Dominant neoantigen verification in hepatocellular carcinoma by a single-plasmid system coexpressing patient HLA and antigen

AUTHORS

Pu Chen[1†], Dongbo Chen[1†*], Dechao Bu[2], Jie Gao[3], Wanying Qin[4], Kangjian Deng[4], Liying Ren[1], Shaoping She[1], Wentao Xu[4], Yao Yang[1], Xingwang Xie[1,5*], Weijia Liao[4*] and Hongsong Chen[1*]

[1]Peking University People's Hospital, Peking University Hepatology Institute, Beijing Key Laboratory of Hepatitis C and Immunotherapy for Liver Disease, Beijing International Cooperation Base for Science and Technology on NAFLD Diagnosis, Beijing 100044, China;

[2]Research Center for Ubiquitous Computing Systems, Institute of Computing Technology, Chinese Academy of Sciences, Beijing 100190, China;

[3]Department of Hepatobiliary Surgery, Peking University People's Hospital, Beijing 100044, China;

[4]Laboratory of Hepatobiliary and Pancreatic Surgery, Affiliated Hospital of Guilin Medical University, Guilin 541001, Guangxi, China;

[5]Corregene Biotechnology Co., Ltd, Beijing 102206, China.

[†]These authors contributed equally to this work.

[*]These authors contributed equally to this work and shared senior authorship.

[*]CORRESPONDENCE

chenhongsong@bjmu.edu.cn (H.S. Chen), chendongbo338@bjmu.edu.cn (D.B. Chen), liaoweijia288@163.com (W.J. Liao), xiexingwang@corregene.com (X.W. Xie).

Chen P, *et al. J Immunother Cancer* 2023; 11:e006334. doi: 10.1136/jitc-2022-006334

TABLE OF CONTENTS

SUPPLEMENTAL MATERIALS AND METHODS

1. Patients and sample collection

We enrolled 14 patients with hepatocellular carcinoma (HCC) who underwent curative resection, including 6 patients from the Peking University People's Hospital and 8 patients from the Affiliated Hospital of Guilin Medical University. All cases were confirmed by pathology reports. The study was approved by the Research Ethics Committees of the Peking University People's Hospital and the Affiliated Hospital of Guilin Medical University. All patients provided written informed consent. Tumor tissues, nontumor liver tissues (nearby tissues > 2 cm away from tumor tissue margin) and portal vein tumor thrombi (PVTTs) were collected and frozen in liquid nitrogen for further processing. Peripheral blood mononuclear cells (PBMCs) were isolated from fresh peripheral blood of patients or healthy donors by Ficoll density gradient centrifugation. They were immediately frozen in -80°C and transferred to liquid nitrogen the next day. COS-7 cells, HEK293T cells, PLC/PRF/5 cells, Hep3B cells and HepG2 cells were purchased from American Type Culture Collection (ATCC). Huh-7 cells were purchased from Cell Resource Center, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences.

2. Extraction and next-generation sequencing (NGS) of DNA and RNA

2.1 Extraction and quality control of DNA and RNA

DNA and RNA were extracted from fresh-frozen samples using AllPrep DNA/RNA Mini Kit (QIAGEN) following the protocol of the manufacturer. The quantity and quality of DNA and RNA were determined by Qubit Fluorometer (Invitrogen) and agarose gel electrophoresis generally. Fragment Analyzer 5400 (Agilent) was used for

accurate verification. At least 1.5 μg high quality genomic DNA and 1.0 μg high quality RNA were prepared for subsequent experiments.

2.2 Whole exome sequencing (WES)

WES was performed using SureSelect Human All Exon V6 (Agilent) according to the manufacturer's instructions. We first used the Covaris to randomly fragment DNA sample to an average of 180 - 280 bp. Fragments were end-repaired, and an extra A base was added to the 3' end. Illumina adaptors were ligated to the fragments. Subsequently, we used SPRI beads to purify and acquire the library. After the solution hybridization of the library and biotin-labeled probes, we used beads to capture exome and then performed PCR amplification. The quality was determined by Qubit Fluorometer (Invitrogen) and Fragment Analyzer 5400 (Agilent). Furthermore, the effective concentration of the library was accurately quantified by quantitative real time PCR (qPCR). The library was sequenced by Illumina NovaSeq 6000 platform. Finally, raw date was filtered to obtain high-quality clean reads for further analysis.

2.3 RNA-sequencing (RNA-seq)

The library was acquired by NEBNext UltraTM RNA Library Prep Kit for Illumina. First, we used beads to capture mRNA from total RNA and fragment it. Then, we used M-MuLV Reverse Transcriptase and random hexamer primer to synthesize first strand cDNA and used RNase H and DNA Polymerase I to perform second strand cDNA synthesis. Remaining overhangs were converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, NEBNext Adaptor with hairpin loop structure were ligated to prepare for hybridization. The library fragments were purified with AMPure XP system

(Beckman Coulter). Subsequently, 3 µl USER Enzyme (NEB) was used with size-selected, adaptor-ligated cDNA at 37°C for 15 min followed by incubation at 95°C for 5 min. Furthermore, we performed PCR to acquire products and used AMPure XP system to purify them. Fragment Analyzer 5400 (Agilent) were used to quantitate the products. The clustering of the index-coded samples was performed on a cBot Cluster Generation System using TruSeq PE Cluster Kit v3-cBot-HS (Illumia). After cluster generation, the library was sequenced on Illumina NovaSeq 6000. Finally, raw data was filtered to obtain high-quality clean reads for subsequent analysis.

3. Variation calling

3.1 Base substitution, mutational signatures, mutated genes and evolutionary tree of the samples

For single nucleotide variants (SNVs), we analyzed the number of 6 different types of base substitutions including A>C, A>G, A>T, C>A, C>G and C>T, and calculated their proportions. Further, each of the substitutions was examined by incorporating information on the bases immediately 5' and 3' to each mutated base generating 96 possible triplet nucleotides (6 types of substitution × 4 types of 5' base × 4 types of 3' base). We calculated the proportion of each triplet nucleotide and identified the 30 mutational signatures from COSMIC database (https://cancer.sanger.ac.uk/cosmic) by the R package "deconstructSigs". Subsequently, we analyzed the abundance of each mutational signatures.

The gene that had at least one mutation was defined as mutated gene. And we focused our analysis on the high-frequency mutated genes, pan-cancer driver mutated genes[1], HCC driver mutated genes (according to previous reports and NCG7.0 database,

http://ncg.kcl.ac.uk/index.php)[2-6], immune-related mutated genes (according to GSEA, https://www.gsea-msigdb.org/gsea/index.jsp) and cytotoxic T lymphocyte (CTL)-evasion mutated genes[7]. The TMB for each sample was calculated as the number of mutations per 36 megabase (Mb) of gene, and the mutated frequency for each gene was the proportion of patients who had mutated genes in all patients.

We constructed an M × N matrix based on the occurrence of mutations in different samples. M was the number of mutations and N was the number of samples. The status of the mutation was 0 or 1, where 0 was unmutated and 1 was mutated. In addition, a negative control sample was added as negative control (NC), and the mutation frequency of all sites was defined as 0. Then phylograms were inferred using the R package "phangorn". The parsimony ratchet method was used to search for the best tree and acctran function was used to get edge length according to the ACCTRAN criterion[8].

3.2 Base substitution and mutated genes of HCC in TCGA database and reference mutational signatures in COSMIC database

Effective mutation analysis is the basis of neoantigen prediction. We used other database to verify the reliability of mutations from our samples. The data for analysis of base substitution and mutated genes of HCC were downloaded from the GDC data portal of TCGA database (https://www.cancer.gov/) and the used R package was "maftools". Reference mutational signatures were downloaded from COSMIC database.

4. Neoantigen prediction

4.1 Affinity prediction between neoantigens and human leukocyte antigens (HLAs)

We used OptiType[9], a new algorithm based on integer linear programming, to

analyze the HLA types of patients from WES data of nontumor liver tissues or PBMCs and used LOHHLA[10] to predict potential loss of heterozygosity (LOH) of HLAs from WES data of tumor tissues. At the same time, we used Variant Effect Predictor (VEP)[11] to predict mutated proteins from somatic mutations and disassembled the mutated proteins to potential mutated peptides. Then, we used Genome Analysis Toolkit (GATK) ASEReadCounter[12] to detect mutation count (MutCount) of potential mutated peptide from RNA sequencing (RNA-seq) data. Subsequently, the NetMHCpan-4.1 algorithm[13] was used to determine the affinity of the mutated peptides to the patient's HLAs. Finally, we filtered the data based on mutated peptide affinity (MutAff) $\leq$ 200 nM or referenced peptide affinity (RefAFF) / MutAff $\geq$ 10 in the case of excluding duplication and LOH of HLAs and predicted potential neoantigens.

4.2 Selection of indexes and filter values

Prediction with computer algorithms aimed at assessing affinity between neoantigens and HLAs is currently the main strategy for clinical neoantigen screening[14]. The common indexes for filtering neoantigens are MutAff, RefAFF / MutAff and the rank of mutated peptide affinity (Mutrank).

The common filter value of MutAff is 500 nM or lower, the RefAFF / MutAff is 1 or higher and the Mutrank is 2 or lower[15-16]. Because neoantigens have high heterogeneity in different tumors and population, the selection of indexes and filter values should be personalized[17].

Single nucleotide polymorphisms (SNPs) are one of the most common types of genetic variation among people. The mutated peptides from SNPs could not induce a strong immune response. We used VEP to predict mutated proteins from SNPs in

nontumor liver tissues and disassembled the mutated proteins to potential mutated peptides as negative dataset[18]. The frequency of the SNPs is 10% or more and the MutCount of potential mutated peptide is 5 or more. Positive dataset consisted of the neoantigens with high confidence collected by Tan et al[19], and the neoantigens without the paired wild types were eliminated. Then we used the negative dataset and the positive dataset to determine appropriate indexes and filter values. We found the increasing filter values of MutAff and Mutrank or the declining filter value of RefAFF / MutAff could induce more candidate neoantigens and the real neoantigens but less proportion of real neoantigens in candidate neoantigens (supplemental figure 6A-C). When the same amount of neoantigens were screened by different indexes, neoantigen proportions screened by MutAff and RefAFF / MutAff were higher than those screened by Mutrank (supplemental figure 7A-C). In our study, we excluded inferior Mutrank and selected MutAff $\leq$ 200 nM and RefAFF / MutAff $\geq$ 10 to balance the number and the proportion of the screened neoantigen for these HCC samples.

5. Establishment, validation and application of the Co-HA system

5.1 Construction of the *KRAS* G12D TCR-T cells

The starting vector was lenti-BSD-T2A-EGFP. This vector was constructed by CorreGene. The vector map is shown in supplemental figure 1A (supplemental plasmid sequence NO. 1). The gene segment of *EGFP* in vector were released from the vector by cleavage with restriction enzymes BfuAI (NEB) and EcoRI (NEB), and the vector without *EGFP* was recovered from the gel. Meanwhile, we entrusted Synbio Technologies to synthesize the gene segment of the *KRAS* G12D TCR, including TK412 Vβ, Cys mTRBC1, P2A, TK412 Vα and LVL_Cys mTRAC, as

described by Wang et al[20]. Gibson Assembly was then performed to assemble the TCR gene segment into the viral vector without *EGFP* to construct the TCR plasmid lenti-BSD-T2A-TK412 (supplemental figure 1A, supplemental plasmid sequence NO. 2). The 3589 bp gene segment was successfully excised from the TCR plasmid by restriction enzymes NotI (NEB) and BamHI (NEB) for verification (supplemental figure 1B). PBMCs from healthy donors were cultured in X-VIVO 15 medium (Lonza) supplemented with 5% Human AB serum (GemCell), 100 U/ml penicillin (Gibco), 100 μg/ml streptomycin (Gibco), 100 IU/ml IL-2 (R&D) and 10 μL T Cell TransAct EA (Miltenyi). According to the methods of production and infection of lentivirus in the previous research of our group[21], the TCR plasmid and assistant plasmid pVSVg (AddGene 8454) and psPAX2 (AddGene 12260) were cotransfected into HEK293T cells. After 48 hours, the supernatant of the virus was collected and centrifuged for 10 min with 2,000 g. The debris was removed by 0.45 μm filter (Millipore). The lentivirus was concentrated with Macrosep Advance Centrifugal Device (100K, PALL) and then the titer was determined by p24 enzyme-linked immunosorbent assay (ELISA). PBMCs were infected by the lentivirus with 20 multiplicity of infection (MOI). After 14 days of cultivation, TCR-T cells recognizing the *KRAS* G12D neoantigen were acquired. DNA was extracted from the TCR-T cells by TIANamp Genomic DNA Kit (TIANGEN) following the protocol of the manufacturer. Sanger sequencing was used to determine the key sequence of the TCR. The sequence of primer was shown as SEQ ID NO. 1 in supplemental table 5. In supplemental figure 1C, the crimson part of the picture represented the matching sequence, and the arrow represented the sequencing direction. In addition, the expression of the TCR was detected by flow cytometry (FCM). The antibodies were PE anti-mouse TCR β chain Antibody (BioLegend), FITC Mouse Anti-Human CD8 (BD) and Cell Viability

Solution (BD).

It is challenging to identify the TCRs of T cells for newfound neoantigens. In general, we produced the specific tetramers to identify the neoantigen-specific T cells. In order to get the sequences of the TCRVα and the TCRVβ of the neoantigen-specific T cells, we need to sort the neoantigen-specific T cells for Sanger sequencing. Besides the TCR-T cells, antigen-specific T cells in peripheral blood and tumor infiltrating lymphocytes (TILs) of patients could be as effector cells in the Co-HA system.

5.2 Construction of the HLA vectors

The HLA vector was the main component of the Co-HA system that contained the HLA subtype linker region, the antigen linker region and the tag sequence. At first, the HLA-A*11:01 vector containing HLA-A*11:01 gene was constructed with the lenti-PURO-T2A-EGFP vector (supplemental figure 3A, supplemental plasmid sequence NO. 3). The steps of constructing the HLA-A*11:01 vector were described in detail as follows. (1) To prevent disturbing subsequent restriction enzyme digestion, the recognition site of restriction enzyme BsmBI on the lenti-PURO-T2A-EGFP was synonymously mutated. (2) We simultaneously entrusted Synbio Technologies to synthesize the gene segment including HLA-A*11:01, E2A, Tag-A*11:01, P2A and *EGFP* we designed. The sequence of HLA-A*11:01 was acquired from the IPD-IMGT/HLA database (https://www.ebi.ac.uk/ipd/imgt/hla/), and the recognition site of restriction enzyme BsmBI in HLA-A*11:01 was synonymously mutated similarly. (3) The gene segment of *EGFP* was excised by restriction enzymes BamHI (NEB) and EcoRI (NEB), and the main part of the vector was recovered from the gel. Then, the synthesized gene segment was assembled into the main part of the vector by Gibson Assembly, and the HLA-A*11:01 vector was constructed and named

lenti-PURO-T2A-(HLA-A*11:01)-E2A-(Tag-A*11:01)-P2A-EGFP (supplemental figure 3A, supplemental plasmid sequence NO. 4). (4) The 2611 bp gene segment was excised from the HLA-A*11:01 vector by restriction enzymes BamHI (NEB) and XhoI (NEB) for verification (supplemental figure 3B). (5) Subsequently, the HLA-A*11:01 vector, and assistant plasmid pVSVg (AddGene 8454) and psPAX2 (AddGene 12260) were cotransfected into HEK293T cells for producing lentivirus. The *EGFP* in vector was used to as reporter gene. Then, COS-7 cells were infected with the lentivirus and cultured with 4 μg/ml puromycin (Sigma) for one week to establish stable cell lines. DNA was extracted from the COS-7 cells by TIANamp Genomic DNA Kit (TIANGEN) following the protocol of the manufacturer. The key sequence of the HLA-A*11:01 vector was analyzed with Sanger sequencing. The sequences of primers were shown as SEQ ID NO. 2-3 in supplemental table 5. In supplemental figure 3C, the crimson parts of the picture represented the matching sequences sequenced by Sanger sequencing, and the arrows represented the sequencing directions. In addition, the expression of HLA-A*11:01 was detected by FCM. The antibodies were FITC Mouse Anti-Human HLA-A (BD) and Cell Viability Solution (BD).

We designed the recognition sites of restriction enzymes BamHI (NEB) and AfeI (NEB) in the HLA-A*11:01 vector to replace the gene segment of the HLA with its tag to construct various HLA vectors. Then, we provided an innovative scheme to design the tag sequences of various HLA vectors. The length of the tag sequences was 15 bp. In order to ensure each tag unique, tag sequence was derived from the corresponding part of the various HLA. In addition, the design of the tag sequences for HLA-A, HLA-B and HLA-C respectively were different and described below. The tag of HLA-A*α:β designed was derived from the first sequence at positions (α × 3 +

1) to (α × 3 + 3) and the second sequence at positions (β × 3 + 1) to (β × 3 + 12) of HLA-A*α:β sequence; The tag of HLA-B*α:β designed was derived from the first sequence at positions (α × 3 + 1) to (α × 3 + 6) and the second sequence at positions (β × 3 + 1) to (β × 3 + 9) of HLA-B*α:β sequence; The tag of HLA-C*α:β designed was derived from the first sequence at positions (α × 3 + 1) to (α × 3 + 9) and the second sequence at positions (β × 3 + 1) to (β × 3 + 6) of HLA-C*α:β sequence. For instance, the tag of HLA-A*11:01 was derived from the first sequence at positions 34 (11 × 3 + 1) to 36 (11 × 3 + 3) and the second sequence at positions 4 (01 × 3 + 1) to 15 (01 × 3 + 12) of the HLA-A*11:01 sequence. Thirty-nine HLA vectors (supplemental table 1), including HLA-A*24:02 and HLA-A*02:01, were constructed for future use.

5.3 Construction of the target cells

We designed overlapping ends on both sides of the antigen linker region (supplemental table 2 SEQ ID NO. 3-4), and different gene segments of antigens can be seamlessly assembled to the HLA vectors at the same time with only one cutting and joining procedure. Specifically, we designed 2 recognition sites of restriction enzyme BsmBI on the HLA vectors for replacing the gene segment of *EGFP* with the gene segment of antigen, which can be used to construct the plasmid with coexpressing patient HLA and antigen.

We first entrusted Synbio Technologies to synthesize the gene segments of the *KRAS* G12D neoantigen (supplemental table 2 SEQ ID NO. 1) and its paired wild antigen (supplemental table 2 SEQ ID NO. 2). Then, we excised the gene segment of *EGFP* by restriction enzyme BsmBI (NEB) and recovered the HLA-A*11:01 vector without *EGFP* from the gel (supplemental figure 4B). Gibson Assembly was performed to

assemble the gene segments of the *KRAS* G12D neoantigen and its paired wild antigen to the HLA-A*11:01 vector without *EGFP* respectively. The target plasmids lenti-(HLA-A*11:01)-KRAS-M and lenti-(HLA-A*11:01)-KRAS-W were constructed (supplemental figure 4A, supplemental plasmid sequence NO. 5-6). The 3290 bp gene segments were excised from the target plasmids respectively by restriction enzymes EcoRI (NEB) and NotI (NEB) for verification (supplemental figure 4C). Subsequently, the target plasmids and assistant plasmid pVSVg (AddGene 8454) and psPAX2 (AddGene 12260) were cotransfected into HEK293T cells for producing lentivirus. Then, COS-7 cells were infected with the lentivirus and cultured with 4 μg/ml puromycin (Sigma) for one week to establish stable target cells. DNA was extracted from the target cells by TIANamp Genomic DNA Kit (TIANGEN) following the protocol of the manufacturer. Sanger sequencing was further performed to analyze the key sequence of the target plasmids. The sequence of primer was shown as SEQ ID NO. 3 in supplemental table 5. In supplemental figure 4D, the crimson parts of the picture represented the matching sequences sequenced by Sanger sequencing, and the arrows represented the sequencing directions.

5.4 Validation and application of the Co-HA system

First, the expression of HLA-A*11:01, HLA-A*24:02, HLA-A*02:01 molecules in the Co-HA system was validated by FCM. The antibodies used to detect the expression of HLA-A*11:01 were FITC Mouse Anti-Human HLA-A (BD) and Cell Viability Solution (BD). The antibodies used to detect the expression of HLA-A*24:02 were Anti-HLA-A24 (Human) mAb-FITC (MBL) and Cell Viability Solution (BD). The antibodies used to detect the expression of HLA-A*02:01 were Mouse Anti-Human HLA-A2 (BD) and Cell Viability Solution (BD). Subsequently, we cocultured 1×10^5 T cells (including 1×10^3 $CD8^+$ TCR-T cells) and 1×10^4 COS-7

cells for 3 days. The COS-7 cells had 3 types: WT COS-7 cells, COS-7 cells expressing the *KRAS* G12D neoantigen and COS-7 cells expressing its paired WT antigen. Then, the specific proliferation of $CD8^+$ TCR-T cells was detected by FCM. The antibodies were PE anti-mouse TCR β chain Antibody (BioLegend), FITC Mouse Anti-Human CD8 (BD) and Cell Viability Solution (BD). In addition, we performed a series of cytotoxicity tests to detect the immunogenicity of the *KRAS* G12D neoantigen in the Co-HA system. The effector cells (1×10^5 TCR-T cells) and the target cells (1×10^4 COS-7 cells) were cocultured for 12 hours. Then, the specific secretion of IFN-γ by the TCR-T cells against the *KRAS* G12D neoantigen was detected by enzyme-linked immunospot assay (ELISPOT) and ELASA. The effector cells (1×10^5 TCR-T cells) and the target cells (1×10^4 COS-7 cells) were cocultured for 3 days. Then, the specific lysis of the COS-7 cells generated by the *KRAS* G12D neoantigen in the Co-HA system was detected by Sanger sequencing. The effector cells (1×10^6 TCR-T cells) and the target cells (1×10^5 COS-7 cells) were cocultured following the protocol of the CytoTox 96® Non-Radioactive Cytotoxicity Assay (Promega). Then, the specific cytotoxicity against COS-7 cells generated by the *KRAS* G12D neoantigen in the Co-HA system was detected by ELISA for LDH levels.

For verification of new HCC-dominant neoantigens by the Co-HA system, the effector cells were T cells amplified by potential neoantigens with PBMCs from peptides. Other steps were same as above.

6. Amplification of neoantigen-specific T cells in peripheral blood

We produced the potential neoantigen peptides in GenScript and coincubated them with 2×10^6 PBMCs/well to promote specific T-cell proliferation. They were cultured in X-VIVO 15 medium (Lonza) supplemented with 5% Human AB serum (GemCell),

100 U/ml penicillin (GIBCO), 100 μg/ml streptomycin (Gibco), and 10 IU/ml IL-2 (R&D) for 3 weeks. Medium was replenished twice a week and 4 μM/ml peptides were replenished weekly.

7. Tetramer staining

7.1 Generation of new specific tetramer using peptide exchange

New specific tetramers were generated by QuickSwitch Quant Tetramer Kit (MBL) following the protocol of peptide exchange experiments provided by the manufacturer. The predicted potential neoantigen peptides were loaded onto the tetramer at 2 mM according to standard procedure. The reference peptide was loaded onto the same tetramer at 1 mM.

7.2 Quantification of peptide exchange using flow cytometric sandwich immunoassay

All control samples were acquired following the protocol of the manufacturer. Then, the following procedure to quantify the peptide exchange efficiency was performed by flow cytometry (FCM): (1) 5 μl of Magnetic Capture Beads were pipetted to a flow cytometer tube containing 200 μl 1× Assay Buffer and run as a "beads" control; (2) Control #1 was bead-captured QuickSwitch Tetramer; (3) Control #2 was beads that have not captured any tetramer and stained with exiting peptide antibody, and control #3 (negative control) was beads that have captured the QuickSwitch Tetramer and stained with exiting peptide antibody. (4) Peptide exchange samples were run, the MFI_{FITC} of each was noted. Peptide-exchanged tetramers displayed various Exiting Peptide amounts, which were inversely proportional to the newly loaded peptide on the HLA molecules. Control #4 was the reference peptide; (5) The percentages of peptide exchange of each peptide exchange samples were calculated. Tetramers bound to T-cell receptors via three HLA/peptide monomers[22-23]. Therefore, the minimal

recommended peptide exchange percentage should be 75%.

7.3 Detection of the neoantigen-specific T cells in peripheral blood by Tetramer staining

The cells tested were re-suspended at a concentration of 2×10^7 cells/ml. 50 μl of samples was prepared for tetramer staining. 10 μl Clear Back (MBL), a human FcR blocking reagent for reducing nonspecific staining, was added to each tube. They were incubated for 5 min at room temperature. 10 μl of tetramer was added and vortexed gently. They were protected from light and incubated for 30 min at room temperature. FITC Mouse Anti-Human CD8 (BD) was added and vortexed gently. They were protected from light and incubated for 20 min at 4 ℃. PBS was used to rinse for 3 times. The cells were resuspended in 500 μl of PBS with Cell Viability Solution (BD) and tested by FCM immediately.

8. Antitumor efficacy of *ENTPD6* neoantigen-specific T cells in vivo

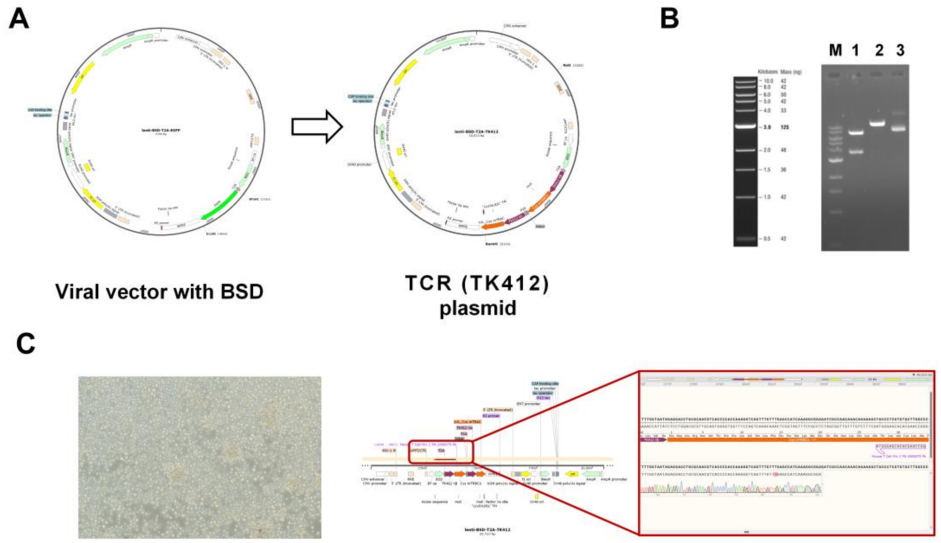
The *ENTPD6* neoantigen-specific T cells from patient 04 were sorted by FCM after tetramer staining (supplemental figure 10A). The survival rate of the neoantigen-specific T cells sorted by FCM and cultivated in vitro (supplemental figure 10B). The Huh-7 cells coexpressing HLA-A*24:02 and *ENTPD6* neoantigen were selected as the target cells (supplemental figure 9A), and then implanted into the B-NDG-$B2m^{tm1}Fcrn^{tm1(mB2m)}$/Bcgen mouse model. When tumor size was approximately 150 ± 50 mm^3, they were treated with the neoantigen-specific T cells (0.5×10^6) through intratumor injection every 2 days. In addition, the key sequences of the *ENTPD6* in tumors were detected by Sanger sequencing.

9. Quantification and statistical analysis

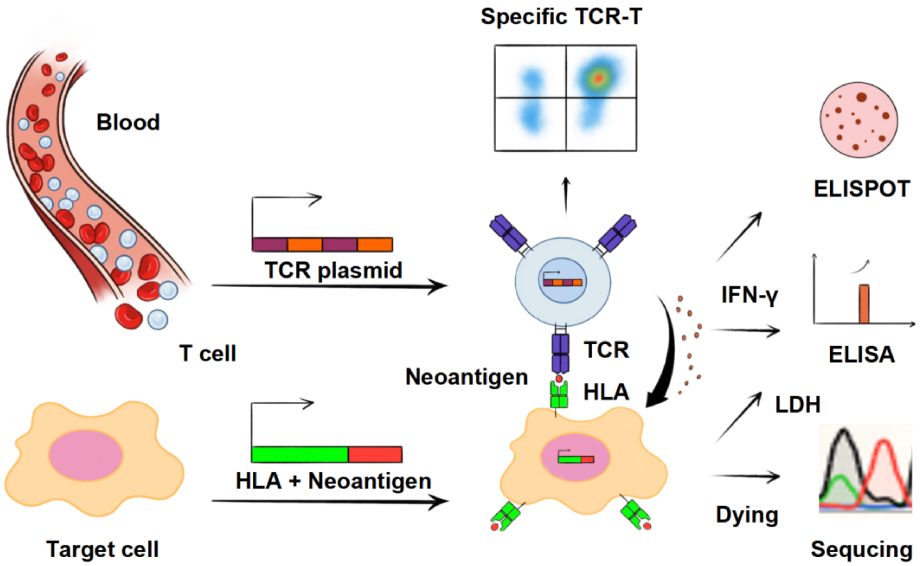
Statistical analyzes were conducted using GraphPad Prism 8.0.2 software. A 2-tailed *P*

value < 0.05 was considered significant. The method for two group comparison is 2-tailed unpaired *t* test.

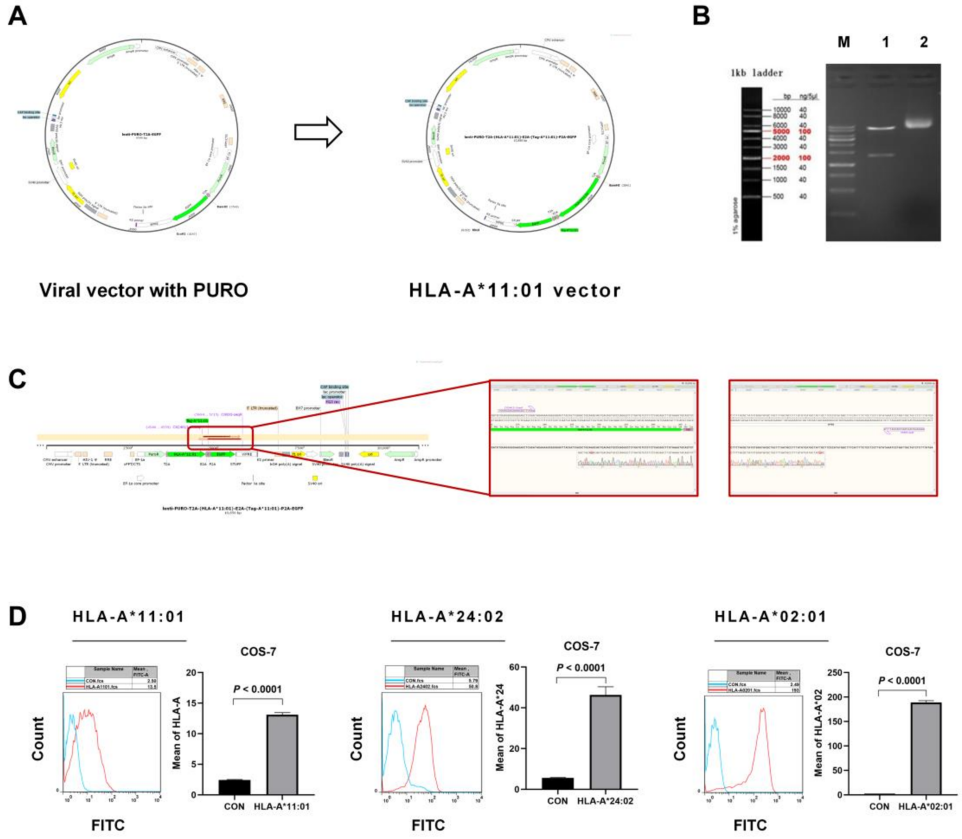
SUPPLEMENTAL FIGURES



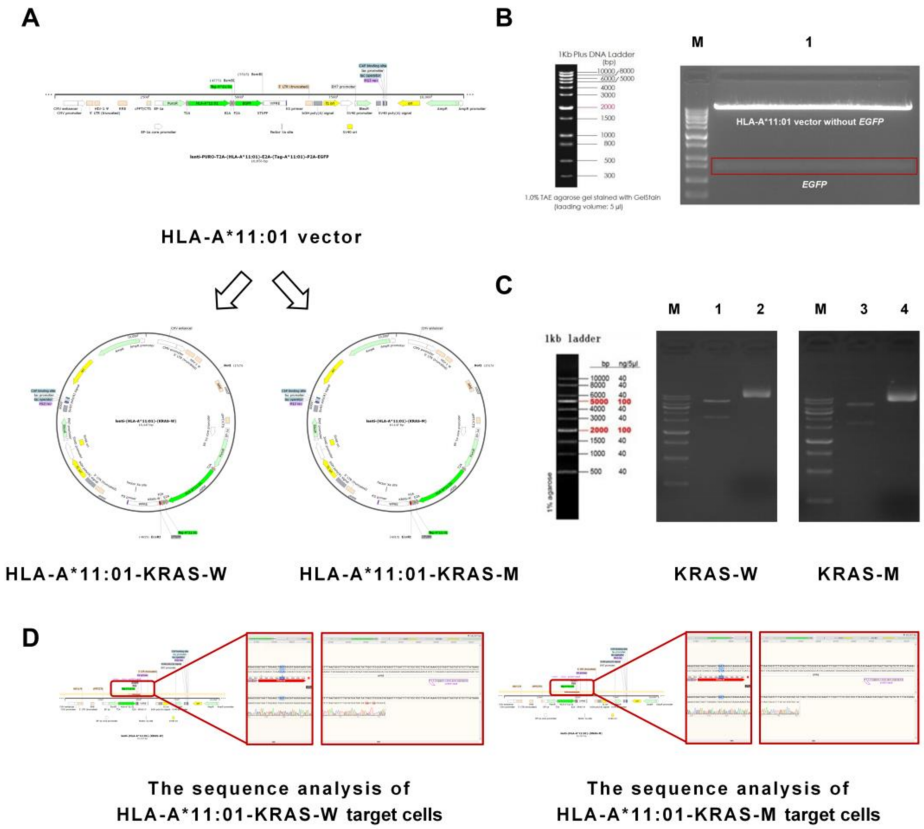
Supplemental figure 1 The construction of the *KRAS* G12D TCR plasmid**.** (A) The map of the *KRAS* G12D TCR plasmid. (B) Validation of the *KRAS* G12D TCR plasmid by gel electrophoresis. Lane M shows the DNA marker, lane 1 shows the TCR plasmid digested by BamHI and NoTI, lane 2 shows the TCR plasmid digested by BamHI, and lane 3 shows the TCR plasmid without digestion. (C) The established *KRAS* G12D TCR-T cells and the key sequence of the TCR-T cells analyzed with Sanger sequencing.



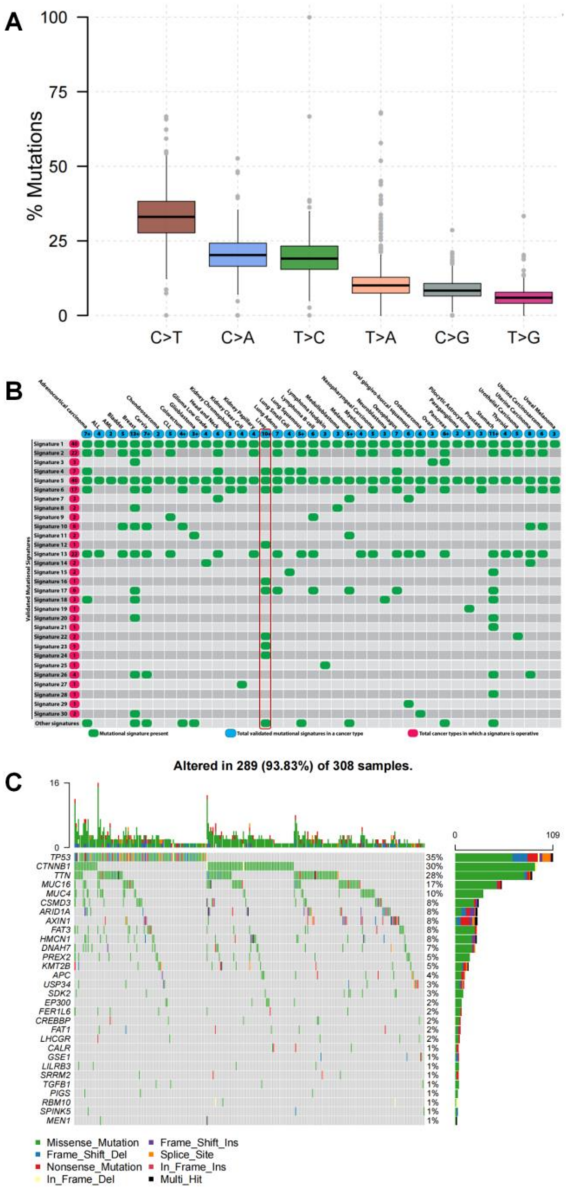
Supplemental figure 2 Schematic for the establishment and validation of the Co-HA system by the *KRAS* G12D TCR-T cells. HLA, human leukocyte antigen; IFN-γ, interferon-γ; LDH, lactate dehydrogenase; ELISPOT, enzyme-linked immunospot assay; ELISA, enzyme-linked immunosorbent assay.



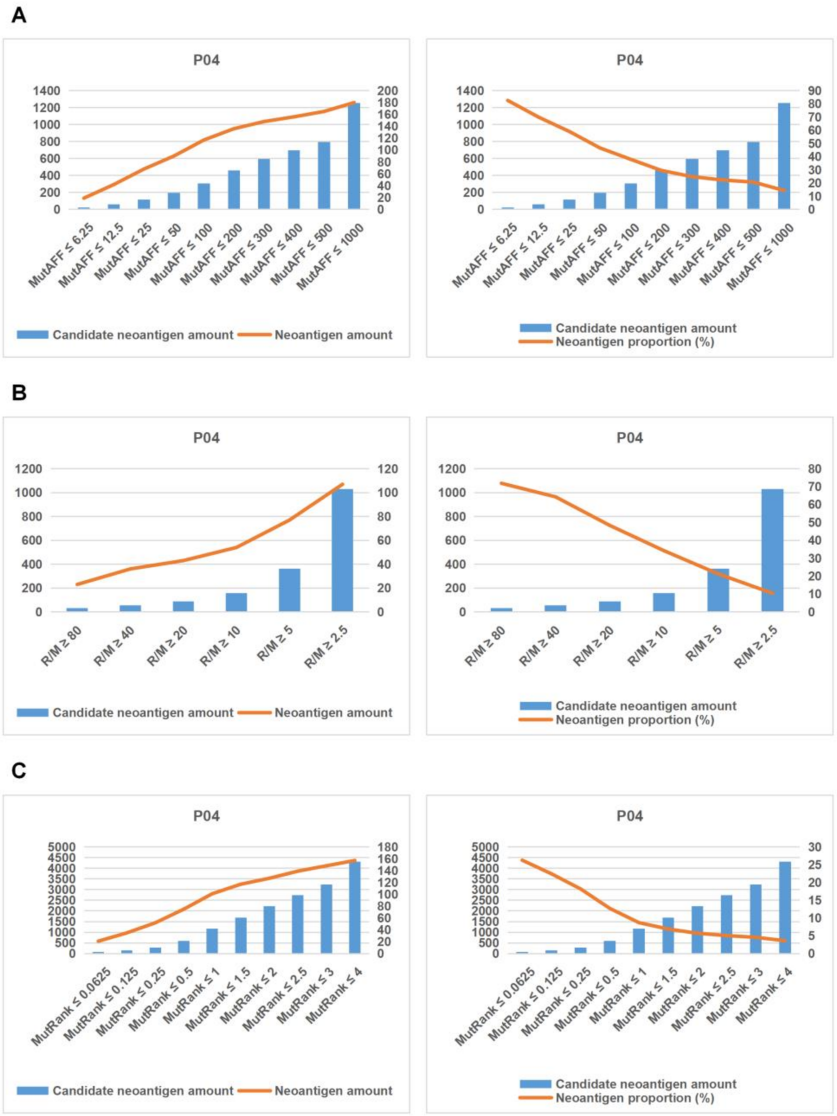
Supplemental figure 3 The construction of the HLA vectors. (A) The map of the HLA-A*11:01 vector. (B) Validation of the HLA-A*11:01 vector by gel electrophoresis. Lane M shows the DNA Marker, lane 1 shows the HLA-A*11:01 vector digested by BamHI and XhoI, and lane 2 shows the HLA-A*11:01 vector without digestion. (C) The key sequence of the HLA-A*11:01 vector analyzed with Sanger sequencing. (D) The expression of prevalent HLA molecules in the COS-7 cells constructed by the Co-HA system. HLA, human leukocyte antigen.



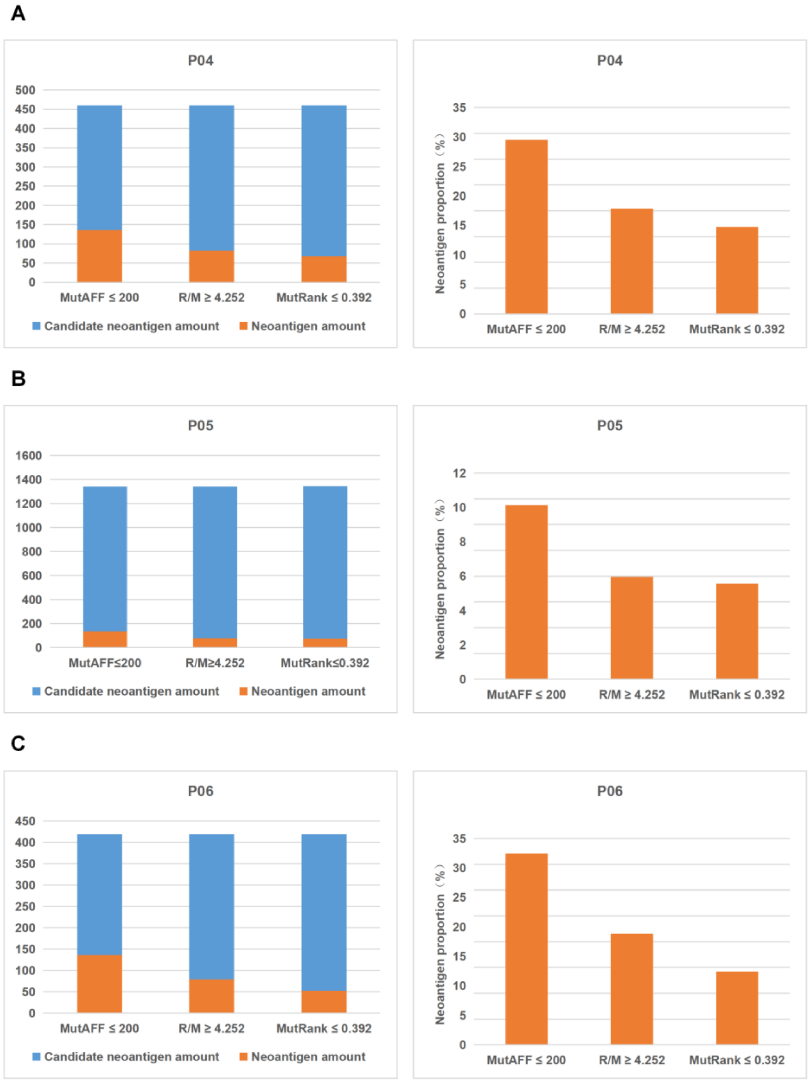
Supplemental figure 4 The construction of target cells coexpressing HLA-A*11:01 and antigens. (A) The maps of the target cell plasmids. (B) The construction of HLA*11:01 vector without *EGFP*. To insert the gene segment of the antigen, the gene segment of *EGFP* in the vector was released from the vector by cleavage with the restriction enzyme BsmBI. Lane M shows the DNA Marker and lane 1 shows the HLA-A*11:01 vector digested by BsmBI. (C) Validation of the target cell plasmids by gel electrophoresis. Lane M shows the DNA marker, lanes 1 and 3 show the target cell plasmids digested by EcoRI and NotI, and lanes 2 and 4 shows the target cell plasmids without digestion. (D) The key sequences of HLA-A*11:01-KRAS-W or HLA-A*11:01-KRAS-M in the COS-7 cells analyzed with Sanger sequencing. HLA, human leukocyte antigen.



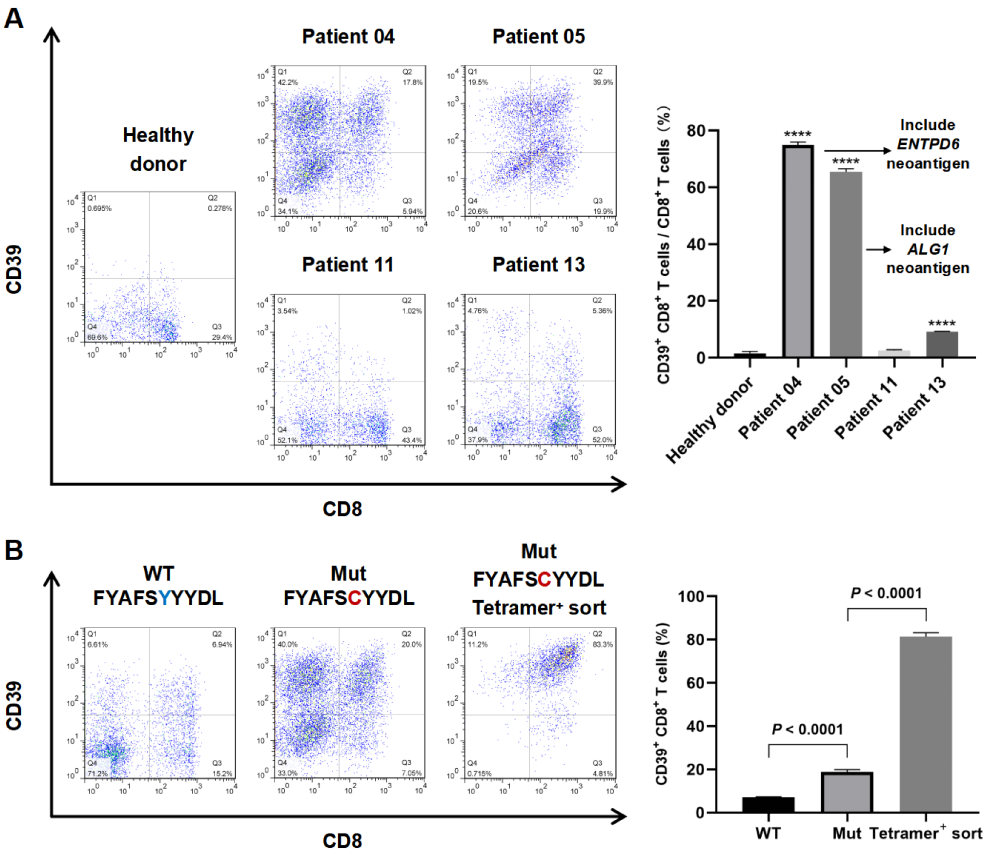
Supplemental figure 5 The mutation spectrum of tumor tissues of HCC patients in databases. (A) The proportions of base substitution subtypes of the samples in TCGA-LIHC dataset. (B) Reference of mutational signatures of tumors in COSMIC database. (C) The key mutated genes and the TMB of the samples in TCGA-LIHC dataset. TCGA-LIHC, The Cancer Genome Atlas Liver Hepatocellular Carcinoma; COSMIC, Catalogue Of Somatic Mutations In Cancer.



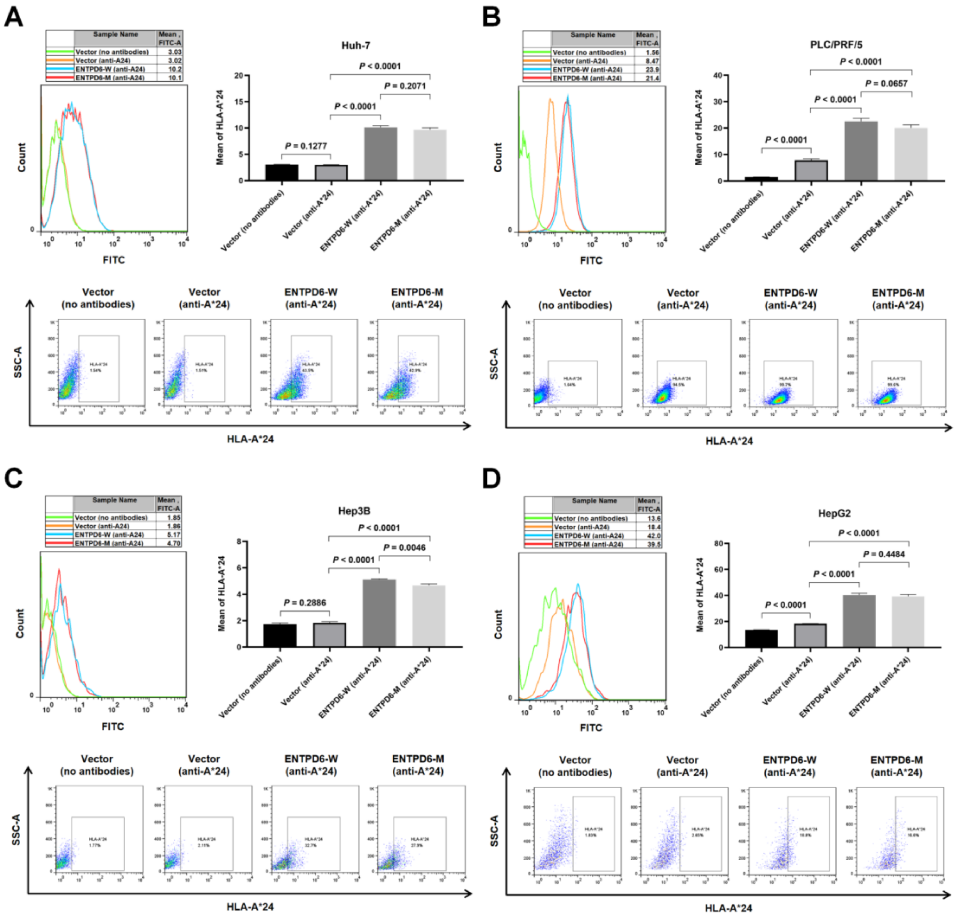
Supplemental figure 6 The screening efficiency of neoantigens screened with different filter values of MutAFF, R/M and MutRank. (A) The candidate neoantigen amount, neoantigen amount and neoantigen proportion screened with different filter values of MutAFF (nM). (B) The candidate neoantigen amount, neoantigen amount and neoantigen proportion screened with different filter values of R/M. (C) The candidate neoantigen amount, neoantigen amount and neoantigen proportion screened with different filter values of MutRank (%). The candidate neoantigen amount is the amount of screened neoantigens. Neoantigen amount is the amount of screened real neoantigens. Neoantigen proportion is the proportion of real neoantigens in candidate neoantigens. MutAFF, mutated peptide affinity; R/M, referenced peptide affinity / mutated peptide affinity. MutRank, the rank of mutated peptide affinity.



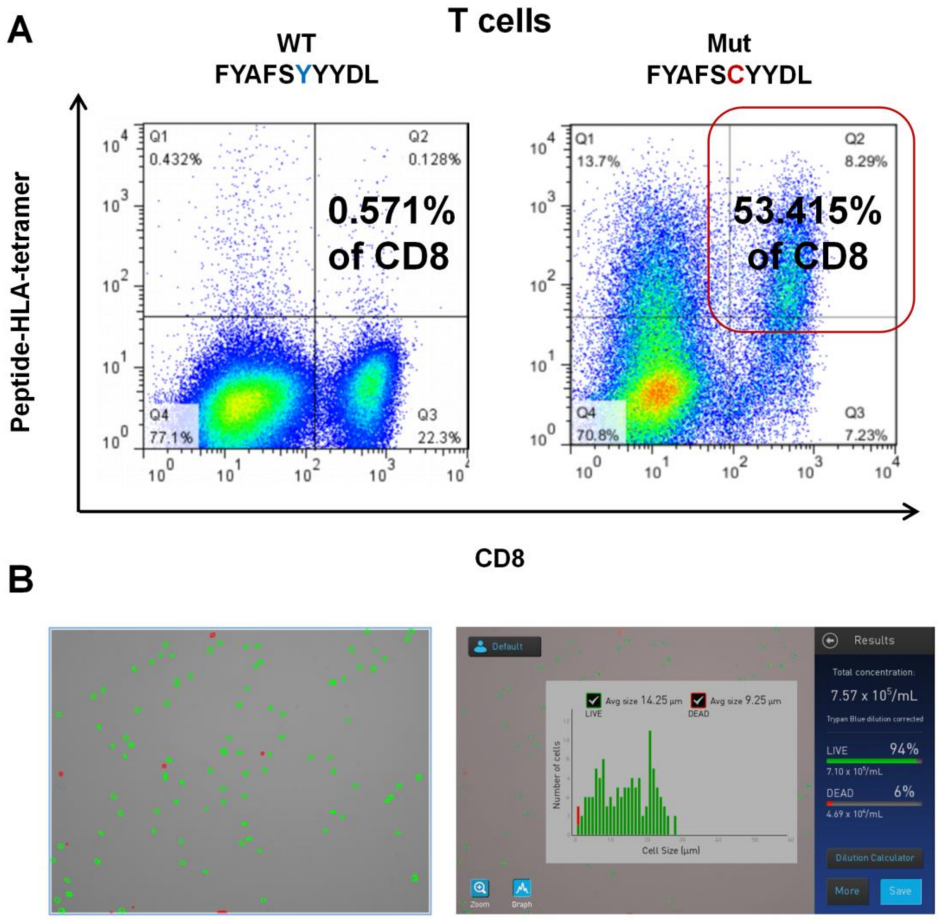
Supplemental figure 7 The comparison of screening efficiency of neoantigens by MutAFF, R/M and MutRank. (A) The comparison of screening efficiency of neoantigens in Patient 04 by MutAFF, R/M and MutRank. (B) The comparison of screening efficiency of neoantigens in Patient 05 by MutAFF, R/M and MutRank. (C) The comparison of screening efficiency of neoantigens in Patient 06 by MutAFF, R/M and MutRank. The candidate neoantigen amount is the amount of screened neoantigens. Neoantigen amount is the amount of screened real neoantigens. Neoantigen proportion is the proportion of real neoantigens in candidate neoantigens. MutAFF, mutated peptide affinity; R/M, referenced peptide affinity / mutated peptide affinity. MutRank, the rank of mutated peptide affinity.



Supplemental figure 8 The high frequency of $CD39^+$ $CD8^+$ T cells in HCC patients with dominant neoantigens. (A) The frequency of $CD39^+$ $CD8^+$ T cells after stimulation with predicted neoantigen peptides in HCC patients. (B) The frequency of $CD39^+$ $CD8^+$ T cells in patient 04 induced by *ENTPD6* neoantigen peptides or its paired WT peptide. The high frequency of $CD39^+$ $CD8^+$ T cells in the tetramer$^+$ *ENTPD6* neoantigen-specific T cells sorted by FCM. FCM, flow cytometry.

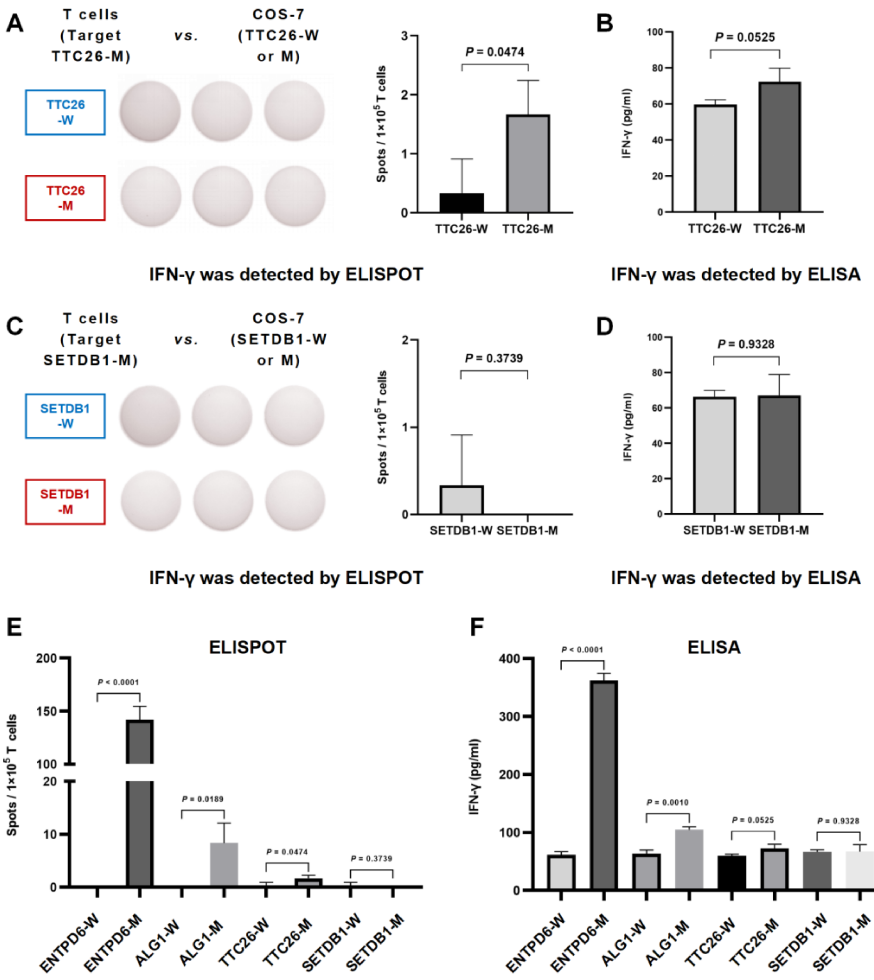


Supplemental figure 9 The construction of target cells in HCC cell lines coexpressing HLA-A*24:02 and *ENTPD6* neoantigen. (A) The expression of HLA-A*24:02 on Huh-7 cells. (B) The expression of HLA-A*24:02 on PLC/PRF/5 cells. (C) The expression of HLA-A*24:02 on Hep3B cells. (D) The expression of HLA-A*24:02 on HepG2 cells. HLA, human leukocyte antigen.

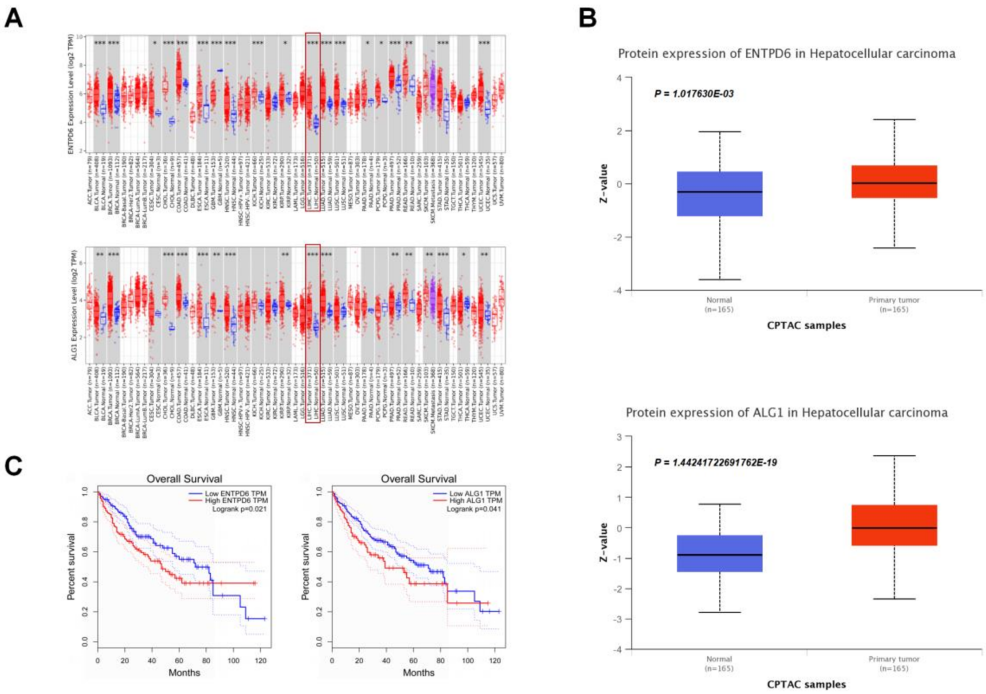


Supplemental figure 10 The *ENTPD6* neoantigen-specific T cells from patient 04. (A) Tetramer staining of PBMCs from patient 04 after stimulation with the *ENTPD6* neoantigens and paired WT peptides. (B) The survival rate of the *ENTPD6* neoantigen-specific T cells acquired by FCM and cultivated in vitro. PBMCs, peripheral blood mononuclear cells; FCM, flow cytometry.

Supplemental figure 11 The frequency of the new HCC-dominant neoantigens in our HCC cohort. (A) The frequency of the neoantigen 5'-FYAFSCYYDL-3' in our HCC cohort determined by Sanger sequencing. (B) The frequency of the neoantigen 5'-WVWCMSPTI-3' in our HCC cohort determined by Sanger sequencing. HLA, human leukocyte antigen.



Supplemental figure 12 Two predicted potential neoantigens are nondominant neoantigens verified in the Co-HA system. (A) The secretion of IFN-γ by T cells from PBMCs of patient 05 against the *TTC26* mutated antigen and the paired WT antigen in the Co-HA system detected by ELISPOT. (B) The secretion of IFN-γ by T cells from PBMCs of patient 05 against the *TTC26* mutated antigen and the paired WT antigen in the Co-HA system detected by ELISA. (C) The secretion of IFN-γ by T cells from PBMCs of patient 05 against the *SETDB1* mutated antigen and the paired WT antigen in the Co-HA system detected by ELISPOT. (D) The secretion of IFN-γ by T cells from PBMCs of patient 05 against the *SETDB1* mutated antigen and the paired WT antigen in the Co-HA system detected by ELISA. (E) The comparison between the dominant neoantigens and nondominant neoantigens detected by ELISPOT in the Co-HA system. (F) The comparison between the dominant neoantigens and nondominant neoantigens detected by ELISA in the Co-HA system. PBMCs, peripheral blood mononuclear cells; ELISPOT, enzyme-linked immunospot assay; ELISA, enzyme-linked immunosorbent assay; IFN-γ, Interferon gamma.



Supplemental figure 13 The expression level and the clinical correlation analysis of *ENTPD6* and *ALG1*. (A) The differential expression between tumor and adjacent normal tissues for *ENTPD6* and *ALG1* in various cancers of TCGA database. Distributions of gene expression levels are displayed using box plots. The statistical significance computed by the Wilcoxon test is annotated by the number of stars ($^{*}P < 0.05$; $^{**}P < 0.01$; $^{***}P < 0.001$). (B) The expression of *ENTPD6* and *ALG1* in the CPTAC-LIHC dataset. (C) Overall survival analysis of HCC patients with high and low expression levels of *ENTPD6* or *ALG1* in TCGA-LIHC dataset. TCGA, The Cancer Genome Atlas; LIHC, Liver Hepatocellular Carcinoma; CPTAC, Clinical Proteomic Tumor Analysis Consortium.

SUPPLEMENTAL TABLES

Supplemental table 1 Summary of constructed HLA vectors

HLA-A		HLA-B		HLA-C	
A*11:01	A*03:01	B*40:01	B*27:01	C*01:02	C*15:02
A*24:02	A*32:01	B*15:01	B*55:01	C*07:02	C*03:03
A*02:01	A*02:06	B*46:01	B*39:01	C*03:04	C*07:04
A*33:01		B*13:01	B*38:01	C*08:01	C*08:01
A*30:01		B*51:01	B*52:01	C*04:01	
A*31:01		B*58:01	B*44:02	C*14:02	
A*26:01		B*35:01	B*15:18	C*06:02	
A*01:01		B*54:01	B*67:01	C*12:02	

Supplemental table 2 Sequence list of antigens and overlaps

SEQ ID	Name	Sequence
NO. 1	KRAS-M	GTAGTTGGAGCTGATGGCGTAGGCAAG
NO. 2	KRAS-W	GTAGTTGGAGCTGGTGGCGTAGGCAAG
NO. 3	Overlap-1	GATGTCGAAGAGAATCCTGGACCG
NO. 4	Overlap-2	TAGCCTAAGAATTCGATATCAAGC

Supplemental table 3 The characteristics of 37 paired mutated and WT peptides restricted by HLA-A*24:02, HLA-A*02:01 or HLA-A*11:01

Patient	Gene	Mut	HLA	MutPeptide	MutAFF (nM)	MutRank	RefPeptide	RefAFF (nM)	RefRank
04	*ENTPD6*	Y/C	HLA-A24:02	FYAFSCYYDL	82.16	1.957	FYAFSYYYDL	51.58	1.101
04	*VPS13D*	Y/F	HLA-A24:02	RFIDTCMVIF	52.99	0.33	RYIDTCMVIF	9.54	0.048
04	*VPS13D*	Y/F	HLA-A24:02	RFIDTCMVI	124.72	0.752	RYIDTCMVI	13.08	0.144
05	*CTNNB1*	D/H	HLA-A02:01	YLHSGIHSGA	93.29	0.397	YLDSGIHSGA	55.69	0.215
05	*SEPT1*	N/S	HLA-A02:01	FLSLRRMLV	63.97	1.192	FLNLRRMLV	69.82	1.119
05	*HEATR6*	I/M	HLA-A02:01	MLMSLEDKSL	56.44	1.958	ILMSLEDKSL	124.57	1.457
05	*ALG1*	G/V	HLA-A02:01	YSIMGLVHV	102.37	1.064	YSIMGLVHG	17767.11	36.417
05	*ALG1*	A/S	HLA-A02:01	WVWCMSPTI	41.2	3.375	WVWCMAPTI	72.26	4.695
05	*TTC26*	G/A	HLA-A02:01	KMAQFYYSA	11.98	0.602	KMGQFYYSA	35.01	1.321
05	*SETDB1*	L/I	HLA-A02:01	KQIAELETWV	113.57	1.531	KQLAELETWV	30.33	0.661
11	*TMEM176B*	R/T	HLA-A11:01	CTAYMQMLR	41.27	0.948	CRAYMQMLR	11832.89	12.191
11	*TMEM176B*	R/T	HLA-A11:01	CTAYMQMLRK	22.17	1.604	CRAYMQMLRK	277.17	3.489
11	*HNRNPA2B1*	D/G	HLA-A11:01	GPVDKIVLQK	172.23	0.31	DPVDKIVLQK	3224.26	2.437
11	*PPFIBP2*	I/K	HLA-A11:01	KLGFSHFGNK	83.75	1.52	KLGFSHFGNI	19571.99	33
11	*TMEM176B*	R/T	HLA-A11:01	TAYMQMLRK	16.58	0.123	RAYMQMLRK	16.33	0.084
11	*HNRNPA2B1*	D/G	HLA-A11:01	VTFDDHGPVDK	104.23	0.17	VTFDDHDPVDK	270.42	0.499
11	*TUBG1*	Q/R	HLA-A11:01	ASIRVALSR	40.43	0.13	ASIQVALSR	73.17	0.112
11	*TUBG1*	Q/R	HLA-A11:01	ASIRVALSRK	17.27	0.239	ASIQVALSRK	20.52	0.104
11	*TUBG1*	Q/R	HLA-A11:01	SIRVALSRK	189.1	0.884	SIQVALSRK	25.38	0.151
11	*OSER1*	S/C	HLA-A11:01	ASSSSCQLK	24.82	0.153	ASSSSSQLK	18.86	0.038
11	*OSER1*	S/C	HLA-A11:01	TIASSSSCQLK	108.54	0.447	TIASSSSSQLK	112.17	0.403
11	*OSER1*	S/C	HLA-A11:01	SSSSCQLKHK	33.3	0.457	SSSSSQLKHK	45.62	0.149
11	*OSER1*	S/C	HLA-A11:01	SSSCQLKHK	143.13	0.714	SSSSQLKHK	89.38	0.141
11	*OSER1*	S/C	HLA-A11:01	IASSSSCQLK	110.36	1.358	IASSSSSQLK	104.67	0.826
13	*FNDC3A*	A/S	HLA-A11:01	LSYSIDFGDK	66.69	1.466	LAYSIDFGDK	189.17	2.481
13	*CKAP4*	R/S	HLA-A11:01	ASCSRSLGR	186.71	0.734	ASCSRRLGR	569.46	1.475
13	*SLC25A15*	L/V	HLA-A11:01	VSTVWSVIK	83.89	0.777	LSTVWSVIK	123.35	1.287
13	*SLC25A15*	L/V	HLA-A11:01	KVSTVWSVIK	25.33	0.281	KLSTVWSVIK	71.25	1.013
13	*GART*	V/F	HLA-A11:01	VTEAVFAGIAK	188.37	1.08	VTEAVVAGIAK	317.35	1.118
13	*SDS*	H/Y	HLA-A11:01	MSGEPLYVK	43.76	0.162	MSGEPLHVK	67.56	0.143
13	*SDS*	H/Y	HLA-A11:01	MMSGEPLYVK	29	0.807	MMSGEPLHVK	76.73	0.694
13	*SDS*	H/Y	HLA-A11:01	GMMSGEPLYVK	73.27	0.823	GMMSGEPLHVK	106.22	0.572
13	*EP400*	P/R	HLA-A11:01	KTDRSAAGRK	172.96	0.704	KTDPSAAGRK	84.51	0.154
13	*AK3*	G/V	HLA-A11:01	ETFSVTETNK	198.61	0.543	ETFSGTETNK	226.36	0.383
13	*TMEM219*	R/H	HLA-A11:01	TAMCFHPHR	183.81	2.211	TAMCFHPRR	223.43	2.507
13	*TMEM219*	R/H	HLA-A11:01	VTAMCFHPHR	132.99	2.72	VTAMCFHPRR	161.63	3.042
13	*DAB2IP*	I/V	HLA-A11:01	IVNSYCVFPR	97.83	3.095	IINSYCVFPR	199.66	4.497

Mut, mutation; MutAFF, mutated peptide affinity; MutRank, the rank of mutated peptide affinity. RefAFF, referenced (WT) peptide affinity; RefRank, the rank of referenced (WT) peptide affinity.

Supplemental table 4 The sequence of potential *ENTPD6* specific TCRs

	TCR Vα	TCR Vβ
S5-1-BA1	ATGACACGAGTTAGCTTGCTGAAGGTGGTCACAGCTTCACTGTGG CTAGGACCTGGCATTGCCCAGAAGATAACTCAAACCCAACCAGGA ATGTTCGTGCAGGAAAAGGAGGCTGTGACTCTGGACTGCACATAT GACACCAGTGATCCAAGTTATGGTCTATTCTGGTACAAGCAGCCC AGCAGTGGGGAAATGATTTTTCTTATTTATCAGGGGTCTTATGACC AGCAAAATGCAACAGAAGGTCGCTACTCATTGAATTTCCAGAAGG CAAGAAAATCCGCCAACCTTGTCATCTCCGCTTCACAACTGGGGG ACTCAGCAATGTACTTCTGTGCAATGAGAGAGATGAGAACCGGTA ACCAGTTCTATTTTGGGACAGGGACAAGTTTGACGGTCATTCCAA AT	ATGGGCCCCGGGCTCCTTGGCTATGTGGTCCTTTGCCTTCTAGGAG CAGGCCCCCTGGAAGCCCAAGTGACCCAGAACCCAAGATACCTCA TCACAGTGACTGGAAAGAAGTTAACAGTGACTTGTTCTCAGAATAT GAACCATGAGTATATGTCCTGGTATCGACAAGACCCAGGGCTGGG CTTAAGGCAGATCTACTATTCAATGAATGTTGAGGTGACTGATAAG GGAGATGTTCCTGAAGGGTACAAAGTCTCTCGAAAAGAGAAGAGG AATTTCCCCCTGATCCTGGAGTCGCCCAGCCCCAACCAGACCTCTC TGTACTTCTGTGCCAGCAGTAGACTAGCGGGGTTCACAGATACGCA GTATTTTGGCCCAGGCACCCGGCTGACAGTGCTC
SP10-2-BA6	ATGGAGACCCTCTTGGGCCTGCTTATCCTTTGGCTGCAGCTGCAAT GGGTGAGCAGCAAACAGGAGGTGACACAGATTCCTGCAGCTCTGA GTGTCCCAGAAGGAGAAAACTTGGTTCTCAACTGCAGTTTCACTG ATAGCGCTATTTACAACCTCCAGTGGTTTAGGCAGGACCCTGGGA AAGGTCTCACATCTCTGTTGCTTATTCAGTCAAGTCAGAGAGAGC AAACAAGTGGAAGACTTAATGCCTCGCTGGATAAATCATCAGGAC GTAGTACTTTATACATTGCAGCTTCTCAGCCTGGTGACTCAGCCAC CTACCTCTGTGCTGTGAACCAGGCAGGAACTGCTCTGATCTTTGGG AAGGGAACCACCTTATCAGTGAGTTCCAAT	ATGGATATCTGGCTCCTCTGCTGTGTGGCCTTTTGTCTCCTGGGAGC AGGCCCAGTGGATTCTGGAGTCACACAAACCCCAAAGCACCTGAT CACAGCAACTGGACAGCGAGTGACGCTGAGATGCTCCCCTAGGTC TGGAGACCTCTCTGTGTACTGGTACCAACAGAGCCTGGACCAGGGC CTCCAGTTCCTCATTCAGTATTATAATGGAGAAGAGAGAGCAAAA GGAAACATTCTTGAACGATTCTCCGCACAACAGTTCCCTGACTTGC ACTCTGAACTAAACCTGAGCTCTCTGGAGCTGGGGGACTCAGCTTT GTATTTCTGTGCCAGCAGCACCCGAGCGGGAGGGCTATACAATGA GCAGTTCTTCGGGCCAGGGACACGGCTCACCGTGCTA
S20-1-BA1	ATGGTCCTGAAATTCTCCGTGTCCATTCTTTGGATTCAGTTGGCAT GGGTGAGCACCCAGCTGCTGGAGCAGAGCCCTCAGTTTCTAAGCA TCCAAGAGGGAGAAAATCTCACTGTGTACTGCAACTCCTCAAGTG TTTTTTCCAGCTTACAATGGTACAGACAGGAGCCTGGGGAAGGTC CTGTCCTCCTGGTGACAGTAGTTACGGGTGGAGAAGTGAAGAAGC TGAAGAGACTAACCTTTCAGTTTGGTGATGCAAGAAAGGACAGTT CTCTCCACATCACTGCGGCCCAGCCTGGTGATACAGGCCTCTACCT CTGTGCAGGCGTAGCTAATGCTGGTGGTACTAGCTATGGAAAGCT GACATTTGGACAAGGGACCATCTTGACTGTCCATCCAAAT	ATGGGCACAAGGCTCCTCTGCTGTGCGGTTCTCTGTCTCCTGGGAG CAGGTCCCATAGACACTGAAGTTACCCAGACACCAAAACACCTGGT CATGGGAATGACAAATAAGAAGTCTTTGAAATGTGAACAACATAT GGGGCACAGGGCTATGTATTGGTACAAGCAGAAAGCTAAGAAGCC ACCGGAGCTCATGTTTGTCTACAGCTATGAGAAACTCTCTATAAAT GAAAGTGTGCCAAGTCGCTTCTCACCTGAATGCCCCAACAGCTCTC TCTTAAACCTTCACCTACACGCCCTGCAGCCAGAAGACTCAGCCCT GTATCTCTGCGCCAGTGGAACCGGGGAGCTGTTTTTTGGAGAAGGC TCTAGGCTGACCGTACTG
S20-1-BA2	ATGGTCCTGAAATTCTCCGTGTCCATTCTTTGGATTCAGTTGGCAT GGGTGAGCACCCAGCTGCTGGAGCAGAGCCCTCAGTTTCTAAGCA TCCAAGAGGGAGAAAATCTCACTGTGTACTGCAACTCCTCAAGTG TTTTTTCCAGCTTACAATGGTACAGACAGGAGCCTGGGGAAGGTC CTGTCCTCCTGGTGACAGTAGTTACGGGTGGAGAAGTGAAGAAGC TGAAGAGACTAACCTTTCAGTTTGGTGATGCAAGAAAGGACAGTT CTCTCCACATCACTGCGGCCCAGCCTGGTGATACAGGCCTCTACCT CTGTGCAGGCGTAGCTAATGCTGGTGGTACTAGCTATGGAAAGCT GACATTTGGACAAGGGACCATCTTGACTGTCCATCCAAAT	ATGGGCACCAGGCTCCTCTGCTGGGTGCTGCTTTGTCTCCTGGGAG CAGGCCCAGTGGACGCTGGAGTCACCCAAAGTCCCACACACCTGA TCAAAACGAGAGGACAGCAAGTGACTCTGAGATGCTCTCCTATCTC TGGGCACAAGAGTGTGTCCTGGTACCAACAGGTCCTGGGTCAGGG GCCCCAGTTTATCTTTCAGTATTATGAGAAAGAAGAGAGAGGAAG AGGAAACTTCCCTGATCGATTCTCAGCTCGCCAGTTCCCTAACTAT AGCTCTGAGCTGAATGTGAACGCCTTGTTGCTGGGGGACTCGGCCC TGTATCTCTGTGCCAGCAGCTTGGAGGTGGATATGAACACTGAAGC TTTCTTTGGACAAGGCACCAGACTCACAGTTGTA
S20-1-BA4	ATGAAGACATTTGCTGGATTTTCGTTCCTGTTTTTGTGGCTGCAGC TGGACTGTATGAGTAGAGGAGAGGATGTGGAGCAGAGTCTTTTCC TGAGTGTCCGAGAGGGAGACAGCTCCGTTATAAACTGCACTTACA CAGACAGCTCCTCCACCTACTTATACTGGTATAAGCAAGAACCTG GAGCAGGTCTCCAGTTGCTGACGTATATTTTTTCAAATATGGACAT GAAACAAGACCAAAGACTCACTGTTCTATTGAATAAAAAGGATAA ACATCTGTCTCTGCGCATTGCAGACACCCAGACTGGGGACTCAGC TATCTACTTCTGTGCAGAGAGAGGGACTGGAGGCTTCAAAACTAT CTTTGGAGCAGGAACAAGACTATTTGTTAAAGCAAAT	ATGGGCACCAGTCTCCTATGCTGTGCGGTTCTCTGTCTCCTGGGAG CAGTTCCCATAGACACTGAAGTTACCCAGACACCAAAACACCTGGT CATGGGAATGACAAATAAGAAGTCTTTGAAATGTGAACAACATAT GGGGCACAGGGCTATGTATTGGTACAAGCAGAAAGCTAAGAAGCC ACCGGAGCTCATGTTTGTCTACAGCTATGAGAAACTCTCTATAAAT GAAAGTGTGCCAAGTCGCTTCTCACCTGAATGCCCCAACAGCTCTC TCTTAAACCTTCACCTACACGCCCTGCAGCCAGAAGACTCAGCCCT GTATCTCTGCGCCAGTGGAACCGGGGAGCTGTTTTTTGGAGAAGGC TCTAGGCTGACCGTACTG
S20-1-BA5	ATGGAGAAAATGTTGGAGTGTGCATTCATAGTCTTGTGGCTTCAGC TTGGCTGGTTGAGTGGAGAAGACCAGGTGACGCAGAGTCCCGAGG CCCTGAGACTCCAGGAGGGAGAGAGTAGCAGTCTCAACTGCAGTT ACACAGTCAGCGGTTTAAGAGGGCTGTTCTGGTATAGGCAAGATC CTGGGAAAGGCCCTGAATTCCTCTTCACCCTGTATTCAGCTGGGGA AGAAAAGGAGAAAGAAAGGCTAAAAGCCACATTAACAAAGAAGG AAAGCTTTCTGCACATCACAGCCCCTAAACCTGAAGACTCAGCCA CTTATCTCTGTGCTGTGCAGGCGCTCACGGGAGGAGGAAACAAAC TCACCTTTGGGACAGGCACTCAGCTAAAAGTGGAACTCAAT	ATGGATATCTGGCTCCTCTGCTGGGTGCTGCTTTGTCTCCTGGGAGC AGGCCCAGTGGACGCTGGAGTCACCCAAAGTCCCACACACCTGAT CAAAACGAGAGGACAGCAAGTGACTCTGAGATGCTCTCCTATCTCT GGGCACAAGAGTGTGTCCTGGTACCAACAGGTCCTGGGTCAGGGG CCCCAGTTTATCTTTCAGTATTATGAGAAAGAAGAGAGAGGAAGA GGAAACTTCCCTGATCGATTCTCAGCTCGCCAGTTCCCTAACTATA GCTCTGAGCTGAATGTGAACGCCTTGTTGCTGGGGGACTCGGCCCT GTATCTCTGTGCCAGCAGCTTGGAGGTGGATATGAACACTGAAGCT TTCTTTGGACAAGGCACCAGACTCACAGTTGTA
SP30-2-BA4	ATGAGGCTGGTGGCAAGAGTAACTGTGTTTCTGACCTTTGGAACT ATAATTGATGCTAAGACCACCCAGCCCACCTCCATGGATTGCGCT GAAGGAAGAGCTGCAAACCTGCCTTGTAATCACTCTACCATCAGT GGAAATGAGTATGTGTATTGGTATCGACAGATTCACTCCCAGGGG CCACAGTATATCATTCATGGTCTAAAAAACAATGAAACCAATGAA ATGGCCTCTCTGATCATCACAGAAGACAGAAAGTCCAGCACCTTG ATCCTGCCCCACGCTACGCTGAGAGACACTGCTGTGTACTATTGCA TCGACCTGGATGCCAGACTCATGTTTGGAGATGGAACTCAGCTGG TGGTGAAGCCCAAT	ATGGGCACCAGGCTCCTCTGCTGTGCGGTTCTCTGTCTCCTGGGAG CAGTTCCCATAGACACTGAAGTTACCCAGACACCAAAACACCTGGT CATGGGAATGACAAATAAGAAGTCTTTGAAATGTGAACAACATAT GGGGCACAGGGCTATGTATTGGTACAAGCAGAAAGCTAAGAAGCC ACCGGAGCTCATGTTTGTCTACAGCTATGAGAAACTCTCTATAAAT GAAAGTGTGCCAAGTCGCTTCTCACCTGAATGCCCCAACAGCTCTC TCTTAAACCTTCACCTACACGCCCTGCAGCCAGAAGACTCAGCCCT GTATCTCTGCGCCAGCAGTATAGGAACTGAAGCTTTCTTTGGACAA GGCACCAGACTCACAGTTGTA
SP30-2-BA6	ATGAGGCTGGTGGCAAGAGTAACTGTGTTTCTGACCTTTGGAACT ATAATTGATGCTAAGACCACCCAGCCCACCTCCATGGATTGCGCT GAAGGAAGAGCTGCAAACCTGCCTTGTAATCACTCTACCATCAGT GGAAATGAGTATGTGTATTGGTATCGACAGATTCACTCCCAGGGG CCACAGTATATCATTCATGGTCTAAAAAACAATGAAACCAATGAA ATGGCCTCTCTGATCATCACAGAAGACAGAAAGTCCAGCACCTTG ATCCTGCCCCACGCTACGCTGAGAGACACTGCTGTGTACTATTGCA TCGACCTGGATGCCAGACTCATGTTTGGAGATGGAACTCAGCTGG TGGTGAAGCCCAAT	ATGGGCACCAGGCTCCTCTGCTGTGCGGTTCTCTGTCTCCTGGGAG CAGTTCCCATAGACACTGAAGTTACCCAGACACCAAAACACCTGGT CATGGGAATGACAAATAAGAAGTCTTTGAAATGTGAACAACATAT GGGGCACAGGGCTATGTATTGGTACAAGCAGAAAGCTAAGAAGCC ACCGGAGCTCATGTTTGTCTACAGCTATGAGAAACTCTCTATAAAT GAAAGTGTGCCAAGTCGCTTCTCACCTGAATGCCCCAACAGCTCTC TCTTAAACCTTCACCTACACGCCCTGCAGCCAGAAGACTCAGCCCT GTATCTCTGCGCCAGCAGTATAGGAACTGAAGCTTTCTTTGGACAA GGCACCAGACTCACAGTTGTA

Supplemental table 5 Sequence list of primers

SEQ ID	Name	Sequence
NO. 1	Mouse T Cell Mix 2 PN-2000079 Pb	GGCCAAGCACACGAGGGTA
NO. 2	CN24613-1VseqF	TGGAGGAGGAAGAGCTCAGA
NO. 3	CN803-seqR	AAGAGACAGCAACCAGGATTTA

SUPPLEMENTAL PLASMID SEQUENCE

Supplemental plasmid sequence No. 1

lenti-BSD-T2A-EGFP:

GTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTAT
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
AATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATT
ATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTA
AATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAG
GGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGT
ACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA
CTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA
TGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGCGCGTTTTGCC
TGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAAT
AAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTA
GTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACG
CAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCG
GAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGG
TTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATC
CTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAC
TTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGAC
AAGATAGAGGAAGAGCAAAACAAAAGTAAGACCACCGCACAGCAAGCGGCCGCTGATCTTCAGACCTGGAGGAGGAGATA
TGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAA
GAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGC
TGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTG
TGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTG
GAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAAT
TACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATA
AATGGGCAAGTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGG
TAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACC
TCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCG
ATTAGTGAACGGATCGGCACTGCGTGCGCCAATTCTGCAGACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGG
GATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAAT
TACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCAGTTTGGTTAATTAGCTAGCTAGGTCTTGAAAGG
AGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCG
GCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCG
AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGG
ACCGGTTCTAGAGCCACCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAAC
AGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATA
TCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATC
GTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCCTGGG
ATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGG
AGGGCGGCTCCGGAGAGGGCAGGGGAAGTCTGCTAACCTGCGGCGACGTGGAGGAAAATCCCGGCCCCGGATCCATGGTG
AGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAG
CGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGT
GCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGA
CTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCG
CGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA
TCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGG
TGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCG

ACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGAT
CACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGAATTCGATATCA
AGCTTATCGGTAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTAT
GTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTG
CTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTG
GTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCC
GCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCT
TTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCG
GACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCC
TTTGGGCCGCCTCCCCGCATCGATACCGTCGACCTCGAGACCTAGAAAAACATGGAGCAATCACAAGTAGCAATACAGCAG
CTACCAATGCTGATTGTGCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAA
GACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTCACTCCC
AACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCC
AGGGATCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCAAGAGAAGGTAGAAGAAGCCAATGA
AGGAGAGAACACCCGCTTGTTACACCCTGTGAGCCTGCATGGGATGGATGACCCGGAGAGAGAAGTATTAGAGTGGAGGTT
TGACAGCCGCCTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGACTGTACTGGGTCTCTCTGGTTAGACCAGATCTGA
GCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTG
CCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCAGGGCCCGTTT
AAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTG
GAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGG
GGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGG
CTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTG
TGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC
ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCC
CAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCC
ACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATT
TTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAG
TTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGT
GGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTA
ACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAG
GCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCC
CGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATAC
GACAAGGTGAGGAACTAAACCATGGCCAAGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGCGACGTCGCCGGAGCGGT
CGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGACTTCGCCGGTGTGGTCCGGGACGACGTGA
CCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAG
CTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACTTCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCA
GCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTCGTGGCCGAGGAGCAGGACTGACACG
TGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATC
CTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAA
TAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCAT
GTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACA
ATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGT
TGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCG
GTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC
TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA
AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGAC
GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC
CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGT
AGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCT
TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG
CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT
ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC
GGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT
CTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT

AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGG
CACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCT
TACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGC
CGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTA
AGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGC
TTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGT
CCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCAT
GCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGC
TCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGG
GGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATC
TTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGA
AATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAA
TGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC

Supplemental plasmid sequence No. 2

lenti-BSD-T2A-TK412:

GTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTAT
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
AATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATT
ATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTA
AATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAG
GGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGT
ACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA
CTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA
TGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGCGCGTTTTGCC
TGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAAT
AAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTA
GTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACG
CAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCG
GAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGG
TTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATC
CTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAC
TTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGAC
AAGATAGAGGAAGAGCAAAACAAAAGTAAGACCACCGCACAGCAAGCGGCCGCTGATCTTCAGACCTGGAGGAGGAGATA
TGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAA
GAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGC
TGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTG
TGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTG
GAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAAT
TACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATA
AATGGGCAAGTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGG
TAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACC
TCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCG
ATTAGTGAACGGATCGGCACTGCGTGCGCCAATTCTGCAGACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGG
GATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAAT
TACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCAGTTTGGTTAATTAGCTAGCTAGGTCTTGAAAGG
AGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCG
GCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCG
AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGG
ACCGGTTCTAGAGCCACCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAAC
AGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATA
TCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATC
GTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCCTGGG
ATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGG
AGGGCGGCTCCGGAGAGGGCAGGGGAAGTCTGCTAACCTGCGGCGACGTGGAGGAAAATCCCGGCCCCATGTCTAACACT
GCCTTCCCTGACCCCGCCTGGAACACCACCCTGCTATCTTGGGTTGCTCTCTTTCTCCTGGGAACAAGTTCAGCAAATTCTG
GGGTTGTCCAGTCTCCAAGATACATAATCAAAGGAAAGGGAGAAAGGTCCATTCTAAAATGTATTCCCATCTCTGGACATCT
CTCTGTGGCCTGGTATCAACAGACTCAGGGGCAGGAACTAAAGTTCTTCATTCAGCATTATGATAAAATGGAGAGAGATAAA
GGAAACCTGCCCAGCAGATTCTCAGTCCAACAGTTTGATGACTATCACTCTGAGATGAACATGAGTGCCTTGGAGCTAGAGG
ACTCTGCCGTGTACTTCTGTGCCAGCTCTCTCACAGATCCGCTAGACTCCGACTACACCTTCGGCTCAGGGACCAGGCTTTT
GGTAATAGAGGACCTGCGCAACGTCACCCCACCAAAGGTCAGTTTGTTTGAGCCATCAAAGGCGGAGATCGCCAACAAACA
GAAAGCTACCCTCGTGTGCTTGGCCCGGGGCTTCTTCCCAGACCACGTAGAACTTTCCTGGTGGGTCAATGGAAAGGAGGT
TCATTCCGGAGTGTGCACTGATCCCCAAGCGTACAAGGAATCCAACTATAGCTACTGTCTCTCATCTCGGCTCCGGGTGAGT
GCGACATTCTGGCATAATCCTCGGAACCACTTTCGATGCCAAGTGCAGTTTCATGGGTTGAGCGAGGAAGACAAGTGGCCC
GAGGGCAGTCCTAAACCAGTCACTCAAAACATAAGCGCCGAGGCATGGGGTAGAGCCGATTGTGGGATTACTAGCGCTTCAT
ACCAACAAGGGGTATTGAGCGCTACAATTCTTTACGAAATTCTCCTCGGCAAGGCGACGCTCTACGCCGTACTGGTGTCTAC
TCTCGTGGTTATGGCAATGGTGAAACGGAAAAACAGCAGAGCCAAAAGAAGTGGTTCTGGCGCCACCAACTTTAGCCTGCT

GAAACAGGCCGGCGACGTGGAAGAGAACCCTGGCCCCATGCAGAGGAACCTGGGAGCTGTGCTGGGGATTCTGTGGGTGC
AGATTTGCTGGGTGAGAGGGGATCAGGTGGAGCAGAGTCCTTCAGCCCTGAGCCTCCACGAGGGAACCGATTCTGCTCTGA
GATGCAATTTTACGACCACCATGAGGAGTGTGCAGTGGTTCCGACAGAATTCCAGGGGCAGCCTCATCAGTTTGTTCTACTT
GGCTTCAGGAACAAAGGAGAATGGGAGGCTAAAGTCAGCATTTGATTCTAAGGAGCGGCGCTACAGCACCCTGCACATCAG
GGATGCCCAGCTGGAGGACTCAGGCACTTACTTCTGTGCTGCTGACTCTTCGAACACGGGTTACCAGAACTTCTATTTTGGG
AAAGGAACAAGTTTGACTGTCATTCCAAACATTCAGAACCCCGAACCAGCCGTATATCAGTTGAAGGACCCAAGATCTCAG
GATAGTACACTCTGCCTGTTCACCGACTTTGACTCACAAATCAACGTCCCGAAGACTATGGAAAGTGGTACGTTCATCACAG
ATAAGTGCGTTCTGGACATGAAGGCTATGGACTCAAAGAGCAACGGGGCAATTGCTTGGTCCAACCAGACAAGCTTTACCT
GTCAGGACATTTTTAAGGAGACTAATGCTACTTATCCCTCCAGCGACGTTCCGTGTGATGCGACTCTTACCGAGAAGTCTTTT
GAGACCGATATGAATCTCAACTTCCAGAATCTGCTGGTGATCGTTCTGCGGATCCTGCTTCTGAAGGTTGCAGGATTCAATCT
TCTTATGACTCTCCGGCTCTGGTCTTCATGATGGAATTCGAATATCAAGCTTATCGGTAATCAACCTCTGGATTACAAAATTTGT
GAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTG
CTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGC
AACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGG
GACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTG
TTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCT
GCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGG
CCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATACCGTCGACCTCG
AGACCTAGAAAAACATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGATTGTGCCTGGCTAGAAGCACAAGA
GGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCA
CTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCAC
ACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTACA
AGCTAGTACCAGTTGAGCAAGAGAAGGTAGAAGAAGCCAATGAAGGAGAGAACACCCGCTTGTTACACCCTGTGAGCCTG
CATGGGATGGATGACCCGGAGAGAGAAGTATTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAGAG
CTGCATCCGGACTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGC
TTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTC
AGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
CAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGA
GGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTG
GGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGG
GGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCA
GCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGG
GGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG
GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGA
ACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTG
ATTTAACAAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGG
CAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTAT
GCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCG
CCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGT
AGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCA
CGTGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGTTGAC
CAGTGCCGTTCCGGTGCTCACCGCGCGCGACGTCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGA
CTTCGTGGAGGACGACTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCC
GGACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACT
TCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCC
GGCAACTGCGTGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAA
AGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCAC
TGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGT
AATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGT
AAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGT
CGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCAC
TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA
GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT
TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT
AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGC
CTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC
TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG
ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTT
GAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA
AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA
GAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGA
TTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATA
TGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGT
TGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGAC
CCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTA
TCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGC
CATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTT
ATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTC
AACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACAT
AGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCA
GTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGG
AAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGA
AGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACA
TTTCCCCGAAAAGTGCCACCTGAC

Supplemental plasmid sequence No. 3

lenti-PURO-T2A-EGFP:

GTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTAT
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
AATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATT
ATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTA
AATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAG
GGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGT
ACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA
CTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA
TGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGCGCGTTTTGCC
TGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAAT
AAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTA
GTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACG
CAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCG
GAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGG
TTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATC
CTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAC
TTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGAC
AAGATAGAGGAAGAGCAAAACAAAAGTAAGACCACCGCACAGCAAGCGGCCGCTGATCTTCAGACCTGGAGGAGGAGATA
TGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAA
GAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGC
TGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTG
TGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTG
GAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAAT
TACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATA
AATGGGCAAGTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGG
TAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACC
TCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCG
ATTAGTGAACGGATCGGCACTGCGTGCGCCAATTCTGCAGACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGG
GATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAAT
TACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCAGTTTGGTTAATTAGCTAGCTAGGTCTTGAAAGG
AGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCG
GCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCG
AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGG
ACCGGTTCTAGAGCCACCATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCCGGGCCGTACGC
ACCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGACCCGGACCGCCACATCGAGCGGGTCACCGAG
CTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAGGTGTGGGTCGCGGACGACGGCGCCGCGGTGGCGGT
CTGGACCACGCCGGAGAGCGTCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTCCC
GGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCGTGGTTCCTGGCCACCGTC
GGCGTCTCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGG
GGTGCCCGCCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACCGTCACCGCCGACGT
CGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCCGGCTCCGGAGAGGGCAGGGGAAGTCTGC
TAACCTGCGGCGACGTGGAGGAAAATCCCGGCCCCGGATCCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTG
CCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTA
CGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTA
CGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGT
CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGG
TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAAC
AGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGAC
GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC
CTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGC
CGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGAATTCGATATCAAGCTTATCGGTAATCAACCTCTGGATTACAAAA
TTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGC
TATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTC
AGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTT
TCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTC
GGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTG
GATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCT
CTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATACCGTCG
ACCTCGAGACCTAGAAAAACATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGATTGTGCCTGGCTAGAAGC
ACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCT
TAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATC
TACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGT
GCTACAAGCTAGTACCAGTTGAGCAAGAGAAGGTAGAAGAAGCCAATGAAGGAGAGAACACCCGCTTGTTACACCCTGTG
AGCCTGCATGGGATGGATGACCCGGAGAGAGAAGTATTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCC
GAGAGCTGCATCCGGACTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCC
ACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGA
TCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCT
AGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATA
AAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTC
TAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACT
TGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAA
ATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGT
AGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC

TGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGA
GCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAG
CAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAA
GTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGT
TCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAG
AAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCA
GCACGTGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGTT
GACCAGTGCCGTTCCGGTGCTCACCGCGCGCGACGTCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCG
GGACTTCGTGGAGGACGACTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGG
TGCCGGACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACG
AACTTCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCC
GGCCGGCAACTGCGTGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTA
TGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTC
GCCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTT
TCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTG
GCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAA
GTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAAC
CTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGC
TCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA
ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTG
GCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTC
CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
AGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGT
AAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTT
CTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA
AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGC
GCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG
GGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTA
TATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCA
TAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCG
AGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAA
CTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTT
GTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCG
AGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCA
GTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAG
TACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGC
CACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAG
ATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAA
CAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTA
TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCG
CACATTTCCCCGAAAAGTGCCACCTGAC

Supplemental plasmid sequence No. 4

lenti-PURO-T2A-(HLA-A*11:01)-E2A-(Tag-A*11:01)-P2A-EGFP:

GTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTAT
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
AATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATT
ATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTA
AATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAG
GGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGT
ACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA
CTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA
TGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGCGCGTTTTGCC
TGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAAT
AAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTA
GTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACG
CAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCG
GAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGG
TTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATC
CTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAC
TTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGAC
AAGATAGAGGAAGAGCAAAACAAAAGTAAGACCACCGCACAGCAAGCGGCCGCTGATCTTCAGACCTGGAGGAGGAGATA
TGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAA
GAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGC
TGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTG
TGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTG
GAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAAT
TACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATA
AATGGGCAAGTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGG
TAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACC
TCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCG
ATTAGTGAACGGATCGGCACTGCGTGCGCCAATTCTGCAGACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGG

GATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAAT
TACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCAGTTTGGTTAATTAGCTAGCTAGGTCTTGAAAGG
AGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCG
GCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCG
AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGG
ACCGGTTCTAGAGCCACCATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCCGGGCCGTACGC
ACCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGACCCGGACCGCCACATCGAGCGGGTCACCGAG
CTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAGGTGTGGGTCGCGGACGACGGCGCCGCGGTGGCGGT
CTGGACCACGCCGGAGAGCGTCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTCCC
GGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCGTGGTTCCTGGCCACCGTC
GGCGTATCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGG
GGTGCCCGCCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACCGTCACCGCCGACGT
CGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCCGGCTCCGGAGAGGGCAGGGGAAGTCTGC
TAACCTGCGGCGACGTGGAGGAAAATCCCGGCCCCGGATCCATGGCCGTCATGGCGCCCCGAACCCTCCTCCTGCTACTCTC
GGGGGCCCTGGCCCTGACCCAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCG
CGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGA
GGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCA
GTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACGGTTCTCACACCATCCAGAT
AATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACAT
CGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCCC
ATGCGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGA
GACACTGCAGCGCACGGACCCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTG
GGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCG
TGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAGAGGAGCAGAGATAC
ACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCTCACCCTGAGATGGGAGCTGTCTTCCCAGCCCACCATCCCCATCG
TGGGCATCATTGCTGGCCTGGTTCTCCTTGGAGCTGTGATCACTGGAGCTGTGGTCGCTGCCGTGATGTGGAGGAGGAAGA
GCTCAGATAGAAAAGGAGGGAGTTACACTCAGGCTGCAAGCAGTGACAGTGCCCAGGGCTCTGATGTGTCTCTCACAGCTT
GTAAAGTGCAGTGTACTAATTATGCTCTCTTGAAATTGGCTGGAGATGTTGAGAGCAACCCAGGTCCCCTAGCCGTCATGGC
GAGCGCTGCAACAAACTTCTCTCTGCTGAAACAAGCCGGAGATGTCGAAGAGAATCCTGGACCGAGAGACGAGATGGTGA
GCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC
GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTG
CCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGAC
TTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGC
GCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACAT
CCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGT
GAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCG
ACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGAT
CACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAACGTCTCATAGCCT
AAGAATTCGATATCAAGCTTATCGGTAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTG
CTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTG
TATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGA
CGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGG
CGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGG
GGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCG
GCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGA
CGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATACCGTCGACCTCGAGACCTAGAAAAACATGGAGCAATCACAA
GTAGCAATACAGCAGCTACCAATGCTGATTGTGCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACAC
CTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAG
GGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTCCCTGATTGGCAGAA
CTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCAAGAGAAGGT
AGAAGAAGCCAATGAAGGAGAGAACACCCGCTTGTTACACCCTGTGAGCCTGCATGGGATGGATGACCCGGAGAGAGAAG
TATTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGACTGTACTGGGTCTCTCTG
GTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTG
CTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTC
TAGCAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTG
CCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTG
TCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATG
CGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCAT
TAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTT
CCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTT
TACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCC
TTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTT
TTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTAATTCT
GTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTA
GTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAAC
CATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTT
TTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGG
CTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATCATCGGCATAGTAT
ATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGC
GACGTCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGACTTCGCCGGTGT
GGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTGGCCTGGGTGTGGG
TGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACTTCCGGGACGCCTCCGGGCCGGCCATG
ACCGAGATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTCGTGGCCGA
GGAGCAGGACTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGG
GACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTTTATTGCAGCTTATAA
TGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAAC
TCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTG
AAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC
TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA
ACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTG

CGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA
GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG
CTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTT
CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCA
GCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC
ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA
GAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA
AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTT
GATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATC
TTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAA
TGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACT
ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAG
CAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTG
CCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGC
TCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGC
GGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATA
ATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGC
GGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGG
AAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAC
TGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATA
AGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGC
GGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC

Supplemental plasmid sequence No. 5

lenti-(HLA-A*11:01)-KRAS-M:

GTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTAT
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
AATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATT
ATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTA
AATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAG
GGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGT
ACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA
CTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA
TGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGCGCGTTTTGCC
TGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAAT
AAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTA
GTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACG
CAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCG
GAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGG
TTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATC
CTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAC
TTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGAC
AAGATAGAGGAAGAGCAAAACAAAAGTAAGACCACCGCACAGCAAGCGGCCGCTGATCTTCAGACCTGGAGGAGGAGATA
TGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAA
GAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGC
TGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTG
TGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTG
GAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAAT
TACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATA
AATGGGCAAGTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGG
TAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACC
TCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCG
ATTAGTGAACGGATCGGCACTGCGTGCGCCAATTCTGCAGACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGG
GATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAAT
TACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCAGTTTGGTTAATTAGCTAGCTAGGTCTTGAAAGG
AGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCG
GCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCG
AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGG
ACCGGTTCTAGAGCCACCATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCCGGGCCGTACGC
ACCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGACCCGGACCGCCACATCGAGCGGGTCACCGAG
CTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAGGTGTGGGCTCGCGGACGACGGCGCCGCGTGGCGGT
CTGGACCACGCCGGAGAGCGTCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTCCC
GGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCGTGGTTCCTGGCCACCGTC
GGCGTATCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGG
GGTGCCCGCCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACCGTCACCGCCGACGT
CGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCCGGCTCCGGAGAGGGCAGGGGAAGTCTGC
TAACCTGCGGCGACGTGGAGGAAAATCCCGGCCCCGGATCCATGGCCGTCATGGCGCCCCGAACCCTCCTCCTGCTACTCTC
GGGGGCCCTGGCCCTGACCCAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCG
CGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGA
GGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCA
GTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACGGTTCTCACACCATCCAGAT
AATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACAT

CGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCCC
ATGCGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGA
GACACTGCAGCGCACGGACCCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTG
GGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCG
TGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAGAGGAGCAGAGATAC
ACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCTCACCCTGAGATGGGAGCTGTCTTCCCAGCCCACCATCCCCATCG
TGGGCATCATTGCTGGCCTGGTTCTCCTTGGAGCTGTGATCACTGGAGCTGTGGTCGCTGCCGTGATGTGGAGGAGGAAGA
GCTCAGATAGAAAAGGAGGGAGTTACACTCAGGCTGCAAGCAGTGACAGTGCCCAGGGCTCTGATGTGTCTCTCACAGCTT
GTAAAGTGCAGTGTACTAATTATGCTCTCTTGAAATTGGCTGGAGATGTTGAGAGCAACCCAGGTCCCCTAGCCGTCATGGC
GAGCGCTGCAACAAACTTCTCTCTGCTGAAACAAGCCGGAGATGTCGAAGAGAATCCTGGACCGGTAGTTGGAGCTGATGG
CGTAGGCAAGTAGCCTAAGAATTCGATATCAAGCTTATCGGTAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGG
TATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTT
TCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTG
TGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCC
CCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCT
TCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTT
CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATACCGTCGACCTCGAGACCTAGAAAAAC
ATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGATTGTGCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGG
GTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAA
GGGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTC
CCTGATTGGCAGAACTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTG
AGCAAGAGAAGGTAGAAGAAGCCAATGAAGGAGAGAACACCCGCTTGTTACACCCTGTGAGCCTGCATGGGATGGATGAC
CCGGAGAGAGAAGTATTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGACTGT
ACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAA
GCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCA
GTGTGGAAAATCTCTAGCAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT
GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGGTATCCCCACGCGCC
CTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGC
TCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTT
CCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAG
ACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTAT
CTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAA
CGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGC
ATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTC
AATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCA
TGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTT
TTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAAT
CATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGTTGACCAGTGCCGTTCCGGT
GCTCACCGCGCGCGACGTCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACG
ACTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTG
GCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACTTCCGGGACGCCTC
CGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGC
ACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCG
GAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATA
GCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCG
CTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCA
GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT
CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG
CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCG
GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGC
ACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC
TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC
TCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA
TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA
GATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTT
GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCC
CCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC
GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATC
CAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGG
CATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCA
TGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGT
TATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATT
CTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTA
AAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAC
CCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGC
CGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGG
GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAA
GTGCCACCTGAC

Supplemental plasmid sequence No. 6

lenti-(HLA-A*11:01)-KRAS-W:

GTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTAT
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
AATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATT
ATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTA
AATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAG
GGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGT
ACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA
CTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA
TGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGCGCGTTTTGCC
TGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAAT
AAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTA
GTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACTTGAAAGCGAAAGGGAAACCAGAGGAGCTCTCTCGACG
CAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCG
GAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGCGATGGGAAAAAATTCGG
TTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATC
CTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAC
TTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGAC
AAGATAGAGGAAGAGCAAAACAAAAGTAAGACCACCGCACAGCAAGCGGCCGCTGATCTTCAGACCTGGAGGAGGAGATA
TGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAA
GAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGC
TGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAATCCTGGCTG
TGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTG
GAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATCACACGACCTGGATGGAGTGGGACAGAGAAATTAACAAT
TACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATA
AATGGGCAAGTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGG
TAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACC
TCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCG
ATTAGTGAACGGATCGGCACTGCGTGCGCCAATTCTGCAGACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGG
GATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAAT
TACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCAGTTTGGTTAATTAGCTAGCTAGGTCTTGAAAGG
AGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCG
GCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCG
AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGG
ACCGGTTCTAGAGCCACCATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCCGGGCCGTACGC
ACCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGACCCGGACCGCCACATCGAGCGGGTCACCGAG
CTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAGGTGTGGGTCGCGGACGACGGCGCCGCGGTGGCGGT
CTGGACCACGCCGGAGAGCGTCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTCCC
GGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCGTGGTTCCTGGCCACCGTC
GGCGTATCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGG
GGTGCCCGCCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACCGTCACCGCCGACGT
CGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCCGGCTCCGGAGAGGGCAGGGGAAGTCTGC
TAACCTGCGGCGACGTGGAGGAAAATCCCGGCCCCGGATCCATGGCCGTCATGGCGCCCCGAACCCTCCTCCTGCTACTCTC
GGGGGCCCTGGCCCTGACCCAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCG
CGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGA
GGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCA
GTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACGGTTCTCACACCATCCAGAT
AATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACAT
CGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCCC
ATGCGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGA
GACACTGCAGCGCACGGACCCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTG
GGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCG
TGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAGAGGAGCAGAGATAC
ACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCTCACCCTGAGATGGGAGCTGTCTTCCCAGCCCACCATCCCCATCG
TGGGCATCATTGCTGGCCTGGTTCTCCTTGGAGCTGTGATCACTGGAGCTGTGGTCGCTGCCGTGATGTGGAGGAGGAAGA
GCTCAGATAGAAAAGGAGGGAGTTACACTCAGGCTGCAAGCAGTGACAGTGCCCAGGGCTCTGATGTGTCTCTCACAGCTT
GTAAAGTGCAGTGTACTAATTATGCTCTCTTGAAATTGGCTGGAGATGTTGAGAGCAACCCAGGTCCCCTAGCCGTCATGGC
GAGCGCTGCAACAAACTTCTCTCTGCTGAAACAAGCCGGAGATGTCGAAGAGAATCCTGGACCGGTAGTTGGAGCTGGTG
GCGTAGGCAAGTAGCCTAAGAATTCGATATCAAGCTTATCGGTAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG
GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCT
TTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGT
GTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTC
CCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACA
ATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCC
TTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCT
TCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATACCGTCGACCTCGAGACCTAGAAAAA
CATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGATTGTGCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTG
GGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAA
AGGGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAAGGCTACTT
CCCTGATTGGCAGAACTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTT
GAGCAAGAGAAGGTAGAAGAAGCCAATGAAGGAGAGAACACCCGCTTGTTACACCCTGTGAGCCTGCATGGGATGGATGA
CCCGGAGAGAGAAGTATTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGACTGT
ACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAA
GCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCA
GTGTGGAAAATCTCTAGCAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT

GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGGTATCCCCACGCGCC
CTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGC
TCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTT
CCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAG
ACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTAT
CTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAA
CGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGC
ATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTC
AATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCA
TGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTT
TTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAAT
CATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGTTGACCAGTGCCGTTCCGGT
GCTCACCGCGCGCGACGTCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACG
ACTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTG
GCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACTTCCGGGACGCCTC
CGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGC
ACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCG
GAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATA
GCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCG
CTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCA
GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT
CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG
CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCG
GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGC
ACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC
TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC
TCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA
TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA
GATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTT
GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCC
CCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC
GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATC
CAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGG
CATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCA
TGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGT
TATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATT
CTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTA
AAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAC
CCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGC
CGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGG
GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAA
GTGCCACCTGAC

REFERENCES

[1] Allegretti M, Fabi A, Buglioni S, et al. Tearing down the walls: FDA approves next generation sequencing (NGS) assays for actionable cancer genomic aberrations. *J Exp Clin Cancer Res* 2018;37:47.

[2] Zhou SL, Zhou ZJ, Hu ZQ, et al. Genomic sequencing identifies WNK2 as a driver in hepatocellular carcinoma and a risk factor for early recurrence. *J Hepatol* 2019;71:1152-1163.

[3] Li X, Xu W, Kang W, et al. Genomic analysis of liver cancer unveils novel driver genes and distinct prognostic features. *Theranostics* 2018;8:1740-1751.

[4] Schulze K, Imbeaud S, Letouzé E, et al. Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. *Nat Genet* 2015;47:505-511.

[5] Totoki Y, Tatsuno K, Covington KR, et al. Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. *Nat Genet* 2014;46:1267-1273.

[6] Sawey ET, Chanrion M, Cai C, et al. Identification of a therapeutic strategy targeting amplified FGF19 in liver cancer by Oncogenomic screening. *Cancer Cell* 2011;19:347-358.

[7] Lawson KA, Sousa CM, Zhang X, et al. Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. *Nature* 2020;586:120-126.

[8] Murugaesu N, Wilson GA, Birkbak NJ, et al. Tracking the genomic evolution of esophageal adenocarcinoma through neoadjuvant chemotherapy. *Cancer Discov* 2015;5:821-831.

[9] Szolek A, Schubert B, Mohr C, et al. OptiType: precision HLA typing from next-generation sequencing data. *Bioinformatics* 2014;30:3310-3316.

[10] McGranahan N, Rosenthal R, Hiley CT, et al. Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. *Cell* 2017;171:1259-1271.

[11] Cunningham F, Allen JE, Allen J, et al. *Ensembl* 2022. Nucleic Acids Res 2022;50:D988-D995.

[12] Jehl F, Degalez F, Bernard M, et al. CisRNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and -Regulation Analysis by Allele-Specific Expression in Livestock Species. *Front Genet* 2021;12:655707.

[13] Reynisson B, Alvarez B, Paul S, et al. NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data. *Nucleic Acids Res* 2020;48:W449-W454.

[14] Lang F, Schrörs B, Löwer M, et al. Identification of neoantigens for individualized therapeutic cancer vaccines. *Nat Rev Drug Discov* 2022;21:261-282.

[15] Boegel S, Castle JC, Kodysh J, et al. Bioinformatic methods for cancer neoantigen prediction. *Prog Mol Biol Transl Sci* 2019;164:25-60.

[16] Cheng Y, Gunasegaran B, Singh HD, et al. Non-terminally exhausted tumor-resident memory HBV-specific T cell responses correlate with relapse-free survival in hepatocellular carcinoma. *Immunity* 2021;54:1825-1840.

[17] Benvenuto M, Focaccetti C, Izzi V, et al. Tumor antigens heterogeneity and

immune response-targeting neoantigens in breast cancer. *Semin Cancer Biol* 2021;72:65-75.

[18] Kim S, Kim HS, Kim E, et al. Neopepsee: accurate genome-level prediction of neoantigens by harnessing sequence and amino acid immunogenicity information. *Ann Oncol* 2018;29:1030-1036.

[19] Tan X, Li D, Huang P, et al. dbPepNeo: a manually curated database for human tumor neoantigen peptides. *Database (Oxford)* 2020;2020:baaa004.

[20] Wang QJ, Yu Z, Griffith K, et al. Identification of T-cell Receptors Targeting KRAS-Mutated Human Tumors. *Cancer Immunol Res* 2016;4:204-214.

[21] Xie X, Wang X, Liao W, et al. MYL6B, a myosin light chain, promotes MDM2-mediated p53 degradation and drives HCC development. *J Exp Clin Cancer Res* 2018;37:28.

[22] Wooldridge L, van den Berg HA, Glick M, et al. Interaction between the CD8 coreceptor and major histocompatibility complex class I stabilizes T cell receptor-antigen complexes at the cell surface. *J Biol Chem* 2005;280:27491-27501.

[23] Wooldridge L, Lissina A, Cole DK, et al. Tricks with tetramers: how to get the most from multimeric peptide-MHC. *Immunology* 2009;126:147-164.