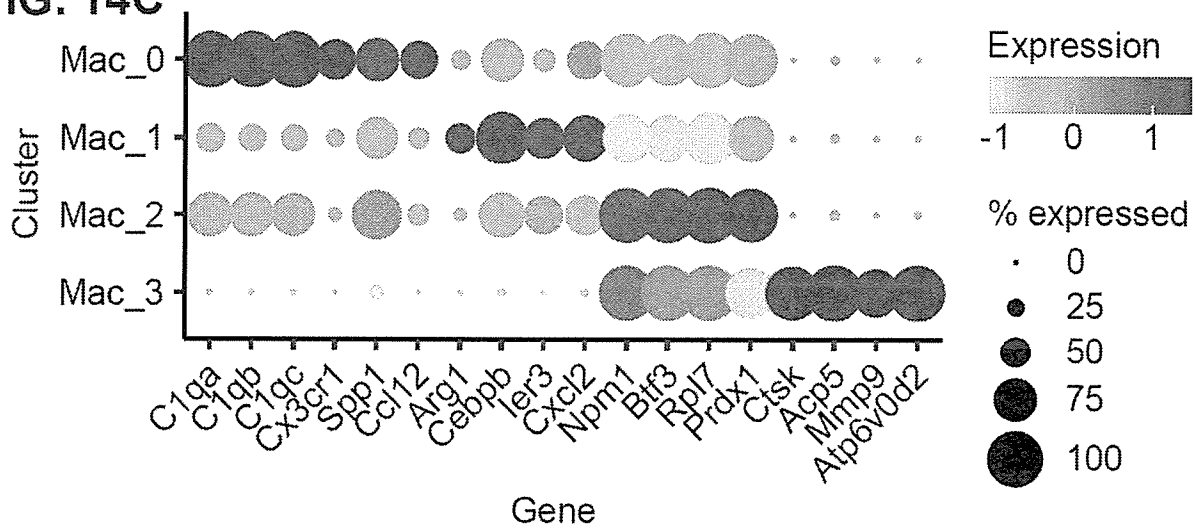


FIG. 14D

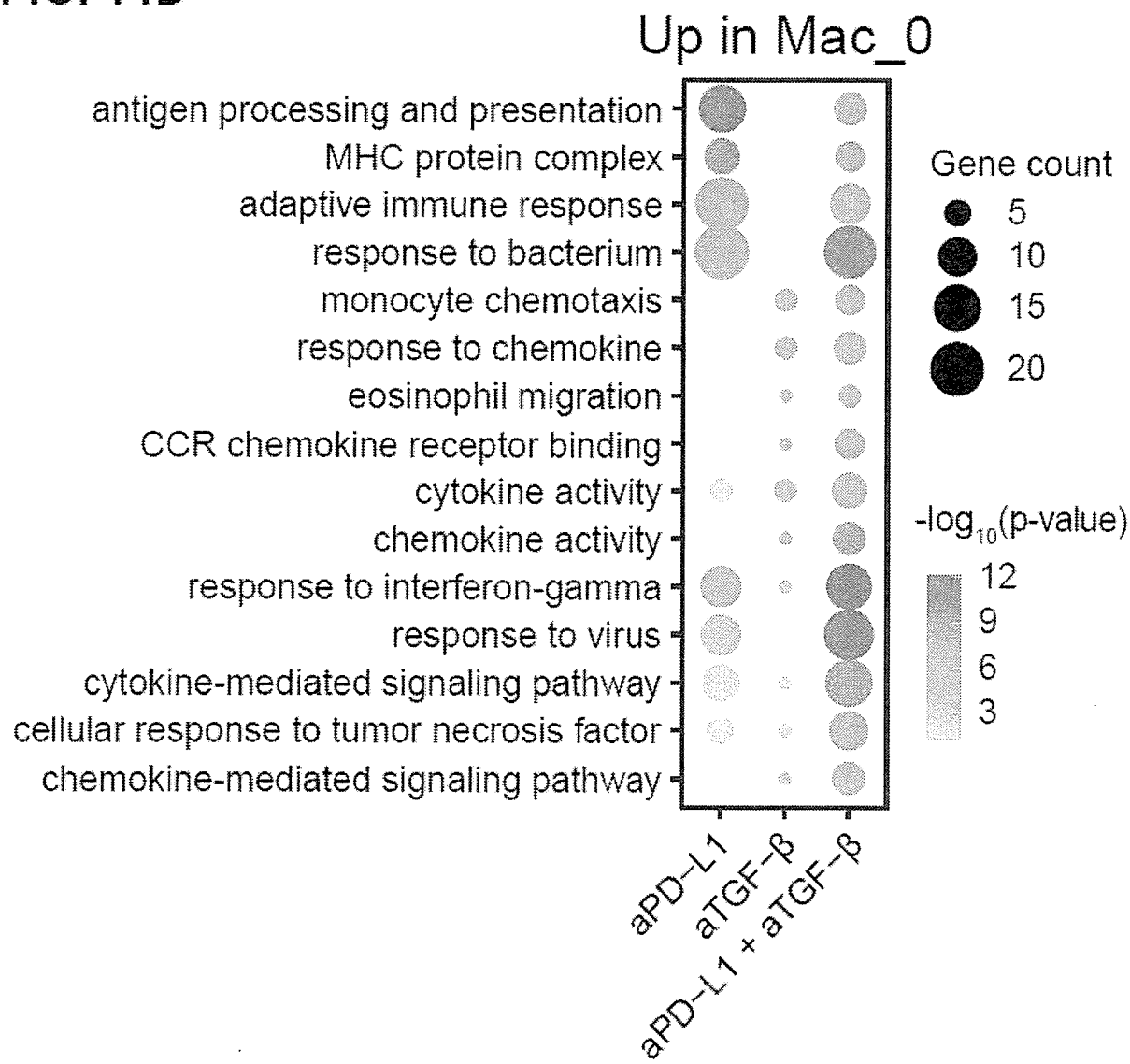


FIG. 14E

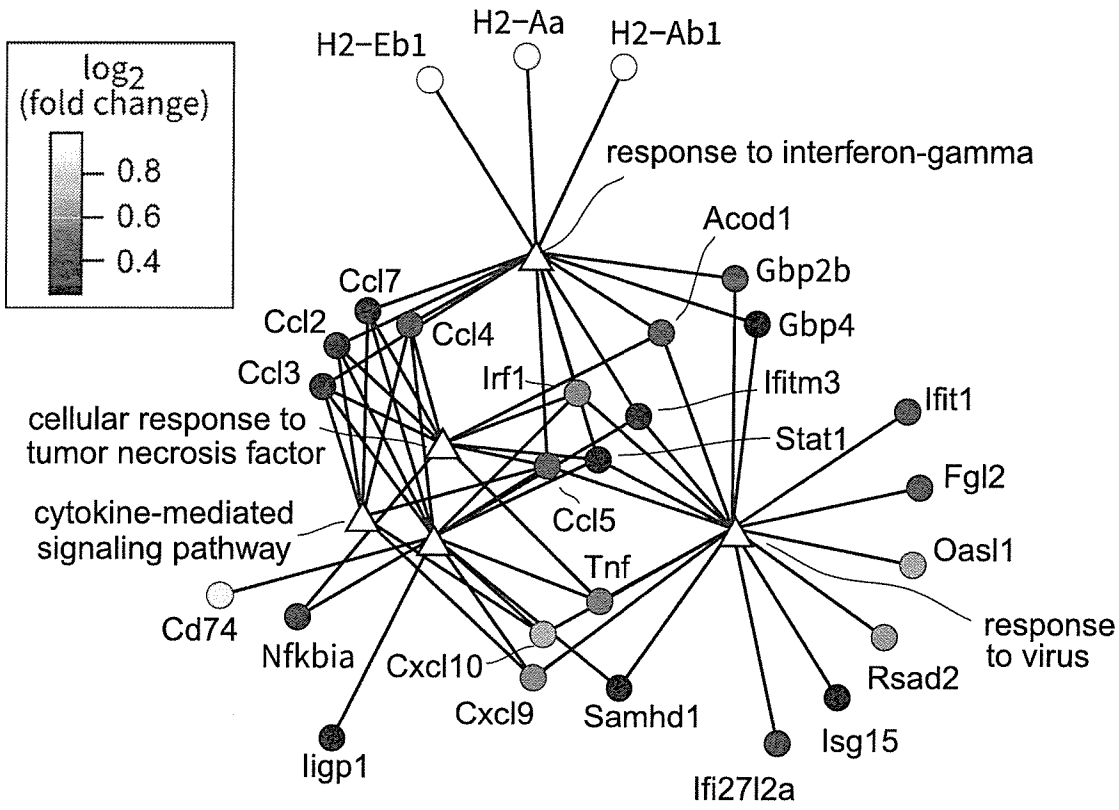


FIG. 14F

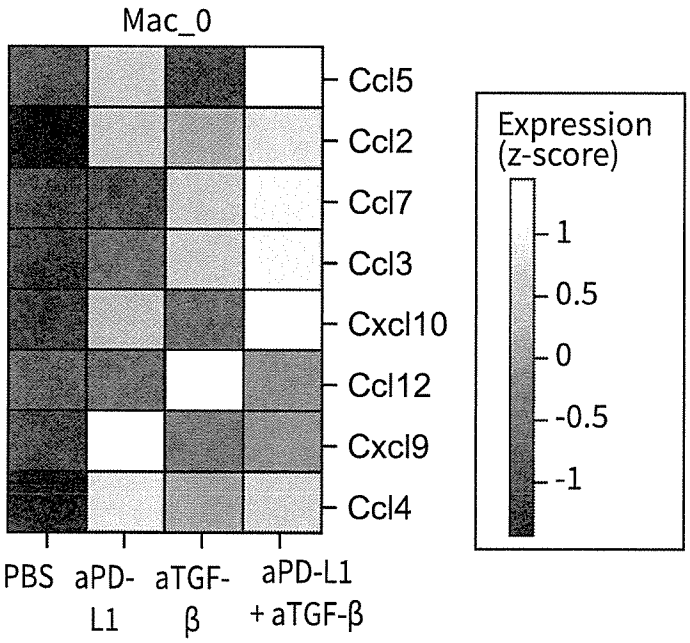


FIG. 15A

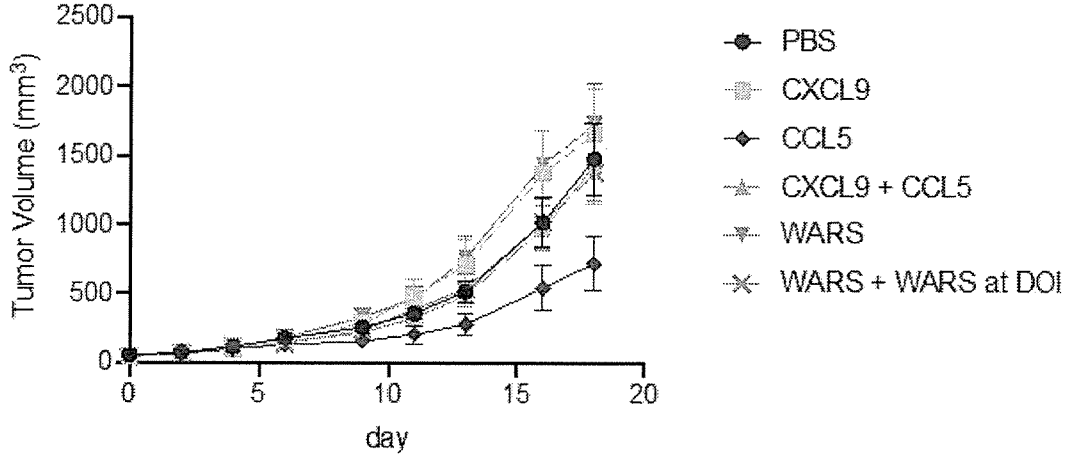


FIG. 15B

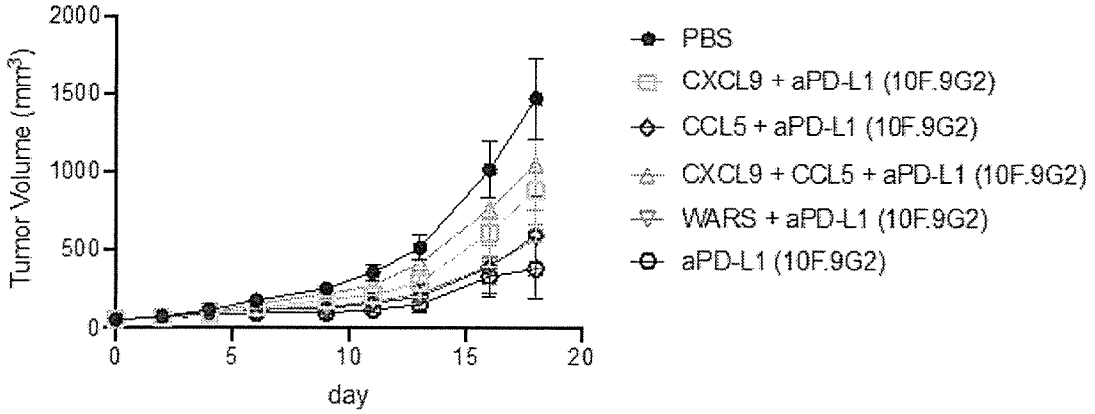


FIG. 15C