Supporting Information Appendix

Tethered IL-15 augments antitumor activity and promotes a stem-cell memory subset in tumor-specific T cells

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SI Appendix Materials and Methods

Plasmid Design. mbIL15: Alternate codon usage and signal peptides can increase expression of IL-15. Therefore, signal peptides for IL-15 and IL-15Rα were omitted and the IgE signal peptide (gb|AAB59424.1) was used for the mbIL15 fusion protein. The mbIL15 construct fuses the human codon-optimized (hCoOp) GeneArt (Regensburg, Germany) IL-15 cDNA sequence (NM_000585.4) to the full-length IL-15Rα cDNA sequence (NM_002189.3) via a 26 amino acid glycine-serine linker [$SG_3(SG_4)_3SG_3SLQ$] and has a C-terminal (FLAG)$_3$ epitope tag (DYKDDDDK, repeated three times). The DNA plasmid expressing IL15-IL15Ra-FLAG_pMK-RQ was synthesized by GeneArt. IL15-IL15Ra-FLAG_pMK-RQ and GlySer-EGFP-mIgG1/pSBSO were digested with *NheI* and *XhoI* to liberate the mbIL15 insert and pSBSO Sleeping Beauty (SB) vector backbone, respectively, to generate IL15-IL15Rα-Flag/pSBSO. Alternatively, a clinically relevant design of mbIL15 (mIL15-IL15Ra(hCoOp)/pSBSO-FRA) was used in the established leukemia mouse model along with the *CAR. The clinical mbIL15 insert consisted of all of the same components as the original mbIL15 but for the removal of the FLAG tag. The clinical mbIL15 insert was codon-optimized and synthesized by GeneArt. Vector 13ABPHSP mIL15-IL15Ra/pMK-T and clinical vector CD19R-CD28Tm-41BBCyt-Z(hCoOp)/pSBSO-FRA were digested with *NheI* and *XhoI* to liberate the mbIL15 insert and pSBSO SB vector backbone, respectively to generate the clinical mIL15-IL15Ra(hCoOp)/pSBSO-FRA plasmid.

SB11: The hyperactive transposase (SB11) is under the control of a cytomegalovirus (CMV) promoter in the pKan-CMV-SB11 SB plasmid (1, 2).

CARs: Generation of the SB transposon encoding the second generation CD19-specific CAR (CD19RCD28/pSBSO) under control of the human elongation factor-1α promoter has been described (1, 2) and is herein referred to as 'CAR'.

A CD19-specific CAR co-expressing *ffLuc*, designated CAR-*ffLuc*, (CD19RCD28-T2A-Flag-ffLuc/pT2SBSO) was used for *in vivo* monitoring of T cells by bioluminescent imaging (BLI). The hCoOp CAR and firefly (*Photinus pyralis)* luciferase reporter genes, linked via a self-cleaving 2A peptide from the *Thosea asigna* virus, were derived from the previously made plasmid CD19RCD28mz-T2A-hΔTK(CoOp)/pΔSBSO. The *SB* inverted-direct repeats (IRs/DRs) T1 were replaced with the hyperactive IRs-DRs T2, to improve transposition, and the firefly luciferase reporter gene replaced the hΔTK transgene. Plasmids CD19RCD28mz-T2A-hΔTK(CoOp)/pΔSBSO and CD19RCD28mZ(CoOp)/pT2SBSO were digested with *Stu* I-*Kpn* I and *ClaI-KpnI* restriction enzymes, respectively, with an extra blunting reaction after the *ClaI* digestion, and ligated using T4 DNA ligase to create intermediate plasmid-I, CD19RCD28mz-T2A-hΔTK(CoOp)/pT2SBSO. The T2A-hΔTK transgene was replaced with a T2A-flag-tag fusion and a multiple cloning site (MCS). T2A-flag-MCS was created by PCR primer annealing and TOPO-TA cloning. Plasmids CD19RCD28mz-T2A-hΔTK(CoOp)/pT2SBSO and T2A-Flag-MCS/TOPO were digested with *BspE1* and *SpeI* and ligated to create intermediate plasmid-II, CD19RCD28mz-T2A-Flag(CoOp)/pT2SBSO. The firefly luciferase gene was excised from the previously made plasmid Flag-FFLuc-HyTK(CoOp)/pT2SBSO using *SnaBI* and *EcoRV* restriction enzymes. The same restriction enzymes were used to digest the accepting pT2SBSO vector. Purified fragments were ligated to create the CD19RCD28mz-T2A-Flag-FFluc(CoOp)/pT2SBSO.

The *SB* transposon encoding *CAR (CD19R-Fcm-CD28m-Z(hCoOp)/pSBSO-SIM), a second generation CD19-specific IgG$_4$-Fc stalk modified CAR, was generated to abrogate unintended binding to innate Fcγ receptors. Source DNA was human codon-optimized and synthesized by GeneArt. The same CD19-specific scFv as used in our previous vectors (2) was connected to modified human IgG4 hinge and Fc regions (the hinge was previously mutated from amino acids CPSC and CPPC to enhance stability of the dimerized IgG4 heavy chain, and amino acid changes L235E, and N297Q were newly made to decrease unintended binding to innate Fcγ receptors). The Fc region was connected to the human CD28 transmembrane and cytoplasmic domains with the cytoplasmic endodomain modification RLLH to RGGH to improve CAR expression; and the CD28 endodomain was connected to the CD3-Z cytoplasmic domain. The GeneArt vector and vector CD19RCD28mZ(hCoOp)/pSBSO-SIM used in clinical trials were digested with *AvrII* and *XmnI* to obtain the insert and vector backbone, which included a portion of the CD19R-CAR. Ligation generated the final *CAR vector (CD19R-Fcm-CD28m-Z(hCoOp)/pSBSO-SIM).

<u>*rLuc*-mKate reporter</u>: *rLuc*8.6-535-T2A-mKateS158A/pLV430G is a lentiviral vector encoding both *Renilla luciferase* (*rLuc*) and mKate. They were created from sequences for *rLuc*8.6-535 and mKateS158A as reported (3, 4), codon-optimized as previously reported (5), and were synthesized by GeneArt to yield a B1 *rLuc*8.6-535-T2A-mKateS158A B2 construct. The B1 and B2 sites are lambda phage recombination sites used in Gateway Recombination Cloning Technology (Invitrogen) synthesizing the construct via BP reaction into pDONR221. Subsequently, *rLuc*8.6-535-T2A-mKateS158A/pDONR221 was recombined into pLV430G (6), a self-inactivating lentivirus encoding an internal U3 promoter from the murine stem cell virus.

Cell lines and propagation. Cell lines were maintained in complete media [CM; RPMI 1640, 10% heat-inactivated fetal bovine serum (Hyclone), and 1% Glutamax-100 (Gibco)] in humidified conditions at 5% CO_2 and 37˚C. NALM-6 (pre-B cell) and THP-1 (human monocyte) were obtained from American Type Culture Collection (Manassas, VA). K562-derived AaPC (designated "clone 9") (7), $CD19^+$EL4 (2), and GFP^+*effLuc*$^+$NALM-6 (8) have been described. The *rLuc*$^+$mKate$^+$NALM-6 cells were generated by lentiviral transduction of NALM-6 with *rLuc*8.6-535-T2A-mKateS158A/pLV430G using standard techniques. Cell lines were negative for mycoplasma. Identity of cell lines was confirmed by STR DNA fingerprinting by the Characterized Cell Line Core, a Cancer Center Support Grant supported facility, at MD Anderson.

Generation and *ex vivo* expansion of genetically modified T cells. The CAR and mbIL15-CAR T cells were generated from mononuclear cell buffy coats from anonymized healthy donors (Gulf Coast Regional Blood Center, Houston, TX) but with modifications to the previously described method of generating clinical-grade CD19-specific CAR T cells (**SI Appendix, Fig. S1**) (2). Briefly, PBMC were co-electroporated with supercoiled DNA plasmids coding for mbIL15 and second-generation CAR seperately expressed as two *Sleeping Beauty* (SB) transposons along with supercoiled DNA plasmid coding for SB11 transposase. Cells were then cocultured on γ-irradiated K562 (clone #9)-derived activating and propagating cells (AaPC), modified to co-express truncated CD19, CD64, CD86, and CD137L, and supplemented with recombinant soluble IL-21 (30 ng/mL). The genetic modification and expansion of CAR T cells (not expressing mbIL15) was similarly performed on AaPC clone #9, but electroporated with only DNA plasmid coding for CAR as SB transposon and DNA plasmid coding for the SB transposase with subsequent cultures supplemented with recombinant soluble IL-21 (30 ng/mL) and IL-2 (50 U/mL) or soluble IL-

15/IL-15Rα-Fc complex (5 ng/mL, IL-15 complex). The AaPC were added once every 8 – 10 days at ratio of 1:1 (T cells to AaPC) and cytokine(s) were supplemented three times per week for all cultures. IL-15/IL15-Rα-Fc (referred to as 'IL-15 complex') was supplemented in CAR T-cell culture medium or used as a control in certain assays. IL-15/IL15-Rα-Fc complex is a 2:1 molar ratio combination of human IL-15 (PeproTech) and human IL-15Rα-Fc chimera (R&D Systems) containing 5 ng/mL of IL-15 (dosing of complex is based on IL-15 content). If CD3^{neg}CD56^{+} NK cell outgrowth exceeded 15%, these were depleted using CD56 microbeads (Miltenyi Biotec) and LS columns (Miltenyi Biotec) per the manufacturer's instructions. Viable T cells were enumerated after each stimulation cycle (8–10 days) based on Trypan blue exclusion. Inferred CAR T cell numbers were calculated by multiplying the CD3^{+}CAR cell fold expansion from the first stimulation with the starting cell number that would then be multiplied by the CAR-specific T cell expansion from subsequent stimulation cycles.

Western Blot of mbIL15. Whole cell lysates (2.4 µg) of propagated mbIL15-CAR T cells were separated by SDS-PAGE under reducing conditions using a "Simple Western" size-based assay (Wes^{TM} System, ProteinSimple, Santa Clara, CA) per the company's protocol. The target protein (mbIL15) was identified using anti-human IL-15 antibody (20ug/mL, R&D Systems) followed by HRP-conjugated rabbit anti-goat secondary antibody (1:250).

Antibodies and Flow Cytometry. Up to 10^6 cells were stained with fluorochrome-conjugated antibodies: fluorescein isothiocyanate (FITC), phycoerythrin (PE), peridinin chlorophyll protein conjugated to cyanine dye (PerCP-Cy5.5), allophycocyanin (APC), AlexaFluor-488, and AlexaFluor-647, which unless otherwise stated, were obtained from BD Biosciences. Unless otherwise stated, antibodies were used at 1:20, 1:40, 1:25, 1:33, 1:20, and 1:20 dilutions, respectively, in a 100 μl volume of buffer. Staining for cell surface markers and corresponding isotype controls was conducted in flow cytometry buffer (phosphate-buffered saline (PBS), 2% fetal bovine serum (FBS), 0.1% sodium azide) for 30 minutes at 4˚C. Intracellular staining was performed following fixation and permeabilization for 20 minutes at 4˚C with BD Cytofix/Cytoperm with antibodies diluted in 1× Perm/Wash buffer for 30 minutes at 4 ˚C (BD Biosciences). Annexin V staining was conducted in 1× annexin binding buffer (BD biosciences). Antibodies used for immunostaining included (against human): Bcl-2 (1:5 dilution, clone Bcl-2/100), Fc (to detect CAR; clone H10104, Invitrogen), IL-15 (1:6.7 dilution for APC; clone 34559, R&D Systems), Blimp-1 (clone 646702, R&D Systems), CD19 CAR idiotype (clone 136.20.1) (9), CD3 (clone SK7), CD4 (cloneRPA-T4), CD8 (clone SK1), CD25 (clone M-A251), CD27 (clone L128), CD28 (clone L293), CD19 (clone HIB19), CD45RA (clone HI100), CD45RO (clone UCHL1), CD56 (clone B159), CD62L (clone DREG-56), CD122 (clone Mik-β3), CD127 (1:8.3 dilution; clone 40131, R&D Systems), CCR7 (1:45 dilution for PerCP-Cy5.5; clone G043H7, BioLegend), IL-2 (clone MQ1-17H12), IFNγ (clone B27), pSTAT5 (pY694) [1:5 dilution; clone 47/Stat5(pY694)], T-bet (1:20 for PerCP-Cy5.5; clone 4B10, BioLegend), and unconjugated rabbit anti-TCF1 (1:20 dilution; clone C725.7, Thermo Scientific). Polyclonal goat anti-rabbit IgG-DyLight650 (1:100 dilution; Thermo Scientific) was used as a secondary antibody to detect TCF1. Annexin V (1:20 dilution; BD Bioscience) and anti-FLAG (1:200 dilution; Prozyme) were also used. Data were acquired using a FACSCalibur with Cell Quest version 3.3 software (BD Biosciences) and analyzed with FlowJo software (version 7.6.5, TreeStar).

Phosflow of pSTAT5. Cells were washed in PBS to remove residual cytokines from culture media. The cells were then transferred to fresh serum-free culture media (RPMI supplemented with 1% Glutamax) at a density of 2×10^6/mL and starved for 12 hours without serum and exogenous cytokine. Serum-starved negative control CAR T cells provided the baseline level of pSTAT5, and positive control CAR T cells were treated with 100 ng/mL IL-15 for one hour after "starving" prior to fixation. Cells were pelleted to remove the supernatant and processed according to the manufacturer's protocol using PhosFlow Lyse/Fix Buffer (BD Biosciences), BD PhosFlow Perm Buffer III (BD Biosciences), and pSTAT5 (pY694, BD Biosciences).

Intracellular cytokine production. Production of cytokines was assessed by intracellular cytokine staining of T cells as described above. T cells were co-cultured with $CD19^+$ or $CD19^{neg}$ targets at an effector to target ratio of 1:5 in 200 μL of CM. T cells were incubated alone (negative control) and with the addition of Leukocyte Activation Cocktail (LAC, containing PMA and ionomycin, BD Biosciences; positive control). Brefeldin-A (GolgiPlug, BD Biosciences) was added, per manufacturer instructions, to all cultures to block exocytosis of cytokines. Cultures were incubated for 6 hours at 37˚C, then stained for surface markers, followed by fixation, permeabilization and staining for expression of intracellular proteins.

Chromium release assay. The antigen-specific cytolytic activity of T cells was assessed in a standard 4-hour chromium release assay (CRA), as previously described (10). Genetically modified T cells were incubated with 2×10^5 of ^{51}Cr-labeled target cells ($CD19^{neg}$ parental EL4, $CD19^+$ EL4, or $CD19^+$ NALM-6). The percentage of specific lysis was calculated from the release of ^{51}Cr using a TopCount NXT (Perkin-Elmer) (10).

In vitro **antigen and cytokine withdrawal assays.** After the fourth stimulation with AaPC, mbIL15$^{\pm}$-CAR T cells were maintained with exogenous cytokine(s) for 10 days, then enumerated and transferred to fresh CM in exogenous cytokine-free (unless otherwise noted) and antigen-free culture conditions. CAR T cells supplemented with IL-15 complex (5 ng/mL, 2×/week) served as a positive control for an assay with cells enumerated on days 15, 30, 50, and 65. T cells persisting in culture for >65 days, referred to as “AWD-T cells”, were assessed for pSTAT5 and Bcl-2. Two days prior to staining for Bcl-2, baseline control CAR T cells were washed and resuspended in CM without cytokine supplementation.

The withdrawal assay assessing CCR7 subset T cell viability was performed as described above, but tested the following treatments: (i) mbIL15-CAR T cells, (ii) CAR T cells supplemented with IL-2 (50 U/ml, 2×/week), and (iii) CAR T cells supplemented with IL-15 (5 ng/ml, 2×/week). Live cell staining of AWD-T cell CCR7 subsets was performed on cells after 65 days. AWD-T cells were first stained with CCR7 antibody and gently washed once with FACS buffer, followed by staining with Annexin V (1:20 dilution; BD Bioscience) per the manufacturer’s protocol.

nCounter system digital gene expression analysis. Day 0 (i.e., 8 days after the fourth AaPC stimulation) CAR and mbIL15-CAR T cells and day 65 AWD-mbIL15-CAR T cells were frozen at -80˚C and later analyzed in batch for gene expression analysis using the nCounter System (NanoString Technologies) according to the manufacturer’s protocol. At the time of analysis, RLT buffer (Qiagen) was added to the samples at a ratio of 166 μL of buffer per 10^6 cells prior to thawing. RNA lysates were immediately processed and analyzed using the nCounter Analysis System (NanoString Technologies) to detect the expression of genes of interest. Multiplexed target-specific, color-coded reporter and biotinylated capture probes for mRNA species of interest were hybridized for >12 hours at 65˚C in a thermocycler (Peltier Thermal Cycler, Bio-Rad), processed in the nCounter PrepStation (NanoString Technologies), and then analyzed using the nCounter Digital Analyzer (NanoString Technologies). Reference genes (*ACTB, G6PD, OAZ1, POLR1B, POLR2A, RPL27, RPS13*, and *TBP*), which together span a dynamic range of RNA expression, were included in the CodeSet and were used to normalize transcript levels to account for variation of transcript levels between samples and of the amount of total RNA present in samples. The count data was positive-, negative-, and housekeeping gene-normalized per nCounter guidelines using the nCounter RCC Collector Worksheet (v1.6.0, NanoString Technologies), as previously described (11), and filtered to remove low-expression genes: those with counts of less than 10 in greater than 60% of samples. A lymphocyte-specific CodeSet (**SI Appendix, Table S1**) was generated from RefSeq accession numbers for chosen mRNA transcripts that were used to generate the reporter and capture probe pairs constituting the lymphocyte gene panel. Statistical analyses were performed using edgeR software (12) via the RobiNA Java interface (13). Statistical evaluation of differential gene expression implemented statistical methods based on a negative binomial dispersion. Genes considered to be significantly differentially expressed demonstrated an absolute fold change ≥2, $P < 0.01$, and a FDR significance value of $q < 0.05$ with the Benjamini-Hochberg method used for multiple testing correction. Significant differentially expressed genes were represented in a heatmap generated using Qlucore Omics Explorer (v.2.3, Qlucore). Digital gene expression analysis for assessing Vα/Vβ repertoire was performed as previously described (14).

G-banded Karyotyping. AWD-mIL15-CAR T cells that were in long-term continuous culture were restimulated with AaPC. Actively dividing T cell samples were submitted for G-banded karyotyping to the Texas Children's Hospital Clinical and Research Cytogenetic Laboratory.

PKH Dilution Assay. AWD-mIL15-CAR T cells that were in long-term continuous culture (1–2 years, depending on the donor) were labeled with PKH (Sigma) per manufacturer's instructions. Labeled cells were assessed for PKH dilution by flow cytometry 10 and 30 days after PKH labeling. The positive PKH dilution control was AWD-mIL15-CAR T cells stimulated with AaPC.

Mouse experiments. *In vivo* experiments used humanized NSG mice (NOD.Cg-Prkdc^{scid}IL2rγ^{tm1Wjl}/SzJ) that were purchased from The Jackson Laboratory (Bar Harbor, ME) or bred at The University of Texas MD Anderson Cancer Center.

Bioluminescence imaging. Serial BLI was performed to measure temporal biodistribution and abundance of mbIL15-CAR and CAR T cells co-expressing *ffLuc* as previously described (8, 15). Serial BLI was used to measure tumor burden of *ffLuc*$^+$ or *rLuc*$^+$NALM-6 cells as previously described (15). Imaging was performed on anesthetized mice using a Xenogen IVIS 100 (Caliper Life Sciences). Imaging for T cells and tumor were performed on alternate days with an initial imaging of background BLI to check that no residual luminescence remained. T cell and tumor flux (photons/s/cm^2/steradian) were quantified by measuring photon signal within a delineated region of interest (ROI) encompassing: (i) the body of the mouse, except the tail and (ii) over the femur. Living Image software (v2.50, Xenogen; Caliper Life Sciences) was used to process the BLI data.

Tissue preparation. Mice were euthanized, and peripheral blood, spleen, and BM from femur and tibia were harvested. Spleens were manually homogenized in 2% FBS/PBS and passed through a 40 μm cell strainer (BD BioSciences). To obtain marrow, the femurs and tibia were flushed with 2% FBS/PBS using 30G needles (BD Biosciences). ACK lysing buffer (Gibco-Invitrogen) was used to lyse red blood cells in all samples.

In vivo persistence and characterization of genetically modified T cells in the absence of CAR activation. CAR T cells (2×10^7per mouse) were injected i.v. into NSG mice in two cohorts (n = 5/group): (i) mbIL15-CAR-*ffLuc* T cells and (ii) CAR-*ffLuc* T cells. Serial bioluminescent imaging (BLI) measured T-cell persistence and biodistribution until sacrifice at days 48-50. Tissues were harvested for analysis.

In vivo characterization of mbIL15-CAR T cells persisting in the absence of CAR activation. NSG mice were engrafted with 2×10^7 mbIL15-CAR T cells (n = 9). After 48-50 days, peripheral blood, spleen, and BM were harvested for flow cytometry analysis by for CD45RO and CCR7 expression. T cells from spleen, liver, and BM samples were *ex vivo* expanded on AaPC at an initial ratio of one isolated cell to five AaPC with subsequent weekly stimulations at a 1:1 ratio. Expanded T cells were tested for antigen-specific function by assessing intracellular staining of IFNγ in response to $CD19^+$ versus $CD19^{neg}$ cell targets.

In vivo persistence and antitumor efficacy of CAR and mbIL15-CAR T Cells in a preventative leukemia model. T cells were engrafted prior to tumor to mimic MRD. On day 0, treatment cohorts of NSG mice (n = 5/group) were injected i.v. with 2×10^7 genetically modified T cells: (i) mbIL15-CAR-*ffLuc* T cells, or (ii) CAR-*ffLuc* T cells (cultured with IL-15 and IL-21). On day 6, 1×10^4 *rLuc*$^+$NALM-6 were injected i.v. T cell and tumor BLI were monitored as described (6) until death or sacrifice, when tissues were harvested for analysis of CD3 and CD19 by flow cytometry. For BLI, background fluorescence was defined by measuring animals given luciferin but without ffLuc-bearing cells (Fig. 5, T cell imaging). To assess therapeutic efficacy, a similar experiment was undertaken with survival at 98 days as the experimental endpoint in cohorts: (i) mbIL15-CAR-*ffLuc* T cells plus NALM-6 ($n = 7$), (ii) CAR-*ffLuc* T cells plus NALM-6 ($n = 8$), and (iii) NALM-6 only ($n = 8$). T-cell persistence and biodistribution was measured by BLI until death or euthanasia. Mice were considered to have reached the experimental endpoint if they developed hind-limb paralysis or were otherwise moribund.

In vivo persistence and antitumor efficacy of CAR and mbIL15-CAR T Cells in an established leukemia model. On day 0, NSG mice were injected i.v. with 1.5×10^4 *ffLuc*$^+$eGFP$^+$NALM-6. After 5 days of tumor engraftment, mice were imaged and randomized into treatment groups ($n = 7$, tumor only group; $n = 6$, all other T cell treatments). On day 6, mice were given 1×10^7 genetically modified T cells via intra-cardiac injection. Infused T cells were CD19-specific CAR T cells (expressing CAR or *CAR) with or without coexpression of mbIL15. The infused cell number was based on the CAR T cell number. Tumor BLI was measured until mortality or sacrifice, when tissues were harvested for analysis as above.

Statistical analysis. Statistical analyses were performed using Prism (GraphPad Software, v.6.02). Cell count and flux values were log-transformed for statistical analysis. Paired (*in vitro* data) and unpaired (*in vivo* data) t-tests were used to compare two groups. One-way ANOVA was used to compare three groups. Two-way ANOVA was used for multiple comparisons of two factors. Two-way RM ANOVA (Tukey’s post-test) compared multiple groups over time. Survival was analyzed with the log-rank test.

SI Appendix References

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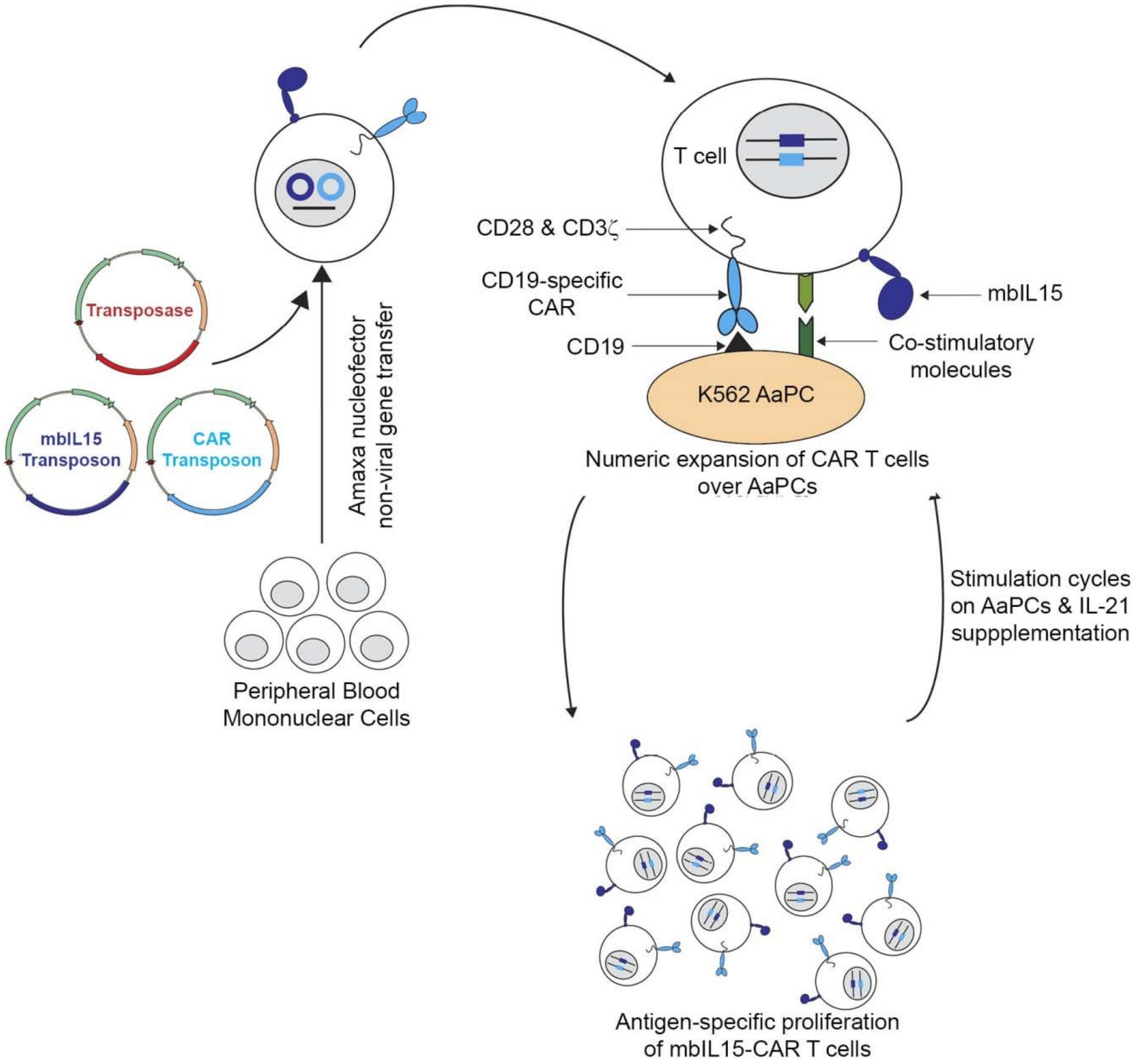

Fig. S1. Generation of CAR^{+}mbIL15$^{\pm}$ CD19-specific T cells using a clinical platform. Schematic of the clinically compliant methods (2) adopted and modified for generating and numerically expanding mbIL15-CAR T cells. PBMC were co-electroporated with mbIL15 and second-generation CAR seperately expressed as two *Sleeping Beauty* (SB) transposons along with the SB11 transposase. Cells were then cocultured on γ-irradiated K562 (clone #9)-derived activating and propagating cells (AaPC), modified to co-express truncated CD19, CD64, CD86, and CD137L, and supplemented with IL-21 (30 ng/mL). The genetic modification and expansion of CAR T cells was similarly performed, but used only CAR SB transposon and SB transposase during electroporation with subsequent cultures supplemented with IL-21 (30 ng/mL) and IL-2 (50 U/mL) or soluble IL-15/IL-15Rα-Fc complex (5 ng/mL, IL-15 complex).

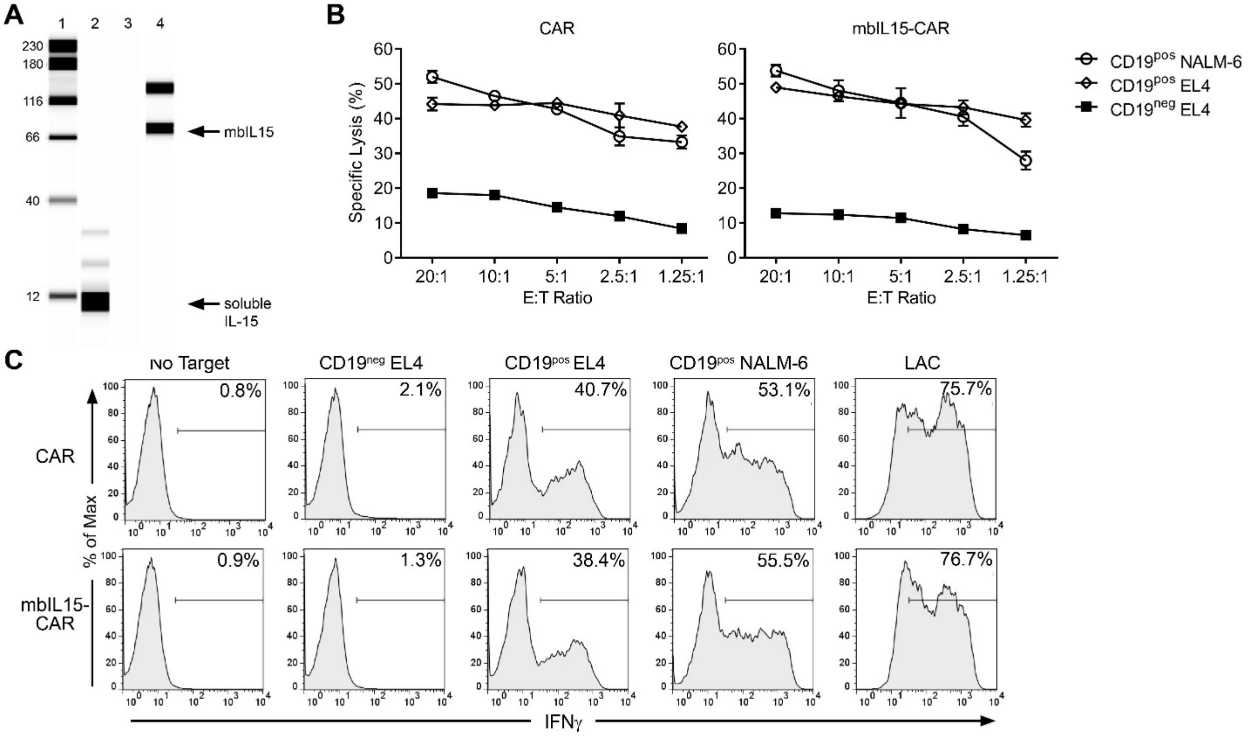

Fig.S2. ***In vitro* phenotype and effector function is not altered by mbIL15 expression. (A)** Western blot analysis of mbIL15 expressed by propagated human T cells. A representative blot from one of three donors is shown. Molecular weight marker (Lane 1), 0.1ng recombinant human IL-15 positive control (Lane 2), CAR T-cell negative control (Lane 3), and mbIL15-CAR T cells (Lane 4). The predicted molecular weight of monomeric recombinant human IL-15 is 14 kDa and that of mIL15 is approximately 72 kDa (incorporating possible post-translational modifications). **(*B*)** CAR T cell (left panel) and mbIL15-CAR T cell (right panel) specific lysis rates of CD19$^+$ or CD19^{neg} targets from a four-hour CRA. Data are represented as mean ± SD for triplicate wells of one of three normal donors. **(C)** IFNγ production by CAR and mbIL15-CAR T cells that were stimulated for 6 hours with CD19$^+$ (tCD19$^+$ EL4 and NALM-6) or CD19^{neg} (EL4) targets, Leukocyte Activating Cocktail (LAC; positive control), or media alone (negative control). Histograms represent CD3$^+$CAR$^+$ cells. Representative histograms are shown for one of four normal donors.

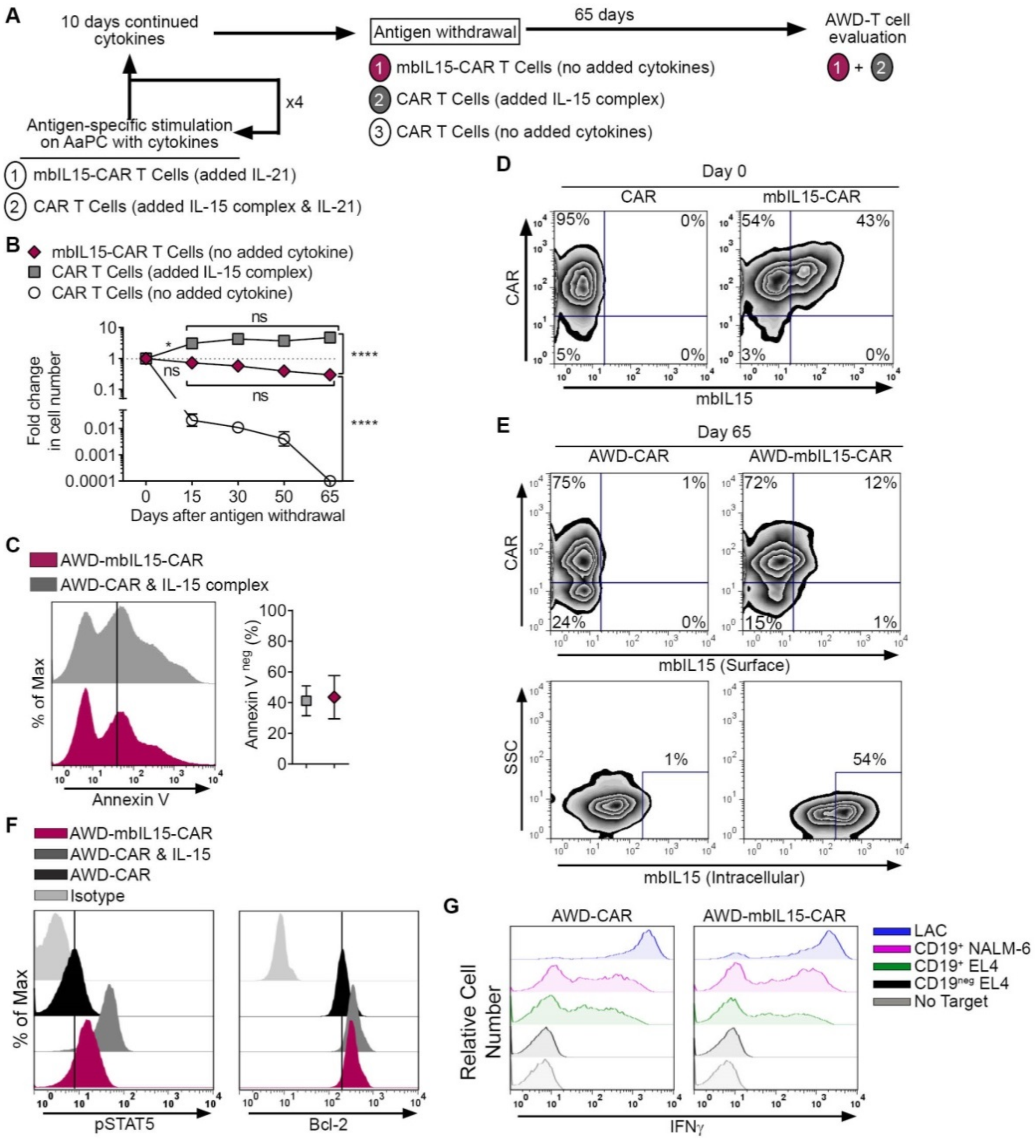

Fig. S3. Prolonged *in vitro* persistence of mbIL15-CAR T cells without CAR activation maintains IL-15 signaling and antigen-specific response. **(*A*)** Schematic summarizing the experimental design. T cells persisting at the end of the assay are termed AWD-T cells. **(*B*)** Fold change in T cell number under antigen and cytokine withdrawal conditions. **P* <0.05, *****P* <0.001, ns = not significant, two-way RM ANOVA (Tukey's post-test). Data displayed as mean ± SD. **(*C*)** Representative histogram showing Annexin V staining (*left panel*) and plotted live T cell (Annexin V^{neg}) frequencies (*right panel*). **(*D, E*)** Representative flow plots showing CAR and mbIL15 expression on T cells on day 0 **(*D*)** and day 65 (*top panel*) **(*E*)** with FLAG staining detecting intracellular localization of mbIL15 (*bottom panel*). **(*F*)** Representative histograms showing fluorescence intensity of pSTAT5 (*left panel*) and Bcl-2 (*right panel*). AWD-CAR T cells cultured with IL-15 complex were left without cytokine or treated with IL-15 to serve as positive and negative controls, respectively. Vertical bar references median fluorescence of the AWD-CAR negative control. **(*G*)** IFNγ production of T cells stimulated with CD19$^+$ or CD19^{neg} targets, Leukocyte Activating Cocktail (LAC), or media alone. Histograms represent cells selected for expression of CD3 and CAR. All data are representative of three donors.

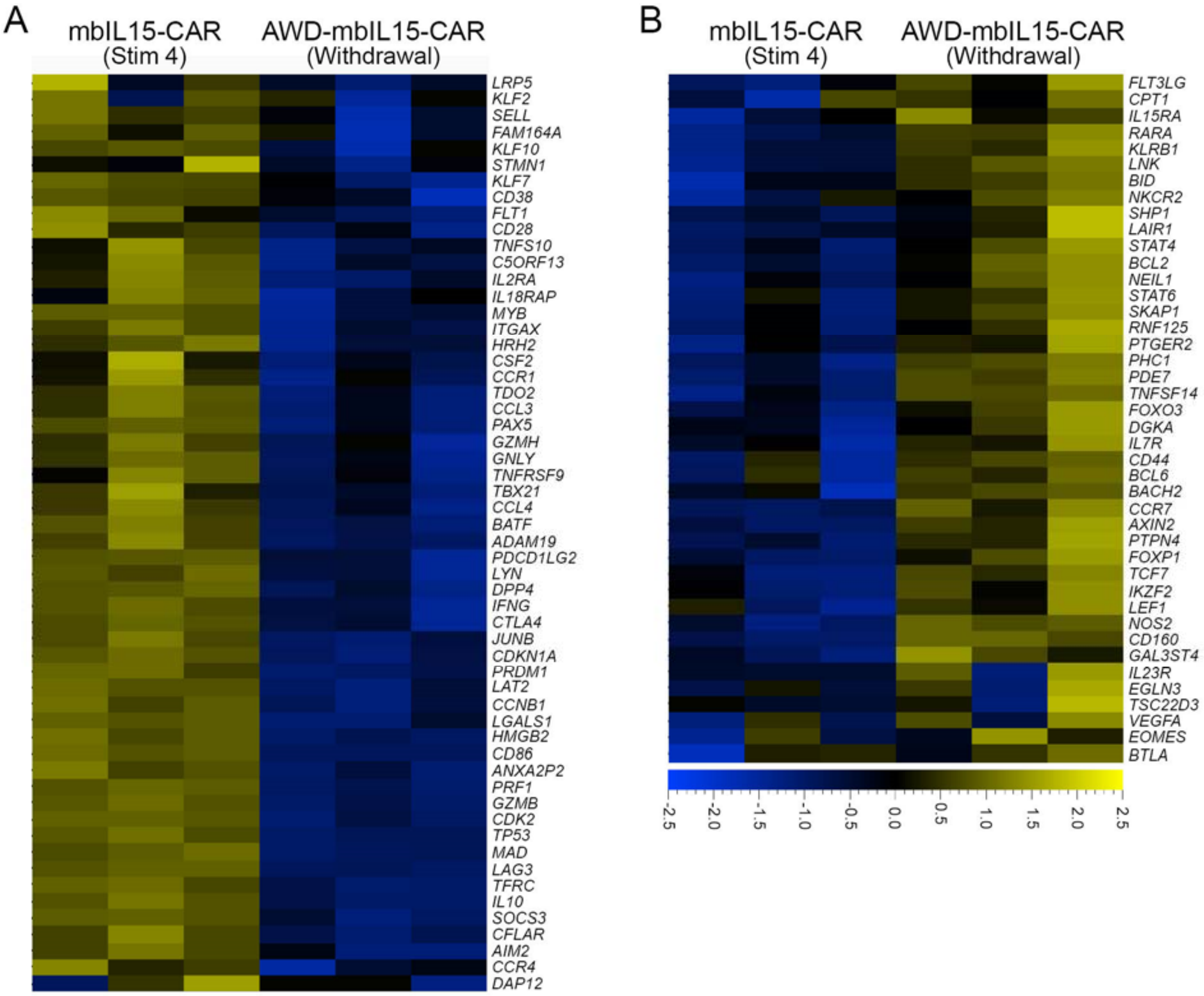

Fig S4. Differentially expressed genes among stim 4 and antigen withdrawal mbIL15-CAR T cells. Heat maps of significantly differentially expressed genes (2-fold cutoff, P <0.01, FDR q value <0.05) that were ***(A)*** downregulated and ***(B)*** upregulated in AWD-mbIL15-CAR T cells relative to mbIL15-CAR T cells, $n = 3$.

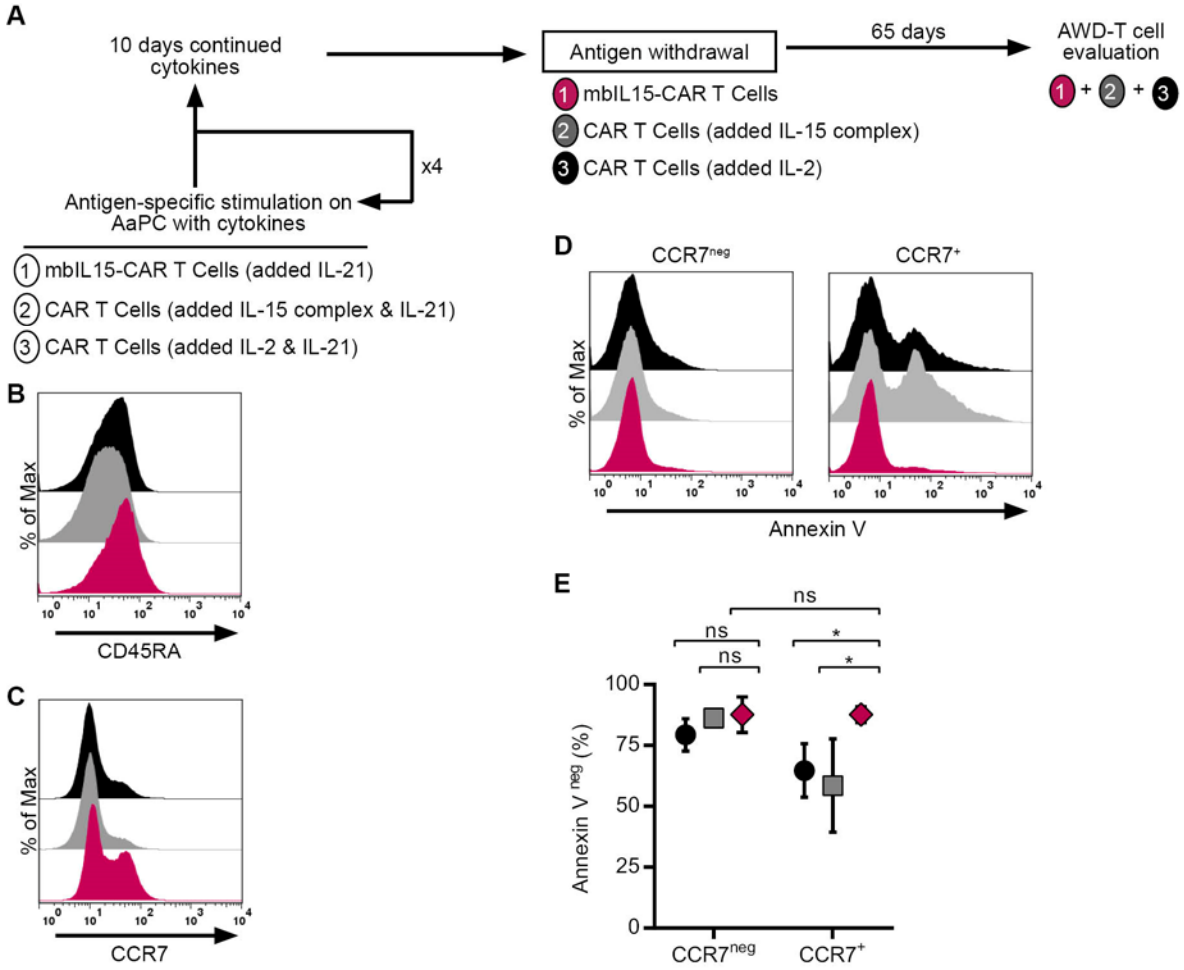

Fig. S5. Tethered IL-15 supports survival of CCR7^{+} T cells. (***A***) Schematic summarizing the antigen withdrawal experiment comparing the impact of IL-2, IL-15/IL15Rα complex, and mbIL15 on CD45RA and CCR7 phenotype. During the 65-day antigen withdrawal, mbIL15-CAR T cells received no exogenous cytokine supplementation, while CAR T cell control treatments received either IL-2 (50 U/ml) or IL-15/IL15Rα complex (5 ng/ml A representative histogram of **(*B*)** CD45RA and **(*C*)** CCR7 expression on AWD-T cells. **(*D*)** Representative histograms showing Annexin V levels in CCR7^{neg} and CCR7^{+} AWD-T cell subsets. Histograms display the lymphocyte population and respective CCR7 subsets selected by gating. **(*E*)** Graph plotting frequencies of live (Annexin V^{neg}) AWD-T cell treatment cohorts in the CCR7^{neg} and CCR7^{+} subsets. Data are represented as mean ± SD. *P <0.05, ns = not significant, two-way ANOVA (Tukey's post-test). All data are representative of three donors. Color legend: CAR T cells supplemented with IL-2 (*black*), CAR T cells supplemented with IL-15/IL15Rα complex (*grey*), and mbIL15-CAR T cells (*magenta*).

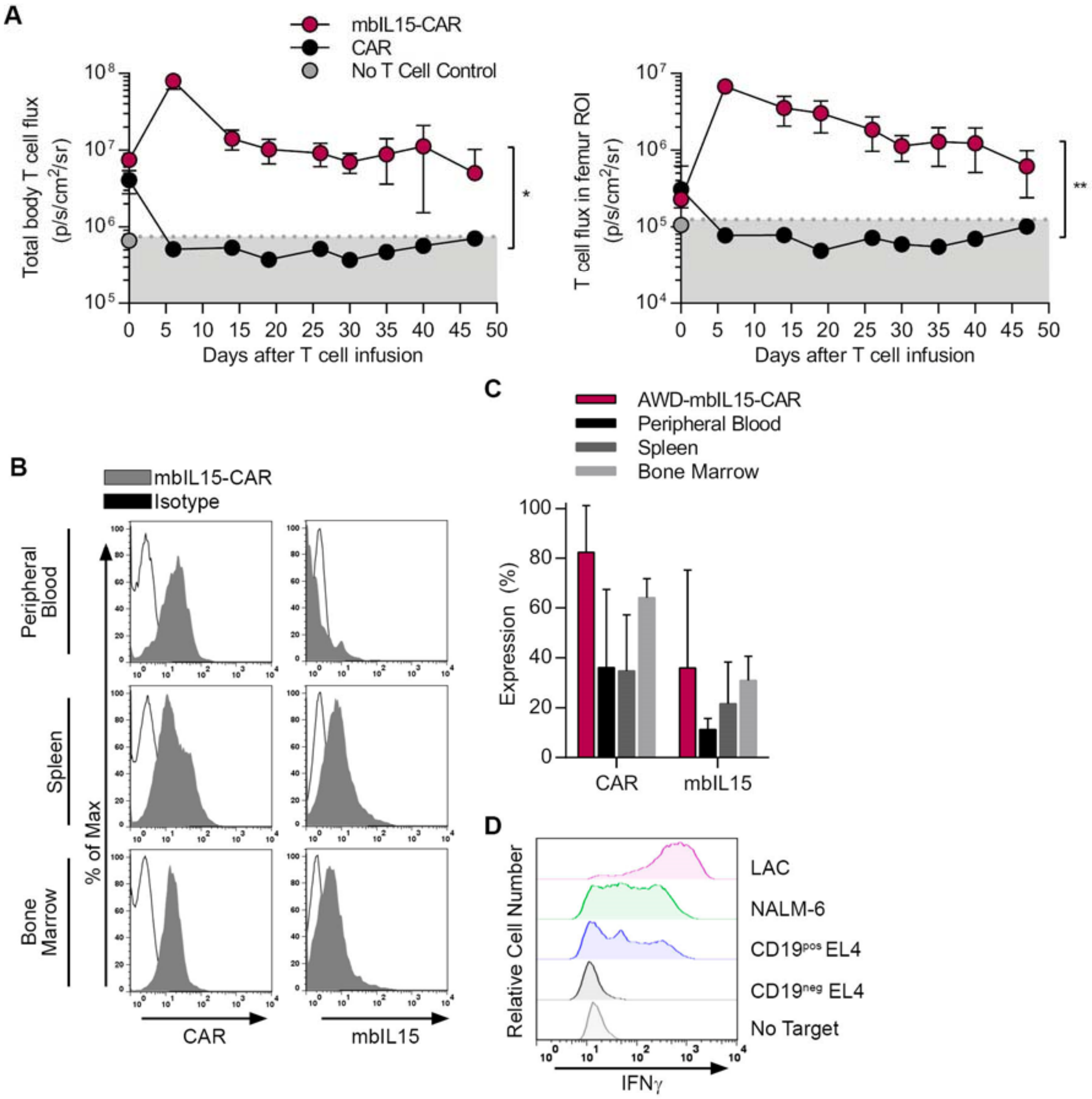

Fig. S6. Long-term *in vivo* engraftment, phenotype, and functionality of mbIL15-CAR T cells independent of CAR signaling. NSG mice were injected i.v. with 2 × 10^7 *ffLuc*$^+$CAR T cells with or without co-expression of mbIL15. Infused T-cell number based on CAR T cells. **(*A*)** Longitudinal plotting of T cell flux. Background BLI (*gray shaded*) was derived by imaging mice without *ffLuc*$^+$ T cells that were treated with D-luciferin. Data are represented as mean ± SD, *n* = 5, and are representative of two experiments. **(*B*)** Peripheral blood, spleen, and bone marrow were analyzed after 48 days *in vivo*. Representative histograms show expression of CAR and mbIL15 and **(*C*)** plotted frequencies of marker expression represented as mean ± SD. Plots and graphs (*B*-*C*) show T cell frequencies after gating on human CD3$^+$ and mouse CD45$^-$ cells in the peripheral blood (*n* = 5), spleen (*n* = 9), and bone marrow (*n* = 9). **(*D*)** Cells isolated from spleen, liver, or bone marrow were *ex vivo* expanded on AaPC to generate cells for assessing intracellular IFNγ production in response to CD19$^-$ and CD19$^+$ targets, *n* = 7 from three tissue sources and four mice. Histograms represent CD3$^+$ cells.

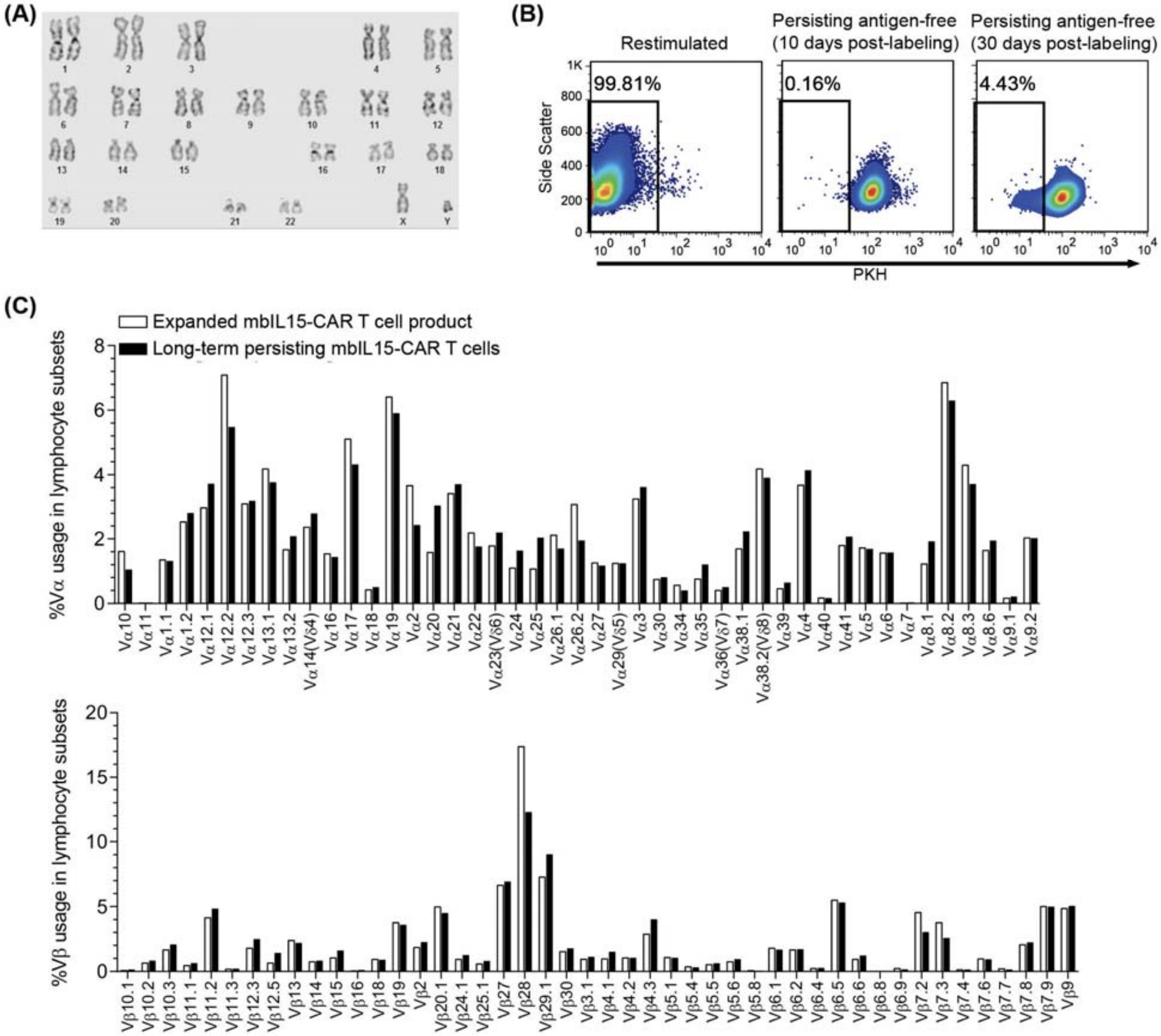

Fig. S7. Prolonged *in vitro* persistence of mbIL15-CAR T cells does not induce aberrant autonomous proliferation or evidence of T-cell transformation. (*A*) G-banding cytogenetic evaluation showing normal karyotype of *ex vivo* propagated mbIL15-CAR T cells persisting *in vitro* long-term (1 year for 3 donors and 2 years for one donor) under antigen-free conditions and without exogenous cytokines. A representative donor is shown. **(*B*)** Homeostatic proliferation, as determined by dilution of the PKH red fluorescent dye, of mbIL15-CAR T cells persisting in long-term continuous culture under antigen-free conditions and without exogenous cytokines ($n = 3$). The proliferation control was the restimulation of the resting T cells with γ-irradiated AaPC clone #9 showing PKH dilution 10 days after labeling (*left panel*). Gates show the percentage of PKH diluted cells. **(*C*)** Assessment of TCR polyclonality of the long-term persisting mbIL15-CAR T cells by quantification of mRNA species coding for Vα and Vβ alleles using a designer TCR expression array as previously described (14). Control TCR Vα and Vβ repertoires are the expanded mbIL15-CAR T cells prior to antigen withdrawal. Bars represent the average percentage of Vα and Vβ allele usage in four normal donors.

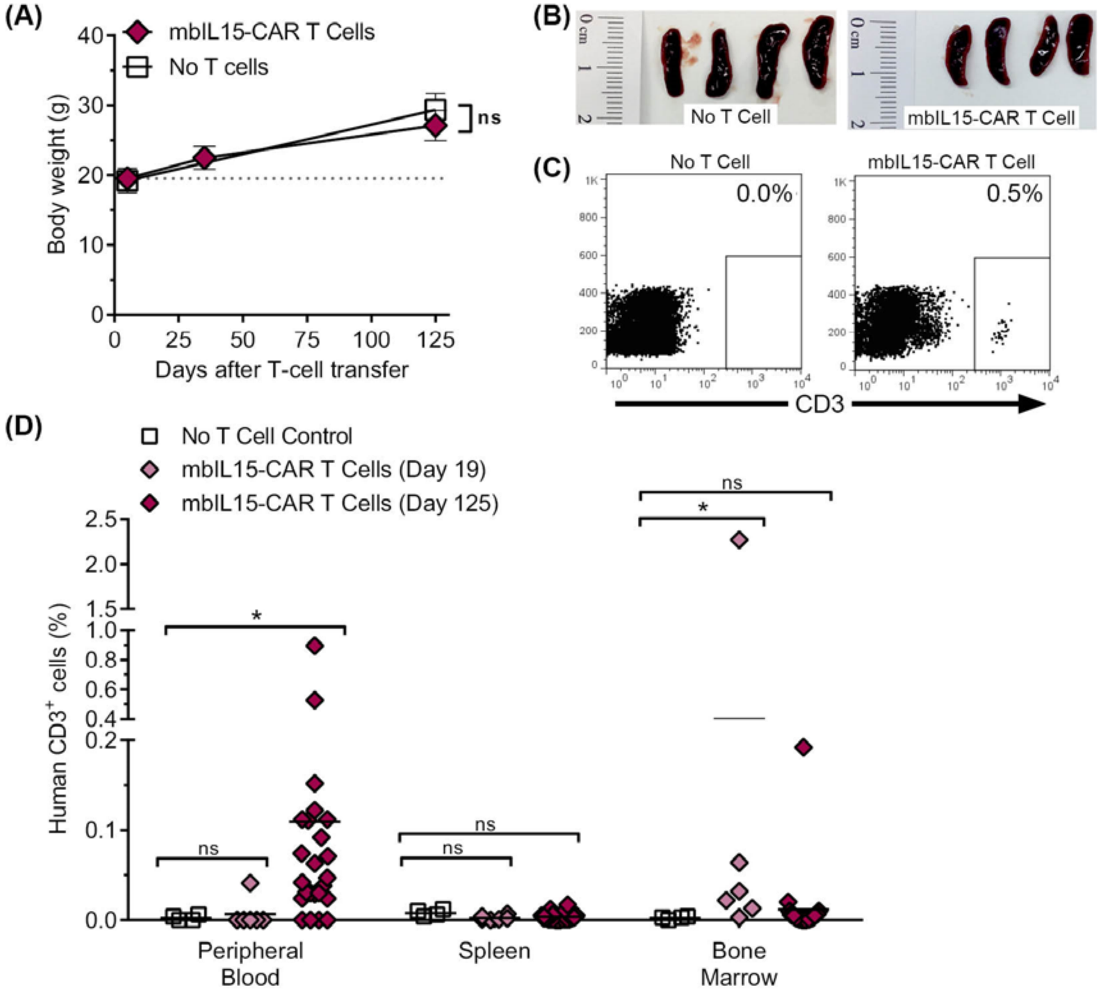

Fig. S8. mbIL15-CAR T cells persisting *in vivo* long-term do not show aberrant autonomous growth or toxicity to recipient mice. NSG mice (tumor-free and no exogenous cytokines) were injected i.v. with 5 × 10^6 mbIL15-CAR T cells to assess long-term safety of persisting T cells. **(*A*)** Body weight to monitor for toxicity from adoptively transferred genetically modified T cells (n = 8, 3 donors). **(*B*)** Representative photos of spleens harvested from mice sacrificed at day 125. **(*C*)** Human CD3$^+$ cell frequencies were assessed by flow cytometry, with representative flow plots from peripheral blood shown. **(*D*)** Human CD3$^+$ cell frequencies observed in the peripheral blood, spleen, and bone marrow at days 19 and 125 of mice treated with mbIL15-CAR T cells. *P <0.05, ns = not significant.

Table S1. nCounter Analysis System Lymphocyte-specific CodeSet

Gene Name	Accession	Target Region	Target Sequence
ABCB1	NM_000927.3	3910-4010	TATAGCACTAAAGTAGGAGACAAAGGAACTCAGCTCTCTGGTGGCCAGAAACAACGCATTGCCATAGCTCGTGCCCTTGTTAGACAGCCTCATATTTTGC
ABCG2	NM_004827.2	285-385	AGGATTTAGGAACGCACCGTGCACATGCTTGGTGGTCTTGTTAAGTGGAAACTGCTGCTTTAGAGTTTGTTTGGAAGGTCCGGGTGACTCATCCCAACAT
ACTB	NM_001101.2	1010-1110	TGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCT
ADAM19	NM_023038.3	1690-1790	GAGAAGGTGAATGTGGCAGGAGACACCTTTGGAAACTGTGGAAAGGACATGAATGGTGAACACAGGAAGTGCAACATGAGAGATGCGAAGTGTGGGAAGA
AGER	NM_001136.3	340-440	GAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAGATTCCTGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCCAA
AHNAK	NM_001620.1	15420-15520	GGATTTGACCTGAATGTTCCTGGGGGTGAAATTGATGCCAGCCTCAAGGCTCCGGATGTAGATGTCAACATCGCAGGGCCGGATGCTGCACTCAAAGTCG
AIF1	NM_032955.1	315-415	AAAAGCGAGAGAAAAGGAAAAGCCAACAGGCCCCCCAGCCAAGAAAGCTATCTCTGAGTTGCCCTGATTTGAAGGGAAAAGGGATGATGGGATTGAAGGG
AIM2	NM_004833.1	607-707	ACGTGCTGCACCAAAAGTCTCTCCTCATGTTAAGCCTGAACAGAAACAGATGGTGGCCCAGCAGGAATCTATCAGAGAAGGGTTTCAGAAGCGCTGTTTG
AIMP2	NM_006303.3	507-607	CCCTCTCCCTGCTTGTGCTGCACAGGCTGCTCTGTGAGCACTTCAGGGTCCTGTCCACGGTGCACACGCACTCCTCGGTCAAGAGCGTGCCTGAAAACCT
AKIP1	NM_020642.3	570-670	GAACATCTCTAAGGACCTCTACATAGAAGTATATCCAGGGACCTATTCTGTCACTGTGGGCTCAAATGACTTAACCAAGAAGACTCATGTGGTAGCAGTT
AKT1	NM_005163.2	1772-1872	TTCTTTGCCGGTATCGTGTGGCAGCACGTGTACGAGAAGAAGCTCAGCCCACCCTTCAAGCCCCAGGTCACGTCGGAGACTGACACCAGGTATTTTGATG
ALDH1A1	NM_000689.3	11-111	ATTGCTGAGCCAGTCACCTGTGTTCCAGGAGCCGAATCAGAAATGTCATCCTCAGGCACGCCAGACTTACCTGTCCTACTCACCGATTTGAAGATTCAAT
ANXA1	NM_000700.1	515-615	GAAATCAGAGACATTAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGC
ANXA2P2	NR_003573.1	257-357	ATATTGTCTTCTCCTACCAGAGAAGGACCAAAAAGGAACTTGCATCAGCACTGAAGTCAGCCTTATCTGGCCACCTGGAGACGGTGATTTTGGGCCTATT
APAF1	NM_181869.1	1160-1260	TTCTGATGAAACTGCAGAATCTTTGCACACGGTTGGATCAGGATGAGAGTTTTTCCCAGAGGCTTCCACTTAATATTGAAGAGGCTAAAGACCGTCTCCG
ARG1	NM_000045.2	505-605	AAGGAACTAAAAGGAAAGATTCCCGATGTGCCAGGATTCTCCTGGGTGACTCCCTGTATATCTGCCAAGGATATTGTGTATATTGGCTTGAGAGACGTGG
ARRB2	NM_004313.3	1652-1752	CATTAATTTTTTGACTGCAGCTCTGCTTCTCCAGCCCCGCCGTGGGTGGCAAGCTGTGTTCATACCTAAATTTTCTGGAAGGGGACAGTGAAAAGAGGAG
ATF3	NM_001030287.2	600-700	GGCTCAGAATGGGAGGACTCCAGAAGATGAGAGAAACCTCTTTATCCAACAGATAAAAGAAGGAACATTGCAGAGCTAAGCAGTCGTGGTATGGGGGCGA
ATM	NM_000051.3	30-130	ACGCTAAGTCGCTGGCCATTGGTGGACATGGCGCAGGCGCGTTTGCTCCGACGGGCCGAATGTTTTGGGGCAGTGTTTTGAGCGCGGAGACCGCGTGATA
ATP2B4	NM_001684.3	7640-7740	CTTCCCATAGTATCATCTGTCCTCTGGAATGACTCTCCTGTCCCTAAAGGGGTTAAGAGAGAGATCACCTAGAAATCCCTCTGGACACTTGTGGGTTCTT
AXIN2	NM_004655.3	1035-1135	CTTGTCCAGCAAAACTCTGAGGGCCACGGCGAGTGTGAGGTCCACGGAAACTGTTGACAGTGGATACAGGTCCTTCAAGAGGAGCGATCCTGTTAATCCT
B2M	NM_004048.2	25-125	CGGGCATTCCTGAAGCTGACAGCATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAGGCTATCCA
B3GAT1	NM_018644.3	145-245	CTGGACAGCGACCCCTTCTCAGACTCCAGTTGGGCCGGACTCTCCAAACCTGCTTCCGCAATGGGTGGGTTGTGAGTGCTGGTAATGAGGAGCCGTGGGT
BACH2	NM_021813.2	3395-3495	TGTGGCACTGTTCATCTGCTGTCCCGAAGAAACCGAGAACACATTTGGTGCACACTACAGCGGTCTTAGCAGCAATACTGTTCCGAAGTATCCTCTCCTC
BAD	NM_004322.2	195-295	CAGCTGTGCCTTGACTACGTAACATCTTGTCCTCACAGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCA
BAG1	NM_004323.3	1490-1590	CTCTTGTGATCGTGTAGTCCCATAGCTGTAAAACCAGAATCACCAGGAGGTTGCACCTAGTCAGGAATATTGGGAATGGCCTAGAACAAGGTGTTTGGCA
BATF	NM_006399.3	825-925	CACTGTGGGTTGCAGGCCCAATGCAGAAGAGTATTAAGAAAGATGCTCAAGTCCCATGGCACAGAGCAAGGCGGGCAGGGAACGGTTATTTTTCTAAATA
BAX	NM_138761.2	694-794	ATTTTTCTGGGAGGGGTGGGGATTGGGGGACATGGGCATTTTTCTTACTTTTGTAATTATTGGGGGGTGTGGGGAAGAGTGGTCTTGAGGGGGTAATAAA
BCL10	NM_003921.2	1250-1350	TGAAAATACCATCTTCTCTTCAACTACACTTCCCAGACCTGGGGACCCAGGGGCTCCTCCTTTGCCACCAGATCTACAGTTAGAAGAAGAAGGAACTTGT
BCL11B	NM_022898.1	3420-3520	GAGATGTAGCACTCATGTCGTCCCGAGTCAAGCGGCCTTTTCTGTGTTGATTTCGGCTTTCATATTACATAAGGGAAACCTTGAGTGGTGGTGCTGGGGG
BCL2	NM_000633.2	1525-1625	CCAAGCACCGCTTCGTGTGGCTCCACCTGGATGTTCTGTGCCTGTAAACATAGATTCGCTTTCCATGTTGTTGGCCGGATCACCATCTGAAGAGCAGACG
BCL2L1	NM_138578.1	1560-1660	CTAAGAGCCATTTAGGGGCCACTTTTGACTAGGGATTCAGGCTGCTTGGGATAAAGATGCAAGGACCAGGACTCCCTCCTCACCTCTGGACTGGCTAGAG
BCL2L1	NM_001191.2	260-360	ATCTTGGCTTTGGATCTTAGAAGAGAATCACTAACCAGAGACGAGACTCAGTGAGTGAGCAGGTGTTTTGGACAATGGACTGGTTGAGCCCATCCCTATT

BCL2L11	NM_138621.2	2825-2925	TGTTGGCACCAGAACTTAAAGCGATGACTGGATGTCTCTGTACTGTATGTATCTGGTTATCAAGATGCCTCTGTGCAGAAAGTATGCCTCCCGTGGGTAT
BCL2L11	NM_138621.4	257-357	CGGACTGAGAAACGCAAGAAAAAAAGACCAAATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAG
BCL6	NM_001706.2	675-775	GTTGTGGACACTTGCCGGAAGTTTATTAAGGCCAGTGAAGCAGAGATGGTTTCTGCCATCAAGCCTCCTCGTGAAGAGTTCCTCAACAGCCGGATGCTGA
BCL6B	NM_181844.3	2135-2235	CTTTATTTGTTCTAGGGCAGCTCTGGGAACATGCGGGATTGTGGAATTGGGTCAGGAACCCTCTCTGGTATTCTGGATGTTGTAGGTTCTCTAGCAGTCT
BHLHE41	NM_030762.2	655-755	CGCCCATTCAGTCCGACTTGGATGCGTTCCACTCGGGATTTCAAACATGCGCCAAAGAAGTCTTGCAATACCTCTCCCGGTTTGAGAGCTGGACACCCAG
BID	NM_197966.1	2095-2195	GCTTAGCTTTAGAAACAGTGCAACACTGGTCTGCTGTTCCAGTGGTAAGCTATGTCCCAGGAATCAGTTTAAAAGCACGACAGTGGATGCTGGGTCCATA
BIRC2	NM_001166.3	1760-1860	TGGGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATCTCCCACCTTGGAACATAGTAGCTTGTTCAGTGGTTCTTACTC
BLK	NM_001715.2	990-1090	AGCTTCTTGCTCCAATCAACAAGGCCGGCTCCTTTCTTATCAGAGAGAGTGAAACCAACAAAGGTGCCTTCTCCCTGTCTGTGAAGGATGTCACCACCCA
BMI1	NM_005180.5	1145-1245	CCTGGAGAAGGAATGGTCCACTTCCATTGAAATACAGAGTTCGACCTACTTGTAAAAGAATGAAGATCAGTCACCAGAGAGATGGACTGACAAATGCTGG
BNIP3	NM_004052.2	325-425	CACCTCGCTCGCAGACACCACAAGATACCAACAGGGCTTCTGAAACAGATACCCATAGCATTGGAGAGAAAAACAGCTCACAGTCTGAGGAAGATGATAT
BTLA	NM_001085357.1	890-990	GCACCAACAGAATATGCATCCATATGTGTGAGGAGTTAAGTCTGTTTCTGACTCCAACAGGGACCATTGAATGATCAGCATGTTGACATCATTGTCTGGG
C21orf33	NM_004649.5	1340-1440	TTGAGTTAATCAGCGTAAGGGGATTTCTAAAGCAGGCAATCCCTGTAGCCGCAGAGAATAAACGCCTTCCCAAAATGGCAACTTCCCACAGCCACATTTC
CA2	NM_000067.2	575-675	AGCTGTGCAGCAACCTGATGGACTGGCCGTTCTAGGTATTTTTTTGAAGGTTGGCAGCGCTAAACCGGGCCTTCAGAAAGTTGTTGATGTGCTGGATTCC
CA9	NM_001216.2	960-1060	CAGGTCCCAGGACTGGACATATCTGCACTCCTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCCAGGGTG
CARD9	NM_052813.2	1850-1950	CGCTGACTTGGCCTGGAACGAGGAATCTGGTGCCCTGAAAGGCCCAGCCGGACTGCCGGGCATTGGGGCCGTTTGTTAAGCGGCACTCATTTTGCGGAGG
CASP1	NM_033292.2	575-675	ACAGGCATGACAATGCTGCTACAAAATCTGGGGTACAGCGTAGATGTGAAAAAAAATCTCACTGCTTCGGACATGACTACAGAGCTGGAGGCATTTGCAC
CAT	NM_001752.2	1130-1230	ATGCTTCAGGGCCGCCTTTTTGCCTATCCTGACACTCACCGCCATCGCCTGGGACCCAATTATCTTCATATACCTGTGAACTGTCCCTACCGTGCTCGAG
CBLB	NM_170662.3	3195-3295	TAATGTCGAAGTTGCCCGGAGCATCCTCCGAGAATTTGCCTTCCCTCCTCCAGTATCCCCACGTCTAAATCTATAGCAGCCAGAACTGTAGACACCAAAA
CCBP2	NM_001296.3	1345-1445	GAACAGATGGGAACCAGCTCAATTGGGTGTCCACTCAAAGTGCTCTCTCCAGGGGCCTCAGTGACTGTGTTGCTAAACCCAGTGGTCAGTTCTCAGTTCT
CCL3	NM_002983.2	681-781	CTGTGTAGGCAGTCATGGCACCAAAGCCACCAGACTGACAAATGTGTATCGGATGCTTTTGTTCAGGGCTGTGATCGGCCTGGGGAAATAATAAAGATGC
CCL4	NM_002984.2	35-135	TTCTGCAGCCTCACCTCTGAGAAAACCTCTTTGCCACCAATACCATGAAGCTCTGCGTGACTGTCCTGTCTCTCCTCATGCTAGTAGCTGCCTTCTGCTC
CCL5	NM_002985.2	280-380	AGTGTGTGCCAACCCAGAGAAGAAATGGGTTCGGGAGTACATCAACTCTTTGGAGATGAGCTAGGATGGAGAGTCCTTGAACCTGAACTTACACAAATTT
CCNB1	NM_031966.2	715-815	AACTTGAGGAAGAGCAAGCAGTCAGACCAAAATACCTACTGGGTCGGGAAGTCACTGGAAACATGAGAGCCATCCTAATTGACTGGCTAGTACAGGTTCA
CCND1	NM_053056.2	690-790	TTGAACACTTCCTCTCCAAAATGCCAGAGGCGGAGGAGAACAAACAGATCATCCGCAAACACGCGCAGACCTTCGTTGCCCTCTGTGCCACAGATGTGAA
CCR1	NM_001295.2	535-635	CATCATTTGGGCCCTGGCCATCTTGGCTTCCATGCCAGGCTTATACTTTTCCAAGACCCAATGGGAATTCACTCACCACACCTGCAGCCTTCACTTTCCT
CCR2	NM_001123041.2	20-120	ACATTCTGTTGTGCTCATATCATGCAAATTATCACTAGTAGGAGAGCAGAGAGTGGAAATGTTCCAGGTATAAAGACCCACAAGATAAAGAAGCTCAGAG
CCR4	NM_005508.4	35-135	GGTCCTTCTTAGCATCGTGCTTCCTGAGCAAGCCTGGCATTGCCTCACAGACCTTCCTCAGAGCCGCTTTCAGAAAAGCAAGCTGCTTCTGGTTGGGCCC
CCR5	NM_000579.1	2730-2830	TAGGAACATACTTCAGCTCACACATGAGATCTAGGTGAGGATTGATTACCTAGTAGTCATTTCATGGGTTGTTGGGAGGATTCTATGAGGCAACCACAGG
CCR6	NM_031409.2	935-1035	CTTTAACTGCGGGATGCTGCTCCTGACTTGCATTAGCATGGACCGGTACATCGCCATTGTACAGGCGACTAAGTCATTCCGGCTCCGATCCAGAACACTA
CCR7	NM_001838.2	1610-1710	TTCCGAAAACCAGGCCTTATCTCCAAGACCAGAGATAGTGGGGAGACTTCTTGGCTTGGTGAGGAAAAGCGGACATCAGCTGGTCAAACAAACTCTCTGA
CD160	NM_007053.2	500-600	TTGATGTTCACCATAAGCCAAGTCACACCGTTGCACAGTGGGACCTACCAGTGTTGTGCCAGAAGCCAGAAGTCAGGTATCCGCCTTCAGGGCCATTTTT
CD19	NM_001770.4	1770-1870	AGATTCACACCTGACTCTGAAATCTGAAGACCTCGAGCAGATGATGCCAACCTCTGGAGCAATGTTGCTTAGGATGTGTGCATGTGTGTAAGTGTGTGTG
CD19R-scfv	SCFV013.1	204-304	GGCACCGACTACAGCCTGACCATCTCCAACCTGGAGCAGGAGGACATCGCCACCTACTTTTGCCAGCAGGGCAACACACTGCCCTACACCTTTGGCGGCG
CD19RCD28	MDA_00002.1	2-102	CAGGTGTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGTGCCAAGCACTACTACTACGGCGGCAGCTACGCCATGGACTACT
CD2	NM_001767.2	1400-1500	TGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTTCTTATGTGCCCTGGTGGACACTTGCCCACCATCCTGTGAGTAAAAGTGAAATA

CD20-scfv (rutuximab)	SCFV002.1	8-108	GCTGTCCCAGAGCCCCGCCATCCTGAGCGCCAGCCCTGGCGAGAAGGTGACCATGACCTGCCGGGCCAGCAGCTCTGTGAGCTACATGCACTGGTATCAG
CD226	NM_006566.2	163-263	TAAACAGGATACGATAAAAGTCCTTAACCAAGACGCAGATGGGAAGAAGCGTTAGAGCGAGCAGCACTCACATCTCAAGAACCAGCCTTTCAAACAGTTT
CD244	NM_016382.2	1150-1250	AAGAGGAACCACAGCCCTTCCTTCAATAGCACTATCTATGAAGTGATTGGAAAGAGTCAACCTAAAGCCCAGAACCCTGCTCGATTGAGCCGCAAAGAGC
CD247	NM_198053.1	1490-1590	TGGCAGGACAGGAAAAACCCGTCAATGTACTAGGATACTGCTGCGTCATTACAGGGCACAGGCCATGGATGGAAAACGCTCTCTGCTCTGCTTTTTTTCT
CD27	NM_001242.4	330-430	CCAGATGTGTGAGCCAGGAACATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACCGGGGGTCTCCTTCTCTCCT
CD274	NM_014143.2	684-784	TAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGGACTCACTTGGTAATTCTG
CD276	NM_001024736.1	2120-2220	ACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATAT
CD28	NM_006139.1	305-405	GCTTGTAGCGTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTTCTCAAGGGAGTTCCGGGCATCCCTTCACAAAGGACTGGATAGT
CD300A	NM_007261.2	0-100	CGGGGAAGTGAGAGTCGGGGATCAGTCCTGCAAGCTACGGAGTCACTACAGGGAGAGGTCTCATCACTAGAAATAGCCGAAGAACCTGCAGCCTCAACCA
CD38	NM_001775.2	1035-1135	CCTTGACTCCTTGTGGTTTATGTCATCATACATGACTCAGCATACCTGCTGGTGCAGAGCTGAAGATTTTGGAGGGTCCTCCACAATAAGGTCAATGCCA
CD3D	NM_000732.4	110-210	TATCTACTGGATGAGTTCCGCTGGGAGATGGAACATAGCACGTTTCTCTCTGGCCTGGTACTGGCTACCCTTCTCTCGCAAGTGAGCCCCTTCAAGATAC
CD3E	NM_000733.2	75-175	AAGTAACAGTCCCATGAAACAAAGATGCAGTCGGGCACTCACTGGAGAGTTCTGGGCCTCTGCCTCTTATCAGTTGGCGTTTGGGGGCAAGATGGTAATG
CD4	NM_000616.3	835-935	AGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAGCATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAGTTGAA
CD40LG	NM_000074.2	1225-1325	GCATTTGATTTATCAGTGAAGATGCAGAAGGGAAATGGGGAGCCTCAGCTCACATTCAGTTATGGTTGACTCTGGGTTCCTATGGCCTTGTTGGAGGGGG
CD44	NM_000610.3	2460-2560	GTGGGCAGAAGAAAAAGCTAGTGATCAACAGTGGCAATGGAGCTGTGGAGGACAGAAAGCCAAGTGGACTCAACGGAGAGGCCAGCAAGTCTCAGGAAAT
CD45R-scfv	SCFV006.1	222-322	TTCACCCTGAACATCCACCCCGTGGAGGAAGAGGACGCCGCCACCTACTACTGCCAGCACAGCAGAGAGCTGCCCTTCACCTTCGGCTCCGGCACCAAGC
CD47	NM_001777.3	897-997	GCCATATTGGTTATTCAGGTGATAGCCTATATCCTCGCTGTGGTTGGACTGAGTCTCTGTATTGCGGCGTGTATACCAATGCATGGCCCTCTTCTGATTT
CD56R-scfv	SCFV008.1	197-297	ATTCAGCGGCTCTGGCTCCGGCACCGACTTCACTCTGATGATCTCTCGGGTGGAGGCCGAGGACCTGGGCGTGTACTACTGCTTTCAGGGCAGCCACGTG
CD58	NM_001779.2	478-578	GTGCTTGAGTCTCTTCCATCTCCCACACTAACTTGTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATACCAGAGCATTACAACAGCCATCGAG
CD63	NM_001780.4	350-450	GTCATCATCGCAGTGGGTGTCTTCCTCTTCCTGGTGGCTTTTGTGGGCTGCTGCGGGGCCTGCAAGGAGAACTATTGTCTTATGATCACGTTTGCCATCT
CD69	NM_001781.1	460-560	AGGACATGAACTTTCTAAAACGATACGCAGGTAGAGAGGAACACTGGGTTGGACTGAAAAAGGAACCTGGTCACCCATGGAAGTGGTCAAATGGCAAAGA
CD7	NM_006137.6	440-540	CCTACACCTGCCAGGCCATCACGGAGGTCAATGTCTACGGCTCCGGCACCCTGGTCCTGGTGACAGAGGAACAGTCCCAAGGATGGCACAGATGCTCGGA
CD80	NM_005191.3	1288-1388	AAAGATCTGAAGGTCCCACCTCCATTTGCAATTGACCTCTTCTGGGAACTTCCTCAGATGGACAAGATTACCCCACCTTGCCCTTTACGTATCTGCTCTT
CD86	NM_006889.3	146-246	TATGGGACTGAGTAACATTCTCTTTGTGATGGCCTTCCTGCTCTCTGGTGCTGCTCCTCTGAAGATTCAAGCTTATTTCAATGAGACTGCAGACCTGCCA
CD8A	NM_001768.5	1320-1420	GCTCAGGGCTCTTTCCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCTTGAGTCTCCAACGGCAAGGGAACAAGTACTT
CDH1	NM_004360.2	1230-1330	CGATAATCCTCCGATCTTCAATCCCACCACGTACAAGGGTCAGGTGCCTGAGAACGAGGCTAACGTCGTAATCACCACACTGAAAGTGACTGATGCTGAT
CDK2	NM_001798.2	220-320	TCGCTGGCGCTTCATGGAGAACTTCCAAAAGGTGGAAAAGATCGGAGAGGGCACGTACGGAGTTGTGTACAAAGCCAGAAACAAGTTGACGGGAGAGGTG
CDK4	NM_000075.2	1055-1155	ACTTTTAACCCACACAAGCGAATCTCTGCCTTTCGAGCTCTGCAGCACTCTTATCTACATAAGGATGAAGGTAATCCGGAGTGAGCAATGGAGTGGCTGC
CDKN1A	NM_000389.2	1975-2075	CATGTGTCCTGGTTCCCGTTTCTCCACCTAGACTGTAAACCTCTCGAGGGCAGGGACCACACCCTGTACTGTTCTGTGTCTTTCACAGCTCCTCCCACAA
CDKN1B	NM_004064.2	365-465	GCTTCCGAGAGGGGTTCGGGCCGCGTAGGGGCGCTTTGTTTTGTTCGGTTTTGTTTTTTTGAGAGTGCGAGAGAGGCGGTCGTGCAGACCCGGGAGAAAG
CDKN2A	NM_000077.3	975-1075	AAGCGCACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACAAGCATTTTGTGAACTAGGGAAGCTCAGGGGGGT
CDKN2C	NM_001262.2	1295-1395	ATAATGTAAACGTCAATGCACAAAATGGATTTGGAAGGACTGCGCTGCAGGTTATGAAACTTGGAAATCCCGAGATTGCCAGGAGACTGCTACTTAGAGG
CEBPA	NM_004364.2	1320-1420	GAGCTGGGAGCCCGGCAACTCTAGTATTTAGGATAACCTTGTGCCTTGGAAATGCAAACTCACCGCTCCAATGCCTACTGAGTAGGGGGAGCAAATCGTG
CFLAR	NM_003879.3	445-545	CAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGC
CFLAR	NM_001127183.1	653-753	TAGAGTGCTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATGGGCCGAGGCAAGATAAGC

CHPT1	NM_020244.2	1303-1403	GATATGGTGATATACTTTAGTGCTTTGTGCCTGCAAATTTCAAGACACCTTCATCTAAATATATTCAAGACTGCATGTCATCAAGCACCTGAACAGGTTC
CIITA	NM_000246.3	470-570	GCCTGAGCAAGGACATTTTCAAGCACATAGGACCAGATGAAGTGATCGGTGAGAGTATGGAGATGCCAGCAGAAGTTGGGCAGAAAAGTCAGAAAAGACC
CITED2	NM_006079.3	965-1065	AGGAGCTGCCCGAACTCTGGCTGGGGCAAAACGAGTTTGATTTTATGACGGACTTCGTGTGCAAACAGCAGCCCAGCAGAGTGAGCTGTTGACTCGATCG
CLIC1	NM_001288.4	310-410	GTGATGGGGCCAAGATTGGGAACTGCCCATTCTCCCAGAGACTGTTCATGGTACTGTGGCTCAAGGGAGTCACCTTCAATGTTACCACCGTTGACACCAA
CLNK	NM_052964.2	1108-1208	GAAGGAGAACAAGGATGGTAGTTTCTTGGTCCGAGATTGTTCCACAAAATCCAAGGAAGAGCCCTATGTTTTGGCTGTGTTTTATGAGAACAAAGTCTAC
c-MET-scfv	SCFV004.1	138-238	CTGATCTACGCCGCCAGCAGCCTGAAGAGCGGCGTGCCCAGCCGGTTTAGCGGCTCTGGCTCTGGCGCCGACTTCACCCTGACCATCAGCAGCCTGCAGC
CREB1	NM_004379.3	4855-4955	TTTGATGGTAGGTCAGCAGCAGTGCTAGTCTCTGAAAGCACAATACCAGTCAGGCAGCCTATCCCATCAGATGTCATCTGGCTGAAGTTTATCTCTGTCT
CREM	NM_001881.2	260-360	CTCCACCTCCTCGCGTCCGTAATCAGTGACGAGGTCCGCTACGTAAATCCCTTTGCGGCGGACAAATGACCATGGAAACAGTTGAATCCCAGCATGATGG
CRIP1	NM_001311.4	269-369	CAACCACCCCTGCTACGCAGCCATGTTTGGGCCTAAAGGCTTTGGGCGGGGCGGAGCCGAGAGCCACACTTTCAAGTAAACCAGGTGGTGGAGACCCCAT
CRLF2	NM_022148.2	1420-1520	CAAGGCAGCACGTCCAAAATGCTGTAAAACCATCTTCCCACTCTGTGAGTCCCCAGTTCCGTCCATGTACCTGTTCCATAGCATTGGATTCTCGGAGGAT
CSAD	NM_015989.4	205-305	TCAAATTCTTCTGCCTAGCCTTAGCCATTAGAGAGAGGTCCTGCTAAAGATGGACTGCAAATGCGCTTGATGGAAGGAGATGTCAATTCCACTGAAGTCC
CSF2	NM_000758.2	475-575	AGATGAGGCTGGCCAAGCCGGGGAGCTGCTCTCTCATGAAACAAGAGCTAGAAACTCAGGATGGTCATCTTGGAGGGACCAAGGGGTGGGCCACAGCCAT
CSNK2A1	NM_177559.2	1930-2030	CCATTCCCACCATTGTTCCTCCACCGTCCCACACTTTAGGGGGTTGGTATCTCGTGCTCTTCTCCAGAGATTACAAAAATGTAGCTTCTCAGGGGAGGCA
CTGF	NM_001901.2	1100-1200	ACCACCCTGCCGGTGGAGTTCAAGTGCCCTGACGGCGAGGTCATGAAGAAGAACATGATGTTCATCAAGACCTGTGCCTGCCATTACAACTGTCCCGGAG
CTLA4	NM_005214.3	405-505	AGTCTGTGCGGCAACCTACATGATGGGGAATGAGTTGACCTTCCTAGATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATC
CTNNA1	NM_001903.2	75-175	TCGCCCAGCTAGCCGCAGAAATGACTGCTGTCCATGCAGGCAACATAAACTTCAAGTGGGATCCTAAAAGTCTAGAGATCAGGACTCTGGCAGTTGAGAG
CTNNB1	NM_001098210.1	1815-1915	TCTTGCCCTTTGTCCCGCAAATCATGCACCTTTGCGTGAGCAGGGTGCCATTCCACGACTAGTTCAGTTGCTTGTTCGTGCACATCAGGATACCCAGCGC
CTNNBL1	NM_030877.3	855-955	TGATGCCAACAAACTGTATTGCAGTGAAGTGCTGGCCATATTGCTCCAGGACAATGATGAAAACAGGGAATTGCTTGGGGAGCTGGATGGAATCGATGTG
CTSC	NM_001114173.1	260-360	TGCTCGGTTATGGGACCACAAGAAAAAAAAGTAGTGGTGTACCTTCAGAAGCTGGATACAGCATATGATGACCTTGGCAATTCTGGCCATTTCACCATCA
CTSD	NM_001909.3	1495-1595	GAAGCCGGCGGCCCAAGCCCGACTTGCTGTTTTGTTCTGTGGTTTTCCCCTCCCTGGGTTCAGAAATGCTGCCTGCCTGTCTGTCTCTCCATCTGTTTGG
CX3CL1	NM_002996.3	140-240	AGCACCACGGTGTGACGAAATGCAACATCACGTGCAGCAAGATGACATCAAAGATACCTGTAGCTTTGCTCATCCACTATCAACAGAACCAGGCATCATG
CX3CR1	NM_001337.3	1040-1140	GGGCGCTCAGTCCACGTTGATTTCTCCTCATCTGAATCACAAAGGAGCAGGCATGGAAGTGTTCTGAGCAGCAATTTTACTTACCACACGAGTGATGGAG
CXCL10	NM_001565.1	40-140	GCAGAGGAACCTCCAGTCTCAGCACCATGAATCAAACTGCGATTCTGATTTGCTGCCTTATCTTTCTGACTCTAAGTGGCATTCAAGGAGTACCTCTCTC
CXCL12	NM_199168.2	505-605	GGGCCTGAGGTTTGCCAGCATTTAGACCCTGCATTTATAGCATACGGTATGATATTGCAGCTTATATTCATCCATGCCCTGTACCTGTGCACGTTGGAAC
CXCL9	NM_002416.1	1975-2075	CACCATCTCCCATGAAGAAAGGGAACGGTGAAGTACTAAGCGCTAGAGGAAGCAGCCAAGTCGGTTAGTGGAAGCATGATTGGTGCCCAGTTAGCCTCTG
CXCR1	NM_000634.2	1950-2050	GCAGCCACCAGTCCATTGGGCAGGCAGATGTTCCTAATAAAGCTTCTGTTCCGTGCTTGTCCCTGTGGAAGTATCTTGGTTGTGACAGAGTCAAGGGTGT
CXCR3	NM_001504.1	80-180	GTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCT
CXCR4	NM_001008540.1	135-235	GTCACTATGGGAAAAGATGGGGAGGAGAGTTGTAGGATTCTACATTAATTCTCTTGTGCCCTTAGCCCACTACTTCAGAATTTCCTGAAGAAAGCAAGCC
DAPL1	NM_001017920.2	190-290	CGAGAAAACAAGTGCCATTGCAAATGTTGCCAAAATACAGACACTGGATGCCCTGAATGACGCACTGGAGAAGCTCAACTATAAATTTCCAGCAACAGTG
DEC1	NM_017418.2	190-290	AGGCCTTACTTTCCAGATCCAGATCCTTGTGCATACAACTGACTTGTGTGGGTGAGGCTTGCAGAAAAAATCAGCTAGAACAGCCTTGGGGGTAGTGGCA
DECTIN-1R	SCFV010.1	270-370	CTGAAGATCGACAGCAGCAACGAGCTGGGCTTCATCGTGAAGCAGGTGTCCAGCCAGCCCGACAACTCCTTCTGGATCGGCCTGAGCAGGCCCCAGACCG
DGKA	NM_001345.4	1375-1475	TTCCTAACACCCACCCACTTCTCGTCTTTGTCAATCCTAAGAGTGGCGGGAAGCAGGGGCAAAGGGTGCTCTGGAAGTTCCAGTATATATTAAACCCTCG
DOCK5	NM_024940.6	630-730	TGCGAGATGACAATGGGAACATCCTAGACCCTGACGAAACCAGCACCATTGCCCTCTTCAAGGCCCATGAGGTGGCCTCCAAAAGGATTGAGGAAAAGAT
DOK2	NM_003974.2	650-750	GCCAGGGACCCAGCTGTACGACTGGCCCTACAGGTTTCTGCGGCGCTTTGGGCGGGACAAGGTAACCTTTTCCTTTGAGGCAGGCCGTCGCTGCGTCTCT
DPP4	NM_001935.3	2700-2800	CAGCAGTCAGCTCAGATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAAGACCATGGAATAGCTAGCAGCACAG

DUSP16	NM_030640.2	615-715	ATGGGTTTAACTCTCCTTTTGCCAGTCACCACCAGCCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACCATTACATCA
EGFR-scfv_ (NIMO CAR)	SCFV015.1	7-107	AGATGACCCAGAGCCCTAGCAGCCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACCTGCCGGTCCAGCCAGAACATCGTGCACAGCAACGGCAACAC
EGLN1	NM_022051.1	3975-4075	AGCAGCATGGACGACCTGATACGCCACTGTAACGGGAAGCTGGGCAGCTACAAAATCAATGGCCGGACGAAAGCCATGGT
EGLN3	NM_022073.3	800-900	AAGCTACATGGTGGGATCCTGCGGATATTTCCAGAGGGGAAATCATTCATAGCAGATGTGGAGCCCATTTTTGACAGACTCCTGTTCTTCTGGTCAGATC
EIF1	NM_005801.3	869-969	CCTGAACAGTCCTCGGTGAATCTGAGAGGAGAGGATGGGGTAAGGCAGAAGCACCAGCTGTACTACTAGAAGGGAGCTTTTGGTGGTAGATCCCCTGGTG
ELF4	NM_001421.3	335-435	AGCTCTGGAGGGCTCTGATAATCCCGTTGTCAGCTCTCTGAAAAGACAGCATGGCTATTACCCTACAGCCCAGTGACCTGATCTTTGAGTTCGCAAGCAA
ELOF1	NM_032377.3	125-225	AGACCCAGTTCACCTGCCCCTTCTGCAACCACGAGAAATCCTGTGATGTGAAAATGGACCGTGCCCGCAACACCGGAGTCATCTCTTGTACCGTGTGCCT
ENTPD1	NM_001776.4	225-325	TTCGAGTAACTTTAGGAAAATGAGCTGCTGGACTCCTCAGTCAATCTGTCCTTTCTAGTCAATGAAAAAGACAGGGTTTGAGGTTCCTTCCGAAACGGGG
EOMES	NM_005442.2	1670-1770	ATCCCATGCCCTGGGGTATTACCCAGACCCAACCTTTCCTGCAATGGCAGGGTGGGGAGGTCGAGGTTCTTACCAGAGGAAGATGGCAGCTGGACTACCA
EPHA2	NM_004431.2	1525-1625	GAGCCGAGTGTGGAAGTACGAGGTCACTTACCGCAAGAAGGGAGACTCCAACAGCTACAATGTGCGCCGCACCGAGGGTTTCTCCGTGACCCTGGACGAC
EPHA4	NM_004438.3	20-120	GCAGCGTTGGCACCGGCGAACCATGGCTGGGATTTTCTATTTCGCCCTATTTTCGTGTCTCTTCGGGATTTGCGACGCTGTCACAGGTTCCAGGGTATAC
EPHB2	NM_017449.2	785-885	CAAAGCAGGCTTCGAGGCCGTTGAGAATGGCACCGTCTGCCGAGGTTGTCCATCTGGGACTTTCAAGGCCAACCAAGGGGATGAGGCCTGTACCCACTGT
ETV6	NM_001987.4	3840-3940	GTATGAATATGAAATCAGAGACCAGGGCATGATGTTGCTAGGATTAGAGCCTCTCAGTCTGGCCTCTTCACCCAAGTGCAAGAACTCAGTCTCTTACTGT
FADD	NM_003824.2	1560-1660	TGAGACTGCTAAGTAGGGGCAGTGATGGTTGCCAGGACGAATTGAGATAATATCTGTGAGGTGCTGATGAGTGATTGACACACAGCACTCTCTAAATCTT
FAM129A	NM_052966.2	3526-3626	TGCCCAATAGATTCAAGAGAAGCTAAGCGGAAATGGAGGGTGGAAGGTGTGATCTGTGGGACTGTCTGGGCCTGTTACTCATCCTGCTATCAATTTCTTA
FANCC	NM_000136.2	2130-2230	GACTCAGTCAGACATGTTCACTAATGACTCAAGTGAGCCTTCGGTACTCCTGGTGCCCGCCCGGCCAGACCGTCAGCTTGATAATTACTAAAGCAAAGGC
FAS	NM_000043.3	90-190	CACCGGGGCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGA
FASLG	NM_000639.1	625-725	TCCATGCCTCTGGAATGGGAAGACACCTATGGAATTGTCCTGCTTTCTGGAGTGAAGTATAAGAAGGGTGGCCTTGTGATCAATGAAACTGGGCTGTACT
FCGR3B	NM_000570.3	73-173	CCTATTCCTGTTCTATGGTGGGGCTCCATTGCGAGACTTCAGATTGAGAAATCAGATGAAGTTTCAAGAAAAGGAAACTGGCAGGTGACAGAGATGGGTG
FGL2	NM_006682.2	250-350	CAATTCAGCAGGATCGAGGAGGTGTTCAAAGAAGTCCAAAACCTCAAGGAAATCGTAAATAGTCTAAAGAAATCTTGCCAAGACTGCAAGCTGCAGGCTG
FLT1	NM_002019.2	5615-5715	TTCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGATGGGAATAGGGAGACAGGGTAGGAAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGG
FLT3LG	NM_001459.2	927-1027	CCTCCCCAGAATGGAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGTACAAAGCCCTTGTCCCCATGAAATTGTATATAAATCATCCT
FOS	NM_005252.2	1475-1575	ACTCAAGTCCTTACCTCTTCCGGAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGTGACACTTCAGAGAGCTGGTAGTTAGTAGCATGTTGAGC
FOXO1	NM_002015.3	1526-1626	TCTCATCACCAACATCATTAACTGTTTCGACCCAGTCCTCACCTGGCACCATGATGCAGCAGACGCCGTGCTACTCGTTTGCGCCACCAAACACCAGTTT
FOXO3	NM_001455.2	1860-1960	CCGGAACGTGATGCTTCGCAATGATCCGATGATGTCCTTTGCTGCCCAGCCTAACCAGGGAAGTTTGGTCAATCAGAACTTGCTCCACCACCAGCACCAA
FOXP1	NM_032682.5	6758-6858	CCTGAAAATCAGATTTACAATGCTGAAGGCATTTCTTGGGCCCAGTGTAGCTCACGCAATCTCTGCTACCCATAAGCCTTGATGAAGATGATACAGTCCG
FOXP3	NM_014009.3	1230-1330	GGGCCATCCTGGAGGCTCCAGAGAAGCAGCGGACACTCAATGAGATCTACCACTGGTTCACACGCATGTTTGCCTTCTTCAGAAACCATCCTGCCACCTG
FYN	NM_002037.3	765-865	GTCTTTGGAGGTGTGAACTCTTCGTCTCATACGGGGACCTTGCGTACGAGAGGAGGAACAGGAGTGACACTCTTTGTGGCCCTTTATGACTATGAAGCAC
FZD1	NM_003505.1	2430-2530	GTGCCAATCCTGACATCTCGAGGTTTCCTCACTAGACAACTCTCTTTCGCAGGCTCCTTTGAACAACTCAGCTCCTGCAAAAGCTTCCGTCCCTGAGGCA
G6PD	NM_000402.2	1155-1255	ACAACATCGCCTGCGTTATCCTCACCTTCAAGGAGCCCTTTGGCACTGAGGGTCGCGGGGGCTATTTCGATGAATTTGGGATCATCCGGGACGTGATGCA
GABPA	NM_002040.3	1160-1260	GACCAAGTCCTGCATTGGGTGGTTTGGGTAATGAAGGAATTCAGCATGACCGATATAGACCTCACCACACTCAACATTTCGGGGAGAGAATTATGTAGTC
GADD45A	NM_001924.2	865-965	GTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCA
GADD45B	NM_015675.2	365-465	TGTGGACCCAGACAGCGTGGTCCTCTGCCTCTTGGCCATTGACGAGGAGGAGGAGGATGACATCGCCCTGCAAATCCACTTCACGCTCATCCAGTCCTTC
GAL3ST4	NM_024637.4	1140-1240	CGAGCCCAAACCCTCAATCCCAATGCCCTCATCCATCCTGTTTCCACTGTTACTGATCATCGCAGCCAGATATCAAGCCCTGCCTCTTTCGATTTGGGGT
GAS2	NM_005256.3	915-1015	GATCTCCCGTGTGGATGGCAAAACATCCCCTATCCAAAGCAAATCTCCAACTCTAAAGGACATGAATCCAGATAACTACTTGGTGGTCTCTGCCAGTTAT

GATA2	NM_032638.3	1495-1595	GAAGAAGGAAGGGATCCAGACTCGGAACCGGAAGATGTCCAACAAGTCCAAGAAGAGCAAGAAAGGGGCGGAGTGCTTCGAGGAGCTGTCAAAGTGCATG
GATA3	NM_001002295.1	2835-2935	AAGAGTCCGGCGGCATCTGTCTTGTCCCTATTCCTGCAGCCTGTGCTGAGGGTAGCAGTGTATGAGCTACCAGCGTGCATGTCAGCGACCCTGGCCCGAC
gBAD-1R-scfv	SCFV001.1	1-101	AGACAGACACCCTGCTCCTCTGGGTGTCCGGCACCTGTGGCGACATCGTGATGAGCAGAAGCCCCAGCAGCCTGGCCGTGTCCGTGGGCGAGAAAGTGAC
GEMIN2	NM_001009182.1	537-637	ACAAGCAACAGTAACTAGTGTCTTGGAATATCTGAGTAATTGGTTTGGAGAAAGAGACTTTACTCCAGAATTGGGAAGATGGCTTTATGCTTTATTGGCT
GFI1	NM_005263.2	2235-2335	TCATCACTGGAGGTAAAAGCACAAGCAATGCCTGTGGACAAGATGTCATTCATTCACTCAGCAAATGTTCATGGATCACCGGCTACCAAGGTACCAGGCA
GLIPR1	NM_006851.2	255-355	CTGCGTTCGAATCCATAACAAGTTCCGATCAGAGGTGAAACCAACAGCCAGTGATATGCTATACATGACTTGGGACCCAGCACTAGCCCAAATTGCAAAA
GLO1	NM_006708.1	1240-1340	GGAAATGATATGGTACCCAGACACTGGGCTAGGCTGCAACTTTATCTCATTTAATACTCCCAGCTGTCATGTGAGAAAGAAAGCAGGCTAGGCATGTGAA
GNLY	NM_006433.2	305-405	CAGGAGCTGGGCCGTGACTACAGGACCTGTCTGACGATAGTCCAAAAACTGAAGAAGATGGTGGATAAGCCCACCCAGAGAAGTGTTTCCAATGCTGCGA
GSK3B	NM_002093.2	925-1025	ACTGATTATACCTCTAGTATAGATGTATGGTCTGCTGGCTGTGTGTTGGCTGAGCTGTTACTAGGACAACCAATATTTCCAGGGGATAGTGGTGTGGATC
GZMA	NM_006144.2	155-255	AGACCCTACATGGTCCTACTTAGTCTTGACAGAAAAACCATCTGTGCTGGGGCTTTGATTGCAAAAGACTGGGTGTTGACTGCAGCTCACTGTAACTTGA
GZMB	NM_004131.3	540-640	ACACTACAAGAGGTGAAGATGACAGTGCAGGAAGATCGAAAGTGCGAATCTGACTTACGCCATTATTACGACAGTACCATTGAGTTGTGCGTGGGGGACC
GZMH	NM_033423.3	705-805	AAAAAAGGGACACCTCCAGGAGTCTACATCAAGGTCTCACACTTCCTGCCCTGGATAAAGAGAACAATGAAGCGCCTCTAACAGCAGGCATGAGACTAAC
HCST	NM_001007469.1	132-232	ATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTT
HDAC1	NM_004964.2	785-885	CAAGCCGGTCATGTCCAAAGTAATGGAGATGTTCCAGCCTAGTGCGGTGGTCTTACAGTGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTC
HDAC2	NM_001527.1	930-1030	AAGCCTATTATCTCAAAGGTGATGGAGATGTATCAACCTAGTGCTGTGGTATTACAGTGTGGTGCAGACTCATTATCTGGTGATAGACTGGGTTGTTTCA
HER2-scfv	SCFV014.1	64-164	CCTGCAGCGCCAGCAGCAGCGTGTCCTACATGCACTGGTATCAGCAGAAGTCCGGCACTAGCCCCAAGCGGTGGATCTACGACACCTACAAGCTCGCCAG
HERV-K 6H5-scfv	SCFV012.1	137-237	CGGCGGCACCAGCTACAACCAGAAGTTCAAGGACAAGGCCATCCTGACCGTGGACAAGAGCAGCAGCACCGCCTACATGGAACTGCGGAGCCTGACCAGC
HLA-A	NM_002116.5	1000-1100	GGAAGAGCTCAGATAGAAAAGGAGGGAGTTACACTCAGGCTGCAAGCAGTGACAGTGCCCAGGGCTCTGATGTGTCCCTCACAGCTTGTAAAGTGTGAGA
HMGB2	NM_001130688.1	125-225	CTGTCAACATGGGTAAAGGAGACCCCAACAAGCCGCGGGGCAAAATGTCCTCGTACGCCTTCTTCGTGCAGACCTGCCGGGAAGAGCACAAGAAGAAACA
HOPX	NM_001145460.1	1117-1217	AACAATAGGAAGCTATGTGTATCTTCTGTGTAAAGCAGTGGCTTCACTGGAAAAATGGTGTGGCTAGCATTTCCCTTTGAGTCATGATGACAGATGGTGT
HOXA10	NM_018951.3	1503-1603	TTCTATAGAGATAGATATTGTCCTAAGTGTCAAGTCCTGACTGGGCTGGGTTTGCTGTCTTGGGGTCCCACTGCTCGAAATGGCCCCTGTCTTCGGCCGA
HOXA9	NM_152739.3	1015-1115	GGCTCTAAACCTCAGGCCACATCTTTTCCAAGGCAAACCCTGTTCAGGCTGGCTCGTAGGCCTGCCGCTTTGATGGAGGAGGTATTGTAAGCTTTCCATT
HOXB3	NM_002146.4	60-160	TGTCCGTTTAAATGCTGCTGGGAGACTCGTAAAAAAATCATCGTGGACCTGGAGGATGAGAGGGGCGAGCTTTATTTCGGTCGGATTGCGGTGTGGTGGT
HOXB4	NM_024015.4	1340-1440	CCTTTCTTTGTCCCCCACTCCCGATACCCAGCGAAAGCACCCTCTGACTGCCAGATAGTGCAGTGTTTTGGTCACGGTAACACACACACACTCTCCCTCA
HPRT1	NM_000194.1	240-340	TGTGATGAAGGAGATGGGAGGCCATCACATTGTAGCCCTCTGTGTGCTCAAGGGGGGCTATAAATTCTTTGCTGACCTGCTGGATTACATCAAAGCACTG
HRH1	NM_000861.2	3055-3155	GTGGCAGCTCAAAATGATATGTTTGAGTAGACGAACAGCTGACATGGAGTTCCCGTGCACCTACGGAAGGGGACGCTTTGAAGGAACCAAGTGCATTTTT
HRH2	NM_022304.1	600-700	GCGGTCCTCATCCTCATCACCGTTGCTGGCAATGTGGTCGTCTGTCTGGCCGTGGGCTTGAACCGCCGGCTCCGCAACCTGACCAATTGTTTCATCGTGT
Human CD19R-scfv	SCFV009.1	215-315	CTTCACCATCAGCAGCCTGCAGCCCGAGGACATCGCCACCTACTACTGCCAGCAGTACCAGAGCCTGCCCTACACCTTCGGCCAGGGCACCAAGCTGCAG
ICOS	NM_012092.2	640-740	AACTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCCTCAACTTGAAGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTAC
ICOSLG	NM_015259.4	1190-1290	CTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTCAAAAGCGTCATCCACACCAAAGGCAAATGTCCCCAAGTGAGTGGGCTCCCCGCTGTCACTG
ID2	NM_002166.4	505-605	CGGATATCAGCATCCTGTCCTTGCAGGCTTCTGAATTCCCTTCTGAGTTAATGTCAAATGACAGCAAAGCACTGTGTGGCTGAATAAGCGGTGTTCATGA
ID3	NM_002167.3	195-295	AGGAAGCCTGTTTGCAATTTAAGCGGGCTGTGAACGCCCAGGGCCGGCGGGGGCAGGGCCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCCAGGC
IDO1	NM_002164.3	50-150	CTATTATAAGATGCTCTGAAAACTCTTCAGACACTGAGGGGCACCAGAGGAGCAGACTACAAGAATGGCACACGCTATGGAAAACTCCTGGACAATCAGT
IFNA1	NM_024013.1	585-685	ATCCCTCTCTTTATCAACAAACTTGCAAGAAAGATTAAGGAGGAAGGAATAACATCTGGTCCAACATGAAAACAATTCTTATTGACTCATACACCAGGTC
IFNG	NM_000619.2	970-1070	ATACTATCCAGTTACTGCCGGTTTGAAAATATGCCTGCAATCTGAGCCAGTGCTTTAATGGCATGTCAGACAGAACTTGAATGTGTCAGGTGACCCTGAT

IFNGR1	NM_000416.1	1140-1240	CCCGGGCAGCCATCTGACTCCAATAGAGAGAGAGAGTTCTTCACCTTTAAGTAGTAACCAGTCTGAACCTGGCAGCATCGCTTTAAACTCGTATCACTCC
IGF1R	NM_000875.2	455-555	TCGGGGGGCCATCAGGATTGAGAAAAATGCTGACCTCTGTTACCTCTCCACTGTGGACTGGTCCCTGATCCTGGATGCGGTGTCCAATAACTACATTGTG
IKZF1	NM_006060.3	4485-4585	CCGCTGTGTACTACTGTGTGCCTAGATTCCATGCACTCTCGTTGTGTTTGAAGTAAATATTGGAGACCGGAGGGTAACAGGTTGGCCTGTTGATTACAGC
IKZF2	NM_001079526.1	945-1045	CCATGTACCTCCTATGGAAGATTGTAAGGAACAAGAGCCTATTATGGACAACAATATTTCTCTGGTGCCTTTTGAGAGACCTGCTGTCATAGAGAAGCTC
IL10	NM_000572.2	230-330	AAGGATCAGCTGGACAACTTGTTGTTAAAGGAGTCCTTGCTGGAGGACTTTAAGGGTTACCTGGGTTGCCAAGCCTTGTCTGAGATGATCCAGTTTTACC
IL10RA	NM_001558.2	150-250	TGCCCAGCCCTCCGTCTGTGTGGTTTGAAGCAGAATTTTTCCACCACATCCTCCACTGGACACCCATCCCAAATCAGTCTGAAAGTACCTGCTATGAAGT
IL12A	NM_000882.2	775-875	CTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCG
IL12B	NM_002187.2	1435-1535	GCAAGGCTGCAAGTACATCAGTTTTATGACAATCAGGAAGAATGCAGTGTTCTGATACCAGTGCCATCATACACTTGTGATGGATGGGAACGCAAGAGAT
IL12RB1	NM_005535.1	1292-1392	AGGAAAAGTGTTACTACATTACCATCTTTGCCTCTGCGCACCCCGAGAAGCTCACCTTGTGGTCTACGGTCCTGTCCACCTACCACTTTGGGGGCAATGC
IL12RB2	NM_001559.2	1315-1415	CCTCCGTGGGACATTAGAATCAAATTTCAAAAGGCTTCTGTGAGCAGATGTACCCTTTATTGGAGAGATGAGGGACTGGTACTGCTTAATCGACTCAGAT
IL13	NM_002188.2	516-616	TTTCTTTCTGATGTCAAAAATGTCTTGGGTAGGCGGGAAGGAGGGTTAGGGAGGGGTAAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCCGTCTTCA
IL15	NM_172174.1	1685-1785	AGGGTGATAGTCAAATTATGTATTGGTGGGGCTGGGTACCAATGCTGCAGGTCAACAGCTATGCTGGTAGGCTCCTGCCAGTGTGGAACCACTGACTACT
IL15RA	NM_002189.2	39-139	CGCTCGCCCGGGGAGTCCAGCGGTGTCCTGTGGAGCTGCCGCCATGGCCCCGCGGCGGGCGCGCGGCTGCCGGACCCTCGGTCTCCCGGCGCTGCTACTG
IL17A	NM_002190.2	240-340	TACTACAACCGATCCACCTCACCTTGGAATCTCCACCGCAATGAGGACCCTGAGAGATATCCCTCTGTGATCTGGGAGGCAAAGTGCCGCCACTTGGGCT
IL17F	NM_052872.3	210-310	GCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTC
IL17RA	NM_014339.4	3020-3120	CTACTATGTGGCGGGCATTTGGGATACCAAGATAAATTGCATGCGGCATGGCCCCAGCCATGAAGGAACTTAACCGCTAGTGCCGAGGACACGTTAAACG
IL18	NM_001562.2	48-148	GACAGTCAGCAAGGAATTGTCTCCCAGTGCATTTTGCCCTCCTGGCTGCCAACTCTGGCTGCTAAAGCGGCTGCCACCTGCTGCAGTCTACACAGCTTCG
IL18R1	NM_003855.2	2025-2125	GAATGAGGGGATTTTAAGTGTCTGAAGAGGCATTTTCTAGGGACCAGTGGGTGACTGAGTAACTGAAATGCTGCTTTCACTCCCTAACACCATGGATCTG
IL18RAP	NM_003853.2	2412-2512	GCTTGATGGACAATGGAGTGGGATTGAGACTGTGGTTTAGAGCCTTTGATTTCCTGGACTGGACTGACGGCGAGTGAATTCTCTAGACCTTGGGTACTTT
IL1A	NM_000575.3	1085-1185	ACTCCATGAAGGCTGCATGGATCAATCTGTGTCTCTGAGTATCTCTGAAACCTCTAAAACATCCAAGCTTACCTTCAAGGAGAGCATGGTGGTAGTAGCA
IL1B	NM_000576.2	840-940	GGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCCTAAAGAGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAA
IL2	NM_000586.2	300-400	AGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTTGTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAACTGGAGC
IL21R	NM_021798.2	2080-2180	CGTGTTTGTGGTCAACAGATGACAACAGCCGTCCTCCCTCCTAGGGTCTTGTGTTGCAAGTTGGTCCACAGCATCTCCGGGGCTTTGTGGGATCAGGGCA
IL22	NM_020525.4	319-419	CTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTG
IL23A	NM_016584.2	411-511	CAGGGACAACAGTCAGTTCTGCTTGCAAAGGATCCACCAGGGTCTGATTTTTTATGAGAAGCTGCTAGGATCGGATATTTTCACAGGGGAGCCTTCTCTG
IL23R	NM_144701.2	710-810	AACTGCAAATTCACCTGGATGATATAGTGATACCTTCTGCAGCCGTCATTTCCAGGGCTGAGACTATAAATGCTACAGTGCCCAAGACCATAATTTATTG
IL27	NM_145659.3	143-243	CAGGAGCTGCGGAGGGAGTTCACAGTCAGCCTGCATCTCGCCAGGAAGCTGCTCTCCGAGGTTCGGGGCCAGGCCCACCGCTTTGCGGAATCTCACCTGC
IL2RA	NM_000417.1	1000-1100	CTTGGTAAGAAGCCGGGAACAGACAACAGAAGTCATGAAGCCCAAGTGAAATCAAAGGTGCTAAATGGTCGCCCAGGAGACATCCGTTGTGCTTGCCTGC
IL2RB	NM_000878.2	1980-2080	GTCCTGCTGCCCGAGCCAGGAACTGTGTGTGTTGCAGGGGGGCAGTAACTCCCCAACTCCCTCGTTAATCACAGGATCCCACGAATTTAGGCTCAGAAGC
IL2RG	NM_000206.1	595-695	CCACAGCTGGACTGAACAATCAGTGGATTATAGACATAAGTTCTCCTTGCCTAGTGTGGATGGGCAGAAACGCTACACGTTTCGTGTTCGGAGCCGCTTT
IL4	NM_000589.2	625-725	GACACTCGCTGCCTGGGTGCGACTGCACAGCAGTTCCACAGGCACAAGCAGCTGATCCGATTCCTGAAACGGCTCGACAGGAACCTCTGGGGCCTGGCGG
IL4R	NM_000418.2	705-805	ATCATCTCACCTATGCAGTCAACATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACCCTCCCTCCGCATCGCAGC
IL5	NM_000879.2	105-205	CCACAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCATCGAACTCTGCTGATAGCCAATGAGACTCTGAGGATTCCTGT
IL6	NM_000600.1	220-320	TGACAAACAAATTCGGTACATCCTCGACGGCATCTCAGCCCTGAGAAAGGAGACATGTAACAAGAGTAACATGTGTGAAAGCAGCAAAGAGGCACTGGCA
IL6R	NM_000565.2	993-1093	CTTTCTACATAGTGTCCATGTGCGTCGCCAGTAGTGTCGGGAGCAAGTTCAGCAAAACTCAAACCTTTCAGGGTTGTGGAATCTTGCAGCCTGATCCGCC

IL7R	NM_002185.2	1610-1710	TTGCTTTGACCACTCTTCCTGAGTTCAGTGGCACTCAACATGAGTCAAGAGCATCCTGCTTCTACCATGTGGATTTGGTCACAAGGTTTAAGGTGACCCA
IL9	NM_000590.1	300-400	AAGTACTAAAGAACAACAAGTGTCCATATTTTTCCTGTGAACAGCCATGCAACCAAACCACGGCAGGCAACGCGCTGACATTTCTGAAGAGTCTTCTGGA
IRF1	NM_002198.1	510-610	CTGTGCGAGTGTACCGGATGCTTCCACCTCTCACCAAGAACCAGAGAAAAGAAAGAAAGTCGAAGTCCAGCCGAGATGCTAAGAGCAAGGCCAAGAGGAA
IRF2	NM_002199.2	1375-1475	CAGTACCTGGAGCTTCTCTTTAACTCAGGACTCCAGCCCATTGGTAGACGTGTGTTTCTAGAGCCTGCTGGATCTCCCAGGGCTACTCACTCAAGTTCAA
IRF4	NM_002460.1	325-425	GGGCACTGTTTAAAGGAAAGTTCCGAGAAGGCATCGACAAGCCGGACCCTCCCACCTGGAAGACGCGCCTGCGGTGCGCTTTGAACAAGAGCAATGACTT
ITCH	NM_031483.4	155-255	ACTGTGAGAACTTCAGGTTTTCCAACCTATTGGTGGTATGTCTGACAGTGGATCACAACTTGGTTCAATGGGTAGCCTCACCATGAAATCACAGCTTCAG
ITGA1	NM_181501.1	1875-1975	AAGTGGCAAGACTATAAGGAAAGAGTATGCACAACGTATTCCATCAGGTGGGGATGGTAAGACACTGAAATTTTTTGGCCAGTCTATCCACGGAGAAATG
ITGA4	NM_000885.4	975-1075	GCCCACTGCCAACTGGCTCGCCAACGCTTCAGTGATCAATCCCGGGGCGATTTACAGATGCAGGATCGGAAAGAATCCCGGCCAGACGTGCGAACAGCTC
ITGA5	NM_002205.2	925-1025	AGAAGACTTTGTTGCTGGTGTGCCCAAAGGGAACCTCACTTACGGCTATGTCACCATCCTTAATGGCTCAGACATTCGATCCCTCTACAACTTCTCAGGG
ITGAL	NM_002209.2	3905-4005	GTGAGGGCTTGTCATTACCAGACGGTTCACCAGCCTCTCTTGGTTTCCTTCCTTGGAAGAGAATGTCTGATCTAAATGTGGAGAAACTGTAGTCTCAGGA
ITGAM	NM_000632.3	515-615	GCCCTCCGAGGGTGTCCTCAAGAGGATAGTGACATTGCCTTCTTGATTGATGGCTCTGGTAGCATCATCCCACATGACTTTCGGCGGATGAAGGAGTTTG
ITGAX	NM_000887.3	700-800	CCCCTCAGCCTGTTGGCTTCTGTTCACCAGCTGCAAGGGTTTACATACACGGCCACCGCCATCCAAAATGTCGTGCACCGATTGTTCCATGCCTCATATG
ITGB1	NM_033666.2	2000-2100	TTTTAACATTACCAAGGTAGAAAGTCGGGACAAATTACCCCAGCCGGTCCAACCTGATCCTGTGTCCCATTGTAAGGAGAAGGATGTTGACGACTGTTGG
ITGB7	NM_000889.1	1278-1378	CAACGTGGTACAGCTCATCATGGATGCTTATAATAGCCTGTCTTCCACCGTGACCCTTGAACACTCTTCACTCCCTCCTGGGGTCCACATTTCTTACGAA
ITK	NM_005546.3	3430-3530	GCCAGTAAAGAAGTCAGTATAGAACCACTAGCGAATAGTGTTGCTCTGGCACAGACCACTGTGGTTGATGGCATGGCCCTCCAACTTGGAATAGGATTTT
JAK1	NM_002227.1	285-385	GAGAACACCAAGCTCTGGTATGCTCCAAATCGCACCATCACCGTTGATGACAAGATGTCCCTCCGGCTCCACTACCGGATGAGGTTCTATTTCACCAATT
JAK2	NM_004972.2	455-555	CTCCTCCCGCGACGGCAAATGTTCTGAAAAAGACTCTGCATGGGAATGGCCTGCCTTACGATGACAGAAATGGAGGGAACATCCACCTCTTCTATATATC
JAK3	NM_000215.2	1715-1815	GTGCTGCTGAAGGTCATGGATGCCAAGCACAAGAACTGCATGGAGTCATTCCTGGAAGCAGCGAGCTTGATGAGCCAAGTGTCGTACCGGCATCTCGTGC
JUN	NM_002228.3	140-240	ACACAGCCAGCCAGCCAGGTCGGCAGTATAGTCCGAACTGCAAATCTTATTTTCTTTTCACCTTCTCTCTAACTGCCCAGAGCTAGCGCCTGTGGCTCCC
JUNB	NM_002229.2	1155-1255	GCGCGCCTGGAGGACAAGGTGAAGACGCTCAAGGCCGAGAACGCGGGGCTGTCGAGTACCGCCGGCCTCCTCCGGGAGCAGGTGGCCCAGCTCAAACAGA
KIR2DL1	NM_014218.2	881-981	GCAGGAAACAGAACAGCGAATAGCGAGGACTCTGATGAACAAGACCCTCAGGAGGTGACATACACACAGTTGAATCACTGCGTTTTCACACAGAGAAAAA
KIR2DL2	NM_014219.2	814-914	TCTCCTTCATCGCTGGTGCTCCAACAAAAAAAATGCTGCGGTAATGGACCAAGAGTCTGCAGGGAACAGAACAGCGAATAGCGAGGACTCTGATGAACAA
KIR2DL3	NM_015868.2	741-841	CTCCGAAACCGGTAACCCCAGACACCTGCATGTTCTGATTGGGACCTCAGTGGTCATCATCCTCTTCATCCTCCTCCTCTTCTTTCTCCTTCATCGCTGG
KIR2DL4	NM_002255.5	15-115	GCGTCCTGGCAGCAGAAGCTGCACCATGTCCATGTCACCCACGGTCATCATCCTGGCATGTCTTGGGTTCTTCTTGGACCAGAGTGTGTGGGCACACGTG
KIR2DL5A	NM_020535.3	1451-1551	GACACGTGCTGTTCCACCTTCCCTCATGCTGTTTCACCTTTCCTCAGACTATTTTCCAGCCTTCTGTCAGTCAGCAGTGAAACTTATAAAATTTTTTGTG
KIR2DS1	NM_014512.1	698-798	CTTCACCCACTGAACCAAGCTCCGAAACCGGTAACCCCAGACACCTACATGTTCTGATTGGGACCTCAGTGGTCAAAATCCCTTTCACCATCCTCCTCTT
KIR2DS2	NM_012312.2	856-956	CAAGAGCCTGCAGGGAACAGAACAGTGAACAGCGAGGATTCTGATGAACAAGACCATCAGGAGGTGTCATACGCATAATTGGATCACTGTGTTTTCACAC
KIR2DS3	NM_012313.1	693-793	GGCCTTCACCCACTGAACCAAGCTCCAAAACCGGTAACCCCAGACACCTACACGTTCTGATTGGGACCTCAGTGGTCAAACTCCCTTTCACCATCCTCCT
KIR2DS4	NM_012314.3	1427-1527	ACATACAAGAGGCTGCCTCTTAACACAGCACTTAGACACGTGCTGTTCCACCTCCCTTCAGACTATCTTTCAGCCTTCTGCCAGCAGTAAAACTTATAAA
KIR2DS5	NM_014513.2	204-304	CTTCCTTCTGCACAGAGAGGGGACGTTTAACCACACTTTGCGCCTCATTGGAGAGCACATTGATGGGGTCTCCAAGGGCAACTTCTCCATCGGTCGCATG
KIR3DL1	NM_013289.2	1054-1154	CCAAATCTGGTAACCCCAGACACCTGCACATTCTGATTGGGACCTCAGTGGTCATCATCCTCTTCATCCTCCTCCTCTTCTTTCTCCTTCATCTCTGGTG
KIR3DL2	NM_006737.2	884-984	TGCCACCCACGGAGGGACCTACAGATGCTTCGGCTCTTTCCGTGCCCTGCCCTGCGTGTGGTCAAACTCAAGTGACCCACTGCTTGTTTCTGTCACAGGA
KIR3DL3	NM_153443.3	508-608	CCTTGCGCCTCGTTGGACAGCTCCACGATGCGGGTTCCCAGGTCAACTATTCCATGGGTCCCATGACACCTGCCCTTGCAGGGACCTACAGATGCTTTGG
KIR3DS1	NM_001083539.1	1000-1100	CTCCAAATCTGGTAACCTCAGACACCTGCACATTCTGATTGGGACCTCAGTGGTCAAAATCCCTTTCACCATCCTCCTCTTCTTTCTCCTTCATCGCTGG
KIT	NM_000222.1	5-105	CATCGCAGCTACCGCGATGAGAGGCGCTCGCGGCGCCTGGGATTTTCTCTGCGTTCTGCTCCTACTGCTTCGCGTCCAGACAGGCTCTTCTCAACCATCT

KLF10	NM_005655.1	570-670	GCTCAGGCAACAAGTGTGATTCGTCATACAGCTGATGCCCAGCTATGTAACCACCAGACCTGCCCAATGAAAGCAGCCAGCATCCTCAACTATCAGAACA
KLF2	NM_016270.2	1015-1115	GGAAGTTTGCGCGCTCAGACGAGCTCACGCGCCACTACCGAAAGCACACGGGCCACCGGCCATTCCAGTGCCATCTGTGCGATCGTGCCTTCTCGCGCTC
KLF4	NM_004235.4	1980-2080	CGAGCATTTTCCAGGTCGGACCACCTCGCCTTACACATGAAGAGGCATTTTTAAATCCCAGACAGTGGATATGACCCACACTGCCAGAAGAGAATTCAGT
KLF6	NM_001008490.1	1165-1265	GGGATGCGTGTTCCAGCCAAAGCATGCCGTTCTGCACCCTACCCAGTTGCCTCCAGGGCCTCTCCTTGGAAGGTCTTTTGAGGGCTAAAAAGGTCCTGTA
KLF7	NM_001270943.1	1546-1646	GTACTATTGAGATCTTTCGCGTCGATCCCAACGGCCTTAGCGGCGGCAGACTGGAATAACACCTTACACCTTTCTGGCCTGCATTTCTGTAGACTTCACT
KLRAP1	NR_028045.1	414-514	CCTTCAGAGTCACAGAATAGATTAAGGCCTGATGATACTCAAAGGCCTGGGAAAACTGATGACAAAGAATTTTCAGTGCCCTGGCACCTCATTGCAGTGA
KLRB1	NM_002258.2	85-185	TGAGTTAAACTTACCCACAGACTCAGGCCCAGAAAGTTCTTCACCTTCATCTCTTCCTCGGGATGTCTGTCAGGGTTCACCTTGGCATCAATTTGCCCTG
KLRC1	NM_002259.3	335-435	ACCTATCACTGCAAAGATTTACCATCAGCTCCAGAGAAGCTCATTGTTGGGATCCTGGGAATTATCTGTCTTATCTTAATGGCCTCTGTGGTAACGATAG
KLRC2	NM_002260.3	942-1042	TATGTGAGTCAGCTTATAGGAAGTACCAAGAACAGTCAAACCCATGGAGACAGAAAGTAGAATAGTGGTTGCCAATGTCTCAGGGAGGTTGAAATAGGAG
KLRC3	NM_002261.2	760-860	ACTCCTGAGCTCAAGAAATCAACACATCTTGGCCTCCCAAGTTGCTGGGATTACTGACACAAGCCACCGCCCCTGAGTGCTCATGTACCATTTAGCTTGT
KLRC4	NM_013431.2	29-129	TTATATTGGTCAACAGCAAAATGAACATTACTACTCAGCCTCCAACACATGCAGTTTGCCTATACCAGGGATCCTGTCAAAATATACACCACTTATAGCT
KLRD1	NM_002262.3	542-642	AGCCTGCTTCAGCTTCAAAACACAGATGAACTGGATTTTATGAGCTCCAGTCAACAATTTTACTGGATTGGACTCTCTTACAGTGAGGAGCACACCGCCT
KLRF1	NM_016523.1	275-375	AAAAAGGAAGTTGTTCAAATGCCACTCAGTATGAGGACACTGGAGATCTAAAAGTGAATAATGGCACAAGAAGAAATATAAGTAATAAGGACCTTTGTGC
KLRG1	NM_005810.3	45-145	TGCCTACGGCAACCCAAGCCCAGAATGACTATGGACCACAGCAAAAATCTTCCTCTTCCAGGCCTTCTTGTTCTTGCCTTGTGGCAATAGCTTTGGGGCT
KLRK1	NM_007360.1	760-860	GGACCAGGATTTACTTAAACTGGTGAAGTCATATCATTGGATGGGACTAGTACACATTCCAACAAATGGATCTTGGCAGTGGGAAGATGGCTCCATTCTC
LAG3	NM_002286.5	1735-1835	CTTTTGGTGACTGGAGCCTTTGGCTTTCACCTTTGGAGAAGACAGTGGCGACCAAGACGATTTTCTGCCTTAGAGCAAGGGATTCACCCTCCGCAGGCTC
LAIR1	NM_002287.3	1195-1295	GCACCTGAGGGTAGAAAGTCACTCTAGGAAAAGCCTGAAGCAGCCATTTGGAAGGCTTCCTGTTGGATTCCTCTTCATCTAGAAAGCCAGCCAGGCAGCT
LAT	NM_001014987.1	1290-1390	TGTGTAATAGAATAAAGGCCTGCGTGTGTCTGTGTTGAGCGTGCGTCTGTGTGTGCCTGTGTGCGAGTCTGAGTCAGAGATTTGGAGATGTCTCTGTGTG
LAT2	NM_014146.3	1863-1963	TGCAGAGCTGATTAAACAGTGTTGTGACTGTCTCATGGGAAGAGCTGGGGCCCAGAGGGACCTTGAGTCAGAAATGTTGCCAGAAAAAGTATCTCCTCCA
LCK	NM_005356.2	1260-1360	ATTAAGTGGACAGCGCCAGAAGCCATTAACTACGGGACATTCACCATCAAGTCAGATGTGTGGTCTTTTGGGATCCTGCTGACGGAAATTGTCACCCACG
LDHA	NM_005566.1	985-1085	CAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAGGAAGAGGCCCGTTTGAAGAAGAGTGCAGATACACTTTGGGGGATCCAAAAGGAGC
LEF1	NM_016269.3	1165-1265	CCGTCACACATCCCATCAGATGTCAACTCCAAACAAGGCATGTCCAGACATCCTCCAGCTCCTGATATCCCTACTTTTTATCCCTTGTCTCCGGGTGGTG
LGALS1	NM_002305.3	60-160	GGTGCGCCTGCCCGGGAACATCCTCCTGGACTCAATCATGGCTTGTGGTCTGGTCGCCAGCAACCTGAATCTCAAACCTGGAGAGTGCCTTCGAGTGCGA
LGALS3	NM_002306.2	120-220	CAGCCGTCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTTCGCTCCATGATGCGTTATCTGGGTCTGGAAACCCAAACCCTCAAGGATGGCCT
LIFR	NM_002310.3	2995-3095	CCTATTGTCCACCCATCATTGAGGAAGAAATACCAAACCCAGCCGCAGATGAAGCTGGAGGGACTGCACAGGTTATTTACATTGATGTTCAGTCGATGTA
LILRB1	NM_001081637.1	2332-2432	AGCTGAGAAAACTAAGTCAGAAAGTGCATTAAACTGAATCACAATGTAAATATTACACATCAAGCGATGAAACTGGAAAACTACAAGCCACGAATGAATG
LOC282997	NR_026932.1	665-765	TGATCACATTCTACCTGGCATTATTTCATCTGAGTCCCTGTCCTAGCCCTTCTGCCCATTAGACTGTAACCTTGTTTAGGGAAAGACCTGTGTCTTACTC
LRP5	NM_002335.1	2515-2615	TGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGA
LRP6	NM_002336.1	2185-2285	CTTAGATTATCCAGAAGGCATGGCAGTAGACTGGCTTGGGAAGAACTTGTACTGGGCAGACACAGGAACGAATCGAATTGAGGTGTCAAAGTTGGATGGG
LRRC32	NM_005512.2	3470-3570	CACCCTGGTGTGGGTTCTCCTGTTCTCTCTGTGCTCTTGCATTCTCTCATTCCCTTTTCCTCTATTGAGCAGAGCCTGGAGTTTGAGACTATGGAATCCA
LTA	NM_000595.2	885-985	CTGATCAAGTCACCGGAGCTTTCAAAGAAGGAATTCTAGGCATCCCAGGGGACCACACCTCCCTGAACCATCCCTGATGTCTGTCTGGCTGAGGATTTCA
LTBR	NM_002342.1	1435-1535	CTAACAGGGGCCCAAGGAACCAATTTATCACCCATGACTGACGGAGTCTGAGAAAAGGCAGAAGAAGGGGGGCACAAGGGCACTTTCTCCCTTGAGGCTG
LYN	NM_002350.1	1285-1385	TCCTGAAGAGCGATGAAGGTGGCAAAGTGCTGCTTCCAAAGCTCATTGACTTTTCTGCTCAGATTGCAGAGGGAATGGCATACATCGAGCGGAAGAACTA
MAD1L1	NM_003550.2	306-406	GAAGACCTGGGGGAAAACACCATGGTTTTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGTGGAGGGAGGCTCTGGACTGGATATTTCTA
MAP2K1	NM_002755.2	970-1070	ACGGAATGGACAGCCGACCTCCCATGGCAATTTTTGAGTTGTTGGATTACATAGTCAACGAGCCTCCTCCAAAACTGCCCAGTGGAGTGTTCAGTCTGGA

MAPK14	NM_001315.1	450-550	TGGGCTCTGGCGCCTATGGCTCTGTGTGTGCTGCTTTTGACACAAAAACGGGGTTACGTGTGGCAGTGAAGAAGCTCTCCAGACCATTTCAGTCCATCAT
MAPK3	NM_002746.2	580-680	AACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCACCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTG
MAPK8	NM_139049.1	945-1045	TCTCTGTAGATGAAGCTCTCCAACACCCGTACATCAATGTCTGGTATGATCCTTCTGAAGCAGAAGCTCCACCACCAAAGATCCCTGACAAGCAGTTAGA
MBD2	NM_003927.3	2015-2115	ATTTACATTCAACTCTGATCCCTGGGCCTTAGGTTTGACATGGAGGTGGAGGAAGATAGCGCATATATTTGCAGTATGAACTATTGCCTCTGGACGTTGT
MCL1	NM_021960.3	1260-1360	GCTGTAACTTCCTAGAGTTGCACCCTAGCAACCTAGCCAGAAAAGCAAGTGGCAAGAGGATTATGGCTAACAAGAATAAATACATGGGAAGAGTGCTCCC
MIF	NM_002415.1	319-419	TCCTACAGCAAGCTGCTGTGCGGCCTGCTGGCCGAGCGCCTGCGCATCAGCCCGGACAGGGTCTACATCAACTATTACGACATGAACGCGGCCAATGTGG
MMP14	NM_004995.2	1470-1570	GACAAGATTGATGCTGCTCTCTTCTGGATGCCCAATGGAAAGACCTACTTCTTCCGTGGAAACAAGTACTACCGTTTCAACGAAGAGCTCAGGGCAGTGG
MPL	NM_005373.2	895-995	CAGTGGCACTTGGACTGCAATGCTTTACCTTGGACCTGAAGAATGTTACCTGTCAATGGCAGCAACAGGACCATGCTAGCTCCCAAGGCTTCTTCTACCA
MTOR	NM_004958.2	5095-5195	TTAGTGTTGCTCCTGGGAGTTGATCCGTCTCGGCAACTTGACCATCCTCTGCCAACAGTTCACCCTCAGGTGACCTATGCCTACATGAAAAACATGTGGA
MXD1	NM_002357.2	880-980	GAGAATAAAGCTGCAGGACAGTCACAAGGCGTGTCTTGGTCTCTAAGAGAGTGGGCACTGCGGCTGTCTCCTTGAAGGTTCTCCCTGTTGGTTCTGATTA
MYB	NM_005375.2	3145-3245	AACTGTTGCATGGATCCTGTGTTTGCAACTGGGGAGACAGAAACTGTGGTTGATAGCCAGTCACTGCCTTAAGAACATTTGATGCAAGATGGCCAGCACT
MYC	NM_002467.3	1610-1710	TCGGACACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCTTGGAGCGCCAGAGGAGGAACGAGCTAAAACGGAGCTTTTTTGCCCTGCGTGACCAGA
MYO6	NM_004999.3	6655-6755	AAGTTGGGGAGATGGCACCTTCTCAGAGGATTGTGAAAATATGAGGAAGAAACAAAACAGTGCATGTAGGAGCACAGGGCCACACAAAGGCATTCTATTG
NANOG	NM_024865.2	1100-1200	CTACTCCATGAACATGCAACCTGAAGACGTGTGAAGATGAGTGAAACTGATATTACTCAATTTCAGTCTGGACACTGGCTGAATCCTTCCTCTCCCCTCC
NBEA	NM_015678.3	8645-8745	CTGAGAGCCCTTGAAGGACCAGAAAACTGCTTATTCCCACGCTTGATATCTGTCTCCAGCGAAGGCCACTGTATCATATACTATGAACGAGGGCGATTCA
NCAM1	NM_000615.5	1620-1720	GGTATTTGCCTATCCCAGTGCCACGATCTCATGGTTTCGGGATGGCCAGCTGCTGCCAAGCTCCAATTACAGCAATATCAAGATCTACAACACCCCCTCT
NCL	NM_005381.2	1492-1592	GAACAGAGATCGATGGGCGATCTATTTCCCTGTACTATACTGGAGAGAAAGGTCAAAATCAAGACTATAGAGGTGGAAAGAATAGCACTTGGAGTGGTGA
NCR1	NM_001145457.1	145-245	TTTCATGGTTCCAAAGGAAAAGCAAGTGACCATCTGTTGCCAGGGAAATTATGGGGCTGTTGAATACCAGCTGCACTTTGAAGGAAGCCTTTTTGCCGTG
NCR2	NM_004828.3	798-898	CTTCAACAGGTCACGGACCTTCCCTGGACCTCAGTTTCCTCACCTGTAGAGAGAGAAATATTATATCACACTGTTGCAAGGACTAAGATAAGCGATGATG
NCR3	NM_147130.1	50-150	GCATCTGTCCTCTCTCCTCAGGGAGGCAAGCATTTGATGCTCGAGGTCCCTGGCAGTTGTGGTCCTTGGCAAGTGATGTGTGAGTCCCGTGTGTCATAGG
NCRNA00185	NR_001544.2	143-243	GAGGCTGTCTGCCAACATCTTTCATCACTCTGCCTGCAACTATGAAAAATTTAGTTCTAAAAAATGCAACCTTGCTAAATTGAGTACTAATAGGATTGGT
NEIL1	NM_024608.2	1675-1775	TTAGCAGGAGGCTCTCCTTGCTTGCACTCACCCTTTCTTATTGTCTTGCCCTGCATCTGGGGGTCTGAATTTTTGGGAGCAGGCAATATCTGAAGGTGCA
NEIL2	NM_145043.2	2570-2670	GCCCGGTGGTGTGTAGAGAAAAGCTGCTTGTTTACTCCTTAAGTCAATGTATTGGTGACTGTTGATTTGTTGAACAATTCAGGAATCAAGGGCTGTGGAG
NFAT5	NM_173214.1	3290-3390	CCCTGACAACTATTCAAACCCAGGACATCTCACAGCCTGGTACTTTTCCAGCAGTTTCTGCTTCTAGTCAGCTGCCCAACAGCGATGCACTATTGCAGCA
NFATC1	NM_172390.1	2510-2610	CCAGTACCAGCGTTTCACCTACCTTCCCGCCAACGGTAACGCCATCTTTCTAACCGTAAGCCGTGAACATGAGCGCGTGGGGTGCTTTTTCTAAAGACGC
NFATC2	NM_012340.3	1815-1915	GACGGACATTGGAAGAAAGAACACGCGGGTGAGACTGGTTTTCCGAGTTCACATCCCAGAGTCCAGTGGCAGAATCGTCTCTTTACAGACTGCATCTAAC
NFATC3	NM_004555.2	2190-2290	GTCCTTGAAGTTCCTCCATATCATAACCCAGCAGTTACAGCTGCAGTGCAGGTGCACTTTTATCTTTGCAATGGCAAGAGGAAAAAAAGCCAGTCTCAAC
NFKB1	NM_001165412.1	2305-2405	CTTGGGTAACTCTGTTTTGCACCTAGCTGCCAAAGAAGGACATGATAAAGTTCTCAGTATCTTACTCAAGCACAAAAAGGCAGCACTACTTCTTGACCAC
NOS2	NM_000625.4	605-705	TTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTC
NOTCH1	NM_017617.3	735-835	CTGCCAGGCTTCACCGGCCAGAACTGTGAGGAAAATATCGACGATTGTCCAGGAAACAACTGCAAGAACGGGGGTGCCTGTGTGGACGGCGTGAACACCT
NR3C1	NM_001018077.1	1665-1765	GCTTTCTCCTCTGGCGGGAGAAGACGATTCATTCCTTTTGGAAGGAAACTCGAATGAGGACTGCAAGCCTCTCATTTTACCGGACACTAAACCCAAAATT
NR4A1	NM_002135.3	155-255	CGGCCGGGTAGGGTGCAGCCTGAGGCTTGTTCAGCAGAACAGGTGCAAGCCACATTGTTGCCAAGACCTGCCTGAAGCCGGATTCTCCCCACTGCCTCCT
NREP	NM_001142474.1	990-1090	AAACTCATTGTTTCCTTGTGGTAAGTGACCGAGATGCTGCCACAGGACCTGAGACACTGATGAATGGTGCTATTTTGGACTTTCAACATGCTCCTTGGCG
NRIP1	NM_003489.2	335-435	TGACTCATGGAGAAGAGCTTGGCTCTGATGTGCACCAGGATTCTATTGTTTTAACTTACCTAGAAGGATTACTAATGCATCAGGCAGCAGGGGGATCAGG
NRP1	NM_003873.5	370-470	GCCTCGCTGCTTTCTTTTCTCCAAGACGGGCTGAGGATTGTACAGCTCTAGGCGGAGTTGGGGCTCTTCGGATCGCTTAGATTCTCCTCTTTGCTGCATT

NT5E	NM_002526.2	1214-1314	ATTCGGGTTTTGAAATGGATAAACTCATCGCTCAGAAAGTGAGGGGTGTGGACGTCGTGGTGGGAGGACACTCCAACACATTTCTTTACACAGGCAATCC
OAZ1	NM_004152.2	313-413	GGTGGGCGAGGGAATAGTCAGAGGGATCACAATCTTTCAGCTAACTTATTCTACTCCGATGATCGGCTGAATGTAACAGAGGAACTAACGTCCAACGACA
OPTN	NM_001008211.1	625-725	TGAAGCTAAATAATCAAGCCATGAAAGGGAGATTTGAGGAGCTTTCGGCCTGGACAGAGAAACAGAAGGAAGAACGCCAGTTTTTTGAGATACAGAGCAA
P2RX7	NM_002562.4	340-440	AGTTGGTGCACAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGGCCAAGA
PAX5	NM_016734.1	2288-2388	CTCCAAGAGGAGCACACTTTGGGGAGATGTCCTGGTTTCCTGCCTCCATTTCTCTGGGACCGATGCAGTATCAGCAGCTCTTTTCCAGATCAAAGAACTC
PDCD1	NM_005018.1	175-275	CTTCTTCCCAGCCCTGCTCGTGGTGACCGAAGGGGACAACGCCACCTTCACCTGCAGCTTCTCCAACACATCGGAGAGCTTCGTGCTAAACTGGTACCGC
PDCD1LG2	NM_025239.3	235-335	TGTGGAGCTGTGGCAAGTCCTCATATCAAATACAGAACATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCTTTATT
PDE3A	NM_000921.3	3010-3110	CTGGCCAACCTTCAGGAATCCTTCATCTCTCACATTGTGGGGCCTCTGTGCAACTCCTATGATTCAGCAGGACTAATGCCTGGAAAATGGGTGGAAGACA
PDE4A	NM_001111307.1	3855-3955	AATAATGGTGTATACCCTCATTCTCATTCCTGGGCAGCCCTTCCTTCCACCCTGGCACCAAAATAATTTCTCCTCCATCCGTACCTTGCCTAGCCTCTCC
PDE7A	NM_002604.2	2210-2310	GTAGCTCAACAAGGAATAGAGGGAGGAGTGTAATTTTGGTAGCTGGTGTTGAATAGGGCCTTTGAGAATCAGACTGAACACAGTGAAATATGTGCCCAAA
PDK1	NM_002610.3	1170-1270	TGGATTGCCCATATCACGTCTTTACGCACAATACTTCCAAGGAGACCTGAAGCTGTATTCCCTAGAGGGTTACGGGACAGATGCAGTTATCTACATTAAG
PDXK	NM_003681.3	580-680	TCCCGGAGGACCTCCTTCCCGTCTACAAAGAAAAAGTGGTGCCGCTTGCAGACATTATCACGCCCAACCAGTTTGAGGCCGAGTTACTGAGTGGCCGGAA
PECAM1	NM_000442.3	1365-1465	ATCTGCACTGCAGGTATTGACAAAGTGGTCAAGAAAAGCAACACAGTCCAGATAGTCGTATGTGAAATGCTCTCCCAGCCCAGGATTTCTTATGATGCCC
PHACTR2	NM_001100164.1	8350-8450	GGCAGAATGCCACTCTACCCTCAGGTCAATTTTATGGTATATGAAAATGCCAGTAATATTTGTGCCACTTGCCAACTCGGGGGAGGAGGGGCTTTTCCCT
PHC1	NM_004426.2	2905-3005	ATACAGCTCCACCTACACCGGAATTACATGGCATCAACCCTGTGTTCCTGTCCAGTAATCCCAGCCGTTGGAGTGTAGAGGAGGTGTACGAGTTTATTGC
POLR1B	NM_019014.3	3320-3420	GGAGAACTCGGCCTTAGAATACTTTGGTGAGATGTTAAAGGCTGCTGGCTACAATTTCTATGGCACCGAGAGGTTATATAGTGGCATCAGTGGGCTAGAA
POLR2A	NM_000937.2	3775-3875	TTCCAAGAAGCCAAAGACTCCTTCGCTTACTGTCTTCCTGTTGGGCCAGTCCGCTCGAGATGCTGAGAGAGCCAAGGATATTCTGTGCCGTCTGGAGCAT
POP5	NM_015918.3	560-660	GCTTCAGGCCCACTTGTTGAACAGAACAATCTGGGTAGCAACAGCATCTTCCACAGTTTTCCAAACTGGATAGCTGCCAACCAGCAGACATTACCCACTT
POU5F1	NM_002701.4	1225-1325	AAGTTCTTCATTCACTAAGGAAGGAATTGGGAACACAAAGGGTGGGGGCAGGGGAGTTTGGGGCAACTGGTTGGAGGGAAGGTGAAGTTCAATGATGCTC
PPARA	NM_001001928.2	5220-5320	GGGTGTGTTTGCTATACGAACATAATGGACGTGAAGTGGGGCAGAAACCCAGAACTCAGCATTCAAGGATGCCCAGGAGAGCTGTCCCTGTTTTAAAGAG
PPP2R1A	NM_014225.3	1440-1540	AACTTAACTCCTTGTGCATGGCCTGGCTTGTGGATCATGTATATGCCATCCGCGAGGCAGCCACCAGCAACCTGAAGAAGCTAGTGGAAAAGTTTGGGAA
PRDM1	NM_182907.1	310-410	CATCCCTGCCAACCAGGAACTTCTTGTGTGGTATTGTCGGGACTTTGCAGAAAGGCTTCACTACCCTTATCCCGGAGAGCTGACAATGATGAATCTCACA
PRF1	NM_005041.3	2120-2220	ACTGTTTTTCAGGGAGGTGGCTGGGTTTACACGCTAATCCCGATTCACCCTGTCCAAACTGCCTAAGCCCTCCGCCATTCTCAAGCCCTGCAGTCACAGC
PRKAA2	NM_006252.2	975-1075	ATAGTGGTGACCCTCAAGACCAGCTTGCAGTGGCTTATCATCTTATCATTGACAATCGGAGAATAATGAACCAAGCCAGTGAGTTCTACCTCGCCTCTAG
PRKCQ	NM_006257.2	1325-1425	GATGGACGATGATGTTGAGTGCACGATGGTAGAGAAGAGAGTTCTTTCCTTGGCCTGGGAGCATCCGTTTCTGACGCACATGTTTTGTACATTCCAGACC
PROM1	NM_006017.1	925-1025	AGCCTGCGGTCATCTCTCAATGACCCTCTGTGCTTGGTGCATCCATCAAGTGAAACCTGCAACAGCATCAGATTGTCTCTAAGCCAGCTGAATAGCAACC
PTGER2	NM_000956.2	1410-1510	GTCAGAAGGAGCTACAAAACCTACCCTCAGTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGCTGCATTGAAGATCCAGCTGCCTATTGATTTAAGC
PTK2	NM_005607.3	1005-1105	GGTTCAAGCTGGATTATTTCAGTGGAACTGGCAATCGGCCCAGAAGAAGGAATCAGTTACCTAACGGACAAGGGCTGCAATCCCACACATCTTGCTGACT
PTPN11	NM_002834.3	4650-4750	TAGTCCCTAGGTTGCTACGGCTTATCATGTGCTTGGTAAAAGGTGATCGCAGGTTCTCAGACGAGTTTACTTTACATGAGATGGAATCAGGCAGAGAGGC
PTPN4	NM_002830.2	705-805	TCGAGGCTTTTTTTCTCCAGCCGAGAGGACGCGGCTGTGATATACGAAGACTTTGTGTGGACAGTAATGACCTCACGTTTCCGATTGCCTGCTGGCAGAA
PTPN6	NM_002831.5	1734-1834	TGGTGCAGACGGAGGCGCAGTACAAGTTCATCTACGTGGCCATCGCCCAGTTCATTGAAACCACTAAGAAGAAGCTGGAGGTCCTGCAGTCGCAGAAGGG
PTPRK	NM_001135648.1	4315-4415	GTGATCAACCGGATTTTTAGGATATGCAATCTAACAAGACCACAGGAAGGTTATCTGATGGTGCAACAGTTTCAGTACCTAGGATGGGCTTCTCATCGAG
RAB31	NM_006868.3	3800-3900	TTTTGTAAAGAGCTTCCATCTGGGCTGGACCCAGTTCTTGCACATACAAGACACCGCTGCAGTCAGCTAGGACCTTTCCGCCATGTATTCTATTCTGTAG
RAC1	NM_198829.1	1250-1350	AAAGACCTTCGTCTTTGAGAAGACGGTAGCTTCTGCAGTTAGGAGGTGCAGACACTTGCTCTCCTATGTAGTTCTCAGATGCGTAAAGCAGAACAGCCTC
RAC2	NM_002872.3	1069-1169	GCTGCCACAACTTGTGTACCTTCAGGGATGGGGCTCTTACTCCCTCCTGAGGCCAGCTGCTCTAATATCGATGGTCCTGCTTGCCAGAGAGTTCCTCTAC

RAF1	NM_002880.2	1990-2090	CCTATGGCATCGTATTGTATGAACTGATGACGGGGGAGCTTCCTTATTCTCACATCAACAACCGAGATCAGATCATCTTCATGGTGGGCCGAGGATATGC
RAP1GAP2	NM_015085.4	4140-4240	CCCACGGCTGGAAAGAGGCCTGTACGTTCTGGACGCGTTTTGTTGGCTGGGCTTCTGGAGGCACTGGCAAGGTCAAACTGCATTTCTTTAAGAACAGTTG
RARA	NM_000964.2	115-215	AGCCACCTAGCTGGGGCCCATCTAGGAGTGGCATCTTTTTTGGTGCCCTGAAGGCCAGCTCTGGACCTTCCCAGGAAAAGTGCCAGCTCACAGAACTGCT
RBPMS	NM_001008710.1	842-942	AAACAGCCTGTAGGTTTTGTCAGTTTTGACAGTCGCTCAGAAGCAGAGGCTGCAAAGAATGCTTTGAATGGCATCCGCTTCGATCCTGAAATTCCGCAAA
RHOA	NM_001664.2	1230-1330	GGTACTCTGGTGAGTCACCACTTCAGGGCTTTACTCCGTAACAGATTTTGTTGGCATAGCTCTGGGGTGGGCAGTTTTTTGAAAATGGGCTCAACCAGAA
RNF125	NM_017831.3	790-890	GCAAGGTGTGTATGTCCCTTTTGTCAGAGGGAACTGTATGAAGACAGCTTGCTGGATCATTGTATTACTCATCACAGATCGGAACGGAGGCCTGTGTTCT
RORA	NM_134261.2	1715-1815	AAAATTAACCGAGACACTTTATATGGCCCTGCACAGACCTGGAGCGCCACACACTGCACATCTTTTGGTGATCGGGGTCAGGCAAAGGAGGGGAAACAAT
RORC	NM_001001523.1	1350-1450	CTCATCAATGCCCATCGGCCAGGGCTCCAAGAGAAAAGGAAAGTAGAACAGCTGCAGTACAATCTGGAGCTGGCCTTTCATCATCATCTCTGCAAGACTC
RPL27	NM_000988.3	23-123	GGGCCGGGTGGTTGCTGCCGAAATGGGCAAGTTCATGAAACCTGGGAAGGTGGTGCTTGTCCTGGCTGGACGCTACTCCGGACGCAAAGCTGTCATCGTG
RPS13	NM_001017.2	331-431	GCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCGTCTGATTCTAATAGAGAGCCGGATTCACCGTTTGGCTCGATATTATAAGACCAAGCGA
RUNX1	NM_001754.4	635-735	CAGCCATGAAGAACCAGGTTGCAAGATTTAATGACCTCAGGTTTGTCGGTCGAAGTGGAAGAGGGAAAAGCTTCACTCTGACCATCACTGTCTTCACAAA
RUNX2	NM_004348.3	1850-1950	GAAGCCACAGCAGTTCCCCAACTGTTTTGAATTCTAGTGGCAGAATGGATGAATCTGTTTGGCGACCATATTGAAATTCCTCAGCAGTGGCCCAGTGGTA
RUNX3	NM_004350.1	2085-2185	GTGGTCTCATAATTCCATTTGTGGAGAGAACAGGAGGGCCAGATAGATAGGTCCTAGCAGAAGGCATTGAGGTGAGGGATCATTTTGGGTCAGACATCAA
S100A4	NM_002961.2	263-363	CAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCC
S100A6	NM_014624.3	539-639	TTCCTGGGGGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGAGACACCCTCTGGGGGTCCTCTCTGAGTCAAAT
SATB1	NM_001131010.1	1335-1435	TTCCGAAATCTACCAGTGGGTACGCGATGAACTGAAACGAGCAGGAATCTCCCAGGCGGTATTTGCACGTGTGGCTTTTAACAGAACTCAGGGCTTGCTT
SCML1	NM_001037540.1	925-1025	GCAACGTATGGTTCTTCTTCAGGGCTCTGCCTTGGCAACCCTCGGGCTGACAGCATCCACAACACTTACTCAACTGACCATGCTTCTGCAGCACCACCTT
SCML2	NM_006089.2	360-460	ATTGGAAGCCCGTGACCCTCGCAATGCCACTTCAGTATGTATTGCTACGGTTATTGGAATTACTGGGGCCAGGTTACGGTTACGACTGGATGGTAGTGAC
SEL1L	NM_005065.4	980-1080	GGGCAATCTAATAGCCCACATGGTTTTGGGTTACAGATACTGGGCTGGCATCGGCGTCCTCCAGAGTTGTGAATCTGCCCTGACTCACTATCGTCTTGTT
SELL	NM_000655.3	110-210	CTCCCTTTGGGCAAGGACCTGAGACCCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAAGAACTAGAGAAGGACCAAGCAAAGCCATGATATTTCCA
SELPLG	NM_003006.3	2297-2397	CATGGGCTGTTAGGTTGACTTCAGTTTTGCCTCTTGGACAACAGGGGGTCTTGTACATCCTTGGGTGACCAGGAAAAGTTCAGGCTATGGGGGGCCAAAG
SERPINE2	NM_006216.2	240-340	CGCTGCCTTCCATCTGCTCCCACTTCAATCCTCTGTCTCTCGAGGAACTAGGCTCCAACACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCC
SH2B3	NM_005475.2	4285-4385	CCTCCAGCCAGAAGTTAAACATCTGGGATATGACGTCTTCATGCCAGGGGCACTCATTTCTTAGCAGCCTCTCTACATACATCTCTCAGGTGGTGCCAAG
SH2D2A	NM_001161443.1	341-441	TGCTGGAGCCCAAGCCTCAGGGGTGCTACTTGGTGCGGTTCAGCGAGAGCGCGGTGACCTTCGTGCTGACTTACAGGAGCCGGACTTGCTGCCGCCACTT
SIT1	NM_014450.2	720-820	GCCCCAGCCCCCCGTAGCAGGGGCATGACTGTTTCCCAACCAGCACCCAAAGACGGGCGCCATTGCCAAGTCACAGGATGTGATCTACCCCGGACTTCCT
SKAP1	NM_003726.3	1360-1460	AAGTGGGAAGAGGCACGTTCATCAAACCTGTTACTAAACCAGCCTAGTCATAGCTCATCCCCATCTCTAAATGTGTCCACACAACCACATCTGCCTTTTC
SKAP2	NM_003930.3	3374-3474	TTTTACAGTTAATCCAGGAGAGGGAGTCCTTTGCCAACTGATGACCAACAGTTCCAAGCCAGATAGTCTCGTGAACAGTGACAATACAGAAATAAGGTGT
SLA2	NM_032214.2	1640-1740	AAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGGTCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAG
SLAMF1	NM_003037.2	580-680	GTGTCTCTTGATCCATCCGAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAGTTTTATCTGGAGAATCTCACCCTGGGGATACGGGAAAGCAGGA
SLAMF7	NM_021181.3	215-315	GGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACTGAAGAAGAATGACTCA
SLC2A1	NM_006516.2	2500-2600	AGGCTCCATTAGGATTTGCCCCTTCCCATCTCTTCCTACCCAACCACTCAAATTAATCTTTCTTTACCTGAGACCAGTTGGGAGCACTGGAGTGCAGGGA
SMAD3	NM_005902.3	4220-4320	TTAAAGGACAGTTGAAAAGGGCAAGAGGAAACCAGGGCAGTTCTAGAGGAGTGCTGGTGACTGGATAGCAGTTTTAAGTGGCGTTCACCTAGTCAACACG
SMAD4	NM_005359.3	1370-1470	AGGTTGCACATAGGCAAAGGTGTGCAGTTGGAATGTAAAGGTGAAGGTGATGTTTGGGTCAGGTGCCTTAGTGACCACGCGGTCTTTGTACAGAGTTACT
SNAI1	NM_005985.2	63-163	GACCACTATGCCGCGCTCTTTCCTCGTCAGGAAGCCCTCCGACCCCAATCGGAAGCCTAACTACAGCGAGCTGCAGGACTCTAATCCAGAGTTTACCTTC
SOCS1	NM_003745.1	1025-1125	TTAACTGTATCTGGAGCCAGGACCTGAACTCGCACCTCCTACCTCTTCATGTTTACATATACCCAGTATCTTTGCACAAACCAGGGGTTGGGGGAGGGTC

SOCS3	NM_003955.3	1870-1970	GGAGGATGGAGGAGACGGGACATCTTTCACCTCAGGCTCCTGGTAGAGAAGACAGGGGATTCTACTCTGTGCCTCCTGACTATGTCTGGCTAAGAGATTC
SOD1	NM_000454.4	35-135	GCCTATAAAGTAGTCGCGGAGACGGGGTGCTGGTTTGCGTCGTAGTCTCCTGCAGCGTCTGGGGTTTCCGTTGCAGTCCTCGGAACCAGGACCTCGGCGT
SOX13	NM_005686.2	3039-3139	ATTTATTGAGTGCCCACTACGTGCCAGGCACTGTTGCTGAGTTCCTGTGGGTGTGTCTCTCGATGCCACTCCTGCTTCTCTGGGGGCCTCTTTCTGTGCT
SOX2	NM_003106.2	151-251	CTTAAGCCTTTCCAAAAAATAATAATAACAATCATCGGCGGCGGCAGGATCGGCCAGAGGAGGAGGGAAGCGCTTTTTTTGATCCTGATTCCAGTTTGCC
SOX4	NM_003107.2	3040-3140	GTTCACGGTCAAACTGAAATGGATTTGCACGTTGGGGAGCTGGCGGCGGCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGAC
SOX5	NM_152989.2	1885-1985	TAGCCATGCAATGATGGATTTCAATCTGAGTGGAGATTCTGATGGAAGTGCTGGAGTCTCAGAGTCAAGAATTTATAGGGAATCCCGAGGGCGTGGTAGC
SPI1	NM_003120.1	730-830	CTCCGCAGCGGCGACATGAAGGACAGCATCTGGTGGGTGGACAAGGACAAGGGCACCTTCCAGTTCTCGTCCAAGCACAAGGAGGCGCTGGCGCACCGCT
SPN	NM_001030288.1	2798-2898	AAGCCAGGCTTCATGGAAAGATCGTATGTGTGACCCAAATATGAGTTCTTCAGCTCAGCCATGGTAATCCCTTCCTTGAAGTCTCCATTTCTGCAGTACA
SPRY2	NM_005842.2	85-185	AAAGAGGAAATACTCCGCGTGCGCTTGTAGAAGGGGAGTCGTCTCCAGCTCCGAACCCCGGAGTGTTCATCAGCGGGGAATCTGGCTCCGAATTCTCTTT
STAT1	NM_007315.2	205-305	TTTGCTGTATGCCATCCTCGAGAGCTGTCTAGGTTAACGTTCGCACTCTGTGTATATAACCTCGACAGTCTTGGCACCTAACGTGCTGTGCGTAGCTGCT
STAT3	NM_139276.2	4535-4635	AGACTTGGGCTTACCATTGGGTTTAAATCATAGGGACCTAGGGCGAGGGTTCAGGGCTTCTCTGGAGCAGATATTGTCAAGTTCATGGCCTTAGGTAGCA
STAT4	NM_003151.2	789-889	AGACAATGGATCAGAGTGACAAGAATAGTGCCATGGTGAATCAGGAAGTTTTGACACTGCAGGAAATGCTTAACAGCCTCGATTTCAAGAGAAAGGAGGC
STAT5A	NM_003152.2	3460-3560	GAGACAGAGAGAGAGAAAGAGAGAGTGTGTGGGTCTATGTAAATGCATCTGTCCTCATGTGTTGATGTAACCGATTCATCTCTCAGAAGGGAGGCTGGGG
STAT5B	NM_012448.3	200-300	AAGGAGAAGCCCTTCATCAGATGCAAGCGTTATATGGCCAGCATTTTCCCATTGAGGTGCGGCATTATTTATCCCAGTGGATTGAAAGCCAAGCATGGGA
STAT6	NM_003153.3	2030-2130	AGAACATCCAGCCATTCTCTGCCAAAGACCTGTCCATTCGCTCACTGGGGGACCGAATCCGGGATCTTGCTCAGCTCAAAAATCTCTATCCCAAGAAGCC
STMN1	NM_203401.1	287-387	CGTGGGTGGCGGCAGGACTTTCCTTATCCCAGTTGATTGTGCAGAATACACTGCCTGTCGCTTGTCTTCTATTCACCATGGCTTCTTCTGATATCCAGGT
SYK	NM_003177.3	1685-1785	CGGACTCTCCAAAGCACTGCGTGCTGATGAAAACTACTACAAGGCCCAGACCCATGGAAAGTGGCCTGTCAAGTGGTACGCTCCGGAATGCATCAACTAC
TAL1	NM_003189.2	4635-4735	ACAGCATCTGTAGTCAGCCGACAACTATTTCGGCCTTTTGGGGGTGGGTCTGGCCGTACTTGTGATTTCGATGGTACGTGACCCTCTGCTGAAGACTTGC
TBP	NM_003194.3	25-125	CGCCGGCTGTTTAACTTCGCTTCCGCTGGCCCATAGTGATCTTTGCAGTGACCCAGCAGCATCACTGTTTCTTGGCGTGTGAAGATAACCCAAGGAATTG
TBX21	NM_013351.1	890-990	ACACAGGAGCGCACTGGATGCGCCAGGAAGTTTCATTTGGGAAACTAAAGCTCACAAACAACAAGGGGGCGTCCAACAATGTGACCCAGATGATTGTGCT
TBXA2R	NM_001060.3	385-485	CACACGCGCTCCTCCTTCCTCACCTTCCTCTGCGGCCTCGTCCTCACCGACTTCCTGGGGCTGCTGGTGACCGGTACCATCGTGGTGTCCCAGCACGCCG
TCF12	NM_207037.1	1105-1205	CACATGACCGCTTGAGTTATCCTCCACACTCAGTTTCACCAACAGACATAAACACGAGTCTTCCACCAATGTCCAGCTTTCATCGCGGCAGTACCAGCAG
TCF3	NM_003200.2	4325-4425	ATACGTGTCAACACAGCTGGCTGGATGATTGGGACTTTAAAACGACCCTCTTTCAGGTGGATTCAGAGACCTGTCCTGTATATAACAGCACTGTAGCAAT
TCF7	NM_003202.2	2420-2520	ATTCCATTTCCAGTTCATCTATGGCAGTCCAGCCAGCTCCTGGGCAGCTTGAGAGGGCAAACCCAAAACCTCATGACAGCCAGAGCCTGTCTTTCAGCAT
TDGF1	NM_003212.2	1567-1667	AAGGAAAGAAAACATCTTTAAGGGGAGGAACCAGAGTGCTGAAGGAATGGAAGTCCATCTGCGTGTGTGCAGGGAGACTGGGTAGGAAAGAGGAAGCAAA
TDO2	NM_005651.1	0-100	AAGGTCAATGATAGCATCTGCCTAGAGTCAAACCTCCGTGCTTCTCAGACAGTGCCTTTTCACCATGAGTGGGTGCCCATTTTTAGGAAACAACTTTGGA
TEK	NM_000459.2	615-715	CGAGTTCGAGGAGAGGCAATCAGGATACGAACCATGAAGATGCGTCAACAAGCTTCCTTCCTACCAGCTACTTTAACTATGACTGTGGACAAGGGAGATA
TERF1	NM_003218.3	1037-1137	CTGAAAGCAGAATACCTGTTTCAAAGAGTCAGCCGGTAACTCCTGAAAAACATCGAGCTAGAAAAAGACAGGCATGGCTTTGGGAAGAAGACAAGAATTT
TERT	NM_198253.1	2570-2670	GGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGA
TF	NM_001063.2	640-740	CTGCTCCACCCTTAACCAATACTTCGGCTACTCGGGAGCCTTCAAGTGTCTGAAGGATGGTGCTGGGGATGTGGCCTTTGTCAAGCACTCGACTATATTT
TFRC	NM_003234.1	1220-1320	CAGTTTCCACCATCTCGGTCATCAGGATTGCCTAATATACCTGTCCAGACAATCTCCAGAGCTGCTGCAGAAAAGCTGTTTGGGAATATGGAAGGAGACT
TGFA	NM_003236.2	780-880	TGCCACAGACCTTCCTACTTGGCCTGTAATCACCTGTGCAGCCTTTTGTGGGCCTTCAAAACTCTGTCAAGAACTCCGTCTGCTTGGGGTTATTCAGTGT
TGFB1	NM_000660.3	1260-1360	TATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGG
TGFB2	NM_003238.2	1125-1225	AAGCCAGAGTGCCTGAACAACGGATTGAGCTATATCAGATTCTCAAGTCCAAAGATTTAACATCTCCAACCCAGCGCTACATCGACAGCAAAGTTGTGAA
TGFBR1	NM_004612.2	4280-4380	GGGGAAATACGACTTAGTGAGGCATAGACATCCCTGGTCCATCCTTTCTGTCTCCAGCTGTTTCTTGGAACCTGCTCTCCTGCTTGCTGGTCCCTGACGC

Thymidine Kinase	SCFV007.1	100-200	TCTACGTACCCGAGCCGATGACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGAT
TIE1	NM_005424.2	2610-2710	CATCGGGGAGGGGAACTTCGGCCAGGTCATCCGGGCCATGATCAAGAAGGACGGGCTGAAGATGAACGCAGCCATCAAAATGCTGAAAGAGTATGCCTCT
TLR2	NM_003264.3	180-280	CTGCTTTCAACTGGTAGTTGTGGGTTGAAGCACTGGACAATGCCACATACTTTGTGGATGGTGTGGGTCTTGGGGGTCATCATCAGCCTCTCCAAGGAAG
TLR8	NM_138636.3	2795-2895	GACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGATCCGGGATTGGCCATCATCGACAACCTCATGCAGAGCATCAACCAAAGCAAGAAAACAG
TNF	NM_000594.2	1010-1110	AGCAACAAGACCACCACTTCGAAACCTGGGATTCAGGAATGTGTGGCCTGCACAGTGAAGTGCTGGCAACCACTAAGAATTCAAACTGGGGCCTCCAGAA
TNFRSF14	NM_003820.2	916-1016	CTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTC
TNFRSF18	NM_004195.2	445-545	AGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTGCCTCGGGGACCTTCTCCGGGGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGCACCCA
TNFRSF1B	NM_001066.2	835-935	CCCAGCTGAAGGGAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGACAGCCTTGGGTCTACTAATAATAGGAGTGGTGAACTGTGTC
TNFRSF4	NM_003327.2	200-300	CCGTGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGCCGTGCAAGCCCTGCACGTGGTGTAACCTCAGAAGTGGGAGTGAGCGGAAGCAGCTGT
TNFRSF9	NM_001561.4	255-355	AGATTTGCAGTCCCTGTCCTCCAAATAGTTTCTCCAGCGCAGGTGGACAAAGGACCTGTGACATATGCAGGCAGTGTAAAGGTGTTTTCAGGACCAGGAA
TNFSF10	NM_003810.2	115-215	GGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAAC
TNFSF11	NM_003701.2	490-590	TACCTGATTCATGTAGGAGAATTAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCACATCAGAGCAGAGAAAGC
TNFSF14	NM_003807.2	270-370	ATTTTCAGAAGCCTCTGGAAAGTCGTGCACAGCCCAGGAGTGTTGAGCAATTTCGGTTTCCTCTGAGGTTGAAGGACCCAGGCGTGTCAGCCCTGCTCCA
TOX	NM_014729.2	3950-4050	AATGAGCAGCTTTGACTTTGACAGGCGGTTTGTGCAGGAAAGCACAGTGCCGTGTTGTTTACAGCTTTTCTAGAGCAGCTGTGCGACCAGGGTAGAGAGT
TP53	NM_000546.2	1330-1430	GGGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC
TRAF1	NM_005658.3	3735-3835	CGAGTGATGGGTCTAGGCCCTGAAACTGATGTCCTAGCAATAACCTCTTGATCCCTACTCACCGAGTGTTGAGCCCAAGGGGGGATTTGTAGAACAAGCC
TRAF2	NM_021138.3	1325-1425	GTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGGGAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTT
TRAF3	NM_145725.1	1795-1895	ATATGATGCCCTGCTTCCTTGGCCGTTTAAGCAGAAAGTGACACTCATGCTGATGGATCAGGGGTCCTCTCGACGTCATTTGGGAGATGCATTCAAGCCC
TSC22D3	NM_198057.2	1400-1500	TTAAGCAGAGGCAACCTCTCTCTTCTCCTCTGTTTCGTGAAGGCAGGGGACACAGATGGGAGAGATTGAGCCAAGTCAGCCTTCTGTTGGTTAATATGGT
TSLP	NM_033035.3	395-495	CCGTCTCTTGTAGCAATCGGCCACATTGCCTTACTGAAATCCAGAGCCTAACCTTCAATCCCACCGCCGGCTGCGCGTCGCTCGCCAAAGAAATGTTCGC
TXK	NM_003328.1	800-900	ATGACTCGTCTCCGATATCCAGTTGGGCTGATGGGCAGTTGTTTACCAGCCACAGCTGGGTTTAGCTACGAAAAGTGGGAGATAGATCCATCTGAGTTGG
TYK2	NM_003331.3	485-585	TCATCGCTGACAGCTGAGGAAGTCTGCATCCACATTGCACATAAAGTTGGTATCACTCCTCCTTGCTTCAATCTCTTTGCCCTCTTCGATGCTCAGGCCC
TYROBP	NM_003332.2	457-557	CTGCACCTCATTCCAACTCCTACCGCGATACAGACCCACAGAGTGCCATCCCTGAGAGACCAGACCGCTCCCCAATACTCTCCTAAAATAAACATGAAGC
UBASH3A	NM_001001895.1	1970-2070	GAGATGCTGCTGTTTCCAGAGGCGTCTTAGTCTCACCCAATGTGATTTGTAGAAGCACGAGACGCACTTTTATATCCCGGAATATTTCCCTCCGGCTTTC
VAX2	NM_012476.2	871-971	CAGCGCCAGCAGCTGCAAGAAAGCTAACACTTAAGACTCCCACCCTGTGACACTGAGTCCCGAGCACAGCACCTTCCCAGTCTCCTGTGCCCCAGCGGAC
VEGFA	NM_001025366.1	1325-1425	GAGTCCAACATCACCATGCAGATTATGCGGATCAAACCTCACCAAGGCCAGCACATAGGAGAGATGAGCTTCCTACAGCACAACAAATGTGAATGCAGAC
WEE1	NM_003390.2	5-105	TGCGTTTGAGTTTGCCGCGAGCCGGGCCAATCGGTTTTGCCAACGCATGCCCACGTGCTGGCGAACAAATGTAAACACGGAGATCGTGTGCCGGGCACTT
XBP1	NM_005080.2	440-540	GGAGTTAAGACAGCGCTTGGGGATGGATGCCCTGGTTGCTGAAGAGGAGGCGGAAGCCAAGGGGAATGAAGTGAGGCCAGTGGCCGGGTCTGCTGAGTCC
XBP1	NM_001079539.1	935-1035	ATTCATTGTCTCAGTGAAGGAAGAACCTGTAGAAGATGACCTCGTTCCGGAGCTGGGTATCTCAAATCTGCTTTCATCCAGCCACTGCCCAAAGCCATCT
YY1AP1	NM_139118.2	755-855	ATGGGAGCTATGCAGCTGATTGAAGACTTCAGCACACATGTCAGCATTGACTGCAGCCCTCATAAAACTGTCAAGAAGACTGCCAATGAATTTCCCTGTT
ZAP70	NM_001079.3	1175-1275	GGAGCTCAAGGACAAGAAGCTCTTCCTGAAGCGCGATAACCTCCTCATAGCTGACATTGAACTTGGCTGCGGCAACTTTGGCTCAGTGCGCCAGGGCGTG
ZBTB16	NM_006006.4	1585-1685	TCCTGGATAGTTTGCGGCTGAGAATGCACTTACTGGCTCATTCAGCGGGTGCCAAAGCCTTTGTCTGTGATCAGTGCGGTGCACAGTTTTCGAAGGAGGA
ZC2HC1A	NM_016010.2	665-765	ACGATTACCGCAGCCAAGTGGCGCTGGCAAAACTGTTGTAGGTGTTCCTTCAGGTAAAGTGTCTTCAAGTAGCAGCTCTTTGGGAAACAAACTTCAGACC
ZEB2	NM_014795.2	20-120	TCCCAGAGAGAAACTTGGCGATCACGTTTTCACATGATGCTCACGCTCAGGGCGCTTCAATTATCCCTCCCCACAAAGATAGGTGGCGCGTGTTTCAGGG
ZNF516	NM_014643.2	4830-4930	GGTGGGGGACGGCTTCATATACCTCTTCCTCAGTAATGCAAATGCGAGTTTTTGTGGTGGGGGTTAAGGCCCATAACAAAGGATCTTAAACCATGCAGTG

Table S2. Fold change in mRNA abundance of mbIL15-CAR T cells relative to CAR T cells

GENE	logFC	PValue	FDR
IL7R	-2.4	1.9E-05	6.7E-03
NRP1	-2.7	1.6E-04	2.9E-02
DAP12	1.9	3.1E-04	3.7E-02
CD4	-1.9	5.5E-04	4.9E-02
TNFRSF4	-1.7	2.5E-03	1.5E-01
TIE1	-1.9	2.6E-03	1.5E-01
HRH2	1.6	4.6E-03	2.2E-01
CPT1	-1.6	5.0E-03	2.2E-01
PDCD1	-1.6	8.6E-03	3.4E-01
ICOSLG	-1.3	1.3E-02	4.2E-01
CMRF35H	-1.7	1.4E-02	4.2E-01
CCR4	-1.4	1.4E-02	4.2E-01
RORC	1.4	2.5E-02	6.4E-01
GILZ	-1.1	2.6E-02	6.4E-01
CD86	-1.3	2.7E-02	6.4E-01
TSLPR	-1.5	3.1E-02	6.8E-01
BCL6	-1.1	3.8E-02	7.9E-01
PAX5	1.1	4.2E-02	8.3E-01
IL23R	1.1	4.8E-02	8.9E-01
KIR2DS2	1.1	5.2E-02	9.2E-01
CD40LG	-1.1	6.3E-02	1.0E+00
IKZF2	-1.0	7.6E-02	1.0E+00
BCL2	0.8	9.2E-02	1.0E+00
SOX5	1.3	1.1E-01	1.0E+00
SOX13	-0.9	1.4E-01	1.0E+00
BNIP3	-0.8	1.5E-01	1.0E+00
GZMH	0.7	1.5E-01	1.0E+00
CD11B	-0.8	1.6E-01	1.0E+00
LEF1	0.9	1.6E-01	1.0E+00
SMAD3	-0.7	1.6E-01	1.0E+00
FLT1	0.7	1.6E-01	1.0E+00
KLRB1	-0.7	1.7E-01	1.0E+00
CCL5	-0.6	1.7E-01	1.0E+00
C5ORF13	-0.8	1.8E-01	1.0E+00
KLF2	-0.6	2.0E-01	1.0E+00
CD276	-0.9	2.0E-01	1.0E+00
LRP5	0.7	2.0E-01	1.0E+00
P2RX7	-0.7	2.1E-01	1.0E+00
NCAM1	0.6	2.1E-01	1.0E+00
ATF3	0.8	2.2E-01	1.0E+00
ANXA1	-0.7	2.2E-01	1.0E+00
EOMES	-0.8	2.3E-01	1.0E+00
NFATC1	-0.6	2.3E-01	1.0E+00
MMP14	-0.8	2.5E-01	1.0E+00
PHACTR2	-0.7	2.6E-01	1.0E+00
GATA3	-0.7	2.6E-01	1.0E+00
CD44	-0.6	2.6E-01	1.0E+00
AIM2	-0.6	2.7E-01	1.0E+00
AGER	-0.6	2.7E-01	1.0E+00
TGFBR1	0.6	2.8E-01	1.0E+00
CSF2	-0.7	2.9E-01	1.0E+00
CD80	-0.6	3.0E-01	1.0E+00
IL10	0.4	3.2E-01	1.0E+00
FGL2	-0.6	3.3E-01	1.0E+00
MYC	-0.5	3.4E-01	1.0E+00
PHC1	-0.6	3.5E-01	1.0E+00
LOC282997	-0.5	3.5E-01	1.0E+00
ITGA5	-0.6	3.6E-01	1.0E+00
SIP1	-0.5	3.7E-01	1.0E+00
ITGA1	-0.5	3.7E-01	1.0E+00
KIR3DL2	-0.8	3.7E-01	1.0E+00
TBXA2R	0.6	3.8E-01	1.0E+00
CCR7	-0.5	3.9E-01	1.0E+00
RNF125	-0.5	3.9E-01	1.0E+00
ITGA4	-0.4	4.1E-01	1.0E+00
IL17RA	0.4	4.1E-01	1.0E+00
NOTCH1	0.4	4.1E-01	1.0E+00
CD28	-0.4	4.2E-01	1.0E+00
BIM	-0.5	4.2E-01	1.0E+00
STMN1	-0.4	4.3E-01	1.0E+00
LYN	0.4	4.3E-01	1.0E+00
KIR2DS1	0.4	4.3E-01	1.0E+00
NKp30	0.4	4.4E-01	1.0E+00
TNFRSF18	-0.5	4.4E-01	1.0E+00
RUNX1	0.4	4.4E-01	1.0E+00
SH2D2A	0.4	4.5E-01	1.0E+00
PDK1	-0.4	4.5E-01	1.0E+00
SELL	-0.4	4.6E-01	1.0E+00
POU5F1	-0.5	4.7E-01	1.0E+00
EGLN1	-0.4	4.7E-01	1.0E+00
TRAF1	-0.4	4.7E-01	1.0E+00
SOCS1	0.4	4.7E-01	1.0E+00
KIR2DL1	-0.7	4.8E-01	1.0E+00
IL23p19	0.4	4.8E-01	1.0E+00
LNK	0.3	4.9E-01	1.0E+00
SKAP1	-0.4	4.9E-01	1.0E+00
BIRC2	-0.3	4.9E-01	1.0E+00
STAT1	-0.2	5.0E-01	1.0E+00
LAIR1	-0.3	5.0E-01	1.0E+00
TNFRSF9	-0.5	5.0E-01	1.0E+00
MYB	-0.4	5.0E-01	1.0E+00
CDK4	0.4	5.0E-01	1.0E+00
XBP1	0.4	5.0E-01	1.0E+00
TFRC	-0.4	5.0E-01	1.0E+00
SLA2	0.4	5.1E-01	1.0E+00
CD69	0.3	5.1E-01	1.0E+00
FAS	-0.4	5.1E-01	1.0E+00
CCL3	0.2	5.1E-01	1.0E+00
EGLN3	-0.3	5.1E-01	1.0E+00
TNF	0.2	5.2E-01	1.0E+00
IGF1R	-0.3	5.2E-01	1.0E+00
BACH2	0.3	5.2E-01	1.0E+00
CD94	-0.4	5.2E-01	1.0E+00
BCL2L1	0.3	5.2E-01	1.0E+00
TXK	0.3	5.2E-01	1.0E+00
IL10RA	-0.3	5.3E-01	1.0E+00
RARA	-0.4	5.3E-01	1.0E+00
XBP1	0.3	5.3E-01	1.0E+00
IL12RB2	0.4	5.3E-01	1.0E+00
DPP4	0.3	5.3E-01	1.0E+00
RUNX3	0.4	5.4E-01	1.0E+00
HVEM	-0.3	5.4E-01	1.0E+00
FLT3LG	-0.3	5.4E-01	1.0E+00
ITGAL	-0.3	5.5E-01	1.0E+00
EPHA4	-0.3	5.5E-01	1.0E+00
IL2RA	-0.4	5.5E-01	1.0E+00
PTGER2	-0.3	5.6E-01	1.0E+00

ID2	0.3	5.6E-01	1.0E+00
DNAM1	-0.2	5.7E-01	1.0E+00
CD7	0.3	5.7E-01	1.0E+00
SLAMF1	-0.4	5.7E-01	1.0E+00
BCLXL	0.2	5.9E-01	1.0E+00
SATB1	0.3	5.9E-01	1.0E+00
TP53	0.2	5.9E-01	1.0E+00
MAD1L1	0.3	6.0E-01	1.0E+00
FOS	0.3	6.0E-01	1.0E+00
NKG2D	-0.3	6.0E-01	1.0E+00
CDK2	0.2	6.0E-01	1.0E+00
GZMB	0.2	6.0E-01	1.0E+00
IFNGR1	0.4	6.0E-01	1.0E+00
CTNNA1	0.2	6.1E-01	1.0E+00
ICOS	-0.2	6.2E-01	1.0E+00
SNAI1	-0.3	6.2E-01	1.0E+00
KIR2DL3	0.2	6.2E-01	1.0E+00
LAG3	0.2	6.2E-01	1.0E+00
HES1	-0.3	6.2E-01	1.0E+00
CD85	-0.3	6.3E-01	1.0E+00
PRF1	0.2	6.4E-01	1.0E+00
CDH1	-0.3	6.5E-01	1.0E+00
VEGFA	-0.2	6.5E-01	1.0E+00
mTOR	0.3	6.6E-01	1.0E+00
AKT1	0.2	6.6E-01	1.0E+00
CD38	-0.2	6.6E-01	1.0E+00
TRAF3	0.3	6.6E-01	1.0E+00
GLIPR1	-0.2	6.6E-01	1.0E+00
Dock5	0.2	6.6E-01	1.0E+00
BCL2L11	-0.3	6.6E-01	1.0E+00
LAT2	-0.3	6.6E-01	1.0E+00
ANXA2P2	0.2	6.7E-01	1.0E+00
p38	0.3	6.7E-01	1.0E+00
ETV6	-0.2	6.7E-01	1.0E+00
ATM	0.3	6.7E-01	1.0E+00
KIR3DL3	0.3	6.8E-01	1.0E+00
CBLB	-0.3	6.8E-01	1.0E+00
IL15RA	-0.2	6.9E-01	1.0E+00
CATHEPSINC	0.2	6.9E-01	1.0E+00
MAPK8	-0.2	6.9E-01	1.0E+00
FYN	-0.2	6.9E-01	1.0E+00
ITGB1	-0.3	6.9E-01	1.0E+00
RUNX2	-0.2	7.0E-01	1.0E+00
CCR1	0.1	7.0E-01	1.0E+00
PTPN4	-0.2	7.0E-01	1.0E+00
FASLG	0.2	7.0E-01	1.0E+00
CD19Rscfv	-0.3	7.0E-01	1.0E+00
PDE4	-0.2	7.1E-01	1.0E+00
STAT5A	-0.2	7.1E-01	1.0E+00
SHP2	0.2	7.1E-01	1.0E+00
E2A	-0.2	7.2E-01	1.0E+00
CREM	0.2	7.2E-01	1.0E+00
LTA	-0.3	7.3E-01	1.0E+00
FOXO3	-0.2	7.3E-01	1.0E+00
CASP1	0.2	7.3E-01	1.0E+00
SHP1	0.2	7.3E-01	1.0E+00
BATF	0.2	7.4E-01	1.0E+00
MAD	-0.1	7.4E-01	1.0E+00
SOCS3	-0.2	7.4E-01	1.0E+00
NKG2F	-0.3	7.4E-01	1.0E+00
IRF4	-0.2	7.4E-01	1.0E+00
RAC2	0.2	7.4E-01	1.0E+00
NFATC2	0.2	7.5E-01	1.0E+00
STAT6	-0.2	7.5E-01	1.0E+00
GNLY	0.2	7.5E-01	1.0E+00
CCL4	0.0	7.5E-01	1.0E+00
CD11C	-0.2	7.5E-01	1.0E+00
CSAD	-0.2	7.5E-01	1.0E+00
ABCB1	-0.2	7.6E-01	1.0E+00
CD8A	0.2	7.6E-01	1.0E+00
BMI1	-0.1	7.6E-01	1.0E+00
RAC1	0.2	7.6E-01	1.0E+00
LAT	-0.1	7.6E-01	1.0E+00
PNK	-0.2	7.6E-01	1.0E+00
AP1	0.2	7.6E-01	1.0E+00
STAT5B	-0.2	7.6E-01	1.0E+00
CD19RCD28CAR	-0.3	7.7E-01	1.0E+00
CITED2	0.2	7.7E-01	1.0E+00
DGKA	-0.2	7.7E-01	1.0E+00
CD274	-0.2	7.7E-01	1.0E+00
YAP	-0.1	7.7E-01	1.0E+00
IL2RG	-0.2	7.7E-01	1.0E+00
POP5	0.2	7.7E-01	1.0E+00
TRF	0.2	7.7E-01	1.0E+00
SLC2A1	-0.2	7.8E-01	1.0E+00
NFATC3	-0.2	7.8E-01	1.0E+00
CFLIP	-0.1	7.9E-01	1.0E+00
SERPINE2	-0.3	7.9E-01	1.0E+00
PDCD1LG2	-0.1	8.0E-01	1.0E+00
CTLA4	-0.2	8.0E-01	1.0E+00
SLAMF7	0.1	8.0E-01	1.0E+00
HOPX	0.1	8.1E-01	1.0E+00
TERT	0.2	8.1E-01	1.0E+00
NFAT5	-0.1	8.1E-01	1.0E+00
SCAP2	0.1	8.1E-01	1.0E+00
TNFRSF1B	-0.1	8.1E-01	1.0E+00
FANCC	0.1	8.1E-01	1.0E+00
JUNB	0.1	8.1E-01	1.0E+00
NT5E	-0.1	8.1E-01	1.0E+00
LGALS1	-0.2	8.1E-01	1.0E+00
ITK	0.1	8.1E-01	1.0E+00
BAX	0.2	8.1E-01	1.0E+00
CCR6	-0.1	8.2E-01	1.0E+00
APAF1	-0.2	8.2E-01	1.0E+00
BTLA	0.2	8.2E-01	1.0E+00
GADD45A	0.1	8.2E-01	1.0E+00
B2M	-0.1	8.2E-01	1.0E+00
LDHA	-0.2	8.2E-01	1.0E+00
CD43	-0.1	8.2E-01	1.0E+00
KLRC1	0.0	8.3E-01	1.0E+00
STS2	-0.2	8.3E-01	1.0E+00
HOXB3	-0.2	8.3E-01	1.0E+00
IL15	0.2	8.3E-01	1.0E+00
RAP46	-0.1	8.3E-01	1.0E+00
CDKN2C	0.1	8.3E-01	1.0E+00
MCL1	-0.1	8.4E-01	1.0E+00
CAT	-0.1	8.4E-01	1.0E+00
HPRT1	0.1	8.4E-01	1.0E+00
IKZF1	0.1	8.4E-01	1.0E+00
JAK2	-0.1	8.4E-01	1.0E+00
NEIL2	-0.2	8.4E-01	1.0E+00
NFkB	-0.1	8.5E-01	1.0E+00

CXCR4	0.1	8.5E-01	1.0E+00
KLF10	0.2	8.5E-01	1.0E+00
DUSP16	-0.1	8.5E-01	1.0E+00
MAP2K1	-0.1	8.6E-01	1.0E+00
IL21R	0.1	8.6E-01	1.0E+00
RAF1	0.1	8.6E-01	1.0E+00
FOXO1	0.1	8.6E-01	1.0E+00
MIF	-0.1	8.6E-01	1.0E+00
FADD	0.1	8.6E-01	1.0E+00
GADD45B	0.2	8.6E-01	1.0E+00
FOXP1	0.1	8.7E-01	1.0E+00
HLAA	-0.1	8.7E-01	1.0E+00
NR3C1	-0.1	8.7E-01	1.0E+00
PRKCQ	0.1	8.8E-01	1.0E+00
TCF12	0.1	8.8E-01	1.0E+00
NR4A1	-0.1	8.8E-01	1.0E+00
BCL10	-0.1	8.8E-01	1.0E+00
ITGB7	0.0	8.8E-01	1.0E+00
MAPK14	0.1	8.8E-01	1.0E+00
HDAC2	0.1	8.8E-01	1.0E+00
CD244	0.0	8.9E-01	1.0E+00
IL18R1	0.1	8.9E-01	1.0E+00
S100A4	0.1	8.9E-01	1.0E+00
HOXB4	-0.1	8.9E-01	1.0E+00
CSNK2A1	0.1	8.9E-01	1.0E+00
BCL11B	0.0	9.0E-01	1.0E+00
CTNNBL1	0.1	9.0E-01	1.0E+00
NCL	0.1	9.0E-01	1.0E+00
ELF1	0.1	9.0E-01	1.0E+00
MBD2	0.1	9.0E-01	1.0E+00
DAP10	-0.1	9.0E-01	1.0E+00
ELF4	0.1	9.0E-01	1.0E+00
GSK3B	-0.1	9.1E-01	1.0E+00
IRF1	0.0	9.1E-01	1.0E+00
CDKN1A	-0.1	9.1E-01	1.0E+00
CREB1	0.0	9.1E-01	1.0E+00
TDO2	0.1	9.1E-01	1.0E+00
STAT3	-0.1	9.1E-01	1.0E+00
AHNAK	0.1	9.1E-01	1.0E+00
CD63	0.0	9.1E-01	1.0E+00
LCK	0.0	9.1E-01	1.0E+00
KLF6	0.1	9.2E-01	1.0E+00
IL2RB	0.0	9.2E-01	1.0E+00
NKp46	0.0	9.2E-01	1.0E+00
EIF1	0.1	9.2E-01	1.0E+00
TRAF2	0.1	9.2E-01	1.0E+00
DOK2	0.1	9.2E-01	1.0E+00
ADAM19	-0.1	9.2E-01	1.0E+00
GFI1	0.0	9.2E-01	1.0E+00
NKG2E	-0.1	9.3E-01	1.0E+00
AIF1	0.0	9.3E-01	1.0E+00
HMGB2	0.0	9.3E-01	1.0E+00
HDAC1	0.1	9.3E-01	1.0E+00
CTNNB1	0.0	9.3E-01	1.0E+00
TYK2	0.1	9.3E-01	1.0E+00
IAP	0.1	9.3E-01	1.0E+00
C80RF70	0.2	9.3E-01	1.0E+00
PPARA	0.0	9.3E-01	1.0E+00
PRDM1	0.0	9.4E-01	1.0E+00
ITCH	0.0	9.4E-01	1.0E+00
CLA	0.0	9.4E-01	1.0E+00
LGALS3	0.1	9.4E-01	1.0E+00
CATHEPSIND	0.0	9.4E-01	1.0E+00
IL18RAP	0.0	9.4E-01	1.0E+00
IL4R	0.0	9.5E-01	1.0E+00
TNFSF10	0.0	9.5E-01	1.0E+00
CD58	0.0	9.5E-01	1.0E+00
BID	0.1	9.5E-01	1.0E+00
JAK1	0.0	9.5E-01	1.0E+00
CD247	0.0	9.5E-01	1.0E+00
SOD1	0.0	9.6E-01	1.0E+00
CIITA	0.1	9.6E-01	1.0E+00
CRIP1	0.1	9.6E-01	1.0E+00
ARRB2	0.1	9.6E-01	1.0E+00
NEIL1	-0.1	9.6E-01	1.0E+00
SMAD4	0.0	9.6E-01	1.0E+00
SELL	0.0	9.6E-01	1.0E+00
C11ORF17	0.0	9.6E-01	1.0E+00
TNFSF14	0.0	9.6E-01	1.0E+00
RHOA	0.0	9.6E-01	1.0E+00
CCR5	-0.1	9.6E-01	1.0E+00
NKG2C	-0.1	9.7E-01	1.0E+00
S100A6	0.0	9.7E-01	1.0E+00
SIT1	0.0	9.7E-01	1.0E+00
KIR2DL4	-0.1	9.7E-01	1.0E+00
CD3E	0.0	9.7E-01	1.0E+00
GZMA	0.0	9.7E-01	1.0E+00
TBX21	0.0	9.7E-01	1.0E+00
GLO1	0.1	9.7E-01	1.0E+00
IFNG	-0.1	9.7E-01	1.0E+00
IL12RB1	0.0	9.7E-01	1.0E+00
CCNB1	-0.1	9.7E-01	1.0E+00
IRF2	0.0	9.7E-01	1.0E+00
PDE7	0.0	9.7E-01	1.0E+00
TNFRSF7	0.0	9.8E-01	1.0E+00
CLIC1	0.0	9.8E-01	1.0E+00
JAK3	0.0	9.8E-01	1.0E+00
OPTN	0.0	9.8E-01	1.0E+00
MAPK3	0.0	9.8E-01	1.0E+00
RORA	0.1	9.8E-01	1.0E+00
KLF7	0.0	9.9E-01	1.0E+00
CDKN1B	0.0	9.9E-01	1.0E+00
PPP2R1A	0.0	9.9E-01	1.0E+00
ATP2B4	0.0	9.9E-01	1.0E+00
CD2	0.0	9.9E-01	1.0E+00
CXCR3	0.0	9.9E-01	1.0E+00
C10RF24	0.0	9.9E-01	1.0E+00
TGFB1	0.0	9.9E-01	1.0E+00
STAT4	0.0	1.0E+00	1.0E+00
ZAP70	0.0	1.0E+00	1.0E+00
CD3D	0.0	1.0E+00	1.0E+00
GABPa	0.0	1.0E+00	1.0E+00
CCR10	-0.1	1.0E+00	1.0E+00
PECAM1	-0.1	1.0E+00	1.0E+00
SOX4	0.1	1.0E+00	1.0E+00