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(54) **Titre : VECTEURS RECOMBINANTS COMPRENANT DES CASSETTES D'EXPRESSION POLYCISTRONIQUE ET LEURS
PROCEDES D'UTILISATION**

(54) **Title: RECOMBINANT VECTORS COMPRISING POLYCISTRONIC EXPRESSION CASSETTES AND METHODS OF USE
THEREOF**

(57) **Abrégé/Abstract:**

Provided herein are vectors comprising a polycistronic expression cassette comprising a polynucleotide that encodes a TCR alpha chain, a polynucleotide that encodes a TCR beta chain, and a polynucleotide that encodes a cytokine, wherein the polynucleotides are separated by polynucleotide sequences that comprise 2A elements.

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Abstract:

Provided herein are vectors comprising a polycistronic expression cassette comprising a polynucleotide that encodes a TCR alpha chain, a polynucleotide that encodes a TCR beta chain, and a polynucleotide that encodes a cytokine, wherein the polynucleotides are separated by polynucleotide sequences that comprise 2A elements.

RECOMBINANT VECTORS COMPRISING POLYCISTRONIC EXPRESSION CASSETTES AND METHODS OF USE THEREOF

1. FIELD

[0001] The instant disclosure relates to polycistronic vectors comprising at least three cistrons and methods of using the same.

2. BACKGROUND

[0002] Co-expression of multiple genes in each cell of a population is critical for a wide variety of biomedical applications. A standard strategy for multigene expression is to incorporate the transgenes into multiple vectors and introduce each vector into the cell. However, the use of multiple vectors often produces a substantially heterogeneous population of engineered cells, wherein not all cells express each of the transgenes or do not express each of the transgenes to a similar degree. Such heterogeneity leads to several problems, particularly for therapeutic applications, including e.g., diminished persistence of the desired engineered cell phenotype *in vivo*, complex manufacturing and purification requirements, and lot-to-lot variability of the engineered cell product.

[0003] Given the problems associated with the use of multiple vectors to co-express multiple genes in single cells, there is an unmet need for single polycistronic vectors capable of not only expressing a plurality of transgenes in a single cell, but also of expressing some or all transgenes to a similar degree across a cell population, resulting in an engineered cell population optimized for therapeutic use.

3. SUMMARY

[0004] The instant disclosure provides recombinant vectors comprising a polycistronic expression cassette comprising a transcriptional regulatory element operably linked to a polycistronic polynucleotide.

[0005] Provided herein is a recombinant vector comprising a polycistronic expression cassette, wherein the polycistronic expression cassette comprises a transcriptional regulatory element operably linked to a polycistronic polynucleotide that comprises: a first polynucleotide sequence that encodes a T cell receptor (TCR) alpha chain comprising an alpha chain variable ($V\alpha$) region and an alpha chain constant ($C\alpha$) region; a second polynucleotide sequence that comprises a first 2A element; a third polynucleotide sequence that encodes a TCR beta chain comprising a beta

chain variable (V β) region and a beta chain constant (C β) region; a fourth polynucleotide sequence that comprises a second 2A element; and a fifth polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof.

[0006] In some embodiments, either or both of the first 2A element and the second 2A element, independently, is a P2A element, a T2A element, an F2A element, or an E2A element.

[0007] In some embodiments, the first 2A element is a P2A element.

[0008] In some embodiments, the P2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 18 or 20, or the amino acid sequence of SEQ ID NO: 18 or 20 comprising 1, 2, or 3 amino acid modifications.

[0009] In some embodiments, the P2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 19 or 21.

[0010] In some embodiments, the second 2A element is a T2A element.

[0011] In some embodiments, the T2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 22 or 24, or the amino acid sequence of SEQ ID NO: 22 or 24 comprising 1, 2, or 3 amino acid modifications.

[0012] In some embodiments, the T2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 23 or 25.

[0013] In some embodiments, either or both of the second polynucleotide sequence and the fourth polynucleotide sequence, independently, encode a furin recognition site.

[0014] In some embodiments, the furin recognition site comprises the amino acid sequence of SEQ ID NO: 2 or 4, or the amino acid sequence of SEQ ID NO: 2 or 4 comprising 1, 2, or 3 amino acid modifications.

[0015] In some embodiments, the furin recognition site is encoded by the polynucleotide sequence of SEQ ID NO: 3 or 5 or the polynucleotide sequence of SEQ ID NO: 3 or 5 comprising 1, 2, or 3 nucleotide modifications.

[0016] In some embodiments, the second polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 10, or the amino acid sequence of SEQ ID NO: 10 comprising 1, 2, or 3 amino acid modifications.

[0017] In some embodiments, the second polynucleotide sequence comprises a polynucleotide

sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 11.

[0018] In some embodiments, the fourth polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 12, or the amino acid sequence of SEQ ID NO: 12 comprising 1, 2, or 3 amino acid modifications.

[0019] In some embodiments, the fourth polynucleotide sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 13.

[0020] In some embodiments, the IL-15, or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 76.

[0021] In some embodiments, the IL-15, or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 77.

[0022] In some embodiments, the IL-15R α , or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 78.

[0023] In some embodiments, the IL-15R α , or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 79.

[0024] In some embodiments, the IL-15, or functional fragment or functional variant thereof, is operably linked to the IL-15R α , or functional fragment or functional variant thereof, via a peptide linker.

[0025] In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 81, or the amino acid sequence of SEQ ID NO: 81 comprising 1, 2, or 3 amino acid modifications.

[0026] In some embodiments, the peptide linker is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 82.

[0027] In some embodiments, the fusion protein is membrane bound.

[0028] In some embodiments, the fusion protein comprises an amino acid sequence at least

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 70 or 73.

[0029] In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 71 or 74.

[0030] In some embodiments, the C α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 40-49.

[0031] In some embodiments, the C α region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 55, 57, or 58.

[0032] In some embodiments, the C β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 50-54 or 60.

[0033] In some embodiments, the C β region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 56 or 59.

[0034] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.

[0035] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.

[0036] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.

[0037] In some embodiments, the first polynucleotide sequence and the second polynucleotide

sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.

[0038] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 181.

[0039] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.

[0040] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 252.

[0041] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.

[0042] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.

[0043] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.

[0044] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; and the third polynucleotide sequence, the second

polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.

[0045] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; and the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 183.

[0046] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.

[0047] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 255.

[0048] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.

[0049] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; or the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164.

[0050] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; or the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238.

[0051] In some embodiments, the first polynucleotide sequence, the second polynucleotide

sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[0052] In some embodiments, the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 184 or 214; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[0053] In some embodiments, the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.

[0054] In some embodiments, the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 258 or 278; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[0055] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.

[0056] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165.

[0057] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the

twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241.

[0058] In some embodiments, the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[0059] In some embodiments, the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 185 or 215; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[0060] In some embodiments, the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.

[0061] In some embodiments, the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 261 or 281; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[0062] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.

[0063] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.

[0064] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.

[0065] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.

[0066] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 187 or 217.

[0067] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; and the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.

[0068] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; and the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 259 or 279.

[0069] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.

[0070] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.

[0071] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.

[0072] In some embodiments, the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; and the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.

[0073] In some embodiments, the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; and the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 189 or 219.

[0074] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.

[0075] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 256 or 276.

[0076] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.

[0077] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; or the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170.

[0078] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the sixth combination polynucleotide sequence

comprises the polynucleotide sequence of SEQ ID NO: 235; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; or the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242.

[0079] In some embodiments, the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[0080] In some embodiments, the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 190; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[0081] In some embodiments, the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[0082] In some embodiments, the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 262; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[0083] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.

[0084] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination

polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171.

[0085] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243.

[0086] In some embodiments, the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[0087] In some embodiments, the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 191; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[0088] In some embodiments, the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[0089] In some embodiments, the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 263; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[0090] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.

[0091] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.

[0092] In some embodiments, the fourth combination polynucleotide sequence comprises the

polynucleotide sequence of SEQ ID NO: 233; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.

[0093] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[0094] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 222; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[0095] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.

[0096] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[0097] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.

[0098] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.

[0099] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; or the eighth combination polynucleotide sequence

comprises the polynucleotide sequence of SEQ ID NO: 237.

[00100] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[00101] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 223; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[00102] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59. In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[00103] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.

[00104] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.

[00105] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.

[00106] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[00107] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 222; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[00108] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[00109] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[00110] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.

[00111] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.

[00112] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237.

[00113] In some embodiments, the third polynucleotide sequence and the second

polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[00114] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 223; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[00115] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[00116] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[00117] In some embodiments, the polycistronic polynucleotide further comprises a sixth polynucleotide sequence that comprises a third 2A element; and a seventh polynucleotide sequence that comprises a marker protein.

[00118] In some embodiments, the third 2A element is a P2A element, a T2A element, an F2A element, or an E2A element.

[00119] In some embodiments, the marker protein comprises domain III of HER1, or a functional fragment or functional variant thereof; an N-terminal portion of domain IV of HER1; and a transmembrane domain of CD28, or a functional fragment or functional variant thereof.

[00120] In some embodiments, the domain III of HER1, or a functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 104.

[00121] In some embodiments, the N-terminal portion of domain IV of HER1 comprises amino acids 1-40, 1-39, 1-38, 1-37, 1-36, 1-35, 1-34, 1-33, 1-32, 1-31, 1-30, 1-29, 1-28, 1-27, 1-26, 1-25,

1-24, 1-23, 1-22, 1-21, 1-20, 1-19, 1-18, 1-17, 1-16, 1-15, 1-14, 1-13, 1-12, 1-11, or 1-10 of SEQ ID NO: 105.

[00122] In some embodiments, the N-terminal portion of domain IV of HER1 comprises amino acids 1-21 of SEQ ID NO: 105.

[00123] In some embodiments, the N-terminal portion of domain IV of HER1 comprises the amino acid sequence of SEQ ID NO: 106, or the amino acid sequence of SEQ ID NO: 106, comprising 1, 2, or 3 amino acid modifications.

[00124] In some embodiments, the transmembrane region of CD28 comprises the amino acid sequence of SEQ ID NO: 107, or the amino acid sequence of SEQ ID NO: 107, comprising 1, 2, or 3 amino acid modifications.

[00125] In some embodiments, the marker protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, or 112.

[00126] In some embodiments, the V α region comprises complementarity determining region 1 α (CDR1 α), CDR2 α , and CDR3 α , comprising the amino acid sequences of SEQ ID NO: 1001 + 10n, 1002 + 10n, and 1003 + 10n, respectively, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00127] In some embodiments, the V β region comprises CDR1 β , CDR2 β , and CDR3 β , comprising the amino acid sequences of SEQ ID NO: 2001 + 10n, 2002 + 10n, and 2003 + 10n, respectively, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00128] In some embodiments, the V α region comprises the CDR1 α , CDR2 α , and CDR3 α from a V α region comprising the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00129] In some embodiments, the V β region comprises the CDR1 β , CDR2 β , and CDR3 β from a V β region comprising the amino acid sequence of SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00130] In some embodiments, the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00131] In some embodiments, the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence

of SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00132] In some embodiments, the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2004 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1005 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2005 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1006 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2006 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1007 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00133] In some embodiments, the TCR alpha chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1008 + 10n, wherein n is an integer from 0 to 79. In some embodiments, the TCR alpha chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1009 + 10n, wherein n is an integer from 0 to 79.

[00134] In some embodiments, the TCR alpha chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1010 + 10n, wherein n is an integer from 0 to 79.

[00135] In some embodiments, the TCR beta chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid

sequence of SEQ ID NO: 2008 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00136] In some embodiments, the TCR beta chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2009 + 10n, wherein n is an integer from 0 to 79.

[00137] In some embodiments, the TCR beta chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2010 + 10n, wherein n is an integer from 0 to 79.

[00138] In some embodiments, transcriptional regulatory element comprises a promoter.

[00139] In some embodiments, the promoter is a human elongation factor 1-alpha (hEF-1 α) hybrid promoter.

[00140] In some embodiments, the promoter comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:150.

[00141] In some embodiments, the recombinant vector further comprises a polyA sequence at the 3' end of the polycistronic expression cassette.

[00142] In some embodiments, the polyA sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:151.

[00143] In some embodiments, the recombinant vector further comprises a Left inverted terminal repeat (ITR) and a Right ITR, wherein the Left ITR and the Right ITR flank the polycistronic expression cassette.

[00144] In some embodiments, the recombinant vector comprises, in order from 5' to 3': the Left ITR; the transcriptional regulatory element; the first polynucleotide sequence; the second polynucleotide sequence; the third polynucleotide sequence; the fourth polynucleotide sequence; the fifth polynucleotide sequence; and the Right ITR.

[00145] In some embodiments, the recombinant vector is a non-viral vector.

[00146] In some embodiments, the non-viral vector is a plasmid.

[00147] In some embodiments, the recombinant vector is a viral vector.

[00148] In some embodiments, the recombinant vector is a polynucleotide.

[00149] Also provided herein is a polynucleotide encoding an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid

sequence selected from the group consisting of SEQ ID NOs: 161, 163, 164, 165, 167, 169, 170, and 171.

[00150] Also provided herein is a polynucleotide comprising a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 232, 235, 236, 238, 239, 241, 242, and 243.

[00151] Also provided herein is a population of cells that comprises any recombinant vector provided herein, or any polynucleotide provided herein.

[00152] In some embodiments, the recombinant vector or the polynucleotide is integrated into the genome of the population of cells.

[00153] In some embodiments, the cells are immune effector cells.

[00154] In some embodiments, the immune effector cells are selected from the group consisting of T cells, natural killer (NK) cells, B cells, mast cells, and myeloid-derived phagocytes.

[00155] In some embodiments, the immune effector cells are T cells.

[00156] In some embodiments, the T cells are selected from the group consisting of naïve T cells (CD4⁺ or CD8⁺); killer CD8⁺ T cells; cytotoxic CD4⁺ T cells; helper CD4⁺ T cells; CD4⁺ T cells corresponding to Th1, Th2, Th9, Th17, Th22, follicular helper (T_{fh}), regulatory (T_{reg}) lineages; tumor infiltrating lymphocytes (TILs); and memory T cells (central memory, effector memory, stem cell memory, stem cell-like memory).

[00157] In some embodiments, the population of cells comprises alpha/beta T cells, gamma/delta T cells, or natural killer T (NKT) cells.

[00158] In some embodiments, the population of cells comprises CD4⁺ T cells, CD8⁺ T cells, or both CD4⁺ T cells and CD8⁺ T cells.

[00159] In some embodiments, the cells are *ex vivo*.

[00160] In some embodiments, the cells are human.

[00161] In some embodiments, the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA⁺CD45RO⁺CD62L⁺CD95⁺ cells.

[00162] In some embodiments, the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA⁺CD45RO⁺CD62L⁺CD95⁺ cells.

[00163] Also provided herein is a population of cells comprising a polycistronic expression cassette comprising a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α ,

or a functional fragment or functional variant thereof; a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95+ cells.

[00164] Also provided herein is a population of cells comprising a polycistronic expression cassette comprising a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof; a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95+ cells.

[00165] Also provided herein is a method of producing a population of engineered cells, comprising introducing into a population of cells any recombinant vector provided herein, and a DNA transposase or a polynucleotide encoding a DNA transposase; and culturing the population of cells under conditions wherein the transposase integrates the polycistronic expression cassette into the genome of the population of cells, thereby producing the population of engineered cells.

[00166] In some embodiments, the Left ITR and the Right ITR are ITRs of a DNA transposon selected from the group consisting of a *Sleeping Beauty* transposon, a piggyBac transposon, a TcBuster transposon, and a Tol2 transposon.

[00167] In some embodiments, the DNA transposon is the *Sleeping Beauty* transposon.

[00168] In some embodiments, the transposase is a *Sleeping Beauty* transposase.

[00169] In some embodiments, the *Sleeping Beauty* transposase is selected from the group consisting of SB11, SB10, SB100X, hSB110, and hSB81.

[00170] In some embodiments, the *Sleeping Beauty* transposase is SB11.

[00171] In some embodiments, the SB11 comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 300.

[00172] In some embodiments, the SB11 is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 301.

[00173] In some embodiments, the polynucleotide encoding the DNA transposase is a DNA vector or an RNA vector.

[00174] In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290 or 291; and the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292, 293 or 294.

[00175] In some embodiments, the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation, sonication, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, or mechanical deformation by passage through a microfluidic device, or a colloidal dispersion system.

[00176] In some embodiments, the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation.

[00177] In some embodiments, the method is completed within 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.

[00178] In some embodiments, wherein the method is completed in less than 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.

[00179] In some embodiments, the population of cells is cryopreserved and thawed before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

[00180] In some embodiments, the population of cells is rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

[00181] In some embodiments, the population of cells is not rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

[00182] In some embodiments, the population of cells comprises expanded human *ex vivo* cells.

[00183] In some embodiments, the population of cells is not activated *ex vivo*.

[00184] In some embodiments, the population of cells comprises T cells.

[00185] Also provided herein is a method of treating cancer in a subject in need thereof comprising administering to the subject a therapeutically effective amount of any of the populations of cells provided herein, thereby treating the cancer.

[00186] In some embodiments, the cancer is selected from lung, cholangiocarcinoma, pancreatic, colorectal, gynecological, and ovarian cancer.

[00187] Also provided herein is a method of treating an autoimmune disease or disorder in a subject in need thereof comprising administering to the subject a therapeutically effective amount any of the populations of cells provided herein, thereby treating the autoimmune disease or disorder.

4. BRIEF DESCRIPTION OF THE RAWINGS

[00188] The accompanying drawings which are incorporated in and constitute a part of this specification, illustrate exemplary embodiments of the present disclosure and, together with the description, serve to explain principles of the present disclosure.

[00189] **FIG. 1** is a set of schematics of the structures of TCR α (A), TCR β (B), and mbIL15 (15), shown from N terminus (left) to C terminus (right).

[00190] **FIG. 2A** is a set of schematics of the ORFs of tricistronic Cassettes APBT15, ATBP15, AP15TB, AT15PB, BPAT15, BTAP15, BP15TA, and BT15PA. **FIG. 2B** is a set of schematics of the ORFs of control Cassettes 15, APB, and BPA.

[00191] **FIG. 3** is a schematic diagram depicting double transposition and single transposition approaches using a *Sleeping Beauty* transposon/transposase system to generate T cells expressing TCR α /TCR β and mbIL15.

[00192] **FIG. 4** is a set of 2-parameter flow plots showing transgene co-expression as assessed after electroporation and overnight incubation for each of Groups 1-14.

[00193] **FIG. 5A** is a set of 2-parameter flow plots showing representative TCR transgene expression in CD3+ cells after overnight incubation for each of Groups 1-14. **FIG. 5B** provides TCR expression data from three donors presented as % mTCR+ cells out of CD3+ cells.

[00194] **FIG. 6A-6C** shows TCR and mbIL15 expression after first phase expansion (Day 13). **FIG. 6A** provides representative TCR and mbIL15 expression data from each of Groups 1-14. **FIG. 6B** provides TCR expression data from three donors presented as % mTCR+ cells out of CD3+ cells. **FIG. 6C** provides TCR and mbIL15 co-expression data from three donors presented as % TCR+mbIL15+ cells out of CD3+ cells.

[00195] **FIG. 7A-7B** shows total numbers of TCR+ and TCR+mbIL15+ cells after first phase expansion (Day 13). **FIG. 7A** provides TCR expression data from three donors presented as total

number of mTCR+ T cells. **FIG. 7B** provides total number of TCR+mbIL15+ T cells from three donors.

[00196] **FIG. 8A-8B** shows cell viability after electroporation (Day 1; **FIG. 8A**) and after first phase expansion (Day 13; **FIG. 8B**) for each of Groups 1-14.

[00197] **FIG. 9A-9B** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 1-14 after first phase expansion (Day 13) with wild-type or mutant neoantigen pulsed T2 cells. Data is presented as % 4-1BB positive cells of CD8+ cells at increasing concentrations of neoantigen peptide.

[00198] **FIG. 10** shows phosphorylated STAT5 levels in transposed CD3+ T cells from each of Groups 1-14 after first phase expansion (Day 13). Isotype negative control and IL-15 treated positive control was included for comparison. (dTp = double transposed with separate mbIL15 and TCR vectors).

[00199] **FIG. 11** shows apoptosis levels in transposed T cells from each of Groups 2-14 after being expanded for 13 days and then activated for 9 days with CD3/CD28 Dynabeads® (ThermoFisher).

[00200] **FIG. 12** is a set of schematics illustrating the differences between the S version and N version of the TCR only and mbIL15 TCR constructs shown from N terminus (left) to C terminus (right).

[00201] **FIG. 13A-13B** shows TCR expression on CD3+ cells (**FIG. 13A**) the day after electroporation (Day 1) and after the first phase expansion prior to enrichment (Day 11 Pre-enrichment) as well as (**FIG. 13B**) after the first phase expansion following enrichment (Day 11 Post-enrichment) and at the end of the second phase expansion. Data from four donors are presented.

[00202] **FIG. 14A-14B** shows TCR and mbIL15 co-expression on CD3+ T cells (**FIG. 14A**) the day after electroporation (Day 1) and after the first phase expansion prior to enrichment (Day 11 Pre-enrichment) as well as after the first phase expansion following enrichment (Day 11 Post-enrichment) and at the end of the second phase expansion. Data from four donors are presented.

[00203] **FIG. 15** is a set of 2-parameter flow plots showing representative TCR and mbIL15 transgenes expression in CD3+ cells after the second phase expansion.

[00204] **FIG. 16A-16B** shows the fold expansion of cells (**FIG. 16A**) after the first expansion phase and (**FIG. 16B**) after the second expansion phase. Data from four donors are presented.

[00205] **FIG. 17A-17B** shows the absolute count of TCR expressing cells in culture (**FIG. 17A**) after the first expansion phase and (**FIG. 17B**) after the second expansion phase. Data from four donors are presented.

[00206] **FIG. 18** shows phosphorylated STAT5 levels after second phase expansion (Day 27) in CD3⁺ T cells transposed with different versions of polycistronic plasmids encoding TCR001. Some containing non-cysteine substituted TCR constant regions (N version) or that are optionally further codon-optimized (NU version). Non-transposed (NT) = NT (Group 2.1); BPA (Group 2.2); BPA-N (Group 2.3); AP15TB (Group 2.4); AP15TB-N (Group 2.5); AP15TB-NU (Group 2.6); BP15TA (Group 2.7); BP15TA-N (Group 2.8); and BP15TA-NU (Group 2.9).

[00207] **FIG. 19A-19B** shows functional data from transposed T cells co-cultured with neoantigen pulsed dendritic cells. **FIG. 19A** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 2.1-2.9 after second phase expansion (Day 27) with wild-type or mutant neoantigen peptide pulsed dendritic cells. Data is presented as % 4-1BB positive cells of CD8⁺ cells at increasing concentrations of neoantigen peptide. **FIG. 19B** shows interferon- γ (IFN- γ) secretion after overnight co-culture of transposed T cells from each of Groups 2.1-2.9 after second phase expansion (Day 27) with wild-type or mutant neoantigen pulsed dendritic cells.

[00208] **FIG. 20A-20B** shows TCR expression and cell survival after 4 weeks of long-term cytokine withdrawal (LTWD) incubation in transposed cells from each of Groups 2.2-2.9. **FIG. 20A** shows the expression of mTCR detected on CD3⁺ gated population with mouse TCR beta antibody and **FIG. 20B** shows cell survival as the percent of live cells recovered relative to initial input number of cells at the beginning of the LTWD.

[00209] **FIG. 21A-21B** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 2.2-2.9 after 4 weeks of LTWD incubation with wild-type or mutant neoantigen (10 μ g/ml) pulsed dendritic cells.

[00210] **FIG. 22A-22B** shows IFN- γ secretion after overnight co-culture of transposed T cells from each of Groups 2.2-2.9 after 4 weeks of LTWD incubation with wild-type or mutant neoantigen (10 μ g/ml) pulsed dendritic cells.

[00211] **FIG. 23A-23C** is a set of pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-expansion (**FIG. 23A**), day 22 post-expansion (**FIG. 23B**), and after 4 weeks of LTWD culture (**FIG. 23C**) in cells transposed with the tested plasmids (Groups 2.2-2.9).

[00212] **FIG. 24** is a set of 2-parameter flow plots showing representative TCR and mbIL15 transgene co-expression in CD3+ cells after overnight incubation (Day 1), after first phase expansion (Day 11, pre- and post-enrichment) and after second phase expansion (Day 22) for each of Groups 3.2-3.4 expressing TCR001 +/- mbIL15 (BPA-N, AP15TB-NU, and BP15TA-NU).

[00213] **FIG. 25A-25C** shows TCR+ population changes during the first expansion phase (Day 1 vs. Day 11 pre-enrichment) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00214] **FIG. 26A-26C** shows TCR+ population changes during the second expansion phase (Day 11 post-enrichment vs. Day 22) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00215] **FIG. 27A-27C** shows TCR+/mbIL15+ population changes during the first expansion phase (Day 1 vs. Day 11 pre-enrichment) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00216] **FIG. 28A-28C** shows TCR+/mbIL15+ population changes during the second expansion phase (Day 11 post-enrichment vs. Day 22) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00217] **FIG. 29A-29I** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 3.1-3.30 after second phase expansion (Day 27) with wild-type (WT) or mutant (Mut) neoantigen pulsed dendritic cells. Data is presented as % 4-1BB positive cells of total CD3+, CD4+ or CD8+ T cells at increasing concentrations of neoantigen peptide. NT = non-transposed; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00218] **FIG. 30A-30I** shows IFN- γ secretion after overnight co-culture of transposed T cells from each of Groups 3.1-3.30 after second phase expansion (Day 27) with wild-type (WT) or mutant (Mut) neoantigen pulsed dendritic cells. Data is presented as IFN- γ level (pg/mL) at increasing concentrations of neoantigen peptide. NT = non-transposed; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00219] **FIG. 31** shows the specific lysis of negative control (Mut+HLA-) tumor cell line AU565 and target tumor cell line TYK-nu (Mut+HLA+) by T cells expressing TCR001 +/- mbIL15. NT = non-transposed; TCR001 only = BPA-N, TCR001 with mbIL15 = AP15TB-NU or BP15TA-NU.

[00220] **FIG. 32A-32B** shows the specific lysis of a tumor cell line by T cells expressing (**FIG. 32A**) TCR022 +/- mbIL15 or (**FIG. 32B**) TCR075 +/- mbIL15. Tumor cell line was transfected with the appropriate HLA-expression plasmid and pulsed with either wild type (WT) or mutant (Mut) peptides and co-cultured with T cells. NT = non-transposed; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00221] **FIG. 33** shows TCR+ population for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD). TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00222] **FIG. 34A-34C** shows cell survival for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD). BPA-N (IL2) = TCR only cultured with IL2, NT = non-transposed, BPA-N = TCR only, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00223] **FIG. 35A-35I** shows specific induction of activation marker, 4-1BB, after overnight co-culture of cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD) with wild-type or mutant neoantigen pulsed dendritic cells. Data are presented as % 4-1BB+ of either CD3+, CD4+, or CD8+ T cells. BPA-N (IL2) = TCR only cultured with IL2, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00224] **FIG. 36A-36C** shows IFN- γ secretion after overnight co-culture of cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD) with wild-type or mutant neoantigen pulsed dendritic cells. BPA-N (IL2) = TCR only cultured with IL2, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00225] **FIG. 37A-37I** shows a comparison of 4-1BB induction in cells transposed with various TCRs + mbIL15 (Groups 3.1-3.30) pre- and post-LTWD culture after overnight co-culture with wild-type or mutant neoantigen pulsed dendritic cells. Data are presented as % 4-1BB+ of either CD3+, CD4+, or CD8+ T cells.

[00226] **FIG. 38** is a set of representative pie charts showing the mean frequency of live CD3+ T cell memory and effector subsets at day 11 post-expansion of cells transposed with TCR001 expressed from either BPA-N or with mbIL15 from either AP15TB-NU or BP15TA-NU.

[00227] **FIG. 39** is a set of representative pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets at day 22 post-expansion of cells transposed with TCR001 expressed from either BPA-N or with mbIL15 from either AP15TB-NU or BP15TA-NU.

[00228] **FIG. 40A-40E** is a set of pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets of in cells transposed with the tested plasmids (Groups 3.1-3.30) after 4 weeks of LTWD culture.

5. DETAILED DESCRIPTION

[00229] The instant disclosure provides recombinant polycistronic nucleic acid vectors comprising at least three cistrons, wherein the first cistron encodes an α chain of an artificial T-cell receptor (TCR), the second cistron encodes a β chain of an artificial TCR, and the third cistron encodes a fusion protein that comprises IL-15 and IL-15R α (e.g., mbIL15), or a functional fragment or functional variant thereof. In some embodiments, the polycistronic nucleic acid further comprises a fourth cistron that encodes a marker protein (e.g., HER1t). In some embodiments, the cistrons are separated by polynucleotide sequence that comprise 2A elements. Also provided are immune effector cells comprising these vectors, immune effector cells engineered *ex vivo* utilizing the vectors to express the three proteins encoded by the vectors, pharmaceutical compositions comprising these vectors or engineered immune effector cells made utilizing these vectors, and methods of treating a subject using these vectors or engineered immune effector cells made utilizing these vectors.

[00230] The polycistronic vectors described herein are particularly useful in methods of manufacturing populations of engineered cells (e.g., immune effector cells) that are substantially homogeneous compared to the prior art systems that utilized at least two vectors for the expression of three proteins.

5.1 Definitions

[00231] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the claimed subject matter belongs. It is to be understood that the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of any subject matter claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise. It must be noted that, as used in the specification and the appended claims, the singular

forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. In this application, the use of “or” means “and/or” unless stated otherwise. Furthermore, use of the term “including” as well as other forms, such as “include,” “includes,” and “included,” is not limiting. The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[00232] As used herein, the terms “about” and “approximately,” when used to modify a numeric value or numeric range, indicate that deviations of 5% to 10% above (*e.g.*, up to 5% to 10% above) and 5% to 10% below (*e.g.*, up to 5% to 10% below) the value or range remain within the intended meaning of the recited value or range.

[00233] As used herein, the terms “T cell receptor” and “TCR” are used interchangeably and refer to molecules comprising CDRs or variable regions from $\alpha\beta$ T cell receptors. Examples of TCRs include, but are not limited to, full-length TCRs, antigen-binding fragments of TCRs, soluble TCRs lacking transmembrane and cytoplasmic regions, single-chain TCRs containing variable regions of TCRs attached by a flexible linker, TCR chains linked by an engineered disulfide bond, single TCR variable domains, single peptide-MHC-specific TCRs, multi-specific TCRs (including bispecific TCRs), TCR fusions, TCRs comprising co-stimulatory regions, human TCRs, humanized TCRs, chimeric TCRs, recombinantly produced TCRs, and synthetic TCRs. In certain embodiments, the TCR is a full-length TCR comprising a full-length α chain and a full-length β chain. In certain embodiments, the TCR is a soluble TCR lacking transmembrane and/or cytoplasmic region(s). In certain embodiments, the TCR is a single-chain TCR (scTCR) comprising $V\alpha$ and $V\beta$ linked by a peptide linker, such as a scTCR having a structure as described in PCT Publication No.: WO 2003/020763, WO 2004/033685, or WO 2011/044186, each of which is incorporated by reference herein in its entirety. In certain embodiments, the TCR comprises a transmembrane region. In certain embodiments, the TCR comprises a co-stimulatory signaling region.

[00234] As used herein, the term “full-length TCR” refers to a TCR comprising a dimer of a first and a second polypeptide chain, each of which comprises a TCR variable region and a TCR constant region comprising a TCR transmembrane region and a TCR cytoplasmic region. In certain embodiments, the full-length TCR comprises one or two unmodified TCR chains, *e.g.*, unmodified α or β TCR chains. In certain embodiments, the full-length TCR comprises one or two altered TCR chains, such as chimeric TCR chains and/or TCR chains comprising one or more amino acid substitutions, insertions, or deletions relative to an unmodified TCR chain. In certain

embodiments, the full-length TCR comprises a mature, full-length TCR α chain and a mature, full-length TCR β chain.

[00235] As used herein, the term “TCR variable region” refers to the portion of a mature TCR polypeptide chain (*e.g.*, a TCR α chain or β chain) which is not encoded by the TRAC gene for TCR α chains, either the TRBC1 or TRBC2 genes for TCR β chains, or the TRDC gene for TCR δ chains. In some embodiments, the TCR variable region of a TCR α chain encompasses all amino acids of a mature TCR α chain polypeptide which are encoded by a TRAV and/or TRAJ gene, and the TCR variable region of a TCR β chain encompasses all amino acids of a mature TCR β chain polypeptide which are encoded by a TRBV, TRBD, and/or TRBJ gene (see, *e.g.*, Lefranc and Lefranc, (2001) “T cell receptor FactsBook.” *Academic Press*, ISBN 0-12-441352-8, which is incorporated by reference herein in its entirety). TCR variable regions generally comprise framework regions (FR) 1, 2, 3, and 4 and complementarity determining regions (CDR) 1, 2, and 3.

[00236] As used herein, the terms “ α chain variable region” and “V α ” are used interchangeably and refer to the variable region of a TCR α chain.

[00237] As used herein, the terms “ β chain variable region” and “V β ” are used interchangeably and refer to the variable region of a TCR β chain.

[00238] As used herein in the context of a TCR, the term “CDR” or “complementarity determining region” means the noncontiguous antigen combining sites found within the variable regions of a TCR chain (*e.g.*, an α chain or a β chain). These regions have been described in Lefranc, (1999) *The Immunologist* 7: 132-136; Lefranc *et al.*, (1999) *Nucleic Acids Res* 27: 209-212; Lefranc (2001) “T cell receptor FactsBook.” *Academic Press*, ISBN 0-12-441352-8; Lefranc *et al.*, (2003) *Dev Comp Immunol.* 27(1):55-77; and in Kabat *et al.*, (1991) “Sequences of protein of immunological interest,” each of which is herein incorporated by reference in its entirety. In certain embodiments, CDRs are determined according to the IMGT numbering system described in Lefranc (1999) *supra*. In certain embodiments, CDRs are defined according to the Kabat numbering system described in Kabat *supra*. In certain embodiments, CDRs are defined empirically, *e.g.*, based upon a structural analysis of the interaction of a TCR with a cognate antigen (*e.g.*, a peptide or a peptide-MHC complex). In certain embodiments, the α chain and β chain CDRs of a TCR are defined according to different conventions (*e.g.*, according to the Kabat or IMGT numbering systems, or empirically based upon structural analysis).

[00239] As used herein, the term “framework amino acid residues” refers to those amino acids in the framework region of a TCR chain (*e.g.*, an α chain or a β chain). The term “framework region” or “FR” as used herein includes the amino acid residues that are part of the TCR variable region, but are not part of the CDRs.

[00240] As used herein, the term “constant region” with respect to a TCR refers to the portion of a TCR that is encoded by the TRAC gene (for TCR α chains) or either the TRBC1 or TRBC2 gene (for TCR β chains), optionally lacking all or a portion of a transmembrane region and/or all or a portion of a cytoplasmic region. In certain embodiments, a TCR constant region lacks a transmembrane region and a cytoplasmic region. A TCR constant region does not include amino acids encoded by a TRAV, TRAJ, TRBV, TRBD, TRBJ, TRDV, TRDD, TRDJ, TRGV, or TRGJ gene (*see, e.g.*, “T cell receptor FactsBook,” *supra*).

[00241] As used herein, the terms “major histocompatibility complex” and “MHC” are used interchangeably and refer to an MHC class I molecule and/or an MHC class II molecule.

[00242] As used herein, the term “MHC class I” refers to a dimer of an MHC class I α chain and a β 2 microglobulin chain and the term “MHC class II” refers to a dimer of an MHC class II α chain and an MHC class II β chain.

[00243] As used herein, the terms “human leukocyte antigen” and “HLA” are used interchangeably and can also refer to the proteins encoded by the MHC genes. HLA-A, HLA-B, HLA-C, HLA-E, HLA-F, and HLA-G refer to major and minor gene products of MHC class I genes. HLA-DP, HLA-DQ, and HLA-DR refer to gene products of MHC class II genes, which are expressed on antigen-presenting cells, B cells, and T cells.

[00244] As used herein, the term “peptide-MHC complex” refers to an MHC molecule (MHC class I or MHC class II) with a peptide bound in the art-recognized peptide binding pocket of the MHC. In some embodiments, the MHC molecule is a membrane-bound protein expressed on the cell surface. In some embodiments, the MHC molecule is a soluble protein lacking transmembrane or cytoplasmic regions.

[00245] As used herein, the term “extracellular” with respect to a recombinant transmembrane protein refers to the portion or portions of the recombinant transmembrane protein that are located outside of a cell.

[00246] As used herein, the term “transmembrane” with respect to a recombinant transmembrane protein refers to the portion or portions of the recombinant transmembrane protein that are embedded in the plasma membrane of a cell.

[00247] As used herein, the term “cytoplasmic” with respect to a recombinant transmembrane protein refers to the portion or portions of the recombinant transmembrane protein that are located in the cytoplasm of a cell.

[00248] As used herein, the term “co-stimulatory signaling region” refers to the intracellular portion of a co-stimulatory molecule that is responsible for mediating intracellular signaling events.

[00249] “Binding affinity” generally refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (*e.g.*, a TCR) and its binding partner (*e.g.*, a peptide-MHC complex). Unless indicated otherwise, as used herein, “binding affinity” refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (*e.g.*, a TCR and a peptide-MHC complex). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured and/or expressed in a number of ways known in the art, including, but not limited to, equilibrium dissociation constant (K_D) and equilibrium association constant (K_A). The K_D is calculated from the quotient of k_{off}/k_{on} , whereas K_A is calculated from the quotient of k_{on}/k_{off} . K_{on} refers to the association rate constant and k_{off} refers to the dissociation rate constant. The k_{on} and k_{off} can be determined by techniques known to one of ordinary skill in the art, such as use of BIAcore® or KinExA. As used herein, a “lower affinity” refers to a larger K_D .

[00250] “Avidity” generally refers to the affinity of binding molecule (*e.g.*, a TCR) and its binding partner (*e.g.*, a peptide-MHC complex). Binding molecules described herein are able to bind antigen via two (or more) sites in which the multiple interactions synergize to enhance the “apparent” affinity. Avidity is the measure of the strength of binding between the binding molecule described herein (*e.g.*, a TCR) and the pertinent antigens (*e.g.*, a peptide-MHC complex). Avidity is related to both the affinity between an antigenic determinant and its antigen binding site on the antigen-binding molecule and the number of pertinent binding sites present on the antigen-binding molecules.

[00251] For example, “specifically binds to” may be used to refer to the ability of a TCR to preferentially bind to a particular antigen (*e.g.*, a specific peptide or a specific peptide-MHC complex combination) as such binding is understood by one skilled in the art. For example, a TCR that specifically binds to an antigen can bind to other antigens, generally with lower affinity as determined by, *e.g.*, BIAcore®, or other immunoassays known in the art (*see, e.g., Savage et al., (1999) Immunity. 10(4):485-92, which is incorporated by reference herein in its entirety*). In a

specific embodiment, a TCR that specifically binds to an antigen binds to the antigen with an association constant (K_a) that is at least 2-fold, 5-fold, 10-fold, 50-fold, 100-fold, 500-fold, 1,000-fold, 5,000-fold, or 10,000-fold greater than the K_a when the TCR binds to another antigen.

[00252] As used herein, an “epitope” is a term in the art and refers to a localized region of an antigen (*e.g.*, a peptide or a peptide-MHC complex) to which a TCR can bind. In certain embodiments, the epitope to which a TCR binds can be determined by, *e.g.*, NMR spectroscopy, X-ray diffraction crystallography studies, ELISA assays, hydrogen/deuterium exchange coupled with mass spectrometry (*e.g.*, liquid chromatography electrospray mass spectrometry), flow cytometry analysis, mutagenesis mapping (*e.g.*, site-directed mutagenesis mapping), and/or structural modeling. For X-ray crystallography, crystallization may be accomplished using any of the known methods in the art (*e.g.*, Giegé R *et al.*, (1994) *Acta Crystallogr D Biol Crystallogr* 50(Pt 4): 339-350; McPherson A, (1990) *Eur J Biochem* 189: 1-23; Chayen NE, (1997) *Structure* 5: 1269-1274; McPherson A, (1976) *J Biol Chem* 251: 6300-6303, each of which is herein incorporated by reference in its entirety). TCR:antigen crystals may be studied using well-known X-ray diffraction techniques and may be refined using computer software such as X-PLOR (Yale University, 1992, distributed by Molecular Simulations, Inc.; *see, e.g.*, *Meth Enzymol* (1985) volumes 114 & 115, eds Wyckoff H. W., *et al.*; U.S. 2004/0014194); and BUSTER (Bricogne G, (1993) *Acta Crystallogr D Biol Crystallogr* 49(Pt 1): 37-60; Bricogne G, (1997) *Meth Enzymol* 276A: 361-423, ed Carter CW; and Roversi P *et al.*, (2000) *Acta Crystallogr D Biol Crystallogr* 56(Pt 10): 1316-1323), each of which is herein incorporated by reference in its entirety. Mutagenesis mapping studies may be accomplished using any method known to one of skill in the art. *See, e.g.*, Champe M *et al.*, (1995) *J Biol Chem* 270: 1388-1394 and Cunningham BC & Wells J A, (1989) *Science* 244: 1081-1085, each of which is herein incorporated by reference in its entirety, for a description of mutagenesis techniques, including alanine scanning mutagenesis techniques. In a specific embodiment, the epitope of an antigen is determined using alanine scanning mutagenesis studies. In a specific embodiment, the epitope of an antigen is determined using hydrogen/deuterium exchange coupled with mass spectrometry. In certain embodiments, the antigen is a peptide-MHC complex. In certain embodiments, the antigen is a peptide presented by an MHC molecule.

[00253] As used herein, the terms “treat,” “treating,” and “treatment” refer to therapeutic or preventative measures described herein. In some embodiments, the methods of “treatment” employ administration of a TCR or a cell expressing a TCR to a subject having a disease or disorder, or

predisposed to having such a disease or disorder, in order to prevent, cure, delay, reduce the severity of, or ameliorate one or more symptoms of the disease or disorder or recurring disease or disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

[00254] As used herein, the term “effective amount” in the context of the administration of a therapy to a subject refers to the amount of a therapy that achieves a desired prophylactic or therapeutic effect.

[00255] As used herein, the term “subject” includes any human or non-human animal. In one embodiment, the subject is a human or non-human mammal. In one embodiment, the subject is a human.

[00256] The determination of “percent identity” between two sequences (*e.g.*, amino acid sequences or nucleic acid sequences) can be accomplished using a mathematical algorithm. A specific, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin S & Altschul S F, (1990) *PNAS* 87: 2264-2268, modified as in Karlin S & Altschul SF, (1993) *PNAS* 90: 5873-5877, each of which is herein incorporated by reference in its entirety. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul SF *et al.*, (1990) *J Mol Biol* 215: 403, which is herein incorporated by reference in its entirety. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, *e.g.*, at score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecule described herein. BLAST protein searches can be performed with the XBLAST program parameters set, *e.g.*, at score=50, wordlength=3 to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul S F *et al.*, (1997) *Nuc Acids Res* 25: 3389-3402, which is herein incorporated by reference in its entirety. Alternatively, PSI BLAST can be used to perform an iterated search which detects distant relationships between molecules. *Id.* When utilizing BLAST, Gapped BLAST, and PSI BLAST programs, the default parameters of the respective programs (*e.g.*, of XBLAST and NBLAST) can be used (*see, e.g.*, National Center for Biotechnology Information (NCBI) on the worldwide web, ncbi.nlm.nih.gov). Another specific, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17, which is herein incorporated by reference in its entirety. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package.

When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

[00257] The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

[00258] As used herein, the terms “antibody” and “antibodies” include full-length antibodies, antigen-binding fragments of full-length antibodies, and molecules comprising antibody CDRs, VH regions, or VL regions. Examples of antibodies include monoclonal antibodies, recombinantly produced antibodies, monospecific antibodies, multi-specific antibodies (including bispecific antibodies), human antibodies, humanized antibodies, chimeric antibodies, immunoglobulins, synthetic antibodies, tetrameric antibodies comprising two heavy chain and two light chain molecules, an antibody light chain monomer, an antibody heavy chain monomer, an antibody light chain dimer, an antibody heavy chain dimer, an antibody light chain-antibody heavy chain pair, intrabodies, heteroconjugate antibodies, antibody-drug conjugates, single domain antibodies, monovalent antibodies, single chain antibodies or single-chain Fvs (scFv), camelized antibodies, affibodies, Fab fragments, F(ab')₂ fragments, disulfide-linked Fvs (sdFv), anti-idiotypic (anti-Id) antibodies (including, *e.g.*, anti-anti-Id antibodies), and antigen-binding fragments of any of the above. In certain embodiments, antibodies described herein refer to polyclonal antibody populations. Antibodies can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA, or IgY), any class (*e.g.*, IgG₁, IgG₂, IgG₃, IgG₄, IgA₁ or IgA₂), or any subclass (*e.g.*, IgG_{2a} or IgG_{2b}) of immunoglobulin molecule. In certain embodiments, antibodies described herein are IgG antibodies, or a class (*e.g.*, human IgG₁ or IgG₄) or subclass thereof. In a specific embodiment, the antibody is a humanized monoclonal antibody. In another specific embodiment, the antibody is a human monoclonal antibody.

[00259] As used herein, the term “cistron” refers to a polynucleotide sequence from which a transgene product can be produced.

[00260] As used herein, the term “polycistronic vector” refers to a polynucleotide vector that comprises a polycistronic expression cassette.

[00261] As used herein, the term “polycistronic expression cassette” refers to a polynucleotide sequence wherein the expression of three or more transgenes is regulated by common transcriptional regulatory elements (*e.g.*, a common promoter) and can simultaneously express three or more separate proteins from the same mRNA. Exemplary polycistronic vectors, without

limitation, include tricistronic vectors (containing three cistrons) and tetracistronic vectors (containing four cistrons).

[00262] As used herein, the term “polycistronic polynucleotide” refers to a polynucleotide that comprises three or more cistrons.

[00263] As used herein, the term “transcriptional regulatory element” refers to a polynucleotide sequence that mediates regulation of transcription of another polynucleotide sequence. Exemplary transcriptional regulatory elements include, but are not limited to, promoters and enhancers.

[00264] As used herein, a “furin recognition site” refers to an amino acid sequence, or a nucleotide sequence encoding the amino acid sequence, which can be cleaved by the furin enzyme. The furin enzyme is also known as PACE. In some embodiments, the furin recognition site comprises the amino acid sequence RXXR (SEQ ID NO: 1), wherein X at position 2 is any amino acid and X at position 3 is arginine or lysine. In some embodiments, the furin recognition site comprises the sequences shown below in Table 1.

[00265] **Table 1. Amino acid sequences of exemplary furin recognition sites and polynucleotide sequences encoding same.**

Description	Sequence	SEQ ID NO:
Furin recognition site	RAKR	2
Furin recognition site polynucleotide coding sequence	CGGGCGAAACGC	3
Furin recognition site (alternative)	RAKRSGSG	4
Furin recognition site (alternative) polynucleotide coding sequence	CGGGCGAAACGCTCTGGAAGCGGA	5

[00266] In some embodiments, the furin recognition site comprises an amino acid sequence that is identical to the amino acid sequence of SEQ ID NO: 2 or 4, or comprises 1, 2, or 3 amino acid modifications, relative to SEQ ID NO: 2 or 4; or is encoded by a polynucleotide sequence 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 3 or 5. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the furin recognition site is capable of mediating the cleavage (via furin) of the first protein from the second protein, resulting in two distinct polypeptides from the same mRNA molecule.

[00267] Responsive to recognition of the furin recognition site by the furin enzyme, the furin enzyme induces cleavage of a given polypeptide on the C-terminal side of the furin recognition site or a portion thereof. Accordingly, polypeptides produced by furin-mediated cleavage at a furin recognition site may retain all or a portion of the furin recognition site on their C-terminus. For example, the C-terminus of a first polypeptide of the present disclosure may comprise the amino acid sequence RAKR (SEQ ID NO: 2) or RA.

[00268] As used herein, a “2A element” refers to a polynucleotide sequence which, when expressed in an mRNA, can induce ribosomal skipping during translation of the mRNA in a cell. Thus, two separate polypeptides may be produced from a single mRNA molecule. An amino acid sequence encoded by a 2A element is referred to as a “self-cleaving peptide.” 2A elements may be viral in origin. Exemplary 2A elements include T2A elements, P2A elements, E2A elements, and F2A elements.

[00269] As used herein, the term “P2A element” refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 19, or 21; (ii) encodes the amino acid sequence of SEQ ID NO: 18, or 20; or (iii) encodes the amino acid sequence of SEQ ID NO: 18, or 20, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the P2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the P2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the P2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the P2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the P2A element can be termed an “fP2A element.” In some embodiments, a fP2A element refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 11; (ii) encodes the amino acid sequence of SEQ ID NO: 10; or (iii) encodes the amino acid sequence of SEQ ID NO: 10, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the P2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 20 and 21).

[00270] As used herein, the term “T2A element” refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 23, or 25; (ii) encodes the amino acid sequence of SEQ ID NO: 22, or 24; or (iii) encodes the amino acid sequence of SEQ ID NO: 22, or 24, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the T2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide

bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the T2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the T2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the T2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the T2A element can be termed an "fT2A element." In some embodiments, an fT2A element refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 13; (ii) encodes the amino acid sequence of SEQ ID NO: 12; or (iii) encodes the amino acid sequence of SEQ ID NO: 12, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the T2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 24 and 25).

[00271] As used herein, the term "F2A element" refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 27, or 29; (ii) encodes the amino acid sequence of SEQ ID NO: 26, or 28; or (iii) encodes the amino acid sequence of SEQ ID NO: 26, or 28, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the F2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the F2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the F2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the F2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the F2A element can be termed an "fF2A element." In some embodiments, a fF2A element refers to a polynucleotide that (i) comprises a polynucleotide

sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 15; (ii) encodes the amino acid sequence of SEQ ID NO: 14; or (iii) encodes the amino acid sequence of SEQ ID NO: 14, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the F2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 28 and 29).

[00272] As used herein, the term “E2A element” refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 31, or 33; (ii) encodes the amino acid sequence of SEQ ID NO: 30, or 32; or (iii) encodes the amino acid sequence of SEQ ID NO: 30, or 32, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the E2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the E2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the E2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the E2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the E2A element can be termed an “fE2A element.” In some embodiments, a fE2A element refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 17; (ii) encodes the amino acid sequence of SEQ ID NO: 16; or (iii) encodes the amino acid sequence of SEQ ID NO: 16, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the E2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 32 and 33).

[00273] Examples of 2A elements comprising furin recognition sites at their N-terminal/5' ends are found below in Table 2. The 2A sites themselves are broken out in Table 3.

Table 2. Polynucleotide sequences of exemplary furin-2A elements and amino acid sequences of translations thereof.

Description	Sequence	SEQ ID NO:
Translation of Furin-P2A element	RAKRSGSGATNFSLLKQAGDVEENPGP	10
Furin-P2A element	CGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGC TGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCCA	11
Translation of Furin-T2A element	RAKRSGSGEGRGSLTTCGDVEENPGP	12
Furin-T2A element	CGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTC TAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	13
Translation of Furin-F2A element	RAKRSGSGVKQTLNFDLLKLAGDVESNPGP	14
Furin-F2A element	CGGGCGAAACGCTCTGGAAGCGGAGTGAAGCAGACCCTGAATT TCGACCTGCTGAAGCTGGCCGGGGACGTGGAGAGCAACCCTGG CCCC	15
Translation of Furin-E2A element	RAKRSGSGQCTNYALLKLAGDVESNPGP	16
Furin-E2A element	CGGGCGAAACGCTCTGGAAGCGGACAGTGTACTAATTATGCTC TCTTGAAATTGGCTGGAGATGTTGAGAGCAACCCAGGTCCC	17

Table 3. Amino acid and polynucleotide sequences of exemplary 2A elements.

Description	Amino Acid Sequence	SEQ ID NO:
P2A (exemplary amino acid sequence)	ATNFSLLKQAGDVEENPGP	18
P2A (exemplary nucleotide sequence)	GCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGATGTGGAGG AGAACCCTGGCCCCA	19
P2A (with flanking residues) (exemplary amino acid sequence)	GSGATNFSLLKQAGDVEENPGP	20
P2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCG ATGTGGAGGAGAACCCTGGCCCCA	21
T2A (exemplary amino acid sequence)	EGRGSLTTCGDVEENPGP	22
T2A (exemplary nucleotide sequence)	GAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGA ATCCCGGCCCT	23
T2A (with flanking residues) (exemplary amino acid sequence)	GSGEGRGSLTTCGDVEENPGP	24
T2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACG TGGAGGAGAATCCCGGCCCT	25
F2A (exemplary amino acid sequence)	VKQTLNFDLLKLAGDVESNPGP	26
F2A (exemplary nucleotide sequence)	GTGAAGCAGACCCTGAATTTTCGACCTGCTGAAGCTGGCCGGGG ACGTGGAGAGCAACCCTGGCCCC	27
F2A (with flanking residues) (exemplary amino acid sequence)	GSGVKQTLNFDLLKLAGDVESNPGP	28
F2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGAGTGAAGCAGACCCTGAATTTTCGACCTGCTGAAGC TGGCCGGGGACGTGGAGAGCAACCCTGGCCCC	29
E2A (exemplary amino acid sequence)	QCTNYALLKLAGDVESNPGP	30
E2A (exemplary nucleotide sequence)	CAGTGTACTAATTATGCTCTCTTGAAATTGGCTGGAGATGTTG AGAGCAACCCAGGTCCC	31
E2A (with flanking residues) (exemplary amino acid sequence)	GSGQCTNYALLKLAGDVESNPGP	32

Description	Amino Acid Sequence	SEQ ID NO:
E2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGACAGTGTACTAATTATGCTCTCTTGAAATTGGCTG GAGATGTTGAGAGCAACCCAGGTCCC	33

[00274] As used herein, the terms “inverted terminal repeat,” “ITR,” “inverted repeat/direct repeat,” and “IR/DR” are used interchangeably and refer to a polynucleotide sequence, *e.g.*, of about 230 nucleotides (*e.g.*, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, or 240 nucleotides), flanking (*e.g.*, with or without an intervening polynucleotide sequence) one end of an expression cassette (*e.g.*, a polycistronic expression cassette) that can be cleaved by a transposase polypeptide when used in combination with a corresponding, *e.g.*, reverse-complementary (*e.g.*, perfectly or imperfectly reverse-complementary) polynucleotide sequence, *e.g.*, of about 230 nucleotides (*e.g.*, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, or 240 nucleotides), flanking (*e.g.*, with or without an intervening polynucleotide sequence) the opposite end of the expression cassette (*e.g.*, a polycistronic expression cassette) (*e.g.*, as described in Cui *et al.*, *J. Mol. Biol.* 2002;318(5):1221-35, the contents of which are incorporated by reference in their entirety herein). In some embodiments, an ITR, *e.g.*, an ITR of a DNA transposon (*e.g.*, a *Sleeping Beauty* transposon, a piggyBac transposon, a TcBuster transposon, and a Tol2 transposon) contains two direct repeats (“DRs”), *e.g.*, imperfect direct repeats, *e.g.*, of about 30 nucleotides (*e.g.*, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleotides), located at each end of the ITR. The terms “ITR” and “DR,” when used in reference to a single- or double-stranded DNA vector, refer to the DNA sequence of the sense strand. A transposase polypeptide may recognize the sense strand and/or the antisense strand of DNA.

[00275] As used herein, the term “Left ITR,” when used in reference to a linear single- or double-stranded DNA vector, refers to the ITR positioned 5’ of the polycistronic expression cassette. As used herein, the term “Right ITR,” when used in reference to a linear single- or double-stranded DNA vector, refers to the ITR positioned 3’ of the polycistronic expression cassette. When a circular vector is used, the Left ITR is closer than the Right ITR to the 5’ end of the polycistronic expression cassette, and the Right ITR is closer than the Left ITR to the 3’ end of the polycistronic expression cassette.

[00276] As used herein, the term “operably linked” refers to a linkage of polynucleotide sequence elements or amino acid sequence elements in a functional relationship. For example, a

polynucleotide sequence is operably linked when it is placed into a functional relationship with another polynucleotide sequence. In some embodiments, a transcription regulatory polynucleotide sequence *e.g.*, a promoter, enhancer, or other expression control element is operably linked to a polynucleotide sequence that encodes a protein if it affects the transcription of the polynucleotide sequence that encodes the protein.

[00277] The term “polynucleotide” as used herein refers to a polymer of DNA or RNA. The polynucleotide sequence can be single-stranded or double-stranded; contain natural, non-natural, or altered nucleotides; and contain a natural, non-natural, or altered internucleotide linkage, such as a phosphoroamidate linkage or a phosphorothioate linkage, instead of the phosphodiester found between the nucleotides of an unmodified polynucleotide sequence. Polynucleotide sequences include, but are not limited to, all polynucleotide sequences which are obtained by any means available in the art, including, without limitation, recombinant means, *e.g.*, the cloning of polynucleotide sequences from a recombinant library or a cell genome, using ordinary cloning technology and polymerase chain reaction, and the like, and by synthetic means.

[00278] The terms “protein” and “polypeptide” are used interchangeably herein and refer to a polymer of amino acids connected by one or more peptide bonds. As used herein, “amino acid sequence” refers to the information describing the relative order and identity of amino acid residues which make up a polypeptide.

[00279] The term “functional variant” as used herein in reference to a protein or polypeptide refers to a protein that comprises at least one amino acid modification (*e.g.*, a substitution, deletion, addition) compared to the amino acid sequence of a reference protein, that retains at least one particular function. In some embodiments, the reference protein is a wild type protein. For example, a functional variant of an IL-15 protein can refer to an IL-15 protein comprising an amino acid substitution compared to a wild type IL-15 protein that retains the ability to bind the IL-15 receptor α chain (IL-15R α). Not all functions of the reference wild type protein need be retained by the functional variant of the protein. In some instances, one or more functions are selectively reduced or eliminated.

[00280] The term “functional fragment” as used herein in reference to a protein or polypeptide refers to a fragment of a reference protein that retains at least one particular function. For example, a functional fragment of an IL-15 protein can refer to a fragment of the protein that retains the ability to specifically bind IL-15R α . Not all functions of the reference protein need be retained by a functional fragment of the protein. In some instances, one or more functions are selectively

reduced or eliminated.

[00281] As used herein, the term “modification,” with reference to a polynucleotide sequence, refers to a polynucleotide sequence that comprises at least one substitution, alteration, inversion, addition, or deletion of nucleotide compared to a reference polynucleotide sequence. As used herein, the term “modification,” with reference to an amino acid sequence, refers to an amino acid sequence that comprises at least one substitution, alteration, inversion, addition, or deletion of an amino acid residue compared to a reference amino acid sequence.

[00282] As used herein, the term “derived from,” with reference to a polynucleotide sequence, refers to a polynucleotide sequence that has at least 85% sequence identity to a reference naturally occurring nucleic acid sequence from which it is derived. The term “derived from,” with reference to an amino acid sequence, refers to an amino acid sequence that has at least 85% sequence identity to a reference naturally occurring amino acid sequence from which it is derived. The term “derived from” as used herein does not denote any specific process or method for obtaining the polynucleotide or amino acid sequence. For example, the polynucleotide or amino acid sequence can be chemically synthesized.

[00283] As used herein, the term “linked to” refers to covalent or noncovalent binding between two molecules or moieties. The skilled worker will appreciate that when a first molecule or moiety is linked to a second molecule or moiety, the linkage need not be direct, but instead, can be via an intervening molecule or moiety.

[00284] As used herein, the term “cytokine” refers to a molecule that mediates and/or regulates a biological or cellular function or process (*e.g.*, immunity, inflammation, and hematopoiesis). As used herein, cytokines include, but are not limited to, lymphokines, chemokines, monokines, and interleukins. The term cytokine as used herein also encompasses functional variants and functional variants of wild type cytokines.

[00285] As used herein, the term “marker protein” or “marker polypeptide” are used interchangeably and refer to a protein or polypeptide that can be expressed on the surface of a cell, which can be utilized to mark or deplete cells expressing the marker protein or polypeptide. In some embodiments, depletion of cells expressing the marker protein or polypeptide is performed through the administration of a molecule that specifically binds the marker protein or polypeptide (*e.g.*, an antibody that mediates antibody dependent cellular cytotoxicity).

[00286] As used herein, the term “immune effector cell” refers to a cell that is involved in the promotion of an immune effector function. Examples of immune effector cells include, but are not

limited to, T cells (*e.g.*, alpha/beta T cells and gamma/delta T cells, CD4⁺ T cells, CD8⁺ T cells, natural killer T (NKT) cells), natural killer (NK) cells, B cells, mast cells, and myeloid-derived phagocytes.

[00287] As used herein, the term, “immune stem cell” refers to a cell that is pluripotent and can differentiate into one or more types of immune cells, including immune effector cells. Immune stem cells include, but are not limited to, bone marrow stem cells, hematopoietic stem cells, embryonic stem cells, induced pluripotent stem cells, umbilical blood stem cells, lymphocyte progenitor cells, stem cell memory T cells, and stem cell memory-like T cells. In certain embodiments, the immune stem cell is isolated and/or enriched from adult and fetal bone marrow, umbilical cord blood, or peripheral blood.

[00288] As used herein, the term “immune effector function” refers to a specialized function of an immune effector cell. The effector function of any given immune effector cell can be different. For example, an effector function of a CD8⁺ T cell is cytolytic activity, and an effector function of a CD4⁺ T cell is secretion of a cytokine.

5.2 T cell Receptors

[00289] In one aspect, the instant disclosure provides TCRs that can be expressed via a polycistronic expression cassette of the present disclosure. In certain embodiments, the TCR comprises a T cell receptor (TCR) alpha chain comprising an alpha chain variable (V α) region and an alpha chain constant (C α) region and a TCR beta chain comprising a beta chain variable (V β) region and a beta chain constant (C β). The amino acid sequences of constant domains comprised in the TCRs disclosed herein are shown in Tables 4 and 5 below.

Table 4. Amino acid sequences of TCR C α regions.

Description	Sequence	SEQ ID NO:
C α (murine, degenerate)	XIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSFTQCQDIFKETNATYPSSDVPDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	40

Description	Sequence	SEQ ID NO:
C α (murine, degenerate) (exemplary nucleotide sequence)	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTC AGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCC TAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACAT CTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTC TGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATG AACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTGCTGCTGA AGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCC NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	57
C α (murine, cysteine- and LIV-substituted)	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVIVLRILLLKLVAGFNLLMTLRLWSS	41
C α (murine, cysteine- and LIV-substituted) (exemplary nucleotide sequence)	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTC AGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCC TAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACAT CTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTC TGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATG AACCTGAATTTTCAGAATCTGCTGGTCACTCGTGCTGAGAATCCTGCTGCTGA AGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCC	55
C α (murine, LIV substituted)	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVIVLRILLLKLVAGFNLLMTLRLWSS	42
C α (murine, LIV substituted) (exemplary nucleotide sequence)	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTC AGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCC TAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACAT CTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTC TGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATG AACCTGAATTTTCAGAATCTGCTGGTCACTCGTGCTGAGAATCCTGCTGCTGA AGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCC	58
C α (murine, cysteine-substituted)	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVSVMLRILLLKLVAGFNLLMTLRLWSS	43
C α (murine, wild type)	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVSVMLRILLLKLVAGFNLLMTLRLWSS	44
C α (human, degenerate)	XIQNPDPVAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKXVLDM RSMDFKSNSAVAWSNKSDFACANAFNNSIIPEDTFFPSPSSCDVKLVEKSF ETDTNLNFQNLXVXXFRILLLKLVAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr X at position 48 is Thr or Cys; X at position 116 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 118 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 119 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	45

Description	Sequence	SEQ ID NO:
C α (human, cysteine- and LIV-substituted; degenerate at position 1)	XIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKCVLDM RSMDFKSNsAVAWsNKsDFACANAFNNSII PEDTFFPSPESsCDVKLVEKsF ETDTNLNFQNLlVIVFRILLlKVAGFNlLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	46
C α (human, LIV-substituted; degenerate at position 1)	XIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDM RSMDFKSNsAVAWsNKsDFACANAFNNSII PEDTFFPSPESsCDVKLVEKsF ETDTNLNFQNLlVIVFRILLlKVAGFNlLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	47
C α (human, cysteine-substituted; degenerate at position 1)	XIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKCVLDM RSMDFKSNsAVAWsNKsDFACANAFNNSII PEDTFFPSPESsCDVKLVEKsF ETDTNLNFQNLsVIGFRILLlKVAGFNlLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	48
C α (human, wild type; degenerate at position 1)	XIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDM RSMDFKSNsAVAWsNKsDFACANAFNNSII PEDTFFPSPESsCDVKLVEKsF ETDTNLNFQNLsVIGFRILLlKVAGFNlLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	49

Table 5. Amino acid sequences of TCR C β regions.

Description	Sequence	SEQ ID NO:
C β (murine, degenerate)	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHLSEEDK WPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNS X at position 57 is Ser or Cys	50
C β (murine, degenerate) (exemplary nucleotide sequence)	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTCGAGCCATCCA AGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGG CTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTG CACTCTGGCGTGNNAACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCG GAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAA TGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGT GGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTTATCAGCAGGGCGTGCT GTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCG GTGCTGGTGTCCACCCTGGTGGT CATGGCGATGGTGAAGAGGAAAACTCT NNN at positions 169-171 make up a codon that encodes Ser or Cys	59
C β (murine, cysteine-substituted)	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHLSEEDK WPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNS	51
C β (murine, cysteine-substituted) (exemplary nucleotide sequence)	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTCGAGCCATCCA AGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGG CTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTG CACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCG GAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAA TGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGT GGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTTATCAGCAGGGCGTGCT GTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCG GTGCTGGTGTCCACCCTGGTGGT CATGGCGATGGTGAAGAGGAAAACTCT	56
C β (murine, wild type)	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHLSEEDK WPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNS	52
C β (human, degenerate)	EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWVWNGKEV HSGVXTDPQPLKEQPALNDSRYCLSSRLRV SATFWQNPRNHFRQVQFYGLS ENDEWTQDRAKPV TQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKA TLYAVLVSAVLVLMAMVKRKDSRG X at position 57 is Ser or Cys	53
C β (human, cysteine-substituted)	EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWVWNGKEV HSGVCTDPQPI.KFQPAI.NDSRYCT.SSRT.RVSATFWQNPRNHFRQVQFYGT.S ENDEWTQDRAKPV TQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKA TLYAVLVSAVLVLMAMVKRKDSRG	54
C β (human, wild type)	EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWVWNGKEV HSGVSTDPQPLKEQPALNDSRYCLSSRLRV SATFWQNPRNHFRQVQFYGLS ENDEWTQDRAKPV TQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKA TLYAVLVSAVLVLMAMVKRKDSRG	60

[00290] As used herein, “LIV-substituted” refers to a C α sequence disclosed herein which, relative to SEQ ID NO: 40, comprises a leucine residue at position 112, an isoleucine residue at

position 114, and a valine residue at position 115. See, for example, SEQ ID Nos: 41 and 42. In some embodiments, and independent of the LIV-substitutions a C α sequence disclosed herein can comprise a cysteine at position 48, replacing the threonine residue. (Compare SEQ ID Nos: 40-44). In some embodiments, the C β sequence disclosed herein has a substitution of the serine at residue 57 with cysteine. This is shown in SEQ ID Nos: 50 and 51.

[00291] Tumor Protein p53 (also referred to as “p53”) acts as a tumor suppressor by, for example, regulating cell division. In some embodiments, wild type full-length p53 has the amino acid sequence of SEQ ID NO: 340, shown below.

```
MEEPQSDPSVEPPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPCP
DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK
SVTCTYSPALNKMFCQLAKTCFVQLWVDSTPPPGTRVRAMAIYKQSQHMTDEVVRRCPHHE
RCSDSDGLAPPQHILIRVEGNLRVEYLLDDRNTFRHSVVVPYEPPEVGSDDCTTIHNYMCNS
SCMGGMNRRPILTIITLEDSSGNLLGRNSFEVVRVCACPGDRDRTEENLRKKGEPHHELP
PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG
GSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD (SEQ ID NO: 340)
```

[00292] Kirsten rat sarcoma viral oncogene homolog (KRAS), also referred to as GTPase Kras, V-Ki-Ras2 Kirsten rat sarcoma viral oncogene, or KRAS2, is a member of the small GTPase superfamily. There are two transcript variants of KRAS: KRAS variant A and KRAS variant B. Hereinafter, references to “KRAS” (mutated or unmutated) refer to both variant A and variant B, unless specified otherwise. In some embodiments, wild type KRAS variant A has the amino acid sequence of SEQ ID NO: 341 and wild type KRAS variant B has the amino acid sequence of SEQ ID NO: 342, both shown below.

```
MTEYKLVVVVGAGGVGKSALTIQLIQNHVFDEYDPTIEDSYRKQVVIDGETCLLDI LD TAG
QEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDS EDVPMVLVGNKCDL
PSRTVDTKQAQDLARSYGIPFIETSAKTRQVEDAFYTLVREIRQYRLKKISKEEKT PGC
VKIKKCIIM (SEQ ID NO: 341)
```

```
MTEYKLVVVVGAGGVGKSALTIQLIQNHVFDEYDPTIEDSYRKQVVIDGETCLLDI LD TAG
QEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDS EDVPMVLVGNKCDL
PSRTVDTKQAQDLARSYGIPFIETSAKTRQGVDDAFYTLVREIRKHKEKMSKDGK KKKKKK
SKTKCVIM (SEQ ID NO: 342)
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[00293] EGFR (also referred to as ERBB1 or HER1) is a transmembrane glycoprotein that belongs to the receptor tyrosine kinase (RTK) super-family of cell surface receptors, which mediate cell signaling by extra-cellular growth factors. Examples of wild type (WT), unmutated human EGFR amino acid sequences include those disclosed in GenBank Accession Nos. NP_001333826.1 (isoform e precursor), NP_001333827.1 (isoform f precursor), NP_001333828.1 (isoform g precursor), NP_001333829.1 (isoform h precursor), NP_001333870.1 (isoform i precursor), NP_005219.2 (isoform a precursor), NP_958439.1 (isoform b precursor), NP_958440.1 (isoform c

precursor), and NP_958441.1 (isoform d precursor). In some embodiments, wild type EGFR has the amino acid sequence of SEQ ID NO: 343

MRPSGTAGAALLALLAALCPASRALEEKVKCQGTSNKLTQLGTFEDHFLSLQRMFNCEV
VLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLLENLQIIRGNMYEENS YALA
VLSNYDANKTGLKELPMRNLQEI LHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDF
QNHLSGCQKCDPSCPNWSCWGAGEENCQKLTII CAQQCSGRCRGKSPSDCCHNQCAAGC
TGPRESCLVCRKFRDEATCKDTCPPMLLYNPTTYQMDVNPGEKYSFGATCVKKCPRNYV
VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLSINATNIKHFK
NCTSI SGLDHLILPVAFRGDSFTHTPPLDPQELDLKTVKEITGFLLIQAWPENRTDLHAF
ENLEIIRGRTKQHGCQFSLAVVSLNITSLGLRSLKEISDGDVVISGNKNLCYANTINWKKL
FGTSGQKTKIISNRGENSCATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCN
LLEGEPPREFVENSECICQHCPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVM
GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVV
ALGIGLFMRRRRHIVRKRTLRRLLQERELVEPLTTPSGEAPNQALLRILKETEFKKIKVLGS
GAFGTVYKGLWIPPEGEKVKI PVAIKELREATSPKANKKEILDEAYVMASVDNPHVCRLGI
CLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAA
RNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVP I KWMALLESILHRIYTHQSDVWSY
GVTVWELMTFGSKPYDGI PASEISSILEKGERLPQPP ICTIDVYIMVMKWMIDADSRPK
FRELIIEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDDDVDADEYLI PQ
QGFFSSPSTSRTPLLSSLSATSNNSTVACIDRNGLOSCPIKEDSFLQRYSSDPTGALTED
SIDDTFLPVPEYINQSVKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLN
TVQPTCVNSTFDS PAHWAQKGS HQISLDNPDYQQDFFPKAKENGIFKGSTAENAEYLRV
APQSSEFIGA (SEQ ID NO: 343)

[00294] The amino acid sequences of exemplary TCRs are set forth in Table 6 herein.

Table 6A. Amino acid sequences of TCR001.

Description	Sequence	SEQ ID NO:
CDR1 α	NYSPAY	1001
CDR2 α	IRENEKE	1002
CDR3 α	ALDIYPHDMR	1003
V α without signal peptide (SignalP)	QKIEQNSEALNIQEGKTATLTTCNYTNYSPAYLQWYRQDPGRGPVFLLLIREN EKEKRKERLKVTFDITLKQSLFHITASQPADSATYLCALDIYPHDMRFGAGT RLTVKP	1004
V α without signal peptide (IMGT)	SQKIEQNSEALNIQEGKTATLTTCNYTNYSPAYLQWYRQDPGRGPVFLLLIRE NEKEKRKERLKVTFDITLKQSLFHITASQPADSATYLCALDIYPHDMRFGAG TRLTVKP	1005
V α	MXSFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTTCNYTNYSPAY LQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDITLKQSLFHITASQPAD SATYLCALDIYPHDMRFGAGTRLTVKP (X = any amino acid)	1006 1007
α chain with WT signal peptide, (substituted) C α	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTTCNYTNYSPAY LQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDITLKQSLFHITASQPAD SATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPQSQDSTLCFL TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRIILLKVAGFNLL MTLRLWSS	1008
α chain with alternative signal peptide, (substituted) C α	MASFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTTCNYTNYSPAY LQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDITLKQSLFHITASQPAD SATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPQSQDSTLCFL TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRIILLKVAGFNLL MTLRLWSS	1009

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAY LQWYRQDPGRGPVFLLLIRENEKEKRERLKVTFD'TTLKQSLFHITASQPAD SATYLCALDIYPHDMRFAGATRLTVKPNIQNPEPAVYQLKDPRSQDSTLCFLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIF KETNATYPSSDVPDCATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1010
CDR1 β	SGHAT	2001
CDR2 β	FQNGV	2002
CDR3 β	ASSLDPGDTGELF	2003
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFF GEGSRLTVL	2004
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGEL FFGEGSRLTVL	2005
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLDPGDTGELFFGEGSRLTVL (X = any amino acid)	2006
		2007
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2008
β chain with alternative signal peptide, (substituted) C β	MATRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2009
β chain with alternative signal peptide, (substituted) C β	MHTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2010

[00295] In some embodiments, TCR001 interacts with and/or is specific for a peptide from the tumor protein p53 (p53). In some embodiments, the peptide is from a neoantigen of p53 and has the amino acid change R175H (in which position 175 of the p53 protein is mutated from Arg to His). In some embodiments, TCR001 interacts with and/or is specific for the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6B. Amino acid sequences of TCR002.

Description	Sequence	SEQ ID NO:
CDR1 α	DSASNY	1011
CDR2 α	IRSNVGE	1012
CDR3 α	AASKSAIMVVLQTSSSL	1013
V α without signal peptide (SignalP)	ENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQV	1014
V α without signal peptide (IMGT)	GENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQV	1015
V α	MXSIRAVFIFLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQV (X = any amino acid)	1016
		1017
α chain with WT signal peptide, (substituted) C α	MTSIRAVFIFLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQVNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1018
α chain alternative peptide, (substituted) with signal C α	MASIRAVFIFLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQVNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1019
α chain alternative peptide, (substituted) with signal C α	MHSIRAVFIFLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQVNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1020
CDR1 β	MNHEY	2011
CDR2 β	SMNVEV	2012
CDR3 β	ASSIQQGADTQY	2013
V β without signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL	2014
V β without signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNV E VTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL	2015
V β	MXPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL (X = any amino acid)	2016
		2017
β chain with WT signal peptide, (substituted) C β	MGPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL E DLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2018

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAPQLLGYYVVLCLLGAGPLEAQTQNPRLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQ TSLYFCASSIQQGADTQYFGPGTRRLTVLEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2019
β chain with alternative signal peptide, C β (substituted)	MHPQLLGYYVVLCLLGAGPLEAQTQNPRLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQ TSLYFCASSIQQGADTQYFGPGTRRLTVLEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2020

[00296] In some embodiments, TCR002 interacts with and/or is specific for a peptide from p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR002 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6C. Amino acid sequences of TCR003.

Description	Sequence	SEQ ID NO:
CDR1 α	NSAFQY	1021
CDR2 α	TYSSGN	1022
CDR3 α	AMSGLKEDSSYKLI	1023
V α w/o signal peptide (SignalP)	QQKEVEQDPGPLSVPEGAIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTY SSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMSGLKEDSSYKLI FGSGTRLLVRP	1024
V α w/o signal peptide (IMGT)	QKEVEQDPGPLSVPEGAIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMSGLKEDSSYKLI F GSGTRLLVRP	1025
V α	MXKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMSGLKEDSSYKLIFGSGTRLLVRP (X = any amino acid)	1026
		1027
α chain w/WT signal peptide, C α (substituted)	MMKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMSGLKEDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLLVIVLRILLKVA GFNLLMTLRLWSS	1028
α chain w/alternative signal peptide, C α (substituted)	MAKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMSGLKEDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLLVIVLRILLKVA GFNLLMTLRLWSS	1029

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMSGLKEDSSYKLIFGSGTRLLVLRPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTQQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVLVLRILLKVA GENLLMTLRLWSS	1030
CDR1 β	MNHEY	2021
CDR2 β	SMNVEV	2022
CDR3 β	ASSIQQGADTQY	2023
V β w/o signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL	2024
V β w/o signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNV E VTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL	2025
V β	MXPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL (X = any amino acid)	2026
		2027
β chain w/WT signal peptide, C β (substituted)	MGPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2028
β chain w/alternative signal peptide, C β (substituted)	MAPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2029
β chain w/alternative signal peptide, C β (substituted)	MHPQLLGYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2030

[00297] In some embodiments, TCR003 interacts with and/or is specific for a peptide from p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR003 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6D. Amino acid sequences of TCR004.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASQS	1031

Description	Sequence	SEQ ID NO:
CDR2 α	VYSSGN	1032
CDR3 α	VVQPGGYQKVT	1033
V α w/o signal peptide (SignalP)	QRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIP	1034
V α w/o signal peptide (IMGT)	RKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIP	1035
V α	MXSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIP (X = any amino acid)	1036
		1037
α chain w/WT signal peptide, C α (substituted)	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIPNIQNPEPAVYQLKDPQRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRIILLKVAGFNLLMTLRLWSS	1038
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIPNIQNPEPAVYQLKDPQRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRIILLKVAGFNLLMTLRLWSS	1039
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIPNIQNPEPAVYQLKDPQRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRIILLKVAGFNLLMTLRLWSS	1040
CDR1 β	MNHNS	2031
CDR2 β	SASEGT	2032
CDR3 β	ASSEGLWQVGDEQY	2033
V β w/o signal peptide (SignalP)	GVTQTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYASASEGTTDKGEVPNGYNVSRNLNKRFSRLRESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVT	2034
V β w/o signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYASASEGTTDKGEVPNGYNVSRNLNKRFSRLRESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVT	2035
V β	MXIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYASASEGTTDKGEVPNGYNVSRNLNKRFSRLRESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVT (X = any amino acid)	2036
		2037
β chain w/WT signal peptide, C β (substituted)	MSIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYASASEGTTDKGEVPNGYNVSRNLNKRFSRLRESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVTETDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2038

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRLNKREFSLRLESAAPSQ TSVYFCASSEGLWQVGDEQYFGPGTRRLTVTEDLRNVTTPPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2039
β chain w/alternative signal peptide, C β (substituted)	MHIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRLNKREFSLRLESAAPSQ TSVYFCASSEGLWQVGDEQYFGPGTRRLTVTEDLRNVTTPPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2040

[00298] In some embodiments, TCR004 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR004 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6E. Amino acid sequences of TCR005.

Description	Sequence	SEQ ID NO:
CDR1 α	TSENNYY	1041
CDR2 α	QEAYKQQN	1042
CDR3 α	AFMGYSGAGSYQLT	1043
V α w/o signal peptide (SignalP)	QTVTQSQPEMSVQEAETVTLSCITYDTSENNYYLFWYKQPPSRQMILVIRQEA YKQQNATENRFSVNFQKAAKSFSLKISDSQLGDTAMYFCAFMGYSGAGSYQL TFGKGTKLSVIP	1044
V α w/o signal peptide (IMGT)	AQTVTQSQPEMSVQEAETVTLSCITYDTSENNYYLFWYKQPPSRQMILVIRQE AYKQQNATENRFSVNFQKAAKSFSLKISDSQLGDTAMYFCAFMGYSGAGSYQ LTFGKGTKLSVIP	1045
V α	MXRVSLWAVVVSTCLESGMAQTVTQSQPEMSVQEAETVTLSCITYDTSENNY YLFYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAAKSFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTTFGKGTKLSVIP (X = any amino acid)	1046
		1047
α chain w/WT signal peptide, C α (substituted)	MTRVSLWAVVVSTCLESGMAQTVTQSQPEMSVQEAETVTLSCITYDTSENNY YLFYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAAKSFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTTFGKGTKLSVIPNIONPEPAVYQLKDPRSQD STLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTF TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRIILLKV AGFNLLMTLRLWSS	1048
α chain w/alternative signal peptide, C α (substituted)	MARVSLWAVVVSTCLESGMAQTVTQSQPEMSVQEAETVTLSCITYDTSENNY YLFYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAAKSFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTTFGKGTKLSVIPNIONPEPAVYQLKDPRSQD STLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTF TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRIILLKV AGFNLLMTLRLWSS	1049

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHRVSLWAVVSTCLESMAQTVTQSQPEMSVQEAETVTLSCITYDTSENNY YLEWYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAAKSFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQD STLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMD SKSNGAIAWSNQTSF TCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKV AGENLLMTLRLWSS	1050
CDR1 β	ENHRY	2041
CDR2 β	SYGVKD	2042
CDR3 β	AISELVTGDSPLH	2043
V β w/o signal peptide (SignalP)	GITQSPRHKVTETGTPVTLRCHQTENHRYMYWYRQDPGHGLRLIHYSYGVKD TDKGEVSDGYSVSRSKTEDFLLTLESATSSQTSVYFCAISELVTGDSPLHFG NGTRLTVT	2044
V β w/o signal peptide (IMGT)	DAGITQSPRHKVTETGTPVTLRCHQTENHRYMYWYRQDPGHGLRLIHYSYGV KDTDKGEVSDGYSVSRSKTEDFLLTLESATSSQTSVYFCAISELVTGDSPLH FNGTRLTVT	2045
V β	MXTRLFFYVALCLLWTHMDAGITQSPRHKVTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRSKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVT (X = any amino acid)	2046
		2047
β chain w/WT signal peptide, C β (substituted)	MGTRLFFYVALCLLWTHMDAGITQSPRHKVTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRSKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVTEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2048
β chain w/alternative signal peptide, C β (substituted)	MATRLFFYVALCLLWTHMDAGITQSPRHKVTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRSKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVTEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2049
β chain w/alternative signal peptide, C β (substituted)	MHTRLFFYVALCLLWTHMDAGITQSPRHKVTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRSKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVTEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2050

[00299] In some embodiments, TCR005 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR005 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6F. Amino acid sequences of TCR006.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1051

Description	Sequence	SEQ ID NO:
CDR2 α	GLKNN	1052
CDR3 α	IVRGSPGAGGTSYGKLT	1053
V α w/o signal peptide (SignalP)	KTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNN ETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRGSPGAGGTSYGKLTFF GQGTILTVHP	1054
V α w/o signal peptide (IMGT)	DAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLK NNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRGSPGAGGTSYGKL TFGQGTILTVHP	1055
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFFGQGTILTVHP (X = any amino acid)	1056
		1057
α chain w/WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFFGQGTILTVHPNIIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1058
α chain w/alternative signal peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFFGQGTILTVHPNIIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1059
α chain w/alternative signal peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFFGQGTILTVHPNIIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1060
CDR1 β	LNHDA	2051
CDR2 β	SQIVND	2052
CDR3 β	ASSIRTEAF	2053
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSIRTEAFFGQGT RLTVV	2054
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSIRTEAFFGQG TRLTVV	2055
V β	MXNQVLCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGTRLTVV (X = any amino acid)	2056
		2057
β chain w/WT signal peptide, C β (substituted)	MSNQVLCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGTRLTVVEDLRNVTPPKVSLFEPKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2058

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGTRLT VVEDLRNVTPPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2059
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGTRLT VVEDLRNVTPPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2060

[00300] In some embodiments, TCR006 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR006 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6G. Amino acid sequences of TCR007.

Description	Sequence	SEQ ID NO:
CDR1 α	TTSDR	1061
CDR2 α	LLSNGAV	1062
CDR3 α	AVAHMDSNYQLI	1063
V α w/o signal peptide (SignalP)	ELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYWYRQDPGKSLES L FVLLSN GAVKQEGRLMASLDTKARLSTLHITA AVHDLSATYFC AVAHMDSNYQLIWGA GTKLI IKP	1064
V α w/o signal peptide (IMGT)	ELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYWYRQDPGKSLES L FVLLSN GAVKQEGRLMASLDTKARLSTLHITA AVHDLSATYFC AVAHMDSNYQLIWGA GTKLI IKP	1065
V α	MXKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYW YRQDPGKSLES L FVLLSNGAVKQEGRLMASLDTKARLSTLHITA AVHDLSAT YFC AVAHMDSNYQLIWGAGTKLI IKP (X = any amino acid)	1066
		1067
α chain w/WT signal peptide, C α (substituted)	MKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYW YRQDPGKSLES L FVLLSNGAVKQEGRLMASLDTKARLSTLHITA AVHDLSAT YFC AVAHMDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLK VAGFNLLM TLRLWSS	1068
α chain w/alternative signal peptide, C α (substituted)	MAKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYW YRQDPGKSLES L FVLLSNGAVKQEGRLMASLDTKARLSTLHITA AVHDLSAT YFC AVAHMDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLK VAGFNLLM TLRLWSS	1069

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYWYRQDPGKSLESLEFVLLSNGAVKQEGRLMASLDTKARLSTLHITAAVHDLSATYFCVAHMDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNLFQNLVLVLRILLKLVAGFNLLMTLRLWSS	1070
CDR1 β	MNHEY	2061
CDR2 β	SVGEGT	2062
CDR3 β	ASSYAGLAAPREQF	2063
V β w/o signal peptide (SignalP)	GVTQTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFFGPGTRLTVL	2064
V β w/o signal peptide (IMGT)	NAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFFGPGTRLTVL	2065
V β	MXLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFFGPGTRLTVL (X = any amino acid)	2066
		2067
β chain w/WT signal peptide, C β (substituted)	MSLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2068
β chain w/alternative signal peptide, C β (substituted)	MALGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2069
β chain w/alternative signal peptide, C β (substituted)	MHLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2070

[00301] In some embodiments, TCR007 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR007 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6H. Amino acid sequences of TCR008.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1071

Description	Sequence	SEQ ID NO:
CDR2 α	GLKNN	1072
CDR3 α	IVRARANAGGTSYGKLT	1073
V α w/o signal peptide (SignalP)	KTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNN ETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLT FGQTILTVHP	1074
V α w/o signal peptide (IMGT)	DAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLK NNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLT FGQTILTVHP	1075
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHP (X = any amino acid)	1076
		1077
α chain w/WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHPNINQNEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1078
α chain w/alternative signal peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHPNINQNEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1079
α chain w/alternative signal peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHPNINQNEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1080
CDR1 β	LNHDA	2071
CDR2 β	SQIVND	2072
CDR3 β	ASLQFNEQF	2073
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASLQFNEQFFGPGTR LTVL	2074
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASLQFNEQFFGPG TRLTVL	2075
V β	MXMSNQVLCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHD AMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVL (X = any amino acid)	2076
V β (alternative)	MXNQVLCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHD AMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKN PTAFYLCASLQFNEQFFGPGTRLTVL (X = any amino acid)	2077
β chain w/WT signal peptide, C β (substituted)	MSMSNQVLCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHD AMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNP RNHFRCCVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVKRNS	2078

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAMSNQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDA MYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVKRKN	2079
β chain w/alternative signal peptide, C β (substituted)	MHMSNQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDA MYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVKRKN	2080

[00302] In some embodiments, TCR008 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR008 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6I. Amino acid sequences of TCR009.

Description	Sequence	SEQ ID NO:
CDR1 α	SSNFYA	1081
CDR2 α	MTLNGDE	1082
CDR3 α	ALITGGGNKLT	1083
V α w/o signal peptide (SignalP)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTL NGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCALITGGGNKLTFGT GTQLKVEL	1084
V α w/o signal peptide (IMGT)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTL NGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCALITGGGNKLTFGT GTQLKVEL	1085
V α	MXKNPLAAPLLILWFHLDVCVSSIILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFGTGTQLKVEL (X = any amino acid)	1086
		1087
α chain w/WT signal peptide, C α (substituted)	MEKNPLAAPLLILWFHLDVCVSSIILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLFQNLVLVIVLRI LLLKVAGF NLLMTLRLWSS	1088
α chain w/alternative signal peptide, C α (substituted)	MAKNPLAAPLLILWFHLDVCVSSIILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLFQNLVLVIVLRI LLLKVAGF NLLMTLRLWSS	1089

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHKNPLAAPLLILWFHLDVCSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFTGTQQLKVELNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQ DIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGF NLLMTLRLWSS	1090
CDR1 β	MNHEY	2081
CDR2 β	SVGEGT	2082
CDR3 β	ASRLQGWN SPLH	2083
V β w/o signal peptide (SignalP)	GVTQTPKFRVLKTGQSM TLLCAQDMNHEYMYWYRQDPGMGLRLIHY SVGEGT TAKGEVPDGYNVSRLKKQNFLLGLESAAPSQT SVYFCASRLQGWN SPLHFGN GTRLTVT	2084
V β w/o signal peptide (IMGT)	NAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMYWYRQDPGMGLRLIHY SVGE GTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQT SVYFCASRLQGWN SPLHF GNGTRLTVT	2085
V β	MXLGLLCCGA FSLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHY SVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVT (X = any amino acid)	2086
		2087
β chain w/WT signal peptide, C β (substituted)	MSLGLLCCGA FSLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHY SVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVTEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2088
β chain w/alternative signal peptide, C β (substituted)	MALGLLCCGA FSLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHY SVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVTEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2089
β chain w/alternative signal peptide, C β (substituted)	MHLGLLCCGA FSLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHY SVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVTEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2090

[00303] In some embodiments, TCR009 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR009 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6J. Amino acid sequences of TCR010.

Description	Sequence	SEQ ID NO:
CDR1 α	TTLSN	1091

Description	Sequence	SEQ ID NO:
CDR2 α	LVKSGEV	1092
CDR3 α	AGPGGAGSYQLT	1093
V α w/o signal peptide (SignalP)	QQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQWYKQRPGGHPVFLIQLVKSG EVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGPGGAGSYQLTFGKG TKLSVIP	1094
V α w/o signal peptide (IMGT)	GQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQWYKQRPGGHPVFLIQLVKSG GEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGPGGAGSYQLTFGKG GTKLSVIP	1095
V α	MXLITSMVLVLMQLSQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGPGGAGSYQLTFGKGTKLSVIP (X = any amino acid)	1096
		1097
α chain w/WT signal peptide, C α (substituted)	MLLITSMVLVLMQLSQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGPGGAGSYQLTFGKGTKLSVIPNINQPEPAVYQLKDPRSQDSTLCCLFT DFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVLVIVLRILLKLVAGFNLLM TLRLWSS	1098
α chain w/alternative signal peptide, C α (substituted)	MALITSMVLVLMQLSQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGPGGAGSYQLTFGKGTKLSVIPNINQPEPAVYQLKDPRSQDSTLCCLFT DFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVLVIVLRILLKLVAGFNLLM TLRLWSS	1099
α chain w/alternative signal peptide, C α (substituted)	MHLITSMVLVLMQLSQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGTYFCAGPGGAGSYQLTFGKGTKLSVIPNINQPEPAVYQLKDPRSQDSTLCCLFT DFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVLVIVLRILLKLVAGFNLLM TLRLWSS	1100
CDR1 β	MNHEY	2091
CDR2 β	SMNVEV	2092
CDR3 β	ASSPFVVGQINEQY	2093
V β w/o signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEV TDKGDVPEGYKVS RKEKRNFP LILES PPNQTS L YFCASSPFVVGQINEQY FGPGTRLTVT	2094
V β w/o signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNV EVTDKGDVPEGYKVS RKEKRNFP LILES PPNQTS L YFCASSPFVVGQINE QYFGPGTRLTVT	2095
V β	MXPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES PPNQ TS L YFCASSPFVVGQINEQYFGPGTRLTVT (X = any amino acid)	2096
		2097
β chain w/WT signal peptide, C β (substituted)	MGPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES PPNQ TS L YFCASSPFVVGQINEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2098

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPQLLGYYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQ TSLYFCASSPFVVIGQINEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKNS	2099
β chain w/alternative signal peptide, C β (substituted)	MHPQLLGYYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQ TSLYFCASSPFVVIGQINEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKNS	2100

[00304] In some embodiments, TCR010 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR010 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6K. Amino acid sequences of TCR011.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1101
CDR2 α	GLKNN	1102
CDR3 α	IVRARANAGGTSYGKLT	1103
V α w/o signal peptide (SignalP)	KTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNN ETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLT FGQTILTVHP	1104
V α w/o signal peptide (IMGT)	DAKTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLK NNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKL TFGQGTILTVHP	1105
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHP (X = any amino acid)	1106
		1107
α chain w/WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1108
α chain w/alternative signal peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1109

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLTFGQGTILT VHPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKS FETDMNLNFQNL LVIVLRILLKLVAGFNLLMTLRLWSS	1110
CDR1 β	LNHDA	2101
CDR2 β	SQIVND	2102
CDR3 β	ATRTGNEAF	2103
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCATRTGNEAFFGQGT RLTVV	2104
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCATRTGNEAFFGQGT RLTVV	2105
V β	MXNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCATRTGNEAFFGQGT RLTVV (X = any amino acid)	2106
		2107
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCATRTGNEAFFGQGT RLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMV KRKNS	2108
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCATRTGNEAFFGQGT RLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMV KRKNS	2109
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCATRTGNEAFFGQGT RLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMV KRKNS	2110

[00305] In some embodiments, TCR011 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR011 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6L. Amino acid sequences of TCR012.

Description	Sequence	SEQ ID NO:
CDR1 α	VS NAYN	1111

Description	Sequence	SEQ ID NO:
CDR2 α	GSKP	1112
CDR3 α	AVEDRRRTALI	1113
V α w/o signal peptide (SignalP)	KDQVFQ PSTVASSEGAVVEIFCNH SVSNAYNFFWYLHFGPCAPRL LVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSVSS	1114
V α w/o signal peptide (IMGT)	KDQVFQ PSTVASSEGAVVEIFCNH SVSNAYNFFWYLHFGPCAPRL LVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSVSS	1115
V α	MXLQSTLGAVWLGLLLNSLWKVAESKDQVFQ PSTVASSEGAVVEIFCNH SVSNAYNFFWYLHFGPCAPRL LVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSVSS (X = any amino acid)	1116
		1117
α chain w/WT signal peptide, C α (substituted)	MALQSTLGAVWLGLLLNSLWKVAESKDQVFQ PSTVASSEGAVVEIFCNH SVSNAYNFFWYLHFGPCAPRL LVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSVSSNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVI VLRI LLLKVAGFNLLMTLRLWSS	1118
		1119
α chain w/alternative signal peptide, C α (substituted)	MHLQSTLGAVWLGLLLNSLWKVAESKDQVFQ PSTVASSEGAVVEIFCNH SVSNAYNFFWYLHFGPCAPRL LVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSVSSNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVI VLRI LLLKVAGFNLLMTLRLWSS	1120
CDR1 β	SNHLY	2111
CDR2 β	FYNNEI	2112
CDR3 β	ASSEYQSQSNEQF	2113
V β w/o signal peptide (SignalP)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDG SNFTLKI RSTKLEDSAMYFCASSEYQSQSNEQFFGPGTRLTVL	2114
V β w/o signal peptide (IMGT)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDG SNFTLKI RSTKLEDSAMYFCASSEYQSQSNEQFFGPGTRLTVL	2115
V β	MXTWLVCWAI FSL LKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDG SNFTLKI RSTKLEDSAMYFCASSEYQSQSNEQFFGPGTRLTVL (X = any amino acid)	2116
		2117
β chain w/WT signal peptide, C β (substituted)	MDTWLVCWAI FSL LKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDG SNFTLKI RSTKLEDSAMYFCASSEYQSQSNEQFFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELS W WNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHN PRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2118
β chain w/alternative signal peptide, C β (substituted)	MATWLVCWAI FSL LKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDG SNFTLKI RSTKLEDSAMYFCASSEYQSQSNEQFFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELS W WNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHN PRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2119

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MHTWLVCWAI F S L L K A G L T E P E V T Q T P S H Q V T Q M G Q E V I L R C V P I S N H L Y F Y W Y R Q I L G Q K V E F L V S F Y N N E I S E K S E I F D D Q F S V E R P D G S N F T L K I R S T K L E D S A M Y F C A S S E Y Q S Q S N E Q F F G P G T R L T V L E D L R N V T P P K V S L F E P S K A E I A N K Q K A T L V C L A R G F F P D H V E L S W W V N G K E V H S G V C T D P Q A Y K E S N Y S Y C L S S R L R V S A T F W H N P R N H F R C Q V Q F H G L S E E D K W P E G S P K P V T Q N I S A E A W G R A D C G I T S A S Y Q Q G V L S A T I L Y E I L L G K A T L Y A V L V S T L V M A M V K R K N S	2120

[00306] In some embodiments, TCR012 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR012 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6M. Amino acid sequences of TCR013.

Description	Sequence	SEQ ID NO:
CDR1 α	T I S G T D Y	1121
CDR2 α	G L T S N	1122
CDR3 α	I L R D N N A R L M	1123
V α w/o signal peptide (SignalP)	K T T Q P N S M E S N E E E P V H L P C N H S T I S G T D Y I H W Y R Q L P S Q G P E Y V I H G L T S N V N N R M A S L A I A E D R K S S T L I L H R A T L R D A A V Y Y C I L R D N N A R L M F G D G T Q L V V K P	1124
V α w/o signal peptide (IMGT)	D A K T T Q P N S M E S N E E E P V H L P C N H S T I S G T D Y I H W Y R Q L P S Q G P E Y V I H G L T S N V N N R M A S L A I A E D R K S S T L I L H R A T L R D A A V Y Y C I L R D N N A R L M F G D G T Q L V V K P	1125
V α	M X L V T S I T V L L S L G I M G D A K T T Q P N S M E S N E E E P V H L P C N H S T I S G T D Y I H W Y R Q L P S Q G P E Y V I H G L T S N V N N R M A S L A I A E D R K S S T L I L H R A T L R D A A V Y Y C I L R D N N A R L M F G D G T Q L V V K P (X = any amino acid)	1126
		1127
α chain w/WT signal peptide, C α (substituted)	M K L V T S I T V L L S L G I M G D A K T T Q P N S M E S N E E E P V H L P C N H S T I S G T D Y I H W Y R Q L P S Q G P E Y V I H G L T S N V N N R M A S L A I A E D R K S S T L I L H R A T L R D A A V Y Y C I L R D N N A R L M F G D G T Q L V V K P N I Q N P E P A V Y Q L K D P R S Q D S T L C L F T D F D S Q I N V P K T M E S G T F I T D K C V L D M K A M D S K S N G A I A W S N Q T S F T C Q D I F K E T N A T Y P S S D V P C D A T L T E K S F E T D M N L N F Q N L L V I V L R I L L L K V A G F N L L M T L R L W S S	1128
α chain w/alternative signal peptide, C α (substituted)	M A L V T S I T V L L S L G I M G D A K T T Q P N S M E S N E E E P V H L P C N H S T I S G T D Y I H W Y R Q L P S Q G P E Y V I H G L T S N V N N R M A S L A I A E D R K S S T L I L H R A T L R D A A V Y Y C I L R D N N A R L M F G D G T Q L V V K P N I Q N P E P A V Y Q L K D P R S Q D S T L C L F T D F D S Q I N V P K T M E S G T F I T D K C V L D M K A M D S K S N G A I A W S N Q T S F T C Q D I F K E T N A T Y P S S D V P C D A T L T E K S F E T D M N L N F Q N L L V I V L R I L L L K V A G F N L L M T L R L W S S	1129
α chain w/alternative signal peptide, C α (substituted)	M H L V T S I T V L L S L G I M G D A K T T Q P N S M E S N E E E P V H L P C N H S T I S G T D Y I H W Y R Q L P S Q G P E Y V I H G L T S N V N N R M A S L A I A E D R K S S T L I L H R A T L R D A A V Y Y C I L R D N N A R L M F G D G T Q L V V K P N I Q N P E P A V Y Q L K D P R S Q D S T L C L F T D F D S Q I N V P K T M E S G T F I T D K C V L D M K A M D S K S N G A I A W S N Q T S F T C Q D I F K E T N A T Y P S S D V P C D A T L T E K S F E T D M N L N F Q N L L V I V L R I L L L K V A G F N L L M T L R L W S S	1130
CDR1 β	M N H E Y	2121

Description	Sequence	SEQ ID NO:
CDR2 β	SMNVEV	2122
CDR3 β	ASGLVGFNQPPQH	2123
V β w/o signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQTS L YFCASGLVGFNQPPQHFGD GTRLSIL	2124
V β w/o signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNV E VTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQTS L YFCASGLVGFNQPPQHFGD GTRLSIL	2125
V β	MXPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQTS L YFCASGLVGFNQPPQHFGD GTRLSIL (X = any amino acid)	2126
		2127
β chain w/WT signal peptide, C β (substituted)	MGPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQTS L YFCASGLVGFNQPPQHFGD GTRLS ILEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRCCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2128
β chain w/alternative signal peptide, C β (substituted)	MAPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQTS L YFCASGLVGFNQPPQHFGD GTRLS ILEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRCCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2129
β chain w/alternative signal peptide, C β (substituted)	MHPQLLG YVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP L ILES P SPNQTS L YFCASGLVGFNQPPQHFGD GTRLS ILEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRCCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2130

[00307] In some embodiments, TCR013 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR013 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6N. Amino acid sequences of TCR014

Description	Sequence	SEQ ID NO:
CDR1 α	VSGNPY	1131
CDR2 α	YITGDNLV	1132
CDR3 α	AVRDGSATSGTYKYI	1133
V α w/o signal peptide (SignalP)	QSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITG DNLVKGSGYGFEEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKY IFGTGTRLKVL	1134

Description	Sequence	SEQ ID NO:
V α w/o signal peptide (IMGT)	AQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVL	1135
V α	MXSAPI SMLAMLF T L SGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVL	1136
	(X = any amino acid)	1137
α chain w/WT signal peptide, C α (substituted)	MASAPI SMLAMLF T L SGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVLANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTCQDIFKETNATYPSSDVPDATLTEKS FETDMNLNFQNLIVIVLRILLKVA GFNLLMTLRLWSS	1138
		1139
α chain w/alternative signal peptide, C α (substituted)	MHSAPI SMLAMLF T L SGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVLANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTCQDIFKETNATYPSSDVPDATLTEKS FETDMNLNFQNLIVIVLRILLKVA GFNLLMTLRLWSS	1140
CDR1 β	SEHNR	2131
CDR2 β	FQNEAQ	2132
CDR3 β	ASSPGLAYEQY	2133
V β w/o signal peptide (SignalP)	DTGVSQDPRHKITKRGQNVTFRCDP I SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CAS SPGLAYEQYFGPGTRLTVT	2134
V β w/o signal peptide (IMGT)	DTGVSQDPRHKITKRGQNVTFRCDP I SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CAS SPGLAYEQYFGPGTRLTVT	2135
V β	MXTSLLCWMALC LLGADHADTGV SQDPRHKITKRGQNVTFRCDP I SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CAS SPGLAYEQYFGPGTRLTVT	2136
	(X = any amino acid)	2137
β chain w/WT signal peptide, C β (substituted)	MGTSLLCWMALC LLGADHADTGV SQDPRHKITKRGQNVTFRCDP I SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CAS SPGLAYEQYFGPGTRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2138
β chain w/alternative signal peptide, C β (substituted)	MATSLLCWMALC LLGADHADTGV SQDPRHKITKRGQNVTFRCDP I SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CAS SPGLAYEQYFGPGTRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2139
β chain w/alternative signal peptide, C β (substituted)	MHTSLLCWMALC LLGADHADTGV SQDPRHKITKRGQNVTFRCDP I SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CAS SPGLAYEQYFGPGTRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2140

[00308] In some embodiments, TCR014 interacts with and/or is specific for p53. In some

embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change Y220C relative to the wild type p53 sequence. In some embodiments, TCR014 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6O. Amino acid sequences of TCR015.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1141
CDR2 α	LYSNGD	1142
CDR3 α	AWNSGGSNYKLT	1143
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAWNSGGSNYKLTFGKGTLLTVNP	1144
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAWNSGGSNYKLTFGKGTLLTVNP	1145
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAWNSGGSNYKLTFGKGTLLTVNP	1146
	(X = any amino acid)	1147
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAWNSGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1148
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAWNSGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1149
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAWNSGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1150
CDR1 β	MNHEY	2141
CDR2 β	SVGEGT	2142
CDR3 β	ASSYSQAWGQPQH	2143
V β w/o signal peptide (SignalP)	GVTQTTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGT TAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYSQAWGQPQHF G DTRLSIL	2144
V β w/o signal peptide (IMGT)	NAGVTQTTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGT TAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQTSVYFCASSYSQAWGQPQHF G D GTRLSIL	2145
V β	MXLGLLCCGAFSLLWAGPVNAGVTQTTPKFRVLKTGQSMTLLCAQDMNHEYMYWYRQDPCMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKKQNFLLGLESAAPSQ	2146

Description	Sequence	SEQ ID NO:
	TSVYFCASSYSQAWGQPQHFGDGTRLSIL (X = any amino acid)	2147
β chain w/WT signal peptide, C β (substituted)	MSLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGETTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASSYSQAWGQPQHFGDGTRLSILEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2148
β chain w/alternative signal peptide, C β (substituted)	MALGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGETTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASSYSQAWGQPQHFGDGTRLSILEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2149
β chain w/alternative signal peptide, C β (substituted)	MHLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSMTLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGETTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASSYSQAWGQPQHFGDGTRLSILEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2150

[00309] In some embodiments, TCR015 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change Y220C relative to the wild type p53 sequence. In some embodiments, TCR015 interacts with the neoantigen in the context of HLA-DRB1*04:01:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6P. Amino acid sequences of TCR016.

Description	Sequence	SEQ ID NO:
CDR1 α	VSGNPY	1151
CDR2 α	YITGDNLV	1152
CDR3 α	AVRVWDYKLS	1153
V α w/o signal peptide (SignalP)	QSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITG DNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRVWDYKLSFGAG TTVTVRA	1154
V α w/o signal peptide (IMGT)	AQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYIT GDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRVWDYKLSFGA GTTVTVRA	1155
V α	MXSAPISMLAMLF ¹ TL ² SLRAQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRVWDYKLSFGAGTTVTVRA (X = any amino acid)	1156
		1157
α chain w/WT signal peptide, C α	MASAPISMLAMLF ¹ TL ² SLRAQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRVWDYKLSFGAGTTVTVRANIQNPEPAVYQLKDP ³ RSQD ⁴ STLCLF	1158

Description	Sequence	SEQ ID NO:
(substituted)	TD FDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIF KETNATYPSSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLL MTLRLWSS	1159
α chain w/alternative signal peptide, C α (substituted)	MHSAPISMLAMLEF T L SGLRAQSV AQPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSTSFHLKKPSALVSD SALYFCAVRVWDYKLSFGAGTTVTVRANIQNPEPAVYQLKDPRSQDSTLCLE TD FDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIF KETNATYPSSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLL MTLRLWSS	1160
CDR1 β	LNHDA	2151
CDR2 β	SQIVND	2152
CDR3 β	ASSISAGGDGYT	2153
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIAEGYSVSREKKESFPLT V T S A Q K N P T A F Y L C A S S I S A G G D G Y T F G S GTRLT V V	2154
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIAEGYSVSREKKESFPLT V T S A Q K N P T A F Y L C A S S I S A G G D G Y T F GSGTRLT V V	2155
V β	MXNQVLCCVVL C F L G A N T V D G G I T Q S P K Y L F R K E G Q N V T L S C E Q N L N H D A M Y WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLT V T S A Q K N P T A F Y L C A S S I S A G G D G Y T F G S G T R L T V V (X = any amino acid)	2156
		2157
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVL C F L G A N T V D G G I T Q S P K Y L F R K E G Q N V T L S C E Q N L N H D A M Y WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLT V T S A Q K N P T A F Y L C A S S I S A G G D G Y T F G S G T R L T V V E D L R N V T P P K V S L F E P S K A E I A N K Q K A T L V C L A R G F F P D H V E L S W W V N G K E V H S G V C T D P Q A Y K E S N Y S Y C L S S R L R V S A T F W H N P R N H F R C Q V Q F H G L S E E D K W P E G S P K P V T Q N I S A E A W G R A D C G I T S A S Y Q Q G V L S A T I L Y E I L L G K A T L Y A V L V S T L V M A M V K R K N S	2158
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVL C F L G A N T V D G G I T Q S P K Y L F R K E G Q N V T L S C E Q N L N H D A M Y WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLT V T S A Q K N P T A F Y L C A S S I S A G G D G Y T F G S G T R L T V V E D L R N V T P P K V S L F E P S K A E I A N K Q K A T L V C L A R G F F P D H V E L S W W V N G K E V H S G V C T D P Q A Y K E S N Y S Y C L S S R L R V S A T F W H N P R N H F R C Q V Q F H G L S E E D K W P E G S P K P V T Q N I S A E A W G R A D C G I T S A S Y Q Q G V L S A T I L Y E I L L G K A T L Y A V L V S T L V M A M V K R K N S	2159
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVL C F L G A N T V D G G I T Q S P K Y L F R K E G Q N V T L S C E Q N L N H D A M Y WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLT V T S A Q K N P T A F Y L C A S S I S A G G D G Y T F G S G T R L T V V E D L R N V T P P K V S L F E P S K A E I A N K Q K A T L V C L A R G F F P D H V E L S W W V N G K E V H S G V C T D P Q A Y K E S N Y S Y C L S S R L R V S A T F W H N P R N H F R C Q V Q F H G L S E E D K W P E G S P K P V T Q N I S A E A W G R A D C G I T S A S Y Q Q G V L S A T I L Y E I L L G K A T L Y A V L V S T L V M A M V K R K N S	2160

[00310] In some embodiments, TCR016 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change Y220C relative to the wild type p53 sequence. In some embodiments, TCR016 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6Q. Amino acid sequences of TCR017.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1161
CDR2 α	NVLDGL	1162
CDR3 α	AVKWTGGFKTI	1163
V α w/o signal peptide (SignalP)	QNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVKWTGGFKTIFGAGTR L FVKA	1164
V α w/o signal peptide (IMGT)	GQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLD G LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVKWTGGFKTIFGAGT R L FVKA	1165
V α	MXGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTR L FVKA	1166
	(X = any amino acid)	1167
α chain w/WT signal peptide, C α (substituted)	MWGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTR L FVKANIQNPEPAVYQLKDP RSQDSTLC LFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETN ATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI LRI LLLKVAGFNLLMTLR LWSS	1168
α chain w/alternative signal peptide, C α (substituted)	MAGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTR L FVKANIQNPEPAVYQLKDP RSQDSTLC LFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETN ATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI LRI LLLKVAGFNLLMTLR LWSS	1169
α chain w/alternative signal peptide, C α (substituted)	MHGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTR L FVKANIQNPEPAVYQLKDP RSQDSTLC LFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETN ATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI LRI LLLKVAGFNLLMTLR LWSS	1170
CDR1 β	MNHEY	2161
CDR2 β	SVGAGI	2162
CDR3 β	ASSYRESHYGYT	2163
V β w/o signal peptide (SignalP)	GVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGI TDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASSYRESHYGYTFGS GTR LTVV	2164
V β w/o signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGA GITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASSYRESHYGYTF GSGTR LTVV	2165
V β	MXIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGS GTR LTVV	2166
	(X = any amino acid)	2167
β chain w/WT signal peptide, C β (substituted)	MSIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGS GTR LTVV EDL RNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2168

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAIGLLCCAALSLLWAGPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2169
β chain w/alternative signal peptide, C β (substituted)	MHIGLLCCAALSLLWAGPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2170

[00311] In some embodiments, TCR017 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR017 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6R. Amino acid sequences of TCR018.

Description	Sequence	SEQ ID NO:
CDR1 α	YGGTVN	1171
CDR2 α	YFSGDPLV	1172
CDR3 α	AVKGDYKLS	1173
V α w/o signal peptide (SignalP)	QSVSQHNHHVILSEAAASLELGCNYSYGGTVNLFWYVQYPGQHLQLLLKYFSG DPLVKGIKGFEEAFIKSKFSFNLRKPSVQWSDTAEYFCAVKGDYKLSFGAGT TVTVRA	1174
V α w/o signal peptide (IMGT)	AQSVSQHNHHVILSEAAASLELGCNYSYGGTVNLFWYVQYPGQHLQLLLKYFS GDPLVKGIKGFEEAFIKSKFSFNLRKPSVQWSDTAEYFCAVKGDYKLSFGAG TTTVRA	1175
V α	MXLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAAASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEEAFIKSKFSFNLRKPSVQWSD TAEYFCAVKGDYKLSFGAGTTTVRA (X = any amino acid)	1176
		1177
α chain w/WT signal peptide, C α (substituted)	MLLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAAASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEEAFIKSKFSFNLRKPSVQWSD TAEYFCAVKGDYKLSFGAGTTTVRANIQNPEPAVYQLKDP RSQDSTLCCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLKLVAGFNLLM TLRLWSS	1178
α chain w/alternative signal peptide, C α (substituted)	MALLLI PVLGMI FALRDARAQSVSQHNHHVILSEAAASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEEAFIKSKFSFNLRKPSVQWSD TAEYFCAVKGDYKLSFGAGTTTVRANIQNPEPAVYQLKDP RSQDSTLCCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLKLVAGFNLLM TLRLWSS	1179

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAA SLELGCNYSYGGTVNL FWYVQYPGQHLQ LLLKYFSGDPLVKGIKGFEAEFIKSKFSFNLRKPSVQWSD TAEYFC AVKGDYKLSFGAGTTVTVRANIQNPEPAVYQLKDPRS QDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVLRI LLLKVAGFNLLM TLRLWSS	1180
CDR1 β	SGHAT	2171
CDR2 β	FQNGV	2172
CDR3 β	ASSLVNTEAF	2173
V β w/o signal peptide (SignalP)	GVAQSPRYKII EKQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLVNTEAFFGQG TRLTVV	2174
V β w/o signal peptide (IMGT)	EAGVAQSPRYKII EKQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLVNTEAFFG QGTRLTVV	2175
V β	MXTRLLCWAALCLLGAE LTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVV (X = any amino acid)	2176
		2177
β chain w/WT signal peptide, C β (substituted)	MGTRLLCWAALCLLGAE LTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEPSKAEIANKQ KATLVCLARGFFPDHVELS W WNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADCGI TSASYQQGVLSATILYE ILLGKATLYAVLVSTLVVMAMVKRKN S	2178
β chain w/alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAE LTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEPSKAEIANKQ KATLVCLARGFFPDHVELS W WNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADCGI TSASYQQGVLSATILYE ILLGKATLYAVLVSTLVVMAMVKRKN S	2179
β chain w/alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAE LTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEPSKAEIANKQ KATLVCLARGFFPDHVELS W WNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADCGI TSASYQQGVLSATILYE ILLGKATLYAVLVSTLVVMAMVKRKN S	2180

[00312] In some embodiments, TCR018 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR018 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6S. Amino acid sequences of TCR019.

Description	Sequence	SEQ ID NO:
CDR1 α	TRDTTYY	1181

Description	Sequence	SEQ ID NO:
CDR2 α	RNSFDEQN	1182
CDR3 α	ALSEGGSNYKLT	1183
V α w/o signal peptide (SignalP)	QKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLTFGKGTLLTVNP	1184
V α w/o signal peptide (IMGT)	AQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLTFGKGTLLTVNP	1185
V α	MXTASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLTFGKGTLLTVNP (X = any amino acid)	1186
		1187
α chain w/WT signal peptide, C α (substituted)	MLTASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVIVLRIILLKLVAGFNLLMTLRLWSS	1188
α chain w/alternative signal peptide, C α (substituted)	MATASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVIVLRIILLKLVAGFNLLMTLRLWSS	1189
α chain w/alternative signal peptide, C α (substituted)	MHTASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVIVLRIILLKLVAGFNLLMTLRLWSS	1190
CDR1 β	LNHNV	2181
CDR2 β	YYDKDF	2182
CDR3 β	ATSRELRGNEQF	2183
V β w/o signal peptide (SignalP)	DAMVIQNPRYQVTQFGKPVTLSCSQTLNHNVMYWYQQKSSQAPKLLFHYDDKDFNNEADTPDNFQSRRPNTSFCFLDIRSPGLGDAAMYLCATSRELRGNEQFFGPGTRRLTVL	2184
V β w/o signal peptide (IMGT)	DAMVIQNPRYQVTQFGKPVTLSCSQTLNHNVMYWYQQKSSQAPKLLFHYDDKDFNNEADTPDNFQSRRPNTSFCFLDIRSPGLGDAAMYLCATSRELRGNEQFFGPGTRRLTVL	2185
V β	MXPGLLHWMALCLLGTGHGDAMVIQNPRYQVTQFGKPVTLSCSQTLNHNVMYWYQQKSSQAPKLLFHYDDKDFNNEADTPDNFQSRRPNTSFCFLDIRSPGLGDAAMYLCATSRELRGNEQFFGPGTRRLTVL (X = any amino acid)	2186
		2187
β chain w/WT signal peptide, C β (substituted)	MGPGLLHWMALCLLGTGHGDAMVIQNPRYQVTQFGKPVTLSCSQTLNHNVMYWYQQKSSQAPKLLFHYDDKDFNNEADTPDNFQSRRPNTSFCFLDIRSPGLGDAAMYLCATSRELRGNEQFFGPGTRRLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVL SATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2188

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPGLLHWMALCLLTGTHGDAMVIQNPRYQVTQFGKPVTLSQSLTNHNVMY WYQQKSSQAPKLLFHYDQDFNNEADTPDNFQSRPNTSFCFLDIRSPGLGD AAMYLCAATSRELRCNEQFFGPGTRTLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2189
β chain w/alternative signal peptide, C β (substituted)	MHPGLLHWMALCLLTGTHGDAMVIQNPRYQVTQFGKPVTLSQSLTNHNVMY WYQQKSSQAPKLLFHYDQDFNNEADTPDNFQSRPNTSFCFLDIRSPGLGD AAMYLCAATSRELRCNEQFFGPGTRTLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2190

[00313] In some embodiments, TCR019 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR019 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6T. Amino acid sequences of TCR020.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1191
CDR2 α	IYSNGD	1192
CDR3 α	AVNDAGNMLT	1193
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIY SNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVNDAGNMLTFGGG TRLMVKP	1194
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYS NGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVNDAGNMLTFGGGT RLMVKP	1195
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCVNDAGNMLTFGGGTRLMVKP	1196
	(X = any amino acid)	1197
α chain with WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCVNDAGNMLTFGGGTRLMVKPNIQNPEPAVYQLKDPKSDSTLCLE TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVGAFNLL MTLRLWSS	1198
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCVNDAGNMLTFGGGTRLMVKPNIQNPEPAVYQLKDPKSDSTLCLE TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVGAFNLL MTLRLWSS	1199

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFEWYRQYSGKSPPELIMFTYNSGDKEDGRFTAQLNKASQYVSLIIRDSQPSD SATYLCVNDAGNMLTFGGGTRLMVKPNIQNPEPAVYQLKDPQRSQDSTLCFLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIF KETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVIRILLKLVAGFNLL MTLRLWSS	1200
CDR1 β	DFQATT	2191
CDR2 β	SNFGSKA	2192
CDR3 β	SAAGQANTEAF	2193
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMA TSNEGSKATYEQQVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSAAGQA NTEAFFGQGTRLTVV	2194
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNE GSKATYEQQVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSAAGQANTEA FFGQGTRLTVV	2195
V β	MXLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQQVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVV (X = any amino acid)	2196
		2197
β chain with WT signal peptide, (substituted) C β	MLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQQVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYYQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN S	2198
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQQVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYYQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN S	2199
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQQVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYYQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN S	2200

[00314] In some embodiments, TCR020 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR020 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6U. Amino acid sequences of TCR021.

Description	Sequence	SEQ ID NO:
CDR1 α	TRDTTY	1201
CDR2 α	RNSFDEQN	1202
CDR3 α	ALSEVDSGNTPLV	1203
V α without signal peptide (SignalP)	QKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEVDSGNTPLVFGKGTRLSVIA	1204
V α without signal peptide (IMGT)	AQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEVDSGNTPLVFGKGTRLSVIA	1205
V α	MXTASLLRAVIASICVVSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEVDSGNTPLVFGKGTRLSVIA	1206
	(X = any amino acid)	1207
α chain with WT signal peptide, (substituted) C α	MLTASLLRAVIASICVVSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEVDSGNTPLVFGKGTRLSVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVA GFNLLMTLRLWSS	1208
α chain alternative peptide, (substituted) with signal C α	MATASLLRAVIASICVVSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEVDSGNTPLVFGKGTRLSVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVA GFNLLMTLRLWSS	1209
α chain alternative peptide, (substituted) with signal C α	MHTASLLRAVIASICVVSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEVDSGNTPLVFGKGTRLSVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVA GFNLLMTLRLWSS	1210
CDR1 β	SGDLS	2201
CDR2 β	YNGEE	2202
CDR3 β	ASSVGSSSSTDTQY	2203
V β without signal peptide (SignalP)	GVTQTPKHLITATGQRVTLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVL	2204
V β without signal peptide (IMGT)	DSGVTQTPKHLITATGQRVTLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVL	2205
V β	MXHFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVL	2206
	(X = any amino acid)	2207
β chain with WT signal peptide, (substituted) C β	MGFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2208

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCSPRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGD SALYFCASSVGSSSSSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2209
β chain with alternative signal peptide, C β (substituted)	MHFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCSPRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGD SALYFCASSVGSSSSSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2210

[00315] In some embodiments, TCR021 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR021 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6V. Amino acid sequences of TCR022.

Description	Sequence	SEQ ID NO:
CDR1 α	NTAFDY	1771
CDR2 α	IRPDVSE	1772
CDR3 α	AAEAGNHRGSTLGRLY	1773
V α w/o signal peptide (SignalP)	QQKEKSDQQQVKQSPQSLIVQKGGISII NCAYENTAFDYFPWYQQFPGKGPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLHIMDSQPGDSATYFCAAEAGNH RGSTLGRLYFGRGTQLTVWP	1774
V α w/o signal peptide (IMGT)	QQQVKQSPQSLIVQKGGISII NCAYENTAFDYFPWYQQFPGKGPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLHIMDSQPGDSATYFCAAEAGNH RGSTLGRLYFGRGTQLTVWP	1775
V α	MXKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISII NCAY ENTAFDYFPWYQQFPGKGPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEAGNH RGSTLGRLYFGRGTQLTVWP (X = any amino acid)	1776 1777
α chain with WT signal peptide, C α (substituted)	MDKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISII NCAY ENTAFDYFPWYQQFPGKGPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEAGNH RGSTLGRLYFGRGTQLTVWP NINPEPAVYQ LKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIV LRIILLKLVAGFNLLMTLRLWSS	1778

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MAKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISIIINCA YENTAFDYFPWYQQFPKGKGPALLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEEAGNHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQ LKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAI AWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIV LRILLKLVAGFNLLMTLRLWSS	1779
α chain with alternative peptide, (substituted) with signal C α	MHKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISIIINCA YENTAFDYFPWYQQFPKGKGPALLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEEAGNHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQ LKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAI AWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIV LRILLKLVAGFNLLMTLRLWSS	1780
CDR1 β	SGHRS	2771
CDR2 β	YFSETQ	2772
CDR3 β	ASSLAAGGYFNEQF	2773
V β w/o signal peptide (SignalP)	GVTQTTPRYLIKTRGQQVTLS CSPISGHRSVSWYQQTPGQGLQFLFEYFSETQ RNKGNFPGRFSGRQFSNSRSEMNVTLELGDSALYLCASSLAAGGYFNEQFF GPGTRLTVL	2774
V β w/o signal peptide (IMGT)	KAGVTQTTPRYLIKTRGQQVTLS CSPISGHRSVSWYQQTPGQGLQFLFEYFSE TQRNKGNFPGRFSGRQFSNSRSEMNVTLELGDSALYLCASSLAAGGYFNEQ FFGPGTRLTVL	2775
V β	MXSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLS CSPISGHRSVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVL (X = any amino acid)	2776
		2777
β chain with WT signal peptide, (substituted) C β	MGSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLS CSPISGHRSVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVLEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2778
β chain with alternative signal peptide, C β (substituted)	MASRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLS CSPISGHRSVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVLEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2779
β chain with alternative signal peptide, C β (substituted)	MHSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLS CSPISGHRSVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVLEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2780

[00316] In some embodiments, TCR022 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR022 interacts with the neoantigen in the context of HLA-A*11:01, as described in International Publication No. WO 2021/163434, incorporated herein by reference in its entirety.

Table 6W. Amino acid sequences of TCR023.

Description	Sequence	SEQ ID NO:
CDR1 α	NSAFQY	1221
CDR2 α	TYSSGN	1222
CDR3 α	AMTSPYNNNDMR	1223
V α without signal peptide (SignalP)	QQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFG AGTRLTVKP	1224
V α without signal peptide (IMGT)	QKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGA GTRLTVKP	1225
V α	MXKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKP (X = any amino acid)	1226
		1227
α chain with WT signal peptide, (substituted) C α	MCKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1228
α chain alternative peptide, (substituted) with signal C α	MAKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1229
α chain alternative peptide, (substituted) with signal C α	MHKSRLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1230
CDR1 β	DFQATT	2221
CDR2 β	SNEGSKA	2222
CDR3 β	SGGLEEAARQFI	2223
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSSVKIECRSLDFQATTMFYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTLSLTITVTS AHPEDSSFYICSGGLEE AARQFIGPGTRLTVL	2224
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTLSLTITVTS AHPEDSSFYICSGGLEEAARQ FIGPGTRLTVL	2225
V β	MXLLLLLLGPGISLLLPGLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVL (X = any amino acid)	2226
		2227

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN S	2228
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN S	2229
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN S	2230

[00317] In some embodiments, TCR023 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR023 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6X. Amino acid sequences of TCR024.

Description	Sequence	SEQ ID NO:
CDR1 α	NSAFQY	1231
CDR2 α	TYSSGN	1232
CDR3 α	AMTSPYNNNDMR	1233
V α without signal peptide (SignalP)	QQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTY SSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFG AGTRLTVKP	1234
V α without signal peptide (IMGT)	QKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGA GTRLTVKP	1235
V α	MXKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKP (X = any amino acid)	1236
		1237

Description	Sequence	SEQ ID NO:
α chain with WT signal peptide, (substituted) $C\alpha$	MCKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFI RDSQPSDSATYLCAMTSPYNNNDMRFGAGTRLT VKPNIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGF NLLMTLRLWSS	1238
α chain with alternative signal peptide, (substituted) $C\alpha$	MAKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFI RDSQPSDSATYLCAMTSPYNNNDMRFGAGTRLT VKPNIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGF NLLMTLRLWSS	1239
α chain with alternative signal peptide, (substituted) $C\alpha$	MHKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFI RDSQPSDSATYLCAMTSPYNNNDMRFGAGTRLT VKPNIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGF NLLMTLRLWSS	1240
CDR1 β	DFQATT	2231
CDR2 β	SNEGSKA	2232
CDR3 β	SGGLEEAARQFI	2233
V β without signal peptide (SignalP)	AVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLT V TSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVL	2234
V β without signal peptide (IMGT)	GAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLT V TSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVL	2235
V β	MXLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLT V TSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVL (X = any amino acid)	2236
		2237
β chain with WT signal peptide, (substituted) $C\beta$	MLLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLT V TSAHPEDSSFYICSGGLEEAARQFIGPGTRLT V LEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2238
β chain with alternative signal peptide, $C\beta$ (substituted)	MALLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLT V TSAHPEDSSFYICSGGLEEAARQFIGPGTRLT V LEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2239
β chain with alternative signal peptide, $C\beta$ (substituted)	MHLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLT V TSAHPEDSSFYICSGGLEEAARQFIGPGTRLT V LEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2240

[00318] In some embodiments, TCR024 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has

the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR024 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6Y. Amino acid sequences of TCR025.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1241
CDR2 α	GLKNN	1242
CDR3 α	IVPNDYKLS	1243
V α without signal peptide (SignalP)	KTTPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTVTVRA	1244
V α without signal peptide (IMGT)	DAKTTPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTVTVRA	1245
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTVTVRA	1246
	(X = any amino acid)	1247
α chain with WT signal peptide, (substituted) C α	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTVTVRANIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVLRLIRILLKVAGFNLLMTLRLWSS	1248
α chain alternative peptide, (substituted) with signal C α	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTVTVRANIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVLRLIRILLKVAGFNLLMTLRLWSS	1249
α chain alternative peptide, (substituted) with signal C α	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTVTVRANIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVLRLIRILLKVAGFNLLMTLRLWSS	1250
CDR1 β	MDHEN	2241
CDR2 β	SYDVKM	2242
CDR3 β	ASSFGTGSIQETQY	2243
V β without signal peptide (SignalP)	SRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIP EGYSVSREKKERFSLILESASTNQTSMYLCASSFGTGSIQETQYFGPGTRLLVL	2244
V β without signal peptide (IMGT)	DVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIP EGYSVSREKKERFSLILESASTNQTSMYLCASSFGTGSIQETQYFGPGTRLLVL	2245
V β	MXIRLLCRVAFCLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIP EGYSVSREKKERFSLILESASTNQTSMYLCASSFGTGSIQETQYFGPGTRLLVL	2246
	(X = any amino acid)	2247

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MGIRLLCRVAFCF ~~FLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF~~ WYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILEASTNQ TSMYLCASSFGTGSIQETQYFGPGTRLLVLEDLRNVT ~~PPKVS~~ LFEP ~~SKAEIA~~ NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR ~~CQVQFHGLSEEDKWPEGS~~ PKPVTQNI ~~SAEAWGRAD~~ CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2248
β chain with alternative signal peptide, C β (substituted)	MAIRLLCRVAFCF ~~FLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF~~ WYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILEASTNQ TSMYLCASSFGTGSIQETQYFGPGTRLLVLEDLRNVT ~~PPKVS~~ LFEP ~~SKAEIA~~ NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR ~~CQVQFHGLSEEDKWPEGS~~ PKPVTQNI ~~SAEAWGRAD~~ CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2249
β chain with alternative signal peptide, C β (substituted)	MHIRLLCRVAFCF ~~FLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF~~ WYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILEASTNQ TSMYLCASSFGTGSIQETQYFGPGTRLLVLEDLRNVT ~~PPKVS~~ LFEP ~~SKAEIA~~ NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR ~~CQVQFHGLSEEDKWPEGS~~ PKPVTQNI ~~SAEAWGRAD~~ CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2250

[00319] In some embodiments, TCR025 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR025 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6Z. Amino acid sequences of TCR026

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1251
CDR2 α	ATKADDK	1252
CDR3 α	ALNPAGGTSYGKLT	1253
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKA DDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALNPAGGTSYGKLT FGQGTILT ~~VHP~~	1254
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATK ADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALNPAGGTSYGKL TFGQGTILT ~~VHP~~	1255
V α	MXYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALNPAGGTSYGKLTFGQGTILT ~~VHP~~ (X = any amino acid)	1256
		1257
α chain with WT signal peptide, C α (substituted)	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALNPAGGTSYGKLTFGQGTILT ~~VHP~~ NIQNPEPAVYQLKDP ~~RSQDST~~ LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT ~~SFTC~~ QDIFKETNATYPS ~~SDVPCD~~ ATLT ~~EKS~~ FETDMNLN ~~FQNL~~ LIVIL ~~RI~~ LLK ~~VAG~~ FNLLMTLRLWSS	1258

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MAYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLQLLLKATKADDKGSNKGFEATYRKETTTFHLEKGSVQVSDSAVYFCALNPAGGTSYGKLTFGQGTLTVHPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRIILLKLVAGFNLLMTLRLWSS	1259
α chain with alternative peptide, (substituted) with signal C α	MHYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLQLLLKATKADDKGSNKGFEATYRKETTTFHLEKGSVQVSDSAVYFCALNPAGGTSYGKLTFGQGTLTVHPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRIILLKLVAGFNLLMTLRLWSS	1260
CDR1 β	SGHTS	2251
CDR2 β	YDEGEE	2252
CDR3 β	ASSSPGATSGGANTGELEF	2253
V β without signal peptide (SignalP)	GVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEEERNRGNFPPRFSGRQFPNYSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVL	2254
V β without signal peptide (IMGT)	EAGVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVL	2255
V β	MXPRLLFWALLCCLLTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVL	2256
	(X = any amino acid)	2257
β chain with WT signal peptide, (substituted) C β	MGPRLLEFWALLCCLLTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVLEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2258
β chain with alternative signal peptide, C β (substituted)	MAPRLLEFWALLCCLLTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVLEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2259
β chain with alternative signal peptide, C β (substituted)	MHPRLLEFWALLCCLLTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVLEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2260

[00320] In some embodiments, TCR026 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR026 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AA. Amino acid sequences of TCR027.

Description	Sequence	SEQ ID NO:
CDR1 α	DSSSTY	1261
CDR2 α	IFSNMDM	1262
CDR3 α	AEIPRDSGGGADGLT	1263
V α without signal peptide (SignalP)	EDVEQSLFSLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSNM DMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEI PRDSGGGADGLTF GKGTHLIIQP	1264
V α without signal peptide (IMGT)	GEDVEQSLFSLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSNM MDMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEI PRDSGGGADGLTF FGKGTHLIIQP	1265
V α	MXTFAGFSFLFLWLQLDCMSRGEDVEQSLFSLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQP (X = any amino acid)	1266
		1267
α chain with WT signal peptide, (substituted) C α	MKTFAGFSFLFLWLQLDCMSRGEDVEQSLFSLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLFQNL LVIVLRILLKVA GFNLLMTLRLWSS	1268
α chain alternative peptide, (substituted) with signal C α	MATEFAGFSFLFLWLQLDCMSRGEDVEQSLFSLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLFQNL LVIVLRILLKVA GFNLLMTLRLWSS	1269
α chain alternative peptide, (substituted) with signal C α	MHTFAGFSFLFLWLQLDCMSRGEDVEQSLFSLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLFQNL LVIVLRILLKVA GFNLLMTLRLWSS	1270
CDR1 β	DFQATT	2261
CDR2 β	SNEGSKA	2262
CDR3 β	SARDLQRSYEQY	2263
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTLSLTITVTSAHPEDSSFYIC SARDLQ RSYEQYFGPGTRLTVT	2264
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTLSLTITVTSAHPEDSSFYIC SARDLQRSYE QYFGPGTRLTVT	2265
V β	MXLLLLLLGPGISLLLPGLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYIC SARDLQRSYEQYFGPGTRLTVT (X = any amino acid)	2266
		2267

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISILLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMEFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSAARDLQRSYEQYFGPGTRLTVTEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYSQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2268
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISILLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMEFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSAARDLQRSYEQYFGPGTRLTVTEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYSQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2269
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISILLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMEFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSAARDLQRSYEQYFGPGTRLTVTEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYSQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2270

[00321] In some embodiments, TCR027 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR027 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AB. Amino acid sequences of TCR028.

Description	Sequence	SEQ ID NO:
CDR1 α	DSSSTY	1271
CDR2 α	IFSNMDM	1272
CDR3 α	AEIPRDSGGGADGLT	1273
V α without signal peptide (SignalP)	EDVEQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSNM DMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEIPRDSGGGADGLTF GKGTHLIIQP	1274
V α without signal peptide (IMGT)	GEDVEQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSN MDMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEIPRDSGGGADGLT FGKGTHLIIQP	1275
V α	MXTFAGFSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQP (X = any amino acid)	1276
		1277

Description	Sequence	SEQ ID NO:
α chain with WT signal peptide, (substituted) $C\alpha$	MKTFAGFSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKVA GFNLLMTLRLWSS	1278
α chain with alternative signal peptide, (substituted) $C\alpha$	MATFAGFSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKVA GFNLLMTLRLWSS	1279
α chain with alternative signal peptide, (substituted) $C\alpha$	MHTFAGFSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEI PRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKVA GFNLLMTLRLWSS	1280
CDR1 β	DFQATT	2271
CDR2 β	SNEGSKA	2272
CDR3 β	SARDLQRSYEQY	2273
V β without signal peptide (SignalP)	AVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEG SKATYEQGVEKDKFLINHASLTLSLTLTVTSAHPEDSSFYIC SARDLQRSYEQ YFGPGTRTLVT	2274
V β without signal peptide (IMGT)	GAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTLSLTLTVTSAHPEDSSFYIC SARDLQRSYEQ YFGPGTRTLVT	2275
V β	MXLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLTVTSAHPEDS SFYIC SARDLQRSYEQYFGPGTRTLVT (X = any amino acid)	2276
		2277
β chain with WT signal peptide, (substituted) $C\beta$	MLLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLTVTSAHPEDS SFYIC SARDLQRSYEQYFGPGTRTLVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2278
β chain with alternative signal peptide, $C\beta$ (substituted)	MALLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLTVTSAHPEDS SFYIC SARDLQRSYEQYFGPGTRTLVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2279
β chain with alternative signal peptide, $C\beta$ (substituted)	MHLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTLTVTSAHPEDS SFYIC SARDLQRSYEQYFGPGTRTLVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2280

[00322] In some embodiments, TCR028 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has

the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR028 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AC. Amino acid sequences of TCR029.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1281
CDR2 α	IRSNMDK	1282
CDR3 α	AEPVGGGLNSGYALN	1283
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTP	1284
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTP	1285
V α	MXGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTP (X = any amino acid)	1286
		1287
α chain with WT signal peptide, (substituted) C α	MAGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRIILLKVAGFNLLMTLRLWSS	1288
		1289
α chain with alternative signal peptide, (substituted) C α	MHGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRIILLKVAGFNLLMTLRLWSS	1290
CDR1 β	SGHKS	2281
CDR2 β	QYYEKEE	2282
CDR3 β	ASSGGRTSGAYEQF	2283
V β without signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPI SGHKSVSWYQQVLGQGPQFI FQYYEKEE RGRGNFPDRFSARQFPNYSSSELNVNALLLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVL	2284
V β without signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPI SGHKSVSWYQQVLGQGPQFI FQYYEK EERGRGNFPDRFSARQFPNYSSSELNVNALLLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVL	2285
V β	MXPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPI SGHKSVSWYQQVLGQGPQFI FQYYEKEEERGRGNFPDRFSARQFPNYSSSELNVNALLLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVL (X = any amino acid)	2286
		2287

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MGPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPISGHKSVS WYQQVLGQGPQFIFQYYEKEERGRGNFPDRFSARQFPNYSSSELNVNALLLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2288
β chain with alternative signal peptide, C β (substituted)	MAPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPISGHKSVS WYQQVLGQGPQFIFQYYEKEERGRGNFPDRFSARQFPNYSSSELNVNALLLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2289
β chain with alternative signal peptide, C β (substituted)	MHPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPISGHKSVS WYQQVLGQGPQFIFQYYEKEERGRGNFPDRFSARQFPNYSSSELNVNALLLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2290

[00323] In some embodiments, TCR029 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR029 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AD. Amino acid sequences of TCR030.

Description	Sequence	SEQ ID NO:
CDR1 α	VSGLRG	1291
CDR2 α	LYSAGEE	1292
CDR3 α	AVTAHRGSTLGRLY	1293
V α without signal peptide (SignalP)	EDQVTQSPEALRLQEGESSSLNCSYTVSGLRGLFWYRQDPGKGPEFLFTLYS AGEEKEKERL KATLT KKESFLHITAPKPEDSATYLCAVTAHRGSTLGRLYFG RGTQLTVWP	1294
V α without signal peptide (IMGT)	EDQVTQSPEALRLQEGESSSLNCSYTVSGLRGLFWYRQDPGKGPEFLFTLYS AGEEKEKERL KATLT KKESFLHITAPKPEDSATYLCAVTAHRGSTLGRLYFG RGTQLTVWP	1295
V α	MXKMLECAFIVLWLQLGWLSGEDQVTQSPEALRLQEGESSSLNCSYTVSGLR GLFWYRQDPGKGPEFLFTLYSAGEEKEKERL KATLT KKESFLHITAPKPEDS ATYLCAVTAHRGSTLGRLYFGRGTQLTVWP	1296
	(X = any amino acid)	1297
α chain with WT signal peptide, C α (substituted)	MEKMLECAFIVLWLQLGWLSGEDQVTQSPEALRLQEGESSSLNCSYTVSGLR GLFWYRQDPGKGPEFLFTLYSAGEEKEKERL KATLT KKESFLHITAPKPEDS ATYLCAVTAHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQ DIFKETNATYPSSDVP CDATLT EKS FETDMNLNFQNL LVIVLRI LLLKVAGF NLLMTLRLWSS	1298

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MAKMLECAFTVLWLQLGWLSGEDQVTQSPEALRLQEGESSSLNCSYTVSGLR GLEWYRQDPGKGPEFLFTLYSAGEEKEKERLKATLTKKESFLHITAPKPEDS ATYLCAVTAHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQLKDPQRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1299
α chain with alternative peptide, (substituted) with signal C α	MHKMLECAFTVLWLQLGWLSGEDQVTQSPEALRLQEGESSSLNCSYTVSGLR GLEWYRQDPGKGPEFLFTLYSAGEEKEKERLKATLTKKESFLHITAPKPEDS ATYLCAVTAHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQLKDPQRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1300
CDR1 β	SGHDT	2291
CDR2 β	YEEEE	2292
CDR3 β	ASSRRGGAYNEQF	2293
V β without signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEE RQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSRRGGAYNEQFFG PGTRLTVL	2294
V β without signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEE EERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSRRGGAYNEQF FGPGTRLTVL	2295
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSRRGGAYNEQFFGPGTRLTVL (X = any amino acid)	2296
		2297
β chain with WT signal peptide, (substituted) C β	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSRRGGAYNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2298
β chain with alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSRRGGAYNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2299
β chain with alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSRRGGAYNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2300

[00324] In some embodiments, TCR030 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR030 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AE. Amino acid sequences of TCR031.

Description	Sequence	SEQ ID NO:
CDR1 α	SSNFYA	1301
CDR2 α	MTLNGDE	1302
CDR3 α	ASVGGGADGLT	1303
V α without signal peptide (SignalP)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLI IQP	1304
V α without signal peptide (IMGT)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLI IQP	1305
V α	MXKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLI IQP (X = any amino acid)	1306
		1307
α chain with WT signal peptide, (substituted) C α	MEKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLI IQPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNLFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1308
α chain with alternative signal peptide, (substituted) C α	MAKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLI IQPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNLFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1309
α chain with alternative signal peptide, (substituted) C α	MHKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLI IQPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNLFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1310
CDR1 β	SGHTA	2301
CDR2 β	FQGNSA	2302
CDR3 β	ASTWDRGSYNEQF	2303
V β without signal peptide (SignalP)	GVSQSPPSNKVTEKGKDVELRCDPISGHTALYWYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLT IQRTQQEDSAVYLCASTWDRGSYNEQFFGPGTRLTVL	2304
V β without signal peptide (IMGT)	GAGVSQSPPSNKVTEKGKDVELRCDPISGHTALYWYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLT IQRTQQEDSAVYLCASTWDRGSYNEQFFGPGTRLTVL	2305
V β	MXTRLLFWVAFCLLGADHTGAGVSQSPPSNKVTEKGKDVELRCDPISGHTALYWYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLT IQRTQQEDSAVYLCASTWDRGSYNEQFFGPGTRLTVL (X = any amino acid)	2306
		2307

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MGTRLLFWVAFCLLGADHTGAGVSQSPSNKVTEKGDVELRCDPI SGHTALY WYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCAS TWD RGSYNEQFFGPGTRLT VLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2308
β chain with alternative signal peptide, C β (substituted)	MATRLLFWVAFCLLGADHTGAGVSQSPSNKVTEKGDVELRCDPI SGHTALY WYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCAS TWD RGSYNEQFFGPGTRLT VLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2309
β chain with alternative signal peptide, C β (substituted)	MHTRLLFWVAFCLLGADHTGAGVSQSPSNKVTEKGDVELRCDPI SGHTALY WYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCAS TWD RGSYNEQFFGPGTRLT VLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2310

[00325] In some embodiments, TCR031 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR031 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AF. Amino acid sequences of TCR032.

Description	Sequence	SEQ ID NO:
CDR1 α	NSMFDY	1311
CDR2 α	ISSIKDK	1312
CDR3 α	AANTGNQFY	1313
V α without signal peptide (SignalP)	QQKNDDQQVKQNSP SLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFL ISISSIKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAANTGNQFY FGTGTSLTVIP	1314
V α without signal peptide (IMGT)	DQQVKQNSP SLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISS I KDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAANTGNQFYFGTGT SLTVIP	1315
V α	MXMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSP SLSVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIV PSQPGDSAVYFCAANTGNQFYFGTGTSLTVIP (X = any amino acid)	1316
		1317
α chain with WT signal peptide, C α (substituted)	MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSP SLSVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIV PSQPGDSAVYFCAANTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVP CDATLTEKS FETDMNLNFQNL LVIVLRILLKVA GFNLLMTLR LWSS	1318
		1319

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSSLVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIV ESQPGDSAVYFCAANTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVLVLRILLKVA GFNLLMTLRLWSS	1320
CDR1 β	SGHAT	2311
CDR2 β	FQNNGV	2312
CDR3 β	ASSHLAGEFYNEQF	2313
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNNGV VDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSHLAGEFYNEQF FGPGTRTLTVL	2314
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNN GVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSHLAGEFYNE QFFGPGTRTLTVL	2315
V β	MXTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSHLAGEFYNEQFFGPGTRTLTVL (X = any amino acid)	2316
		2317
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSHLAGEFYNEQFFGPGTRTLTVLEDLRNVTTPPKVSLFEPSKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2318
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSHLAGEFYNEQFFGPGTRTLTVLEDLRNVTTPPKVSLFEPSKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2319
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSHLAGEFYNEQFFGPGTRTLTVLEDLRNVTTPPKVSLFEPSKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2320

[00326] In some embodiments, TCR032 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR032 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AG. Amino acid sequences of TCR033.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFYG	1321
CDR2 α	NALDGL	1322
CDR3 α	AFAYGQNFV	1323
V α without signal peptide (SignalP)	QSLEQPSSEVTAVEGAIVQINCTYQTSIFYGLSWYQQHGGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLLQELQMKDSASYFCAFAYGQNFVFGPGTRLSSVLP	1324
V α without signal peptide (IMGT)	QGSLEQPSSEVTAVEGAIVQINCTYQTSIFYGLSWYQQHGGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLLQELQMKDSASYFCAFAYGQNFVFGPGTRLSSVLP	1325
V α	MXGAFLLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSIFYGLSWYQQHGGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLLQELQMKDSASYFCAFAYGQNFVFGPGTRLSSVLP (X = any amino acid)	1326
		1327
α chain with WT signal peptide, (substituted) C α	MWGAFLLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSIFYGLSWYQQHGGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLLQELQMKDSASYFCAFAYGQNFVFGPGTRLSSVLPNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1328
α chain alternative peptide, (substituted) with signal C α	MAGAFLLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSIFYGLSWYQQHGGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLLQELQMKDSASYFCAFAYGQNFVFGPGTRLSSVLPNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1329
α chain alternative peptide, (substituted) with signal C α	MHGAFLLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSIFYGLSWYQQHGGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLLQELQMKDSASYFCAFAYGQNFVFGPGTRLSSVLPNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1330
CDR1 β	SGDLS	2321
CDR2 β	YYNGEE	2322
CDR3 β	ASSPLGDSGNTIY	2323
V β without signal peptide (SignalP)	GVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGD SALYFCASSPLGDSGNTIYFGEGSWLTVV	2324
V β without signal peptide (IMGT)	DSGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGD SALYFCASSPLGDSGNTIYFGEGSWLTVV	2325
V β	MXFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGD SALYFCASSPLGDSGNTIYFGEGSWLTVV (X = any amino acid)	2326
		2327
β chain with WT signal peptide, (substituted) C β	MGFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGD SALYFCASSPLGDSGNTIYFGEGSWLTVVVDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNSS	2328

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCSPRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLS SLELGD SALYFCASSPLGDSGNTIYFGEGSWLTVVEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2329
β chain with alternative signal peptide, C β (substituted)	MHFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCSPRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLS SLELGD SALYFCASSPLGDSGNTIYFGEGSWLTVVEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2330

[00327] In some embodiments, TCR034 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR034 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AH. Amino acid sequences of TCR034.

Description	Sequence	SEQ ID NO:
CDR1 α	TSINN	1331
CDR2 α	IRSNERE	1332
CDR3 α	ATDAWNNDMR	1333
V α without signal peptide (SignalP)	QQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIR SNE REKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDAWNNDMRFGAGTR LTVKP	1334
V α without signal peptide (IMGT)	SQQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIR SN EREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDAWNNDMRFGAGT RLTVKP	1335
V α	MXTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDAWNNDMRFGAGTRLTVKP (X = any amino acid)	1336
		1337
α chain with WT signal peptide, C α (substituted)	METLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDAWNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDP RSQDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFK ETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGFNLLM TLRLWSS	1338
α chain with alternative signal peptide, C α (substituted)	MATLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDAWNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDP RSQDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFK ETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGFNLLM TLRLWSS	1339

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDAWNNDMRFAGATRLTVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLK VAGFNLLMTLRLWSS	1340
CDR1 β	MNHNS	2331
CDR2 β	SASEG	2332
CDR3 β	ASSESQGNTEAF	2333
V β without signal peptide (SignalP)	GVTQTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAEGTTDKGEVPNGYNVSRNLNKRFSRLLESAAPSQTSVYFCASSESQGNTEAFFGQGTRLTVV	2334
V β without signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAEGTTDKGEVPNGYNVSRNLNKRFSRLLESAAPSQTSVYFCASSESQGNTEAFFGQGTRLTVV	2335
V β	MXIGLLCCVAFSLLWASPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAEGTTDKGEVPNGYNVSRNLNKRFSRLLESAAPSQTSVYFCASSESQGNTEAFFGQGTRLTVV (X = any amino acid)	2336
		2337
β chain with WT signal peptide, (substituted) C β	MSIGLLCCVAFSLLWASPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAEGTTDKGEVPNGYNVSRNLNKRFSRLLESAAPSQTSVYFCASSESQGNTEAFFGQGTRLTVVEDLRNVTTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2338
β chain with alternative signal peptide, C β (substituted)	MAIGLLCCVAFSLLWASPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAEGTTDKGEVPNGYNVSRNLNKRFSRLLESAAPSQTSVYFCASSESQGNTEAFFGQGTRLTVVEDLRNVTTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2339
β chain with WT signal peptide, (substituted) C β	MHIGLLCCVAFSLLWASPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAEGTTDKGEVPNGYNVSRNLNKRFSRLLESAAPSQTSVYFCASSESQGNTEAFFGQGTRLTVVEDLRNVTTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2340

[00328] In some embodiments, TCR034 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR034 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AI. Amino acid sequences of TCR035.

Description	Sequence	SEQ ID NO:
CDR1 α	VSPFSN	1341
CDR2 α	MTFSENT	1342
CDR3 α	VVSSYKII	1343
V α without signal peptide (SignalP)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIMTF SENTKSNGRYTATLDADTKQSSLHITASQLSDSASYICVVSSYKIIIFGTGTRLHVFP	1344
V α without signal peptide (IMGT)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIMTF SENTKSNGRYTATLDADTKQSSLHITASQLSDSASYICVVSSYKIIIFGTGTRLHVFP	1345
V α	MXKHLTTFVLVILWLWLYFYRGNKGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFP	1346
	(X = any amino acid)	1347
α chain with WT signal peptide, (substituted) C α	MKKHLTTFVLVILWLWLYFYRGNKGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFPNIQNPEPAVYQLKDPRSQDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLM TRLWSS	1348
α chain alternative peptide, (substituted) with signal C α	MAKHLTTFVLVILWLWLYFYRGNKGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFPNIQNPEPAVYQLKDPRSQDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLM TRLWSS	1349
α chain alternative peptide, (substituted) with signal C α	MKKHLTTFVLVILWLWLYFYRGNKGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFPNIQNPEPAVYQLKDPRSQDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLM TRLWSS	1350
CDR1 β	SGHTA	2341
CDR2 β	FQGNSA	2342
CDR3 β	ASSPIQGENSPLH	2343
V β without signal peptide (SignalP)	GVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SA PDKSGLP SDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHF GNGTRLTVT	2344
V β without signal peptide (IMGT)	GAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLP SDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPL HFGNGTRLTVT	2345
V β	MXTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLP SDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVT	2346
	(X = any amino acid)	2347
β chain with WT signal peptide, (substituted) C β	MGTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLP SDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2348

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPI SGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLT IQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLT VTEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2349
β chain with alternative signal peptide, C β (substituted)	MHTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPI SGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLT IQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLT VTEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2350

[00329] In some embodiments, TCR035 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR035 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AJ. Amino acid sequences of TCR036.

Description	Sequence	SEQ ID NO:
CDR1 α	VSPFSN	1351
CDR2 α	MTFSENT	1352
CDR3 α	VVSSYKLI	1353
V α without signal peptide (SignalP)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIMTF SENTKSNGRYTATLDADTKQSSLHITASQLSDSASYICVVSSYKLI FGTGTR LQVFP	1354
V α without signal peptide (IMGT)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIMTF SENTKSNGRYTATLDADTKQSSLHITASQLSDSASYICVVSSYKLI FGTGTR LQVFP	1355
V α	MXKHLTTFLVILWLWLYFYRGN GKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKLI FGTGTRLQVFP (X = any amino acid)	1356
		1357
α chain with WT signal peptide, C α (substituted)	MKKHLTTFLVILWLWLYFYRGN GKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKLI FGTGTRLQVFPNIQNPEPAVYQLKDP RSQDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFK ETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGFNLLM TLRWSS	1358
α chain with alternative signal peptide, C α (substituted)	MAKHLTTFLVILWLWLYFYRGN GKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKLI FGTGTRLQVFPNIQNPEPAVYQLKDP RSQDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFK ETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKVAGFNLLM TLRWSS	1359

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHKHLTTFVLVLWLYFYRGNKGKQVEQSPQSLIILEGKNCTLQCNYTVSPFSLNLRWYKQDTGRGPVSLTIMTFSENTKSNGRYTATLDADTKQSSLHITASQLSDSASYICVVSSYKLIFGTGTRLQVFPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNLFQNLVLVLRILLKLVAGFNLLMTLRLWSS	1360
CDR1 β	SGHTA	2351
CDR2 β	FQGN SA	2352
CDR3 β	ASSPIQGENSPLH	2353
V β without signal peptide (SignalP)	GVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHFGNGTRLTVT	2354
V β without signal peptide (IMGT)	GAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHFGNGTRLTVT	2355
V β	MXTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHFGNGTRLTVT (X = any amino acid)	2356
		2357
β chain with WT signal peptide, (substituted) C β	MGTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2358
β chain with alternative signal peptide, C β (substituted)	MATRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2359
β chain with alternative signal peptide, C β (substituted)	MHTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2360

[00330] In some embodiments, TCR036 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR036 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AK. Amino acid sequences of TCR037.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVSVY	1361
CDR2 α	YLSGSTLV	1362
CDR3 α	AVSKGTGAQKLV	1363
V α without signal peptide (SignalP)	QSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINP	1364
V α without signal peptide (IMGT)	AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINP	1365
V α	MXLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINP (X = any amino acid)	1366
		1367
α chain with WT signal peptide, (substituted) C α	MLLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1368
α chain alternative peptide, (substituted) with signal C α	MALLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1369
α chain alternative peptide, (substituted) with signal C α	MHLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1370
CDR1 β	LNHDA	2361
CDR2 β	SQIVND	2362
CDR3 β	ASEAF	2363
V β without signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCEQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTIVV	2364
V β without signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTIVV	2365
V β	MXNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTIVV (X = any amino acid)	2366
		2367
β chain with WT signal peptide, (substituted) C β	MSNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTIVVEDLRNVTTPKVSLEFESKAEIANKQKATLVC LARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFW HNPRNHFRQVQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQ QGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2368

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MANQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNP TASYLCASEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVC LARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFW HNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQ QGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2369
β chain with alternative signal peptide, C β (substituted)	MHNQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNP TASYLCASEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVC LARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFW HNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQ QGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2370

[00331] In some embodiments, TCR037 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR037 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AL. Amino acid sequences of TCR038.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGTDY	1371
CDR2 α	GLTSN	1372
CDR3 α	ILASGAGSYQLT	1373
V α without signal peptide (SignalP)	KTTPNSMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAAVYYCILASGAGSYQLTFGKGTK LSVIP	1374
V α without signal peptide (IMGT)	DAKTTPNSMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLT SNVNNRMASLAIAEDRKSSTLILHRATLRDAAVYYCILASGAGSYQLTFGKG TKLSVIP	1375
V α	MXLVTSITVLLSLGIMGDAKTTPNSMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAAVYY CILASGAGSYQLTFGKGTKLSVIP	1376
	(X = any amino acid)	1377
α chain with WT signal peptide, C α (substituted)	MKLVTSTITVLLSLGIMGDAKTTPNSMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAAVYY CILASGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDP RSQDSTLC LFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDI FKET NATYPSSDVPCDATLTLEKSFETDMNLNFQNLIVLRI LLLKVAGFNLLMTL RLWSS	1378
α chain with alternative signal peptide, C α (substituted)	MALVTSTITVLLSLGIMGDAKTTPNSMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAAVYY CILASGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDP RSQDSTLC LFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDI FKET NATYPSSDVPCDATLTLEKSFETDMNLNFQNLIVLRI LLLKVAGFNLLMTL RLWSS	1379

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHLVTSITVLLSLGIMGDAKTTQPNMESNEEEEPVHLPCNHSTISGTDYIHWYRQLPSQGP EYVIHGLTSNVNRMASLAIAEDRKSSTLI LHRATLRDAAVYYCII LASGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQT SFTCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLK VAGFNLLMTLRLWSS	1380
CDR1 β	LGHD	2371
CDR2 β	YNNKFTI	2372
CDR3 β	ASRTIGYNTEAF	2373
V β without signal peptide (SignalP)	QTPKYLVTQMGN DKSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETV PNRFS PKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGTR LTVV	2374
V β without signal peptide (IMGT)	DTAVSQTPKYLVTQMGN DKSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETV PNRFS PKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGTR LTVV	2375
V β	MXCRLLCVVFC LLQAGPLDTAVSQTPKYLVTQMGN DKSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETV PNRFS PKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGTR LTVV (X = any amino acid)	2376
		2377
β chain with WT signal peptide, (substituted) C β	MGCRLLCVVFC LLQAGPLDTAVSQTPKYLVTQMGN DKSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETV PNRFS PKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGTR LTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2378
β chain with alternative signal peptide, C β (substituted)	MACRLLCVVFC LLQAGPLDTAVSQTPKYLVTQMGN DKSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETV PNRFS PKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGTR LTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2379
β chain with alternative signal peptide, C β (substituted)	MHCRLLCVVFC LLQAGPLDTAVSQTPKYLVTQMGN DKSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETV PNRFS PKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGTR LTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2380

[00332] In some embodiments, TCR038 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR038 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AM. Amino acid sequences of TCR039.

Description	Sequence	SEQ ID NO:
CDR1 α	VGISA	1381
CDR2 α	LSSGK	1382
CDR3 α	AALSYNTDKLI	1383
V α without signal peptide (SignalP)	AKNEVEQSPQNLTAEGEFITINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFP	1384
V α without signal peptide (IMGT)	KNEVEQSPQNLTAEGEFITINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFP	1385
V α	MXKIRQFLLAILLWLQQLSCVSAKNEVEQSPQNLTAEGEFITINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFP (X = any amino acid)	1386
		1387
α chain with WT signal peptide, (substituted) C α	MKKIRQFLLAILLWLQQLSCVSAKNEVEQSPQNLTAEGEFITINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFPNIQNPEPAVYQLKDPQSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDCLATLEKSFETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1388
α chain alternative peptide, (substituted) with signal C α	MAKIRQFLLAILLWLQQLSCVSAKNEVEQSPQNLTAEGEFITINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFPNIQNPEPAVYQLKDPQSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDCLATLEKSFETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1389
α chain alternative peptide, (substituted) with signal C α	MHKIRQFLLAILLWLQQLSCVSAKNEVEQSPQNLTAEGEFITINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFPNIQNPEPAVYQLKDPQSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPDCLATLEKSFETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1390
CDR1 β	SGHTA	2381
CDR2 β	FQGTGA	2382
CDR3 β	ASSLSGLLQETQY	2383
V β without signal peptide (SignalP)	GVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVL	2384
V β without signal peptide (IMGT)	GAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVL	2385
V β	MXTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVL (X = any amino acid)	2386
		2387
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVLEDLRNVTPEKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2388

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPI SGHTALY WYRQSLGQGPEFLIYFQGTGAADD SGLPNDRFFAVRPEGSVSTLKIQRTERG DSAVYLCASSLSGLLQETQYFGPGTRLLVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2389
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPI SGHTALY WYRQSLGQGPEFLIYFQGTGAADD SGLPNDRFFAVRPEGSVSTLKIQRTERG DSAVYLCASSLSGLLQETQYFGPGTRLLVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2390

[00333] In some embodiments, TCR039 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR039 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AN. Amino acid sequences of TCR040.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1391
CDR2 α	ATKADDK	1392
CDR3 α	ALSHTGSSNTGKLI	1393
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIFGQGTRLQVKP	1394
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIFGQGTRLQVKP	1395
V α	MXYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIFGQGTRLQVKP (X = any amino acid)	1396
		1397
α chain with WT signal peptide, C α (substituted)	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTLEKSFETDMNLNLFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1398
α chain with alternative signal peptide, C α (substituted)	MAYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTLEKSFETDMNLNLFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1399

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHYSPIGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSHTGSSNTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQ DIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVI VLRILLLKVAGF NLLMTLRLWSS	1400
CDR1 β	SGHAT	2391
CDR2 β	FQNGV	2392
CDR3 β	ASSTGGGRHQPH	2393
V β without signal peptide (SignalP)	GVAQSPRYKII EKQSVAFWCNPI SGHATLYWYQQI LGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHF GDGTRLSIL	2394
V β without signal peptide (IMGT)	EAGVAQSPRYKII EKQSVAFWCNPI SGHATLYWYQQI LGQGPKLLIQFQNN GVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPH HFGDGTRLSIL	2395
V β	MXTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQI LGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHF GDGTRLSIL (X = any amino acid)	2396
		2397
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQI LGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHF GDGTRLSILEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2398
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQI LGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHF GDGTRLSILEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2399
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLY WYQQI LGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHF GDGTRLSILEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2400

[00334] In some embodiments, TCR040 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR040 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AO. Amino acid sequences of TCR041.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1401
CDR2 α	ATKADDK	1402
CDR3 α	ALSQTGSSSKTGKLI	1403
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSSKTGKLI FGQGTRLQVKP	1404
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSSKTGKLI FGQGTRLQVKP	1405
V α	MXYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSSKTGKLI FGQGTRLQVKP (X = any amino acid)	1406
		1407
α chain with WT signal peptide, (substituted) C α	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSSKTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGFNLLMTLRLWSS	1408
α chain alternative peptide, (substituted) with signal C α	MAYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSSKTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGFNLLMTLRLWSS	1409
α chain alternative peptide, (substituted) with signal C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSSKTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGFNLLMTLRLWSS	1410
CDR1 β	SGHAT	2401
CDR2 β	FQNGV	2402
CDR3 β	ASSTGGGRHQPH	2403
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSIL	2404
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSIL	2405
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSIL (X = any amino acid)	2406
		2407
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSILEDLRNVTPEKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2408

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAEELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHFGDGTRLSILEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2409
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAEELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHFGDGTRLSILEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2410

[00335] In some embodiments, TCR041 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR041 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AP. Amino acid sequences of TCR042.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1411
CDR2 α	ATKADDK	1412
CDR3 α	ALSQTGSSNTGKLI	1413
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKA DDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSNTGKLI F GQGTRLQVKP	1414
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKA ADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSNTGKLI FGQGTRLQVKP	1415
V α	MXYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSQTGSSNTGKLI FGQGTRLQVKP (X = any amino acid)	1416
		1417
α chain with WT signal peptide, C α (substituted)	MNYSPLGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSQTGSSNTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDPQRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPDATLTLEKSFETDMNLNLFQNLIVIVLRI LLLKVAGF NLLMTLRLWSS	1418
α chain with alternative signal peptide, C α (substituted)	MAYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSQTGSSNTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDPQRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPDATLTLEKSFETDMNLNLFQNLIVIVLRI LLLKVAGF NLLMTLRLWSS	1419

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHYSPIGLVSLILLLLGRTRGNSVLTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSNTGKLIFGQGTRELQVKPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGFNLLMTLRLWSS	1420
CDR1 β	SGHAT	2411
CDR2 β	FQNGV	2412
CDR3 β	ASSTGGGRHQPH	2413
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSIL	2414
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSIL	2415
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSIL (X = any amino acid)	2416
		2417
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2418
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2419
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2420

[00336] In some embodiments, TCR042 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR042 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AQ. Amino acid sequences of TCR043.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1421
CDR2 α	ATKADDK	1422
CDR3 α	ALSTTGSSNTGKLI	1423
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKP	1424
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKP	1425
V α	MXYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKP (X = any amino acid)	1426
		1427
α chain with WT signal peptide, (substituted) C α	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKPNIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGFNLLMTLRLWSS	1428
α chain alternative peptide, (substituted) with signal C α	MAYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKPNIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGFNLLMTLRLWSS	1429
α chain alternative peptide, (substituted) with signal C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKPNIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVLVLRILLLKVAGFNLLMTLRLWSS	1430
CDR1 β	SGHAT	2421
CDR2 β	FQNGV	2422
CDR3 β	ASSTGGGRHQPH	2423
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDTRLISIL	2424
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDTRLISIL	2425
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDTRLISIL (X = any amino acid)	2426
		2427
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDTRLISILEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2428

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQ PQHF GDGTRLSILEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2429
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQ PQHF GDGTRLSILEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2430

[00337] In some embodiments, TCR043 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR043 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AR. Amino acid sequences of TCR044.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1431
CDR2 α	IYSNGD	1432
CDR3 α	AVSWYSTLT	1433
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYV SLLIRDSQPSDSATYLC AVSWYSTLT FKGKT MLLVSP	1434
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIYS NGDKEDGRFTAQLNKASQYV SLLIRDSQPSDSATYLC AVSWYSTLT FKGKTM LLVSP	1435
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYV SLLIRDSQPSD SATYLC AVSWYSTLT FKGKTMLLVSP (X = any amino acid)	1436
		1437
α chain with WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYV SLLIRDSQPSD SATYLC AVSWYSTLT FKGKTMLLVSPNIQNPEPAVYQLK DPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSK SNGAI AWSNQTSFT CQDIFK ETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLR ILLK VAGFNLLM TLRLWSS	1438
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYV SLLIRDSQPSD SATYLC AVSWYSTLT FKGKTMLLVSPNIQNPEPAVYQLK DPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSK SNGAI AWSNQTSFT CQDIFK ETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLR ILLK VAGFNLLM TLRLWSS	1439

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFEWYRQYSGKSPELIMFTYNSGDKEDGRFTAQLNKASQYVSLLIRDSQPSD SATYLCVSWYSTLTFTGKGTMLLVSPNIQNPEPAVYQLKDPRSQDSTLCCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNSGAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKVVAGFNLLM TLRLWSS	1440
CDR1 β	WSHSY	2431
CDR2 β	SAAADT	2432
CDR3 β	ASSGSRTDTQY	2433
V β without signal peptide (SignalP)	GITQSPRYKITETGRQVTLMCHQTWSHSYMFWYRQDLGHGLRLIYYSAADIT TDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSGSRTDTQYFGPG TRLTVL	2434
V β without signal peptide (IMGT)	DAGITQSPRYKITETGRQVTLMCHQTWSHSYMFWYRQDLGHGLRLIYYSAAD DITDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSGSRTDTQYFG EGTRLTVL	2435
V β	MXTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVL (X = any amino acid)	2436
		2437
β chain with WT signal peptide, (substituted) C β	MGTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2438
β chain with alternative signal peptide, C β (substituted)	MATRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2439
β chain with alternative signal peptide, C β (substituted)	MHTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2440

[00338] In some embodiments, TCR044 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR044 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AS. Amino acid sequences of TCR045.

Description	Sequence	SEQ ID NO:
CDR1 α	SVFSS	1441
CDR2 α	VVTGGEV	1442
CDR3 α	AGEFAGNQFY	1443
V α without signal peptide (SignalP)	QLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQWYRQEPGEGPVLLVTVVTTGG EVKKLKRLLTFQFGDARKDSSLHITAAQPGDTGLYLCAGEFAGNQFYFGTGTSLTVIP	1444
V α without signal peptide (IMGT)	TQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQWYRQEPGEGPVLLVTVVTTG GEVKKLKRLLTFQFGDARKDSSLHITAAQPGDTGLYLCAGEFAGNQFYFGTGTSLTVIP	1445
V α	MXLKFSVSI LWIQLAWVSTQ LLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTTGGEVKKLKRLLTFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIP (X = any amino acid)	1446
		1447
α chain with WT signal peptide, (substituted) C α	MVLKFSVSI LWIQLAWVSTQ LLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTTGGEVKKLKRLLTFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1448
α chain alternative peptide, (substituted) with signal C α	MALKFSVSI LWIQLAWVSTQ LLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTTGGEVKKLKRLLTFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1449
α chain alternative peptide, (substituted) with signal C α	MHLKFSVSI LWIQLAWVSTQ LLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTTGGEVKKLKRLLTFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1450
CDR1 β	MGHRA	2441
CDR2 β	YSYEKL	2442
CDR3 β	ASSQVGLTYEQY	2443
V β without signal peptide (SignalP)	EVTQTTPKHLVMGMTNKKSLKCEQHMGHRAMYWYKQKAKKPELMFVYSYEKL SINESVPSRFSPECNSSLNLHLHALQPEDSALYLCASSQVGLTYEQYFGP GTRLTVT	2444
V β without signal peptide (IMGT)	DTEVTQTTPKHLVMGMTNKKSLKCEQHMGHRAMYWYKQKAKKPELMFVYSYE KLSINESVPSRFSPECNSSLNLHLHALQPEDSALYLCASSQVGLTYEQYF GPGTRLTVT	2445
V β	MXCRLCCAVLCLLGAVPIDTEVTQTTPKHLVMGMTNKKSLKCEQHMGHRAMY WYKQKAKKPELMFVYSYEKL SINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRLTVT (X = any amino acid)	2446
		2447
β chain with WT signal peptide, (substituted) C β	MGCRLCCAVLCLLGAVPIDTEVTQTTPKHLVMGMTNKKSLKCEQHMGHRAMY WYKQKAKKPELMFVYSYEKL SINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRLTVTIEDLRNVTTPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2448

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MACRLCCAVLCLLGAVPIDTEVTQTPKHLVMGMTNKKSLKCEQHMGRAMY WYKQKAKKPPPELMFVYSYEKLSINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2449
β chain with alternative signal peptide, C β (substituted)	MHCRLCCAVLCLLGAVPIDTEVTQTPKHLVMGMTNKKSLKCEQHMGRAMY WYKQKAKKPPPELMFVYSYEKLSINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2450

[00339] In some embodiments, TCR045 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR045 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AT. Amino acid sequences of TCR046.

Description	Sequence	SEQ ID NO:
CDR1 α	VSGNPY	1451
CDR2 α	YITGDNLV	1452
CDR3 α	AVRDNSGGSNYKLT	1453
V α without signal peptide (SignalP)	QSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITG DNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDNSGGSNYKLT FGKGTLLTVNP	1454
V α without signal peptide (IMGT)	AQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYIT GDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDNSGGSNYKL TFGKGTLLTVNP	1455
V α	MXSAPISMLAMLFLLSGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRDNSGGSNYKLTFGKGTLLTVNP (X = any amino acid)	1456
		1457
α chain with WT signal peptide, C α (substituted)	MASAPISMLAMLFLLSGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRDNSGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPQSQDST LCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTC QDIFKETNATYPSSDVPFCDATLTEKSFETDMNLNFQNLVIVLRIILLKVAG FNLLMTLRLWSS	1458
		1459

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSAPISMLAMLF'TLSGLRAQSVAPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRGLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRDNSGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPRSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFC QDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRILLKLVAG ENLLMTLRLWSS	1460
CDR1 β	SGHAT	2451
CDR2 β	FQNGV	2452
CDR3 β	ASSLGQGQTQY	2453
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLGQGQTQYFGP GTRLLVL	2454
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNN GVDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLGQGQTQYF GPGTRLLVL	2455
V β	MXTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVL (X = any amino acid)	2456
		2457
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVLEDLRNVTTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2458
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVLEDLRNVTTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2459
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQIILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVLEDLRNVTTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2460

[00340] In some embodiments, TCR046 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR046 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AU. Amino acid sequences of TCR047.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVSVY	1461
CDR2 α	YLSGSTLV	1462
CDR3 α	AVRGSSGTYYKI	1463
V α without signal peptide (SignalP)	QSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYYKIFGTGTRLKVL	1464
V α without signal peptide (IMGT)	AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYYKIFGTGTRLKVL	1465
V α	MXLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYYKIFGTGTRLKVL (X = any amino acid)	1466
		1467
α chain with WT signal peptide, (substituted) C α	MLLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYYKIFGTGTRLKVLNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGLAIWSNQTSFTCQD I FKETNATYPSSDVPDCLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1468
α chain alternative peptide, (substituted) with signal C α	MALLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYYKIFGTGTRLKVLNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGLAIWSNQTSFTCQD I FKETNATYPSSDVPDCLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1469
α chain alternative peptide, (substituted) with signal C α	MHLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYYKIFGTGTRLKVLNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGLAIWSNQTSFTCQD I FKETNATYPSSDVPDCLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1470
CDR1 β	MDHEN	2461
CDR2 β	SYDVKM	2462
CDR3 β	ASKGDQNTAEAF	2463
V β without signal peptide (SignalP)	SRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLLILESASTNQTSMYLCASKGDQNTAEAFGGQTRLT V	2464
V β without signal peptide (IMGT)	DVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDV KMKEKGD IPEGYSVSREKKERFSLLILESASTNQTSMYLCASKGDQNTAEAF GGQTRLT V	2465
V β	MXIRLLCRVAFCFILAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLLILESASTNQ TSMYLCASKGDQNTAEAFGGQTRLT V	2466
	(X = any amino acid)	2467
β chain with WT signal peptide, (substituted) C β	MGIRLLCRVAFCFILAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLLILESASTNQ TSMYLCASKGDQNTAEAFGGQTRLT VVEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2468

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAIRLLCRVAFCFILAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQ TSMYLCASKGQDQNTAEFFGQGTSLTVVEDLRNVTPPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVKRKN	2469
β chain with alternative signal peptide, C β (substituted)	MHIRLLCRVAFCFILAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQ TSMYLCASKGQDQNTAEFFGQGTSLTVVEDLRNVTPPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVKRKN	2470

[00341] In some embodiments, TCR047 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR047 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AV. Amino acid sequences of TCR048.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1471
CDR2 α	NVLDGL	1472
CDR3 α	AVRDLQGTGANNLF	1473
V α without signal peptide (SignalP)	QNIDQPTTEMTATEGAIVQINCTYQTSFGNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVRDLQGTGANNLFFGTG TRLTVIP	1474
V α without signal peptide (IMGT)	GQNIDQPTTEMTATEGAIVQINCTYQTSFGNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVRDLQGTGANNLFFGT GTRLTVIP	1475
V α	MXGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSFGNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVRDLQGTGANNLFFGTGTRLTVIP	1476
	(X = any amino acid)	1477
α chain with WT signal peptide, C α (substituted)	MWGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSFGNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVRDLQGTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPRSQDSTLCFTD FDSQINVEKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKS FETDMNLNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1478

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MAGVFLLYVSMKMGTTGQNIQDQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVRDLQGTGANNLFFGTGTRLTVPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVEPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1479
α chain with alternative peptide, (substituted) with signal C α	MHG VFLLYVSMKMGTTGQNIQDQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVRDLQGTGANNLFFGTGTRLTVPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVEPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1480
CDR1 β	MDHEN	2471
CDR2 β	SYDVKM	2472
CDR3 β	ASSLTFGTTEAF	2473
V β without signal peptide (SignalP)	SRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIP EGYSVSREKKERFSLILESASTNQTSMYLCASSLTFGTTEAFFGQGTRLTVV	2474
V β without signal peptide (IMGT)	DVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDV KMKEKGDIP EGYSVSREKKERFSLILESASTNQTSMYLCASSLTFGTTEAFFGQGTRLTVV	2475
V β	MXIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDV KMKEKGDIP EGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVV	2476
	(X = any amino acid)	2477
β chain with WT signal peptide, (substituted) C β	MGIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDV KMKEKGDIP EGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2478
β chain with alternative signal peptide, C β (substituted)	MAIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDV KMKEKGDIP EGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2479
β chain with alternative signal peptide, C β (substituted)	MHIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDV KMKEKGDIP EGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2480

[00342] In some embodiments, TCR048 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR048 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AW. Amino acid sequences of TCR049.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1481
CDR2 α	NVLDGL	1482
CDR3 α	AFYYGGSQGNLI	1483
V α without signal peptide (SignalP)	QNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKGT KLSVKP	1484
V α without signal peptide (IMGT)	GQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKG TKLSVKP	1485
V α	MXGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKGT KLSVKP (X = any amino acid)	1486
		1487
α chain with WT signal peptide, (substituted) C α	MWGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKGT KLSVKPNIQNPEPAVYQLKDPRSQDSTLCFLTFD DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1488
α chain alternative peptide, (substituted) with signal C α	MAGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKGT KLSVKPNIQNPEPAVYQLKDPRSQDSTLCFLTFD DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1489
α chain alternative peptide, (substituted) with signal C α	MHG VFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKGT KLSVKPNIQNPEPAVYQLKDPRSQDSTLCFLTFD DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1490
CDR1 β	SGHVS	2481
CDR2 β	FQNEAQ	2482
CDR3 β	ASSFGSGSTDTQY	2483
V β without signal peptide (SignalP)	GVSQSPRYKVAKRQDVALRCDPISGHVSLFWYQQALGQGPEFLTYFQNEAQ LDKSGLPSPDRFFAERPEGSVSTLKIQRTOQEDSAVYLCASSFGSGSTDTQYF GPGTRLTVL	2484
V β without signal peptide (IMGT)	GAGVSQSPRYKVAKRQDVALRCDPISGHVSLFWYQQALGQGPEFLTYFQNEAQ LDKSGLPSPDRFFAERPEGSVSTLKIQRTOQEDSAVYLCASSFGSGSTDTQ YFGPTRLTVL	2485
V β	MXTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPISGHVSLF WYQQALGQGPEFLTYFQNEAQ LDKSGLPSPDRFFAERPEGSVSTLKIQRTOQE DSAVYLCASSFGSGSTDTQYF GPGTRLTVL (X = any amino acid)	2486
		2487
β chain with WT signal peptide, (substituted) C β	MGTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPISGHVSLF WYQQALGQGPEFLTYFQNEAQ LDKSGLPSPDRFFAERPEGSVSTLKIQRTOQE DSAVYLCASSFGSGSTDTQYF GPGTRLTVLEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2488

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQGDVALRCDPI SGHVS LF WYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQR TQQE DSAVYLCASSFGSGSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2489
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQGDVALRCDPI SGHVS LF WYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQR TQQE DSAVYLCASSFGSGSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2490

[00343] In some embodiments, TCR049 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR049 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AX. Amino acid sequences of TCR050.

Description	Sequence	SEQ ID NO:
CDR1 α	VTNFRS	1491
CDR2 α	LTSSGIE	1492
CDR3 α	AGQNYGGSQGNLI	1493
V α without signal peptide (SignalP)	EDKVVQSPLSLVVHEGDTVTLNCSYEVTNFRSLLWYKQEKKAPTFLFMLTSS GIEKKSGRLSSI LDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFG KGTKLSVKP	1494
V α without signal peptide (IMGT)	EDKVVQSPLSLVVHEGDTVTLNCSYEVTNFRSLLWYKQEKKAPTFLFMLTSS GIEKKSGRLSSI LDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFG KGTKLSVKP	1495
V α	MXKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSI LDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKP (X = any amino acid)	1496
		1497
α chain with WT signal peptide, C α (substituted)	MMKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSI LDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQ DIFKETNATYPSSDVP CDATLTEKSFETDMNLN FQNLLVIVLRI LLLKVAGF NLLMTLRLWSS	1498
α chain with alternative signal peptide, C α (substituted)	MAKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSI LDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQ DIFKETNATYPSSDVP CDATLTEKSFETDMNLN FQNLLVIVLRI LLLKVAGF NLLMTLRLWSS	1499

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSIILDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDPQRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1500
CDR1 β	SNHLY	2491
CDR2 β	FYNNE	2492
CDR3 β	ASRDPAYEQY	2493
V β without signal peptide (SignalP)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLEDSAMYFCASRDPAYEQYFG PGTRLTVT	2494
V β without signal peptide (IMGT)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLEDSAMYFCASRDPAYEQYFG PGTRLTVT	2495
V β	MXTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVT (X = any amino acid)	2496
		2497
β chain with WT signal peptide, (substituted) C β	MDTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWWNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2498
β chain with alternative signal peptide, C β (substituted)	MATWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWWNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2499
β chain with alternative signal peptide, C β (substituted)	MHTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWWNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2500

[00344] In some embodiments, TCR050 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR050 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AY. Amino acid sequences of TCR051.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1501
CDR2 α	IYSNGD	1502
CDR3 α	AVTLCGGYNKLI	1503
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVTLCGGYNKLIFGAGTRLAVHP	1504
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVTLCGGYNKLIFGAGTRLAVHP	1505
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVTLCGGYNKLIFGAGTRLAVHP (X = any amino acid)	1506
		1507
α chain with WT signal peptide, (substituted) C α	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVTLCGGYNKLIFGAGTRLAVHPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQD I FKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1508
α chain alternative peptide, (substituted) with signal C α	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVTLCGGYNKLIFGAGTRLAVHPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQD I FKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1509
α chain alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVTLCGGYNKLIFGAGTRLAVHPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQD I FKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1510
CDR1 β	LNHDA	2501
CDR2 β	SQIVND	2502
CDR3 β	ASSSRDYEQY	2503
V β without signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2504
V β without signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2505
V β	MXNQVLCVVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT (X = any amino acid)	2506
		2507
β chain with WT signal peptide, (substituted) C β	MSNQVLCVVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVTEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2508

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MANQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTPPKVSLEFESKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2509
β chain with alternative signal peptide, C β (substituted)	MHNQVLCCVVLCLFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTPPKVSLEFESKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2510

[00345] In some embodiments, TCR051 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR051 interacts with the neoantigen in the context of HLA-DPA1*03:01/ DPB1*02:01:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AZ. Amino acid sequences of TCR052.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVSVY	1511
CDR2 α	YLSGSTLV	1512
CDR3 α	AVSDLVRDDKII	1513
V α without signal peptide (SignalP)	QSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSG STLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSDLVRDDKIIIFG KGTRLHILP	1514
V α without signal peptide (IMGT)	AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLS GSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSDLVRDDKIIIF GKGTRLHILP	1515
V α	MXLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYLSGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRDDKIIIFGKGTRLHILP	1516
	(X = any amino acid)	1517
α chain with WT signal peptide, C α (substituted)	MLLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYLSGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRDDKIIIFGKGTRLHILPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSSKNGAIASWNSQTSFTCDQ IFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLIVIVLRILLKLVAGFN LLMTLRLWSS	1518

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MALLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYLSGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRRDKIIFGKGTRLHI LPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLKLVAGFN LLMTLRLWSS	1519
α chain with alternative peptide, (substituted) with signal C α	MHLLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYLSGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRRDKIIFGKGTRLHI LPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLKLVAGFN LLMTLRLWSS	1520
CDR1 β	MNHNS	2511
CDR2 β	SASEGT	2512
CDR3 β	ASIGGFEEAF	2513
V β without signal peptide (SignalP)	GVTQTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSA SEGTTDKGEVPNGYNVSRNLN KREFSLRLESAAPSQT SVYFCASIGGFEEAFFGQ GTR LTVV	2514
V β without signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSA SEGTTDKGEVPNGYNVSRNLN KREFSLRLESAAPSQT SVYFCASIGGFEEAFFGQ GTR LTVV	2515
V β	MXIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSA SEGTTDKGEVPNGYNVSRNLN KREFSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGTR LTVV (X = any amino acid)	2516 2517
β chain with WT signal peptide, (substituted) C β	MSIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSA SEGTTDKGEVPNGYNVSRNLN KREFSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGTR LTVV VEDLRNVTPPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVKRKN S	2518
β chain with alternative signal peptide, C β (substituted)	MAIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSA SEGTTDKGEVPNGYNVSRNLN KREFSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGTR LTVV VEDLRNVTPPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVKRKN S	2519
β chain with alternative signal peptide, C β (substituted)	MHIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSA SEGTTDKGEVPNGYNVSRNLN KREFSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGTR LTVV VEDLRNVTPPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVKRKN S	2520

[00346] In some embodiments, TCR052 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR052 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BA. Amino acid sequences of TCR053.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1521
CDR2 α	NVLDGL	1522
CDR3 α	AVYPGGSQGNLI	1523
V α without signal peptide (SignalP)	QNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKGT KLSVKP	1524
V α without signal peptide (IMGT)	GQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKG TKLSVKP	1525
V α	MXGVFLLYVSMKMGGTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKGT KLSVKP (X = any amino acid)	1526
		1527
α chain with WT signal peptide, (substituted) C α	MWGVFLLYVSMKMGGTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKGT KLSVKPNIQNPEPAVYQLKDPRSQDSTLCFLTFD DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDI FKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1528
α chain alternative peptide, (substituted) with signal C α	MAGVFLLYVSMKMGGTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKGT KLSVKPNIQNPEPAVYQLKDPRSQDSTLCFLTFD DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDI FKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1529
α chain alternative peptide, (substituted) with signal C α	MHG VFLLYVSMKMGGTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKGT KLSVKPNIQNPEPAVYQLKDPRSQDSTLCFLTFD DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDI FKET NATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTL RLWSS	1530
CDR1 β	SGHAT	2521
CDR2 β	FQNGV	2522
CDR3 β	ASSLGTGSTDTQY	2523
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGTGSTDTQYF GPGTRLTVL	2524
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGTGSTDTQ YFGPTRLTVL	2525
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGTGSTDTQYF GPGTRLTVL (X = any amino acid)	2526
		2527
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGTGSTDTQYF GPGTRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2528

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGTGSTD TQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2529
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGTGSTD TQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2530

[00347] In some embodiments, TCR053 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR053 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BB. Amino acid sequences of TCR054.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1531
CDR2 α	IYSNGD	1532
CDR3 α	AVTLSGGYNKLI	1533
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQSFFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLC AVTLSGGYNKLI FGA GTRLAVHP	1534
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYS DRGSQSFFWYRQYSGKSP ELIMFIYS NGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLC AVTLSGGYNKLI FGA GTRLAVHP	1535
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC AVTLSGGYNKLI FGA GTRLAVHP (X = any amino acid)	1536
		1537
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC AVTLSGGYNKLI FGA GTRLAVHPNIQNPEPAVYQLK DPRS QDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILL LKVGAFN LLMTLRLWSS	1538
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC AVTLSGGYNKLI FGA GTRLAVHPNIQNPEPAVYQLK DPRS QDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILL LKVGAFN LLMTLRLWSS	1539

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFEWYRQYSGKSPELIMFTYNSGDKEDGRFTAQLNKASQYVSLLIRDSQPSD SATYLCVAVTLSSGGYNKLIIFGAGTRLAVHPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQD IFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1540
CDR1 β	LNHDA	2531
CDR2 β	SQIVND	2532
CDR3 β	ASSSRDYEQY	2533
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCEQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2534
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGP GTRLTVT	2535
V β	MXNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVT (X = any amino acid)	2536
		2537
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTPPKVSLEFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2538
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTPPKVSLEFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2539
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTPPKVSLEFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2540

[00348] In some embodiments, TCR054 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR054 interacts with the neoantigen in the context of DPA1*01:03/DBP1*02:01 as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BC. Amino acid sequences of TCR055.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1541
CDR2 α	IRSNMDK	1542
CDR3 α	AEYIQGAQKLV	1543
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINP	1544
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINP	1545
V α	MXGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINP (X = any amino acid)	1546
		1547
α chain with WT signal peptide, (substituted) C α	MAGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPQRSQDSTLCLETDDFSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTLEKS FETDMNLNLFQNLIVIVLRILLKLVAGFNL LMTLRLWSS	1548
α chain with alternative signal peptide, (substituted) C α	MAGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPQRSQDSTLCLETDDFSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTLEKS FETDMNLNLFQNLIVIVLRILLKLVAGFNL LMTLRLWSS	1549
α chain with alternative signal peptide, (substituted) C α	MHGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPQRSQDSTLCLETDDFSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTLEKS FETDMNLNLFQNLIVIVLRILLKLVAGFNL LMTLRLWSS	1550
CDR1 β	LGHNA	2541
CDR2 β	YSLEER	2542
CDR3 β	ASSQEDNEQF	2543
V β without signal peptide (SignalP)	ELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVL	2544
V β without signal peptide (IMGT)	ETGVTQTTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVL	2545
V β	MXCRLCCAVLCLLGAGELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVL (X = any amino acid)	2546
		2547
β chain with WT signal peptide, (substituted) C β	MGCRLCCAVLCLLGAGELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2548

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MACRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHN AMYWKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSLFLHLHTLQ PEDSALYLCASSQEDNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPСКАEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2549
β chain with alternative signal peptide, C β (substituted)	MHCRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHN AMYWKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSLFLHLHTLQ PEDSALYLCASSQEDNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPСКАEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2550

[00349] In some embodiments, TCR055 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR055 interacts with the neoantigen in the context of HLA-C*01:02, as described in International Publication No. WO 2021/163477, incorporated herein by reference in its entirety.

Table 6BD. Amino acid sequences of TCR056.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1551
CDR2 α	IYSNGD	1552
CDR3 α	AVNPPVKTSYDKVI	1553
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIY SNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVNPPVKTSYDKVI FGPGTSLSVIP	1554
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYS NGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVNPPVKTSYDKVI FGPGTSLSVIP	1555
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIP (X = any amino acid)	1556
		1557
α chain with WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIPNIQNPEPAVYQLKDPRSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASNSQTSFTC QDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLIVILRLILLKVAG ENLLMTLRLWSS	1558
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIPNIQNPEPAVYQLKDPRSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASNSQTSFTC QDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLIVILRLILLKVAG ENLLMTLRLWSS	1559

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFEWYRQYSGKSPELIMFTYNSGDKEDGRFTAQLNKASQYVSLLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIPNIQNPEPAVYQLKDPRSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSSKNGAIASWNSQTSFTC QDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIVILRILLKLVAG ENLLMTLRLWSS	1560
CDR1 β	SGHVS	2551
CDR2 β	FNYFA	2552
CDR3 β	ASSHREPHTGELF	2553
V β without signal peptide (SignalP)	GVSQSPRYKVTKRGQDVALRCDPISGHVSLYWYRQALGQGPEFLTYFNIEAQ QDKSGLPNDRFSAERPEGSISTLTIQRTEQRDSAMYRCASSHREPHTGELFF GEGSRLTVL	2554
V β without signal peptide (IMGT)	GAGVSQSPRYKVTKRGQDVALRCDPISGHVSLYWYRQALGQGPEFLTYFNIE AQQDKSGLPNDRFSAERPEGSISTLTIQRTEQRDSAMYRCASSHREPHTGEL FFGEGSRLTVL	2555
V β	MXTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRGQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNIEAQQDKSGLPNDRFSAERPEGSISTLTIQRTEQR DSAMYRCASSHREPHTGELFFGEGSRLTVL (X = any amino acid)	2556
		2557
β chain with WT signal peptide, (substituted) C β	MGTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRGQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNIEAQQDKSGLPNDRFSAERPEGSISTLTIQRTEQR DSAMYRCASSHREPHTGELFFGEGSRLTVLEDLRNVTTPKVSLEFESKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2558
β chain with alternative signal peptide, C β (substituted)	MATSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRGQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNIEAQQDKSGLPNDRFSAERPEGSISTLTIQRTEQR DSAMYRCASSHREPHTGELFFGEGSRLTVLEDLRNVTTPKVSLEFESKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2559
β chain with alternative signal peptide, C β (substituted)	MHTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRGQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNIEAQQDKSGLPNDRFSAERPEGSISTLTIQRTEQR DSAMYRCASSHREPHTGELFFGEGSRLTVLEDLRNVTTPKVSLEFESKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2560

[00350] In some embodiments, TCR056 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR056 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BE. Amino acid sequences of TCR057.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1561

Description	Sequence	SEQ ID NO:
CDR2 α	NVLDGL	1562
CDR3 α	AVYTGGFKTI	1563
V α without signal peptide (SignalP)	QNIDQPTMTATEGAI VQINCTYQTS GFNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYTGGFKTIFGAGTRL FVKA	1564
V α without signal peptide (IMGT)	GQNIDQPTMTATEGAI VQINCTYQTS GFNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYTGGFKTIFGAGTR L FVKA	1565
V α	MXGVFLLYVSMKMGTTGQNIDQPTMTATEGAI VQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKA (X = any amino acid)	1566
		1567
α chain with WT signal peptide, (substituted) C α	MWGVFLLYVSMKMGTTGQNIDQPTMTATEGAI VQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLCCLFTDFDS QINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRL WSS	1568
α chain with alternative signal peptide, (substituted) C α	MAGVFLLYVSMKMGTTGQNIDQPTMTATEGAI VQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLCCLFTDFDS QINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRL WSS	1569
α chain with alternative signal peptide, (substituted) C α	MHG VFLLYVSMKMGTTGQNIDQPTMTATEGAI VQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLCCLFTDFDS QINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRL WSS	1570
CDR1 β	SGHAT	2561
CDR2 β	FQNGV	2562
CDR3 β	ASNLGGGSTDTQY	2563
V β without signal peptide (SignalP)	GVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASNLGGGSTDTQYF GPGTRLTVL	2564
V β without signal peptide (IMGT)	EAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASNLGGGSTDTQ YFGPGTRLTVL	2565
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASNLGGGSTDTQYFGPGTRLTVL (X = any amino acid)	2566
		2567
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASNLGGGSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRAD CCITSASYQQCVLSATILYEILLGKATLYAVLVSTLVVMAMVKRNS	2568

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAEELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASNLGGGSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2569
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAEELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASNLGGGSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2570

[00351] In some embodiments, TCR057 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR057 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BF. Amino acid sequences of TCR058.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASQS	1571
CDR2 α	VYSSGN	1572
CDR3 α	AVNPKYTGGFKTI	1573
V α without signal peptide (SignalP)	QRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVY SSGNEDGRFTAHLNRSQYISLLIRDSKLSDSATYLCVAVNPKYTGGFKTIFG AGTRLFVKA	1574
V α without signal peptide (IMGT)	RKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYS SGNEDGRFTAHLNRSQYISLLIRDSKLSDSATYLCVAVNPKYTGGFKTIFGA GTRLFVKA	1575
V α	MXSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGGFKTIFGAGTRLFVKA (X = any amino acid)	1576 1577
α chain with WT signal peptide, C α (substituted)	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1578
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1579

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFEWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRRASQYISLLIRDSKLSDS ATYLCVAVNPKYTGGEKTFIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1580
CDR1 β	LGHNA	2571
CDR2 β	YSLEER	2572
CDR3 β	ASSQDVTSEWVDTIY	2573
V β without signal peptide (SignalP)	ELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHNAMYWKQSAKKPLELMF VYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQDVTSEWVDTIYFGE GSWLTVV	2574
V β without signal peptide (IMGT)	ETGVTQTTPRHLVMGMTNKKSLKCEQHLGHNAMYWKQSAKKPLELMFVYSLE ERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQDVTSEWVDTIYFGE GSWLTVV	2575
V β	MXCRLCCAVLCCLGAGELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHN AMYWKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGE GSWLTVV (X = any amino acid)	2576
		2577
β chain with WT signal peptide, (substituted) C β	MGCRLCCAVLCCLGAGELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHN AMYWKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGE GSWLTVV VEDLRNVT PPKVS LFEPSK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPK PVTQNI SAEAW GRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2578
β chain with alternative signal peptide, C β (substituted)	MACRLCCAVLCCLGAGELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHN AMYWKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGE GSWLTVV VEDLRNVT PPKVS LFEPSK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPK PVTQNI SAEAW GRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2579
β chain with alternative signal peptide, C β (substituted)	MHCRLCCAVLCCLGAGELVPMETGVTQTTPRHLVMGMTNKKSLKCEQHLGHN AMYWKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGE GSWLTVV VEDLRNVT PPKVS LFEPSK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPK PVTQNI SAEAW GRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2580

[00352] In some embodiments, TCR058 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR058 interacts with the neoantigen in the context of HLA-C*01:02, as described in International Publication No. WO 2021/163477, incorporated herein by reference in its entirety.

Table 6BG. Amino acid sequences of TCR059.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASQS	1581

Description	Sequence	SEQ ID NO:
CDR2 α	VYSSGN	1582
CDR3 α	VVDDQGTGANNLF	1583
V α without signal peptide (SignalP)	QRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVDDQGTGANNLFFGTGTRLTVIP	1584
V α without signal peptide (IMGT)	RKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVDDQGTGANNLFFGTGTRLTVIP	1585
V α	MXSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVDDQGTGANNLFFGTGTRLTVIP (X = any amino acid)	1586
		1587
α chain with WT signal peptide, (substituted) C α	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVDDQGTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTLEKS FETDMNLNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1588
α chain alternative peptide, (substituted) with signal C α	MASLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVDDQGTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTLEKS FETDMNLNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1589
α chain alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVDDQGTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTLEKS FETDMNLNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1590
CDR1 β	MNHEY	2581
CDR2 β	SVGAGI	2582
CDR3 β	ASRN LGDTQY	2583
V β without signal peptide (SignalP)	GVTQTPKFQVLKTGQSM TLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRN LGDTQYFGPGTRTLV	2584
V β without signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSM TLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRN LGDTQYFGPGTRTLV	2585
V β	MXIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRN LGDTQYFGPGTRTLV (X = any amino acid)	2586
		2587
β chain with WT signal peptide, (substituted) C β	MSIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRN LGDTQYFGPGTRTLVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATEFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGIT SASYQQGVL SATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2588

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, Cβ (substituted)	MAIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQ TSVYFCASRNLDGTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2589
β chain with alternative signal peptide, Cβ (substituted)	MHIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQ TSVYFCASRNLDGTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2590

[00353] In some embodiments, TCR059 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR059 interacts with the neoantigen in the context of HLA-C*01:02, as described in International Publication No. WO 2021/163477, incorporated herein by reference in its entirety.

Table 6BH. Amino acid sequences of TCR060.

Description	Sequence	SEQ ID NO:
CDR1α	TSINN	1591
CDR2α	IRSNERE	1592
CDR3α	ATDGETSGSRLT	1593
Vα without signal peptide (SignalP)	QQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIRSN REKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEG TQLTVNP	1594
Vα without signal peptide (IMGT)	SQQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIRSN EREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGE GTQLTVNP	1595
Vα	MXTLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINN LQ WYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNP (X = any amino acid)	1596
		1597
α chain with WT signal peptide, Cα (substituted)	METLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINN LQ WYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPQSQDSTLCF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLT EKS FETDMNLNFQNL LVI VLRI LLLKVAGFNLL MTLRLWSS	1598
α chain with alternative signal peptide, Cα (substituted)	MATLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINN LQ WYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPQSQDSTLCF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLT EKS FETDMNLNFQNL LVI VLRI LLLKVAGFNLL MTLRLWSS	1599

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHTLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINNLO WYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFEGGTQLTVNPNIQNPEPAVYQLKDPRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIF KETNATYPSSDVPDATLTEKSFETDMNLNFQNL LVI VLRILLK VAGFNLL MTLRLWSS	1600
CDR1 β	DFQATT	2591
CDR2 β	SNFGSKA	2592
CDR3 β	SASRGATGQPQH	2593
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSASRGA TGQPQHFGDGTRLSIL	2594
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSASRGATGQP QHFGDGTRLSIL	2595
V β	MXLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSIL (X = any amino acid)	2596
		2597
β chain with WT signal peptide, (substituted) C β	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSILEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NS	2598
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSILEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NS	2599
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSILEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NS	2600

[00354] In some embodiments, TCR060 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR060 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

Table 6BI. Amino acid sequences of TCR061.

Description	Sequence	SEQ ID NO:
CDR1 α	SSNFYA	1601
CDR2 α	MTLNGDE	1602
CDR3 α	AFTTGNQFY	1603
V α w/o signal peptide (SignalP)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIP	1604
V α w/o signal peptide (IMGT)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIP	1605
V α	MXKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIP	1606
	(X = any amino acid)	1607
α chain w/WT signal peptide, C α (substituted)	MEKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLT EKS FETDMNLNLFQNL LVIVLRILLKLVAGFNL LMTLRLWSS	1608
α chain w/alternative signal peptide, C α (substituted)	MAKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLT EKS FETDMNLNLFQNL LVIVLRILLKLVAGFNL LMTLRLWSS	1609
α chain w/alternative signal peptide, C α (substituted)	MHKNPLAAPLLILWFHLDVCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLT EKS FETDMNLNLFQNL LVIVLRILLKLVAGFNL LMTLRLWSS	1610
CDR1 β	SGHDYL	2601
CDR2 β	FNNNVF	2602
CDR3 β	ASSSYGGYSNQPH	2603
V β w/o signal peptide (SignalP)	GVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKI QPSEPRDSAVYFCASSSYGGYSNQPHFGDGTRLSIL	2604
V β w/o signal peptide (IMGT)	DAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKI QPSEPRDSAVYFCASSSYGGYSNQPHFGDGTRLSIL	2605
V β	MXSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKI QPSEPRDSAVYFCASSSYGGYSNQPHFGDGTRLSIL	2606
	(X = any amino acid)	2607
β chain w/WT signal peptide, C β (substituted)	MGSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKI QPSEPRDSAVYFCASSSYGGYSNQPHFGDGTRLSILEDLRNVT PPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATLFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2608

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MASWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLF WYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFSAKMPNASFSTLKIQPSEPR DSAVYFCASSSYGGYSNQPHFGDGTRLSILEDLRNVTTPKVSLEFESKAIEI ANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKNS	2609
β chain w/alternative signal peptide, C β (substituted)	MHSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLF WYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFSAKMPNASFSTLKIQPSEPR DSAVYFCASSSYGGYSNQPHFGDGTRLSILEDLRNVTTPKVSLEFESKAIEI ANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKNS	2610

[00355] In some embodiments, TCR061 interacts with and/or is specific for tumor protein KRAS (KRAS). In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12C relative to the wild type KRAS sequence. In some embodiments, TCR061 interacts with the neoantigen in the context of HLA-DRB1*11:01 as described in International Publication No. WO 2019/060349, incorporated herein by reference in its entirety.

Table 6BJ. Amino acid sequences of TCR062.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1611
CDR2 α	GYKTK	1612
CDR3 α	LVGDMDQAGTALI	1613
V α w/o signal peptide (SignalP)	KTTPQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTK VTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGT TSLSVSS	1614
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYK TKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGK GTTLSVSS	1615
V α	MXQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMDQAGTALIFGKGTTLVSS (X = any amino acid)	1616
		1617
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMDQAGTALIFGKGTTLVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVLVIVLRILLKLVAGFNLLMT LRLWSS	1618
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMDQAGTALIFGKGTTLVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVLVIVLRILLKLVAGFNLLMT LRLWSS	1619

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPREFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDDQAGTALIFGKGTTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVEKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVIVLRILLKLVAGFNLLMTLRLWSS	1620
CDR1 β	SGHDT	2611
CDR2 β	YEEEE	2612
CDR3 β	ASSLGEGRVDGYT	2613
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDSALYLCASSLGEGRVDGYTFGSGTRLTVV	2614
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDSALYLCASSLGEGRVDGYTFGSGTRLTVV	2615
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDSALYLCASSLGEGRVDGYTFGSGTRLTVV (X = any amino acid)	2616
		2617
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDSALYLCASSLGEGRVDGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2618
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDSALYLCASSLGEGRVDGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2619
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDSALYLCASSLGEGRVDGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2620

[00356] In some embodiments, TCR062 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR062 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BK. Amino acid sequences of TCR063.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1621

Description	Sequence	SEQ ID NO:
CDR2 α	GYKTK	1622
CDR3 α	LVGDMDQAGTALI	1623
V α w/o signal peptide (SignalP)	KTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFP SQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSS	1624
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFP SQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSS	1625
V α	MXQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFP SQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSS (X = any amino acid)	1626
		1627
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFP SQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDP RSQDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL LVIVLRILLKLVAGFNLLMTLRLWSS	1628
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFP SQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDP RSQDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL LVIVLRILLKLVAGFNLLMTLRLWSS	1629
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFP SQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDP RSQDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL LVIVLRILLKLVAGFNLLMTLRLWSS	1630
CDR1 β	SGHDT	2621
CDR2 β	YEEEE	2622
CDR3 β	ASSLGRASNQPOH	2623
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCS PKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPOHFGDGTRLSIL	2624
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCS PKSGHDTVSWYQQALGQGPQFI FQYEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPOHFGDGTRLSIL	2625
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCS PKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPOHFGDGTRLSIL (X = any amino acid)	2626
		2627
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCS PKSGHDTVSWYQQALGQGPQFI FQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPOHFGDGTRLSILEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITSASYQQGVL SATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2628

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYQQALGQGPQFIFQYEEEEERQGRNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPOHFQDGTSLILEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2629
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYQQALGQGPQFIFQYEEEEERQGRNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPOHFQDGTSLILEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2630

[00357] In some embodiments, TCR063 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR063 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BL. Amino acid sequences of TCR064.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1631
CDR2 α	GYKTK	1632
CDR3 α	LVGDRDQAGTALI	1633
V α w/o signal peptide (SignalP)	KTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTK VTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDRDQAGTALIFGKGT TSLSVSS	1634
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYK TKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDRDQAGTALIFGK GTTLVSVSS	1635
V α	MXQVARVIVFLTSLTSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLVSVSS (X = any amino acid)	1636
		1637
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTSLTSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLVSVSSNIQNPEPAVYQLKDPKSDSTLCCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1638
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTSLTSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLVSVSSNIQNPEPAVYQLKDPKSDSTLCCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1639

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTSLTSLAKTTQPISMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPREFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDRDQAGTALIFGKGTTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVEKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1640
CDR1 β	SGHDT	2631
CDR2 β	YEEEE	2632
CDR3 β	ASSFGQSSTYGYT	2633
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSFGQSSTYGYTFGSGTRLTVV	2634
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSFGQSSTYGYTFGSGTRLTVV	2635
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSFGQSSTYGYTFGSGTRLTVV (X = any amino acid)	2636
		2637
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSFGQSSTYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2638
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSFGQSSTYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2639
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQRGNFDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSFGQSSTYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2640

[00358] In some embodiments, TCR064 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR064 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BM. Amino acid sequences of TCR065.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1641

Description	Sequence	SEQ ID NO:
CDR2 α	GYKTK	1642
CDR3 α	LVGDMDQAGTALI	1643
V α w/o signal peptide (SignalP)	KTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFI PADRKSSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSS	1644
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFI PADRKSSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSS	1645
V α	MXQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFI PADRKSSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSS (X = any amino acid)	1646
		1647
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFI PADRKSSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1648
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFI PADRKSSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1649
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFI PADRKSSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1650
CDR1 β	SGHDT	2641
CDR2 β	YEEEE	2642
CDR3 β	ASSLGQTNNGYT	2643
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSLGQTNNGYTFGSGTRLTVV	2644
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSLGQTNNGYTFGSGTRLTVV	2645
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSLGQTNNGYTFGSGTRLTVV (X = any amino acid)	2646
		2647
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLLGDLSALYLCASSLGQTNNGYTFGSGTRLTVVVEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2648

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYQQALGQGPQFIFQYEEEEERQRGNFDPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGQTNYG YTFGSGTRLT VVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2649
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYQQALGQGPQFIFQYEEEEERQRGNFDPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGQTNYG YTFGSGTRLT VVEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2650

[00359] In some embodiments, TCR065 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR065 interacts with the neoantigen in the context of HLA-Cw*08:02 as described in International Publication No. WO 2017/048593, incorporated herein by reference in its entirety.

Table 6BN. Amino acid sequences of TCR066.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1651
CDR2 α	IYSNGD	1652
CDR3 α	AAAMDSSYKLI	1653
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIY SNGDKEDGRFTAQLNKASQYVSLLRDSQPSDSATYLCAAAMDSSYKLIFGSG GTRLLVRP	1654
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYS NGDKEDGRFTAQLNKASQYVSLLRDSQPSDSATYLCAAAMDSSYKLIFGSG GTRLLVRP	1655
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLLRDSQPSD SATYLCAAAMDSSYKLIFGSGTRLLVRP (X = any amino acid)	1656
		1657
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLLRDSQPSD SATYLCAAAMDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPKSDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1658
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLLRDSQPSD SATYLCAAAMDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPKSDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1659

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFEWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSD SATYLCAAAMDSSYKLIFGSGTRLLVVRNIQNPEPAVYQLKDPRSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRIILLKVAGFNL LMTLRLWSS	1660
CDR1 β	WSHSY	2651
CDR2 β	SAAADI	2652
CDR3 β	ASSDPGTEAF	2653
V β w/o signal peptide (SignalP)	GITQSPRYKITETGRQVTLMCHQTWSHSYMFWYRQDLGHGLRLIYYSAAADI TDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSDPGTEAFFGQGT RLTVV	2654
V β w/o signal peptide (IMGT)	DAGITQSPRYKITETGRQVTLMCHQTWSHSYMFWYRQDLGHGLRLIYYSAA DITDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSDPGTEAFFGQ GTRLTVV	2655
V β	MXTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVV (X = any amino acid)	2656
		2657
β chain w/WT signal peptide, C β (substituted)	MGTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVVEDLRNVTPPKVSLEFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATEFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2658
β chain w/alternative signal peptide, C β (substituted)	MATRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVVEDLRNVTPPKVSLEFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATEFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2659
β chain w/alternative signal peptide, C β (substituted)	MHTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYYSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVVEDLRNVTPPKVSLEFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATEFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2660

[00360] In some embodiments, TCR066 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR066 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BO. Amino acid sequences of TCR067.

Description	Sequence	SEQ ID NO:
CDR1 α	TIYSNPF	1661

Description	Sequence	SEQ ID NO:
CDR2 α	SFTDNKR	1662
CDR3 α	ALRGNAGAKLT	1663
V α w/o signal peptide (SignalP)	DGDSVTQTTEGLVTLTEGLPVMNLCTYQTIYSNPFLFWYVQHLNESPRLLKSF FTDNKRTEHQGFHATLHKSSSSSFHLQKSSAQLSDSALYYCALRGNAGAKLTF GGGTRLTVRPD	1664
V α w/o signal peptide (IMGT)	GDSVTQTTEGLVTLTEGLPVMNLCTYQTIYSNPFLFWYVQHLNESPRLLKSF TDNKRTEHQGFHATLHKSSSSSFHLQKSSAQLSDSALYYCALRGNAGAKLTFG GGTRLTVRPD	1665
V α	MXPVTCSVLVLLMLRRSNGDGDSVTQTTEGLVTLTEGLPVMNLCTYQTIYSN PFLFWYVQHLNESPRLLKSF FTDNKRTEHQGFHATLHKSSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPD (X = any amino acid)	1666
		1667
α chain w/WT signal peptide, C α (substituted)	MRPVTCSVLVLLMLRRSNGDGDSVTQTTEGLVTLTEGLPVMNLCTYQTIYSN PFLFWYVQHLNESPRLLKSF FTDNKRTEHQGFHATLHKSSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPDIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIASWNTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVSMGLRI LLLKVAGF NLLMTLRLWSS	1668
α chain w/alternative signal peptide, C α (substituted)	MAPVTCSVLVLLMLRRSNGDGDSVTQTTEGLVTLTEGLPVMNLCTYQTIYSN PFLFWYVQHLNESPRLLKSF FTDNKRTEHQGFHATLHKSSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPDIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIASWNTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVSMGLRI LLLKVAGF NLLMTLRLWSS	1669
α chain w/alternative signal peptide, C α (substituted)	MHPVTCSVLVLLMLRRSNGDGDSVTQTTEGLVTLTEGLPVMNLCTYQTIYSN PFLFWYVQHLNESPRLLKSF FTDNKRTEHQGFHATLHKSSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPDIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIASWNTSFTCQ DIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVSMGLRI LLLKVAGF NLLMTLRLWSS	1670
CDR1 β	LGHDT	2661
CDR2 β	YNNKQL	2662
CDR3 β	ASSSRDWSAETLY	2663
V β w/o signal peptide (SignalP)	AVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNKQL IVNETVPRRFSPQSSDKAHLNLRIKSVEPEDSAVYLCASSSRDWSAETLYFG SGTRLTVL	2664
V β w/o signal peptide (IMGT)	ETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNK QLIVNETVPRRFSPQSSDKAHLNLRIKSVEPEDSAVYLCASSSRDWSAETLY FGSGTRLTVL	2665
V β	MXCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVL (X = any amino acid)	2666
		2667
β chain w/WT signal peptide, C β (substituted)	MGCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVLEDLRNVTTPPKVSLFEPKAEIAN KQKATLVCLARGFPPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC CITSASYHQCVLSATILYETILLGKATLYAVLVSGVLVLMAMVKKKNS	2668

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MACRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC GITSASYHQGVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS	2669
β chain w/alternative signal peptide, C β (substituted)	MHCRLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADC GITSASYHQGVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS	2670

[00361] In some embodiments, TCR067 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR067 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BP. Amino acid sequences of TCR068.

Description	Sequence	SEQ ID NO:
CDR1 α	DPNSYY	1671
CDR2 α	VFSSTEL	1672
CDR3 α	AVSGGTNSAGNKLT	1673
V α w/o signal peptide (SignalP)	EQVEQRPPHLSVREGDSAVITCTYTDPN SYFFWYKQEPGASLQLLMKVFS TEINEGQGFTVLLNKKDKRLSLNLTA AHPGDSAAYFCAVSGGTNSAGNKLT FGIGTRVLVRP	1674
V α w/o signal peptide (IMGT)	GEQVEQRPPHLSVREGDSAVITCTYTDPN SYFFWYKQEPGASLQLLMKVFS STEINEGQGFTVLLNKKDKRLSLNLTA AHPGDSAAYFCAVSGGTNSAGNKLT FGIGTRVLVRP	1675
V α	MXTVTGPLFLCFWLQ LNCVSRGEQVEQRPPHLSVREGDSAVITCTYTDPN SY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTA AHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRP (X = any amino acid)	1676
		1677
α chain w/WT signal peptide, C α (substituted)	MKTVTGPLFLCFWLQ LNCVSRGEQVEQRPPHLSVREGDSAVITCTYTDPN SY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTA AHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRPDIQNPEPAVYQLKDPRSQDS TLCFLTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVPDATLT EKS FETDMNLNFQNL SVMGLRILLKVA GFNLLMTLRLWSS	1678

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MATVTGPLFLCFWLQINCVSERGEQVEQRPPHLSVREGDSAVITCTYTDPN SY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTA AHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRPDIQNPEPAVYQLKDPRS QDS TLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQT SFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL SVMGLRI LLLKVA GENLLMTLRLWSS	1679
α chain w/alternative signal peptide, C α (substituted)	MHTVTGPLFLCFWLQINCVSERGEQVEQRPPHLSVREGDSAVITCTYTDPN SY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTA AHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRPDIQNPEPAVYQLKDPRS QDS TLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQT SFT CQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL SVMGLRI LLLKVA GENLLMTLRLWSS	1680
CDR1 β	LGHDT	2671
CDR2 β	YNNKQL	2672
CDR3 β	ASSRDWGP AEQF	2673
V β w/o signal peptide (SignalP)	AVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNKQL IVNETVPRRFSPQSSDKAHLNLRIKSVEPEDSAVYLCASSRDWGP AEQFFGP GTRLTVL	2674
V β w/o signal peptide (IMGT)	ETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNK QLIVNETVPRRFSPQSSDKAHLNLRIKSVEPEDSAVYLCASSRDWGP AEQFF GP GTRLTVL	2675
V β	MXCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSRDWGP AEQFFGP GTRLTVL (X = any amino acid)	2676
		2677
β chain w/WT signal peptide, C β (substituted)	MGCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSRDWGP AEQFFGP GTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYHQGVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS	2678
β chain w/alternative signal peptide, C β (substituted)	MACRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSRDWGP AEQFFGP GTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYHQGVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS	2679
β chain w/alternative signal peptide, C β (substituted)	MHCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSRDWGP AEQFFGP GTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCG ITSASYHQGVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS	2680

[00362] In some embodiments, TCR068 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR068 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BQ. Amino acid sequences of TCR069.

Description	Sequence	SEQ ID NO:
CDR1 α	NDMFDY	1681
CDR2 α	VRSNVDK	1682
CDR3 α	AAGDSGGSNYKLT	1683
V α w/o signal peptide (SignalP)	QQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWYKKYPDNSPTLLISVRSNVDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLC AAGDSGGSNYKLTFGKGTLLTVTP	1684
V α w/o signal peptide (IMGT)	QQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWYKKYPDNSPTLLISVRSNVDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLC AAGDSGGSNYKLTFGKGTLLTVTP	1685
V α	MXGFLKALLLVLCRLPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWYKKYPDNSPTLLISVRSNVDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLC AAGDSGGSNYKLTFGKGTLLTVTP (X = any amino acid)	1686
		1687
α chain w/WT signal peptide, C α (substituted)	MTGFLKALLLVLCRLPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWYKKYPDNSPTLLISVRSNVDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLC AAGDSGGSNYKLTFGKGTLLTVTPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL SVMGLRILL LKVAGFNLLMTLRLWSS	1688
α chain w/alternative signal peptide, C α (substituted)	MAGFLKALLLVLCRLPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWYKKYPDNSPTLLISVRSNVDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLC AAGDSGGSNYKLTFGKGTLLTVTPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL SVMGLRILL LKVAGFNLLMTLRLWSS	1689
α chain w/alternative signal peptide, C α (substituted)	MHGFLKALLLVLCRLPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWYKKYPDNSPTLLISVRSNVDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLC AAGDSGGSNYKLTFGKGTLLTVTPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL SVMGLRILL LKVAGFNLLMTLRLWSS	1690
CDR1 β	NSHNY	2681
CDR2 β	SYGAGN	2682
CDR3 β	ASASWGGYAEQF	2683
V β w/o signal peptide (SignalP)	AVTQSPRNKVTVTGGNVTLSQRQTNSHNYMYWYRQDTGHGLRLIHYSYAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTSLYFCASASWGGYAEQFFGPGTRRLTVL	2684
V β w/o signal peptide (IMGT)	EAAVTQSPRNKVTVTGGNVTLSQRQTNSHNYMYWYRQDTGHGLRLIHYSYAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTSLYFCASASWGGYAEQFFGPGTRRLTVL	2685
V β	MXSRLFLVLSLLCTKHMEAAVTQSPRNKVTVTGGNVTLSQRQTNSHNYMYWYRQDTGHGLRLIHYSYAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTSLYFCASASWGGYAEQFFGPGTRRLTVL (X = any amino acid)	2686
		2687

Description	Sequence	SEQ ID NO:
β chain w/WT signal peptide, C β (substituted)	MGSRLFLVLSSLCTKHMEAAVTQSPRNKVTVTGGNVTLSQRQTNSHNYMYWY RQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRITTQEDFFLLLELASPSQTS LYFCASASWGGYAEQFFGPGTRLTVLEDLRNVTTPPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGIT SASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2688
β chain w/alternative signal peptide, C β (substituted)	MASRLFLVLSSLCTKHMEAAVTQSPRNKVTVTGGNVTLSQRQTNSHNYMYWY RQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRITTQEDFFLLLELASPSQTS LYFCASASWGGYAEQFFGPGTRLTVLEDLRNVTTPPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGIT SASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2689
β chain w/alternative signal peptide, C β (substituted)	MHSRLFLVLSSLCTKHMEAAVTQSPRNKVTVTGGNVTLSQRQTNSHNYMYWY RQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRITTQEDFFLLLELASPSQTS LYFCASASWGGYAEQFFGPGTRLTVLEDLRNVTTPPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGIT SASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2690

[00363] In some embodiments, TCR069 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR069 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BR. Amino acid sequences of TCR070.

Description	Sequence	SEQ ID NO:
CDR1 α	TTMRS	1691
CDR2 α	LASGT	1692
CDR3 α	AADSSNTGYQNFY	1693
V α w/o signal peptide (SignalP)	DQVEQSPSALS LHEGTD SALRCNFTTTTMRSVQWFRQNSRGSLISLFY LASGT KENGRLKSAFDSKERRYSTLHIRDAQLED SGTYFCAADSSNTGYQNFYFGKG TSLTVIP	1694
V α w/o signal peptide (IMGT)	GDQVEQSPSALS LHEGTD SALRCNFTTTTMRSVQWFRQNSRGSLISLFY LASG TKENGRLKSAFDSKERRYSTLHIRDAQLED SGTYFCAADSSNTGYQNFYFGK GTSLTVIP	1695
V α	MXRNLGAVLGILWVQICWVRGDQVEQSPSALS LHEGTD SALRCNFTTTTMRSV QWFRQNSRGSLISLFY LASG TKENGRLKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTGYQNFYFGKG TSLTVIP (X = any amino acid)	1696
		1697

Description	Sequence	SEQ ID NO:
α chain w/WT signal peptide, C α (substituted)	MQRNLGAVLGILWVQICWVRGDQVEQSPSALS LHEGTD SALRCNFTTTMRSV QWFRQNSRGLISLFY LASG TKENGR LKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTGYQNFYFGKGTSLTVI PNIQNPEPAVYQLKDPRS QDSTLCL ETD FDSQINVPKTMESGTFITDKTVLDMKAMDSK SNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS	1698
α chain w/alternative signal peptide, C α (substituted)	MARNLGAVLGILWVQICWVRGDQVEQSPSALS LHEGTD SALRCNFTTTMRSV QWFRQNSRGLISLFY LASG TKENGR LKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTGYQNFYFGKGTSLTVI PNIQNPEPAVYQLKDPRS QDSTLCL ETD FDSQINVPKTMESGTFITDKTVLDMKAMDSK SNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS	1699
α chain w/alternative signal peptide, C α (substituted)	MHRNLGAVLGILWVQICWVRGDQVEQSPSALS LHEGTD SALRCNFTTTMRSV QWFRQNSRGLISLFY LASG TKENGR LKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTGYQNFYFGKGTSLTVI PNIQNPEPAVYQLKDPRS QDSTLCL ETD FDSQINVPKTMESGTFITDKTVLDMKAMDSK SNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS	1700
CDR1 β	SGHLS	2691
CDR2 β	IYDKME	2692
CDR3 β	ASSLTDP L DSDYT	2693
V β w/o signal peptide (SignalP)	NSGVVQSPRYIIKGK GERSILKCIPI SGHLSVAWYQQTQGQELKFFIQHYDK MERDKGNLPSRFSVQQFDDYHSE MNMSALELED SAVYFCASSLTDP L DSDYT FGS GTRLLVI	2694
V β w/o signal peptide (IMGT)	SGVVQSPRYIIKGK GERSILKCIPI SGHLSVAWYQQTQGQELKFFIQHYDKM ERDKGNLPSRFSVQQFDDYHSE MNMSALELED SAVYFCASSLTDP L DSDYT FGS GTRLLVI	2695
V β	MXNTAFPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELED SAVYFCASSLTDP L DSDYT FGS GTRLLVI (X = any amino acid)	2696
		2697
β chain w/WT signal peptide, C β (substituted)	MSNTAFPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELED SAVYFCASSLTDP L DSDYT FGS GTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSAS YQQGVLSATILYEI LLGKATLYAVLVSTLVMMAMVK RKNS	2698
β chain w/alternative signal peptide, C β (substituted)	MANTAFPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELED SAVYFCASSLTDP L DSDYT FGS GTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSAS YQQGVLSATILYEI LLGKATLYAVLVSTLVMMAMVK RKNS	2699
β chain w/alternative signal peptide, C β (substituted)	MHNTAFPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELED SAVYFCASSLTDP L DSDYT FGS GTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSAS YQQGVLSATILYEI LLGKATLYAVLVSTLVMMAMVK RKNS	2700

[00364] In some embodiments, TCR070 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR070 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BS. Amino acid sequences of TCR071.

Description	Sequence	SEQ ID NO:
CDR1 α	TTMRS	1701
CDR2 α	LASGT	1702
CDR3 α	AADSSNTZYQNFY (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1703
V α w/o signal peptide (SignalP)	DQVEQSPSALS LHEGTD SALRCNFTTTMRSVQWFRQNSRGS LISLFY LASGT KENGRLKSAFDSKERRYSTLHIRDAQLED SGTYFCAADSSNTZYQNFYFGKG TSLTVIP (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1704
V α w/o signal peptide (IMGT)	GDQVEQSPSALS LHEGTD SALRCNFTTTMRSVQWFRQNSRGS LISLFY LASGT TKENGRLKSAFDSKERRYSTLHIRDAQLED SGTYFCAADSSNTZYQNFYFGKG GTSLTVIP (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1705
V α	MXRNLGAVLGILWVQICWVRGDQVEQSPSALS LHEGTD SALRCNFTTTMRSV QWFRQNSRGS LISLFY LASGT KENGRLKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTZYQNFYFGKG TSLTVIP (X = any amino acid) (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1706
		1707
α chain w/WT signal peptide, C α (substituted)	MQRNLGAVLGILWVQICWVRGDQVEQSPSALS LHEGTD SALRCNFTTTMRSV QWFRQNSRGS LISLFY LASGT KENGRLKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTZYQNFYFGKG TSLTVIPNIQNPEPAVYQLKDP RSQDSTLCL FTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLSVMGLRILLK VAGFNL LMTLRLWSS (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1708

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MARNLGAVLGILWVQICWVRGDQVEQSPSALSLHEGTDLSALRCNFTTTMRSV QWFRQNSRGSLSISLFYLASGTKENGRKLSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTZ YQNFYFGKGTSLTVI PNIQNPEPAVYQLKDPRS QDSTLCL FTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1709
α chain w/alternative signal peptide, C α (substituted)	MHRNLGAVLGILWVQICWVRGDQVEQSPSALSLHEGTDLSALRCNFTTTMRSV QWFRQNSRGSLSISLFYLASGTKENGRKLSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTZ YQNFYFGKGTSLTVI PNIQNPEPAVYQLKDPRS QDSTLCL FTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1710
CDR1 β	SGHLS	2701
CDR2 β	HYDKME	2702
CDR3 β	CASSLTDPDLSDYTF	2703
V β w/o signal peptide (SignalP)	NSGVVQSPRYIIKGKERSILKCIPISGHLSVAWYQQTQGGQELKFFIQHYDK MERDKGNLPSRFSVQQFDDYHSEMNMSALELEDSAVYFCASSLTDPDLSDYT FGSGTRLLVI	2704
V β w/o signal peptide (IMGT)	SGVVQSPRYIIKGKERSILKCIPISGHLSVAWYQQTQGGQELKFFIQHYDKM ERDKGNLPSRFSVQQFDDYHSEMNMSALELEDSAVYFCASSLTDPDLSDYTF GSGTRLLVI	2705
V β	MXNTAFDPDPAWNTTLLSWVALFLLGTSSANS SGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPDLSDYTFGSGTRLLVI (X = any amino acid)	2706
		2707
β chain w/WT signal peptide, C β (substituted)	MSNTAFDPDPAWNTTLLSWVALFLLGTSSANS SGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPDLSDYTFGSGTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGITSAS YQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVK RKNS	2708
β chain w/alternative signal peptide, C β (substituted)	MANTAFDPDPAWNTTLLSWVALFLLGTSSANS SGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPDLSDYTFGSGTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGITSAS YQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVK RKNS	2709
		2710

[00365] In some embodiments, TCR071 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some

embodiments, TCR071 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BT. Amino acid sequences of TCR072.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1711
CDR2 α	IYSNGD	1712
CDR3 α	AVEGAGSYQLT	1713
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIP	1714
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIP	1715
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIP (X = any amino acid)	1716
		1717
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1718
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1719
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1720
CDR1 β	DFQATT	2711
CDR2 β	SNEGSKA	2712
CDR3 β	SASNRLAVNEQF	2713
V β w/o signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNESKATYEQGVEKDKFLINHASLTLSLTITVTSAPEDSSFYICASNRLAVNEQFFGPGTRLTVL	2714
V β w/o signal peptide (IMGT)	GAVVSQHPSWVICKSGTSSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNESKATYEQGVEKDKFLINHASLTLSLTITVTSAPEDSSFYICASNRLAVNEQFFGPGTRLTVL	2715
V β	MXLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNESKATYEQGVEKDKFLINHASLTLSLTITVTSAPEDSSFYICASNRLAVNEQFFGPGTRLTVL (X = any amino acid)	2716
		2717

Description	Sequence	SEQ ID NO:
β chain w/WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMEFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSA SNRLAVNEQFFGPGTRLTVLEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2718
β chain w/alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMEFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSA SNRLAVNEQFFGPGTRLTVLEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2719
β chain w/alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSSVKIECRSLD FQATTMEFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTL TVTSAHPEDSSFYICSA SNRLAVNEQFFGPGTRLTVLEDLRNVT PPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2720

[00366] In some embodiments, TCR072 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12R relative to the wild type KRAS sequence. In some embodiments, TCR072 interacts with the neoantigen in the context of HLA-DQA1*05:05:HLA-DQB1*03:01 heterodimer as described in International Publication No. WO 2020/154275, incorporated herein by reference in its entirety.

Table 6BU. Amino acid sequences of TCR073.

Description	Sequence	SEQ ID NO:
CDR1 α	NSMFDY	1721
CDR2 α	ISISSIKDK	1722
CDR3 α	AASGNTGTASKLT	1723
V α w/o signal peptide (SignalP)	QQKNDDQQVKQNSP SLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFL ISISSIKDKNEDGRETFVFLNKS AKHLSLHIVPSQPGDSAVYFCAASGNTGTAS SKLTFGTGTRLQVTL	1724
V α w/o signal peptide (IMGT)	DQQVKQNSP SLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISS IKDKNEDGRETFVFLNKS AKHLSLHIVPSQPGDSAVYFCAASGNTGTASKLTF GTGTRLQVTL	1725
V α	MXMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSP SLSVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRETFVFLNKS AKHLSLHIV PSQPGDSAVYFCAASGNTGTASKLTFGTGTRLQVTL (X = any amino acid)	1726
		1727

Description	Sequence	SEQ ID NO:
α chain w/WT signal peptide, C α (substituted)	MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISSISKDNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAASGNTGTASKLTFTGTGTRLQVTLNIQNPEPAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVLRILL LKVAGFNLLMTLRLWSS	1728
α chain w/alternative signal peptide, C α (substituted)	MHMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISSISKDNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAASGNTGTASKLTFTGTGTRLQVTLNIQNPEPAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVLRILL LKVAGFNLLMTLRLWSS	1729 1730
CDR1 β	LNHDA	2721
CDR2 β	SQIVND	2722
CDR3 β	ASSNQIVTGGYGYT	2723
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLV TGGYGYTFGSGTRLTVV	2724
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLV TGGYGYTFGSGTRLTVV	2725
V β	MXNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLV TGGYGYTFGSGTRLTVV (X = any amino acid)	2726 2727
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLV TGGYGYTFGSGTRLTVVEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNTISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2728
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLV TGGYGYTFGSGTRLTVVEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNTISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2729
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLV TGGYGYTFGSGTRLTVVEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNTISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2730

[00367] In some embodiments, TCR073 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12R relative to the wild type KRAS sequence. In some embodiments, TCR073 interacts with the neoantigen in the context of HLA-DRB5*01:HLA-DRA*01 :01 heterodimer as described in International Publication No. WO 2020/154275, incorporated herein

by reference in its entirety.

Table 6BV. Amino acid sequences of TCR074.

Description	Sequence	SEQ ID NO:
CDR1 α	TIYSNAF	1731
CDR2 α	SSTDNKR	1732
CDR3 α	ALSEGGNYKYV	1733
V α w/o signal peptide (SignalP)	DGDSVTQKEGLVTLTEGLPVMLNCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIA	1734
V α w/o signal peptide (IMGT)	GDSVTQKEGLVTLTEGLPVMLNCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIA	1735
V α	MXPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMLNCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIA (X = any amino acid)	1736
		1737
α chain w/WT signal peptide, C α (substituted)	MRPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMLNCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1738
α chain w/alternative signal peptide, C α (substituted)	MAPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMLNCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1739
α chain w/alternative signal peptide, C α (substituted)	MHPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMLNCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1740
CDR1 β	NSQYPW	2731
CDR2 β	LRSPGD	2732
CDR3 β	TCSARHSAETLY	2733
V β w/o signal peptide (SignalP)	DPTVTLLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRITLYCTCSARHSAETLYFGSGTRITVL	2734
V β w/o signal peptide (IMGT)	VTLLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRITLYCTCSARHSAETLYFGSGTRITVL	2735
V β	MXQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRITLYCTCSARHSAETLYFGSGTRITVL (X = any amino acid)	2736
		2737

Description	Sequence	SEQ ID NO:
β chain w/WT signal peptide, C β (substituted)	MWQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRCILKNSQYP WMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANM SQGRTLYCTCSARHSAETLYFGSGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2738
β chain w/alternative signal peptide, C β (substituted)	MAQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRCILKNSQYP WMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANM SQGRTLYCTCSARHSAETLYFGSGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2739
β chain w/alternative signal peptide, C β (substituted)	MHQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRCILKNSQYP WMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANM SQGRTLYCTCSARHSAETLYFGSGTRLTVLEDLRNVT PPKVSLFEPSKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2740

[00368] In some embodiments, TCR074 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR074 interacts with the neoantigen in the context of HLA-A3 heterodimer as described in International Publication No. WO 2020/086827, incorporated herein by reference in its entirety.

Table 6BW. Amino acid sequences of TCR075.

Description	Sequence	SEQ ID NO:
CDR1 α	TSDEPSYG	1741
CDR2 α	QGSYDQQN	1742
CDR3 α	AMRGASQGGSEKLV	1743
V α w/o signal peptide (SignalP)	QKITQTQPGMFVQEKEAVTLDCTYDTS DPSYGLFWYKQPSSGEMIFLIYQGS YDQQNATEGGRYS LNFQKARKSANLVI SASQLGDSAMYFCAMRGASQGGSEKL VFGKGT KLT VNP	1744
V α w/o signal peptide (IMGT)	AQKITQTQPGMFVQEKEAVTLDCTYDTS DPSYGLFWYKQPSSGEMIFLIYQG SYDQQNATEGGRYS LNFQKARKSANLVI SASQLGDSAMYFCAMRGASQGGSEK LVFGKGT KLT VNP	1745
V α	MXLSSLLKVVTASLWLGP GIAQKITQTQPGMFVQEKEAVTLDCTYDTS DPSY GLFWYKQPSSGEMIFLIYQGSYDQQNATEGGRYS LNFQKARKSANLVI SASQL GDSAMYFCAMRGASQGGSEKLVFGKGT KLT VNP	1746
	(X = any amino acid)	1747
α chain w/WT signal peptide, C α (substituted)	MSLSSLLKVVTASLWLGP GIAQKITQTQPGMFVQEKEAVTLDCTYDTS DPSY GLFWYKQPSSGEMIFLIYQGSYDQQNATEGGRYS LNFQKARKSANLVI SASQL GDSAMYFCAMRGASQGGSEKLVFGKGT KLT VNPNIQNPEPAVYQLKDP RSQD STLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMD SKNGAIAWSNQTSF TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNL LVIVLRI LLLKV AGFNLLMTLR LWSS	1748

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MALSSLLKVV TASLWLGP GIAQKITQTQPGMFVQEKEAVTLDCTYDTS DPSY GLEWYKQPSSGEMIFLIYQGSYDQQNATEGRYSLNFQKARKSANLVISASQL GDSAMYFCAMRGASQGGSEKLVFGKGT KLT VNPNIQNPEPAVYQLKDPRS QD STLCLFTDFDSQINVPKTME SGT FITDKCVLDMKAMDSKSN GAI A WSNQTSF TCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKV AGENLLMTLRLWSS	1749
α chain w/alternative signal peptide, C α (substituted)	MHLSSLLKVV TASLWLGP GIAQKITQTQPGMFVQEKEAVTLDCTYDTS DPSY GLEWYKQPSSGEMIFLIYQGSYDQQNATEGRYSLNFQKARKSANLVISASQL GDSAMYFCAMRGASQGGSEKLVFGKGT KLT VNPNIQNPEPAVYQLKDPRS QD STLCLFTDFDSQINVPKTME SGT FITDKCVLDMKAMDSKSN GAI A WSNQTSF TCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNL LVIVLRI LLLKV AGENLLMTLRLWSS	1750
CDR1 β	SGHRS	2741
CDR2 β	YFSETQ	2742
CDR3 β	ASSLTSGGFDEQF	2743
V β w/o signal peptide (SignalP)	GVTQT P RYLIKTRGQQVTLS CSPISGHR SVSWYQQTPGQGLQFLFEYFSETQ RNKGNFPGRFSGRQFSNSRSE MNVSTLELGDSALYLCASSLTSGGFDEQFFG PGTRLTVL	2744
V β w/o signal peptide (IMGT)	KAGVTQT P RYLIKTRGQQVTLS CSPISGHR SVSWYQQTPGQGLQFLFEYFSE TQRNKGNFPGRFSGRQFSNSRSE MNVSTLELGDSALYLCASSLTSGGFDEQF FGPTRLTVL	2745
V β	MXSRLLCWVLLC LLGAGPVKAGVTQT P RYLIKTRGQQVTLS CSPISGHR SVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSE MNVSTLELGD SALYLCASSLTSGGFDEQFFGPGTRLTVL (X = any amino acid)	2746
		2747
β chain w/WT signal peptide, C β (substituted)	MGSRLLCWVLLC LLGAGPVKAGVTQT P RYLIKTRGQQVTLS CSPISGHR SVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSE MNVSTLELGD SALYLCASSLTSGGFDEQFFGPGTRLT VLEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELS W W VNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADC GITSASYQQGVLSATI LYEILLGKATLYAVLVSTLVVMAMVKR KNS	2748
β chain w/alternative signal peptide, C β (substituted)	MASRLLCWVLLC LLGAGPVKAGVTQT P RYLIKTRGQQVTLS CSPISGHR SVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSE MNVSTLELGD SALYLCASSLTSGGFDEQFFGPGTRLT VLEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELS W W VNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADC GITSASYQQGVLSATI LYEILLGKATLYAVLVSTLVVMAMVKR KNS	2749
β chain w/alternative signal peptide, C β (substituted)	MHSRLLCWVLLC LLGAGPVKAGVTQT P RYLIKTRGQQVTLS CSPISGHR SVS WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSE MNVSTLELGD SALYLCASSLTSGGFDEQFFGPGTRLT VLEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELS W W VNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADC GITSASYQQGVLSATI LYEILLGKATLYAVLVSTLVVMAMVKR KNS	2750

[00369] In some embodiments, TCR075 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR075 interacts with the neoantigen in the context of HLA-A*11:01, as described in International Publication No. WO 2019/112941, incorporated herein by reference in its entirety.

Table 6BX. Amino acid sequences of TCR076.

Description	Sequence	SEQ ID NO:
CDR1 α	DSASNY	1751
CDR2 α	IRSNVGE	1752
CDR3 α	AASTGGGNKLT	1753
V α w/o signal peptide (SignalP)	ENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFGTG TQLKVEL	1754
V α w/o signal peptide (IMGT)	GENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFGT GTQLKVEL	1755
V α	MXSIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYF PWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDS AVYFCAASTGGGNKLTFGTGTQLKVEL	1756
	(X = any amino acid)	1757
α chain w/WT signal peptide, C α (substituted)	MTSIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYF PWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDS AVYFCAASTGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPQRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLL MTLRLWSS	1758
α chain w/alternative signal peptide, C α (substituted)	MASIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYF PWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDS AVYFCAASTGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPQRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLL MTLRLWSS	1759
α chain w/alternative signal peptide, C α (substituted)	MHSIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYF PWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDS AVYFCAASTGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPQRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLL MTLRLWSS	1760
CDR1 β	DFQATT	2751
CDR2 β	SNEGSKA	2752
CDR3 β	SAREGAGGMGTQY	2753
V β w/o signal peptide (SignalP)	AVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEG SKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAAREGAGGMGT QYFGPGTRLLVL	2754
V β w/o signal peptide (IMGT)	GAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAAREGAGGMG TQYFGPGTRLLVL	2755
V β	MXLLLLLLGPGAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDS SFYICSAAREGAGGMGTQYFGPGTRLLVL	2756
	(X = any amino acid)	2757
β chain w/WT signal peptide, C β (substituted)	MLLLLLLLGPGAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDS SFYICSAAREGAGGMGTQYFGPGTRLLVLEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2758

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MALLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDS SFYICSAAREGAGGMGTQYFGPGTRLLVLEDLRNVTPPKVSLFEPKSAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2759
β chain w/alternative signal peptide, C β (substituted)	MHLLLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDS SFYICSAAREGAGGMGTQYFGPGTRLLVLEDLRNVTPPKVSLFEPKSAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2760

[00370] In some embodiments, TCR076 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR076 interacts with the neoantigen in the context of HLA-DRB1*07:01, as described in International Publication No. WO 2019/060349, incorporated herein by reference in its entirety.

Table 6BY. Amino acid sequences of TCR077.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVPPY	1761
CDR2 α	Y TSAATLV	1762
CDR3 α	AVSEDSNYQLI	1763
V α w/o signal peptide (SignalP)	QSVTQLGSHVSVSEGAIVLLRCNYSSSVPPPYLFWYVQYPNQGLQQLLKYTSA ATLVKGINGFEAEFFKKSETSFHLTKPSAHMSDAAEYFCAVSEDSNYQLIWGA GTKLI IKP	1764
V α w/o signal peptide (IMGT)	AQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPPYLFWYVQYPNQGLQQLLKYTSA AATLVKGINGFEAEFFKKSETSFHLTKPSAHMSDAAEYFCAVSEDSNYQLIWG AGTKLI IKP	1765
V α	MXLLLVVPVLEVI FTLGGTTRAQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPPYL FWYVQYPNQGLQQLLKYTSAATLVKGINGFEAEFFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKP (X = any amino acid)	1766
		1767
α chain w/WT signal peptide, C α (substituted)	MLLLLVVPVLEVI FTLGGTTRAQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPPYL FWYVQYPNQGLQQLLKYTSAATLVKGINGFEAEFFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1768
α chain w/alternative signal peptide, C α (substituted)	MALLLVVPVLEVI FTLGGTTRAQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPPYL FWYVQYPNQGLQQLLKYTSAATLVKGINGFEAEFFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1769

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHLLLVVPVLEVI FTTLGGTRAQSVTQLGSHVSVSEGA LVLLRCNYSSSVPPYL FWYVQYPNQGLQ LLLKYTSAATLVKGINGF EA EFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRS QDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVIVLRILLK VAGFNL LMTLR LWSS	1770
CDR1 β	GTSNPN	2761
CDR2 β	SVGTG	2762
CDR3 β	AYSPGLASDTQY	2763
V β w/o signal peptide (SignalP)	QTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYWYRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAYSPGLASDTQYFG PGTRLTVL	2764
V β w/o signal peptide (IMGT)	SQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYWYRQAAGRGLQLLFYSVG IGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAYSPGLASDTQYF GPGTRLTVL	2765
V β	MXCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLTVL (X = any amino acid)	2766
		2767
β chain w/WT signal peptide, C β (substituted)	MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2768
β chain w/alternative signal peptide, C β (substituted)	MACSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2769
β chain w/alternative signal peptide, C β (substituted)	MHCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2770

[00371] In some embodiments, TCR077 interacts with and/or is specific for the epidermal growth factor receptor (EGFR) tumor protein. In some embodiments, the peptide is from a neoantigen of EGFR. In some embodiments, the neoantigen has the amino acid changes E746-A750del relative to the wild type EGFR sequence. In some embodiments, TCR077 interacts with the neoantigen in the context of a heterodimer of HLA-DPA1*02:01 and HLA-DPB1*01:01, as described in International Publication No. WO 2019/213195, incorporated herein by reference in its entirety.

Table 6BZ. Amino acid sequences of TCR078.

Description	Sequence	SEQ ID NO:
CDR1 α	TSINN	1771
CDR2 α	IRSNERE	1772
CDR3 α	ATDGETSGSRLT	1773
V α without signal peptide (SignalP)	QQGEEDPQALSIQEGENATMNCSYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEGTQLTVNP	1774
V α without signal peptide (IMGT)	SQQGEEDPQALSIQEGENATMNCSYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEGTQLTVNP	1775
V α	MXTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNCSYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEGTQLTVNP (X = any amino acid)	1776
		1777
α chain with WT signal peptide, (substituted) C α	METLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNCSYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1778
α chain alternative peptide, (substituted) with signal C α	MATLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNCSYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1779
α chain alternative peptide, (substituted) with signal C α	MHTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNCSYKTSINNLLQWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1780
CDR1 β	DFQATT	2771
CDR2 β	SNEGSKA	2772
CDR3 β	SASRGATGQPQH	2773
V β without signal peptide (SignalP)	AVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASARGATGQPQHFGDGTRLSIL	2774
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASARGATGQPQHFGDGTRLSIL	2775
V β	MXLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASARGATGQPQHFGDGTRLSIL (X = any amino acid)	2776
		2777
β chain with WT signal peptide, (substituted) C β	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASARGATGQPQHFGDGTRLSILEDLRNVTPPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2778

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MALLLLLLLPGSGLGAVVSQHPSPWICKSGTSVKIECRSLDFQATTMFWYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSS FYICSAARGATGQPQHFGDGTRLSILEDLRNVTPPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2779
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLLLPGSGLGAVVSQHPSPWICKSGTSVKIECRSLDFQATTMFWYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSS FYICSAARGATGQPQHFGDGTRLSILEDLRNVTPPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2789

[00372] In some embodiments, TCR078 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR078 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

Table 6CA. Amino acid sequences of TCR079.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1781
CDR2 α	IRSNMDK	1782
CDR3 α	AERGRGGKLI	1783
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSN MDKRQGGQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKP	1784
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSN NMDKRQGGQRVTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQG TELSVKP	1785
V α	MXGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPPQFIIDIRSNMDKRQGGQRVTVLLNKTVKHLSLQIAATQPGD SAVYFCAERGRGGKLIFGQGT (X = any amino acid)	1786
		1787
α chain with WT signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPPQFIIDIRSNMDKRQGGQRVTVLLNKTVKHLSLQIAATQPGD SAVYFCAERGRGGKLIFGQGT TELSEKPNIQNPEPAVYQLKDPKQDSTLCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTCQDIF KETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRIILLKVAGFNLL MTLRLWSS	1788
α chain with alternative signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPPQFIIDIRSNMDKRQGGQRVTVLLNKTVKHLSLQIAATQPGD SAVYFCAERGRGGKLIFGQGT TELSEKPNIQNPEPAVYQLKDPKQDSTLCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTCQDIF KETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRIILLKVAGFNLL MTLRLWSS	1789

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGQRTVLLNKTVKHLSQLIAATQPGDSAVYFCAERGRGGKLI FGQGTLSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI VLRI LLLKVAGFNLLMTLRLWSS	1790
CDR1 β	DFQATT	2781
CDR2 β	SNEGSKA	2782
CDR3 β	SAGRASTDQY	2783
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNESGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVL	2784
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNESGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVL	2785
V β	MXLLLLLLGPGIS LLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNESGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVL (X = any amino acid)	2786
		2787
β chain with WT signal peptide, (substituted) C β	MLLLLLLLGPGIS LLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNESGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGITSAS YQQGVLSATILYEI LLLGKATLYAVLVSTLVMMAMVKRKN S	2788
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGIS LLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNESGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGITSAS YQQGVLSATILYEI LLLGKATLYAVLVSTLVMMAMVKRKN S	2789
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGIS LLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNESGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGITSAS YQQGVLSATILYEI LLLGKATLYAVLVSTLVMMAMVKRKN S	2790

[00373] In some embodiments, TCR079 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR079 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

Table 6CB. Amino acid sequences of TCR080

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1791
CDR2 α	IRSNMDK	1792
CDR3 α	AERGRGGKLI	1793
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKP	1794
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKP	1795
V α	MXGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKP (X = any amino acid)	1796
		1797
α chain with WT signal peptide, (substituted) C α	MAGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLLMTLRLWSS	1798
α chain alternative peptide, (substituted) with signal C α	MAGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLLMTLRLWSS	1799
α chain alternative peptide, (substituted) with signal C α	MHGIRALEFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLLVIVLRILLKLVAGFNLLMTLRLWSS	1800
CDR1 β	DFQATT	2791
CDR2 β	SNEGSKA	2792
CDR3 β	SAGRASTDQY	2793
V β without signal peptide (SignalP)	AVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYIC SAGRASTDQYFGPGTRLTVL	2794
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYIC SAGRASTDQYFGPGTRLTVL	2795
V β	MXLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYIC SAGRASTDQYFGPGTRLTVL (X = any amino acid)	2796
		2797
β chain with WT signal peptide, (substituted) C β	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYIC SAGRASTDQYFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2798

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MALLLLLLLGPSSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTTLVTSAPHPEDSS FYICSAGRASTDTQYFGPGTRTLTVLEDLRNVTPPKVSLFEPKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2799
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLLLGPSSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTTLVTSAPHPEDSS FYICSAGRASTDTQYFGPGTRTLTVLEDLRNVTPPKVSLFEPKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2800

[00374] In some embodiments, TCR080 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR080 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

[00375] The disclosure also provides for the use of other TCR V α and V β sequences, as well as any other alpha or beta chains, in the polycistronic vectors, engineered cells or pharmaceutical compositions described herein. These TCR V α and V β sequences and alpha or beta chains include those described in International Publication Nos. WO 2016/085904, WO 2017/048593, WO 2018/026691, WO 2019/060349, WO 2019/067243, WO 2019/070435, WO 2019/112941, WO 2019/213195, WO 2020/086827, WO 2020/154275, WO 2020/264269, WO 2021/163434, WO 2021/163477, and WO 2021/173902 incorporated by reference herein in their entireties.

[00376] The CDRs of a TCR disclosed herein can be defined using any art recognized numbering convention. Additionally or alternatively, the CDRs can be defined empirically, *e.g.*, based upon structural analysis of the interaction of the TCR with a cognate antigen (*e.g.*, a peptide or a peptide-MHC complex). In some embodiments, CDR3 of the TCR can further comprise an N-terminal cysteine and/or a C-terminal phenylalanine or tryptophan.

[00377] The TCRs disclosed herein can be used in any TCR structural format. For example, in certain embodiments, the TCR is a full-length TCR comprising a full-length α chain and a full-length β chain. The transmembrane regions (and optionally also the cytoplasmic regions) can be removed from a full-length TCR to produce a soluble TCR. Accordingly, in certain embodiments, the TCR is a soluble TCR lacking transmembrane and/or cytoplasmic region(s). The methods of

producing soluble TCRs are well-known in the art. In some embodiments, the soluble TCR comprises an engineered disulfide bond that facilitates dimerization, see, *e.g.*, U.S. Patent No. 7,329,731, which is incorporated by reference herein in its entirety. In some embodiments, the soluble TCR is generated by fusing the extracellular domain of a TCR described herein to other protein domains, *e.g.*, maltose binding protein, thioredoxin, human constant kappa domain, or leucine zippers, see, *e.g.*, Løset et al., Front Oncol. 2014; 4: 378, which is incorporated by reference herein in its entirety. A single-chain TCR (scTCR) comprising V α and V β linked by a peptide linker can also be generated. Such scTCRs can comprise V α and V β , each linked to a TCR constant region. Alternatively, the scTCRs can comprise V α and V β , where either the V α , the V β , or both the V α and V β are not linked to a TCR constant region. Exemplary scTCRs are described in PCT Publication Nos. WO 2003/020763, WO 2004/033685, and WO 2011/044186, each of which is incorporated by reference herein in its entirety. Furthermore, the TCRs disclosed herein can comprise two polypeptide chains (*e.g.*, an α chain and a β chain) in which the chains have been engineered to each have a cysteine residue that can form an interchain disulfide bond. Accordingly, in certain embodiments, the TCRs disclosed herein comprise two polypeptide chains linked by an engineered disulfide bond. Exemplary TCRs having an engineered disulfide bond are described in U.S. Patent Nos. 8,361,794 and 8,906,383, each of which is incorporated by reference herein in its entirety.

[00378] In certain embodiments, the TCRs disclosed herein comprise one or more chains (*e.g.*, an α chain and/or a β chain) having a transmembrane region. In certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) having a transmembrane region. The transmembrane region can be the endogenous transmembrane region of that TCR chain, a variant of the endogenous transmembrane region, or a heterologous transmembrane region. In certain embodiments, the TCRs disclosed herein comprise an α chain and a β chain having endogenous transmembrane regions.

[00379] In certain embodiments, the TCRs disclosed herein comprise one or more chains (*e.g.*, an α chain and/or a β chain) having a cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) each having a cytoplasmic region. The cytoplasmic region can be the endogenous cytoplasmic region of that TCR chain, variant of the endogenous cytoplasmic region, or a heterologous cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) where both chains have transmembrane regions, but one chain is lacking a cytoplasmic region. In

certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) where both chains have endogenous transmembrane regions but lack an endogenous cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise an α chain and a β chain where both chains have endogenous transmembrane regions but lack an endogenous cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise a co-stimulatory signaling region from a co-stimulatory molecule; see, *e.g.*, PCT Publication Nos.: WO 1996/018105, WO 1999/057268, and WO 2000/031239, and U.S. Patent No. 7,052,906, all of which are incorporated herein by reference in their entireties.

[00380] In certain embodiments, the instant disclosure provides a polypeptide comprising an α chain variable region ($V\alpha$) and a β chain variable region ($V\beta$) of a TCR fused together. For example, such polypeptide may comprise, in order, the $V\alpha$ and $V\beta$, or the $V\beta$ and the $V\alpha$, optionally with a linker (*e.g.*, a peptide linker) between the two regions. For example, a Furin and/or a 2A cleavage site (*e.g.*, one of the sequences in Tables 2 or 3), or combinations thereof, may be used in the linker for the $V\alpha/V\beta$ fusion polypeptide. In certain embodiments, the instant disclosure provides a polypeptide comprising an α chain and a β chain of a TCR fused together. For example, such polypeptide may comprise, in order, an α chain and a β chain, or a β chain and an α chain, optionally with a linker (*e.g.*, a peptide linker) between the two chains. For example, a Furin and/or a 2A cleavage site (*e.g.*, one of the sequences in Tables 2 or 3), or combinations thereof, may be used in the linker for the α/β fusion polypeptide. For example, a fusion polypeptide may comprise, from the N-terminus to the C-terminus: the α chain of a TCR, a furin cleavage site, a 2A cleavage site, and the β chain of the TCR. In certain embodiments, the polypeptide comprises, from the N-terminus to the C-terminus: the β chain of a TCR, a furin cleavage site, a 2A element, and the α chain of the TCR.

5.3 Methods of Use

[00381] In another aspect, the instant disclosure provides a method of treating a subject using the polycistronic polynucleotides, recombinant vectors, engineered cells (*e.g.*, a cell comprising a heterologous and/or recombinant nucleic acid), or pharmaceutical compositions disclosed herein. Any disease or disorder in a subject that would benefit from treatment with a recombinant cell of the present disclosure, or a polynucleotide or vector of the present disclosure can be treated using the methods disclosed herein.

[00382] In certain embodiments, the method comprises administering to the subject an effective amount of a recombinant cell or population thereof as disclosed herein.

[00383] As disclosed *infra*, cells administered to the subject can be autologous or allogeneic to the subject. In certain embodiments, autologous cells are obtained from a cancer patient directly following a cancer treatment. In this regard, it has been observed that following certain cancer treatments, in particular treatments with drugs that damage the immune system, shortly after treatment during the period when patients would normally be recovering from the treatment, the quality of T cells obtained may be optimal or improved for their ability to expand *ex vivo*. Likewise, following *ex vivo* manipulation using the methods described herein, these cells may be in a preferred state for enhanced engraftment and *in vivo* expansion. Thus, in certain embodiments, cells are collected from blood, bone marrow, lymph node, thymus, or another tissue or bodily fluid, or an apheresis product, during this recovery phase. Further, in certain aspects, mobilization and conditioning regimens can be used to create a condition in a subject wherein repopulation, recirculation, regeneration, and/or expansion of particular cell types is favored, especially during a defined window of time following therapy.

[00384] The number of cells that are employed will depend upon a number of circumstances including, the lifetime of the cells, the protocol to be used (*e.g.*, the number of administrations), the ability of the cells to multiply, the stability of the recombinant construct, and the like. In certain embodiments, the cells are applied as a dispersion, generally being injected at or near the site of interest. The cells may be administered in any physiologically acceptable medium.

[00385] In certain embodiments, the cancer is cancer of the lung, bile duct cancer (*e.g.*, cholangiocarcinoma), pancreatic cancer, colorectal cancer, ovarian, or gynecologic cancer. In certain embodiments, the cancer is leukemia (*e.g.*, mixed lineage leukemia, acute lymphocytic leukemia, acute myeloid leukemia, chronic lymphocytic leukemia, or chronic myeloid leukemia), alveolar rhabdomyosarcoma, bone cancer, brain cancer (*e.g.*, glioma, *e.g.*, glioblastoma), breast cancer, cancer of the anus, anal canal, or anorectum, cancer of the eye, cancer of the intrahepatic bile duct (*e.g.*, intrahepatic cholangiocellular cancer), cancer of the joints, cancer of the neck, gallbladder, or pleura, cancer of the nose, nasal cavity, or middle ear, cancer of the oral cavity, cancer of the vulva, myeloma (*e.g.*, chronic myeloid cancer), colon cancer, esophageal cancer, cervical cancer, gastrointestinal cancer, gastrointestinal carcinoid tumor, Hodgkin's lymphoma, hypopharynx cancer, kidney cancer, larynx cancer, liver cancer (*e.g.*, hepatocellular carcinoma), lung cancer (*e.g.*, non-small cell lung cancer), malignant mesothelioma, melanoma, multiple myeloma, nasopharynx cancer, non-Hodgkin's lymphoma, ovarian cancer, pancreatic cancer, peritoneum, omentum, and mesentery cancer, pharynx cancer, prostate cancer, rectal cancer, renal

cancer (*e.g.*, renal cell carcinoma (RCC)), gastric cancer, small intestine cancer, soft tissue cancer, stomach cancer, carcinoma, sarcoma (*e.g.*, synovial sarcoma, rhabdomyosarcoma), skin cancer, testicular cancer, thyroid cancer, head and neck cancer, ureter cancer, and urinary bladder cancer. In certain embodiments, the cancer is melanoma, breast cancer, lung cancer, prostate cancer, thyroid cancer, ovarian cancer, or synovial sarcoma. In one embodiment, the cancer is synovial sarcoma or liposarcoma (*e.g.*, myxoid/round cell liposarcoma). In certain embodiments, the cancer is lung, cholangiocarcinoma, pancreatic, colorectal, gynecological or ovarian cancer.

[00386] A polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein may be delivered to a subject by a variety of routes. These include, but are not limited to, parenteral, intranasal, intratracheal, oral, intradermal, topical, intramuscular, intraperitoneal, transdermal, intravenous, intratumoral, conjunctival, intrathecal, and subcutaneous routes. Pulmonary administration can also be employed, *e.g.*, by use of an inhaler or nebulizer, and formulation with an aerosolizing agent for use as a spray. In certain embodiments, the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein is delivered intravenously. In certain embodiments, the polycistronic polynucleotide, vector, engineered cell, or pharmaceutical composition described herein is delivered subcutaneously. In certain embodiments, the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein is delivered intratumorally. In certain embodiments, the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein is delivered into a tumor draining lymph node.

[00387] The amount of the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition which will be effective in the treatment and/or prevention of a condition will depend on the nature of the disease, and can be determined by standard clinical techniques.

[00388] The precise dose to be employed in a composition will also depend on various factors, including but not limited to the route of administration, and the seriousness of the infection or disease caused by it, and should be decided according to the judgment of the practitioner and each subject's circumstances. For example, effective doses may also vary depending upon means of administration, target site, physiological state of the patient (including age, body weight, and health), whether the patient is a human or an animal, other medications administered, or whether treatment is prophylactic or therapeutic. Usually, the patient is a human but non-human mammals

including transgenic mammals can also be treated. Treatment dosages are optimally titrated to optimize safety and efficacy.

5.4 IL-15/IL-15R α Fusion Proteins

[00389] The disclosure also provides recombinant vectors that include cytokines. In some embodiments, the cytokine is an interleukin. In some embodiments, the cytokine is membrane bound. In some embodiments, the cytokine is a fusion protein comprising a soluble cytokine, or a functional fragment or functional variant thereof, operably linked to a cognate receptor of the cytokine, or a functional fragment or functional variant thereof, optionally a membrane-bound form thereof. In some embodiments, the fusion protein comprises human IL-15 (hIL-15) operably linked to human IL-15R α (hIL-15R α). In membrane-bound form, this fusion protein is referred to herein as membrane bound IL-15 (mbIL15). In some embodiments, hIL-15 is directly operably linked to hIL-15R α . In some embodiments, hIL-15 is indirectly operably linked to hIL-15R α . In some embodiments, hIL-15 is indirectly operably linked to hIL-15R α via a peptide linker.

[00390] In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 81, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 81. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 81. In some embodiments, the amino acid of the linker consists of the amino acid sequence of SEQ ID NO: 81, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 81. In some embodiments, the amino acid of the linker consists of the amino acid sequence of SEQ ID NO: 81.

[00391] In some embodiments, the linker is encoded by a polynucleotide sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 82. In some embodiments, the linker is encoded by the polynucleotide sequence of SEQ ID NO: 82. In some embodiments, hIL-15 comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 76. In some embodiments, hIL-15 comprises the amino acid sequence of SEQ ID NO: 76. In some embodiments, the amino acid sequence of hIL-15 consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 76. In some embodiments, the amino acid sequence of hIL-15 consists of the amino acid sequence of SEQ ID NO: 76.

[00392] In some embodiments, hIL-15 is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence

of SEQ ID NO: 77. In some embodiments, hIL-15 is encoded by the polynucleotide sequence of SEQ ID NO: 77.

[00393] In some embodiments, hIL-15R α comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 78. In some embodiments, hIL-15R α comprises the amino acid sequence of SEQ ID NO: 78. In some embodiments, the amino acid sequence of hIL-15R α consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 78. In some embodiments, the amino acid sequence of hIL-15R α consists of the amino acid sequence of SEQ ID NO: 78.

[00394] In some embodiments, hIL-15R α is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 79. In some embodiments, hIL-15R α is encoded by the polynucleotide sequence of SEQ ID NO: 79.

[00395] In some embodiments, the fusion protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 70 or 73. In some embodiments, the fusion protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 70. In some embodiments, the fusion protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 73. In some embodiments, the fusion protein comprises the amino acid sequence of SEQ ID NO: 70 or 73. In some embodiments, the fusion protein comprises the amino acid sequence of SEQ ID NO: 70. In some embodiments, the fusion protein comprises the amino acid sequence of SEQ ID NO: 73.

[00396] In some embodiments, the amino acid sequence of the fusion protein consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 70 or 73. In some embodiments, the amino acid sequence of the fusion protein consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 70. In some embodiments, the amino acid sequence of the fusion protein consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 73. In some embodiments, the amino acid sequence of the fusion protein consists of the amino acid sequence of SEQ ID NO: 70 or 73. In some embodiments, the amino acid sequence of the fusion protein consists of the amino acid sequence of SEQ ID NO: 70. In some embodiments, the amino acid sequence of the fusion protein consists of the amino acid sequence of SEQ ID NO: 73.

[00397] In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polynucleotide sequence of SEQ ID NO: 71 or 74. In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polynucleotide sequence of SEQ ID NO: 71. In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polynucleotide sequence of SEQ ID NO: 74.

[00398] In some embodiments, the fusion protein is encoded by the polynucleotide sequence of SEQ ID NO: 71 or 74. In some embodiments, the fusion protein is encoded by the polynucleotide sequence of SEQ ID NO: 71. In some embodiments, the fusion protein is encoded by the polynucleotide sequence of SEQ ID NO: 74.

[00399] Exemplary cytokine fusion proteins and components thereof are disclosed in Table 7. Additional exemplary mbIL15 fusions are disclosed in Hurton *et al.*, “Tethered IL-15 augments antitumor activity and promotes a stem-cell memory subset in tumor-specific T cells,” PNAS, 113(48) E7788-E7797 (2016), the entire contents of which are incorporated by reference herein.

[00400] The amino acid sequence and polynucleotide sequence of exemplary cytokine fusion proteins and component polypeptides are provided in Table 7, herein.

Table 7. Amino acid and polynucleotide sequences of exemplary IL-15/IL-15R α fusion proteins and components thereof.

Description	Sequence	SEQ ID NO
mbIL15 (with N-terminal signal sequence) (exemplary amino acid sequence)	MDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCK VTAMKCFLLLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEE LEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCP PFMSVEHADIWVKSYSYLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRD PALVHQR PAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAAT TAAIVPGSQLMP SKSPSTGTTEI SSHESSHGTPSQTTAKNWELTASASHQPPGV YPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAMEALPVT WGTSSRDEDLNCSHHL	70
mbIL15 (with N-terminal signal sequence) (exemplary nucleotide sequence)	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGC AACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGC ATGCACATTGATGCCACCCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAA GTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGA GGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCT CCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCCTACAGCCTGTAC AGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGACCTCT TCTCTGACAGAGTGCCTGTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACA CCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCT CCATCTACAGTGACAACAGCCGAGTGACACCTCAGCCTGAATCTCTGAGCCCT	71

Description	Sequence	SEQ ID NO
	TCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACA ACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACA GGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTG TATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTG CTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAG ACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	
mbIL15 (without N-terminal signal sequence) (exemplary amino acid sequence)	NWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLLELQVISLES GDASIHDVTENLIILANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQ MFINTSSGGSGGGSGGGSGGGSGGGSLQITCPPPMSVEHADIWVKSYSLSY SRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPLSKCIRD PALVHQRPAP PSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAIVPGSQLMPKSPST GTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVL LCGLSAVSL LACYLKS RQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	73
mbIL15 (without N-terminal signal sequence) (exemplary nucleotide sequence)	AACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGC ATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAA GTGACCGCCATGAAGTGTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGCGGATCTGGAGGA GGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCT CCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTACAGCCTGTAC AGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGGCACCTCT TCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACA CCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCT CCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCT TCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACA ACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACA GGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTG TATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTG CTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAG ACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	74
Soluble hIL-15 (exemplary amino acid sequence)	NWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLLELQVISLES GDASIHDVTENLIILANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQ MFINTS	76
Soluble hIL-15 (exemplary nucleotide sequence)	AACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGC ATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAA GTGACCGCCATGAAGTGTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCAATACAAGC	77
hIL-15R α (exemplary amino acid sequence)	ITCPPPMSVEHADIWVKSYSLSYSRERYICNSGFKRKAGTSSLTECVLNKATNVA HWTTPLSKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNN TAATTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVL LCGLSAVSLLACYLKS RQTPPLASVEMEAMEA LPVTWGTSSRDEDLENC SHHL	78
hIL-15R α (exemplary nucleotide sequence)	ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGGCTGCTGAATAAGGCCACAAATGTGGCC CACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAG AGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAA	79

Description	Sequence	SEQ ID NO
	TCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAAT ACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAG TCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACA CCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAG CCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACA TCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTG AAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCC CTGCCTGTGACATGGGGAAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCT CACCACCTG	
Linker (exemplary amino acid sequence)	SGGSGGGSGGGSGGGSGGGSLQ	81
Linker (exemplary nucleotide sequence)	TCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGA GGATCTGGCGGAGGATCTCTGCAG	82
IgE N-terminal signal sequence (exemplary amino acid sequence)	MDWTWILFLVAAATRVHS	83
IgE N-terminal signal sequence (exemplary nucleotide sequence)	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGC	84

5.5 Marker Proteins

[00401] The marker proteins described herein function to allow for the selective depletion of cells contacted with the recombinant vector disclosed herein (*e.g.*, “recombinant cells”) *in vivo*, through the administration of an agent, *e.g.*, an antibody, that specifically binds to the marker protein and may mediate or catalyze killing of a recombinant cell. In some embodiments, marker proteins are expressed on the surface of the recombinant cell.

[00402] In some embodiments, the marker protein comprises the extracellular domain of a cell surface protein, or a functional fragment or functional variant thereof. In some embodiments, the cell surface protein is human epidermal growth factor receptor 1 (hHER1). In some embodiments, the marker protein comprises a truncated HER1 protein that is able to be bound by an anti-hHER1 antibody. In some embodiments, the marker protein comprises a variant of a truncated hHER1 protein that is able to be bound by an anti-hHER1 antibody. In some embodiments, the hHER1 marker protein provides a safety mechanism by allowing for depletion of infused recombinant cells through administering an antibody that recognizes the hHER1 marker protein expressed on the surface of recombinant cells. An exemplary antibody that binds the hHER1 marker protein is cetuximab.

[00403] In some embodiments, the hHER1 marker protein comprises from N terminus to C terminus: domain III of hHER1, or a functional fragment or functional variant thereof; an N-terminal portion of domain IV of hHER1; and the transmembrane region of human CD28.

[00404] In some embodiments, domain III of hHER1 comprises the amino acid sequence of SEQ ID NO: 104; or the amino acid sequence of SEQ ID NO: 104, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the amino acid sequence of domain III of hHER1 consists of the amino acid sequence of SEQ ID NO: 104; or the amino acid sequence of SEQ ID NO: 10, comprising 1, 2, or 3 amino acid modifications.

[00405] In some embodiments, the N-terminal portion of domain IV of hHER1 comprises amino acids 1-40, 1-39, 1-38, 1-37, 1-36, 1-35, 1-34, 1-33, 1-32, 1-31, 1-30, 1-29, 1-28, 1-27, 1-26, 1-25, 1-24, 1-23, 1-22, 1-21, 1-20, 1-19, 1-18, 1-17, 1-16, 1-15, 1-14, 1-13, 1-12, 1-11, or 1-10 of SEQ ID NO: 105. In some embodiments, the C terminus of domain III of hHER1 is directly fused to the N terminus of the N-terminal portion of domain IV of hHER1.

[00406] In some embodiments, the C terminus of the N-terminal portion of domain IV of hHER1 is indirectly fused to the N terminus of the CD28 transmembrane domain via a peptide linker. In some embodiments, the peptide linker comprises glycine and serine amino acid residues. In some embodiments, the peptide linker is from about 5-25, 5-20, 5-15, 5-10, 10-20, or 10-15 amino acids in length.

[00407] In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 108, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 108. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 108. In some embodiments, the amino acid sequence of the peptide linker consists of the amino acid sequence of SEQ ID NO: 108, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 108. In some embodiments, the amino acid sequence of the peptide linker consists of the amino acid sequence of SEQ ID NO: 108.

[00408] In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, 112, or 113. In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 103. In some

embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 112. In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 113.

[00409] In some embodiments, the marker protein comprises the amino acid sequence of SEQ ID NO: 100 or 103. In some embodiments, the marker protein comprises the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein comprises the amino acid sequence of SEQ ID NO: 103.

[00410] In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, 112, or 113. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 103. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 112. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 113.

[00411] In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 100, 103, 112, or 113. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 103. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 112. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 113.

[00412] In some embodiments, the marker protein is derived from human CD20 (hCD20). In some embodiments, the marker protein comprises a truncated hCD20 protein that comprises the extracellular region (hCD20t), or a functional fragment or functional variant thereof. In some embodiments, the hCD20 marker protein provides a safety mechanism by allowing for depletion of infused recombinant cells through administering an antibody that recognizes the hCD20 marker

protein expressed on the surface of recombinant cells. An exemplary antibody that binds the hCD20 marker protein is rituximab.

[00413] The amino acid sequences of exemplary marker proteins are provided in Table 8, herein.

Table 8. Amino acid sequences of exemplary marker proteins.

Description	Amino Acid Sequence	SEQ ID NO
HER1t (with N-terminal signal sequence) (exemplary amino acid sequence)	MRLPAQLLGLLMLWVPGSSGRKVCNGIGIGEFKDSLSINATNI KHFKNCTSI SGDLHILPVAFRGDSFTHTPPLDPQELDI LKTVK EITGFLLIQAWPENRTDLHAFENLEIIRGR TKQH GQFSLAVVS LNITSLGLRSLKEISDGDV IISGNKNLCYANTINWKKLFGTSG QKTKIISNRGENSCKATGQVCHALCSPEG CWGPEPRDCVSGGG GSGGGGSGGGGSGGGGSFWVLVVVGVLACYSLLVTVAFIIFW VRSKRS	100
HER1t (without N-terminal signal sequence) (exemplary amino acid sequence)	RKVCNGIGIGEFKDSLSINATNIKHFKNCTSI SGDLHILPVAF RGDSFTHTPPLDPQELDI LKTVKEITGFLLIQAWPENRTDLHA FENLEIIRGR TKQH GQFSLAVVSLNITSLGLRSLKEISDGDV I ISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQV CHALCSPEG CWGPEPRDCVSGGGGSGGGGSGGGGSGGGGSFWV LVVGVLACYSLLVTVAFIIFWVRSKRS	103
Domain III of hHER1 (exemplary amino acid sequence)	RKVCNGIGIGEFKDSLSINATNIKHFKNCTSI SGDLHILPVAF RGDSFTHTPPLDPQELDI LKTVKEITGFLLIQAWPENRTDLHA FENLEIIRGR TKQH GQFSLAVVSLNITSLGLRSLKEISDGDV I ISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQ	104
Domain IV of hHER1 (exemplary amino acid sequence)	VCHALCSPEG CWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPR EFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPH CVKTC PAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLE GCPTNGPKIPS	105
Truncated domain IV of hHER1 (exemplary amino acid sequence)	VCHALCSPEG CWGPEPRDCVS	106
CD28 transmembrane domain (exemplary amino acid sequence)	FWVLVVVGVLACYSLLVTVAFIIFWVRSKRS	107
Linker (exemplary amino acid sequence)	GGGGSGGGGSGGGGSGGGGS	108
Igk N-terminal signal sequence (exemplary amino acid sequence)	MRLPAQLLGLLMLWVPGSSG	109
Igk Variant 1 N-terminal signal sequence (exemplary amino acid sequence)	MRMLPAQLLGLLMLWVPGSSG	110
Igk Variant 2 N-terminal signal sequence (exemplary amino acid sequence)	PRMLPAQLLGLLMLWVPGSSG	111
HER1t-2 (with N-terminal signal sequence) (exemplary amino acid sequence)	MRLPAQLLGLLMLWVPGSSGRKVCNGIGIGEFKDSLSINATNI KHFKNCTSI SGDLHILPVAFRGDSFTHTPPLDPQELDI LKTVK EITGFLLIQAWPENRTDLHAFENLEIIRGR TKQH GQFSLAVVS LNITSLGLRSLKEISDGDV IISGNKNLCYANTINWKKLFGTSG QKTKIISNRGENSCKATGQVCHALCSPEG CWGPEPRDCVSCRN VSRGRECVDKCNLLEGEPRFVENSECIQCHPECLPQAMNITC TGRGPDNCIQCAHYIDGPHCVKTC PAGVMGENNTLVWKYADAG HVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMV GALLLL	112

Description	Amino Acid Sequence	SEQ ID NO
	LVVALGIGLFLM	
HER1t-2 (without N-terminal signal sequence) (exemplary amino acid sequence)	RKVCNGIGIGIEFKDLSLSINATNIKHFKNCTSSISGDLHLIPVAF RGDSFTHTPPLDPQELDIKTVKEITGFLLIQAWPENRTDLHA FENLEIIRGRTKQHGGQFSLAVVSLNITSLGLRSLKEISDGDVI ISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQV CHALCSPEGCGWPEPRDCVSCRNVSRGECVDKCNLLEGEPRE FVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHC VKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLE GCPTNGPKIPSIATGMVGALLLLLVVALGIGLFLM	113
hCD20 (full length) (exemplary amino acid sequence)	MTTPRNSVNGTFFPAEPMKGPIAMQSGPKPLFRMSSLVGPTQS FFMRESKTLGAVQIMNGLFHIALGGLLMI PAGIYAPICVTWVY PLWGGIMYIISGSLAATEKNSRKCLVKGKMIMNSLSLFAAIS GMILS IMDILNIIKISHFLKMESLNFI RAHTPYINIYNCEPANP SEKNSPSTQYCYSIQSLFLGILSVMLIFAFFQELVIAGIVENE WKRTCSRPKSNIVLLSAEEKKEQTIEIKEEVVGLTETSSQPKN EEDIEIPIQEEEEETETNFPPEPPQDQESSPIENDSSP	114
hCD20t-1 (exemplary amino acid sequence)	MTTPRNSVNGTFFPAEPMKGPIAMQSGPKPLFRMSSLVGPTQS FFMRESKTLGAVQIMNGLFHIALGGLLMI PAGIYAPICVTWVY PLWGGIMYIISGSLAATEKNSRKCLVKGKMIMNSLSLFAAIS GMILS IMDILNIIKISHFLKMESLNFI RAHTPYINIYNCEPANP SEKNSPSTQYCYSIQSLFLGILSVMLIFAFFQELVIAGIVENE WKRTCSRPKSNIVLLSAEEKKEQTIEIKEEVVGLTETSSQPKN EEDIE	115

5.6 Vectors

[00414] In one aspect, provided herein are recombinant vectors comprising a polycistronic expression cassette that comprises at least three cistrons. In some embodiments, the polycistronic expression cassette comprises at least 4, 5, or 6 cistrons. In some embodiments, the polycistronic expression cassette comprises 3 cistrons. In some embodiments, the polycistronic expression cassette comprises 4 cistrons. In some embodiments, the polycistronic expression cassette comprises 5 cistrons. In some embodiments, the polycistronic expression cassette comprises 6 cistrons.

[00415] In some embodiments, the vector is a non-viral vector. Exemplary non-viral vectors include, but are not limited to, plasmid DNA, transposons, episomal plasmids, minicircles, ministrings, and oligonucleotides (*e.g.*, mRNA, naked DNA). In some embodiments, the polycistronic vector is a DNA plasmid vector.

[00416] In some embodiments, the vector is a viral vector. Viral vectors can be replication competent or replication incompetent. Viral vectors can be integrating or non-integrating. A number of viral based systems have been developed for gene transfer into mammalian cells, and a suitable viral vector can be selected by a person of ordinary skill in the art. Exemplary viral vectors include, but are not limited to, adenovirus vectors (*e.g.*, adenovirus 5), adeno-associated virus

(AAV) vectors (*e.g.*, AAV2, 3, 5, 6, 8, 9), retrovirus vectors (MMSV, MSCV), lentivirus vectors (*e.g.*, HIV-1, HIV-2), gammaretrovirus vectors, herpes virus vectors (*e.g.*, HSV1, HSV2), alphavirus vectors (*e.g.*, SFV, SIN, VEE, M1), flavivirus (*e.g.*, Kunjin, West Nile, Dengue virus), rhabdovirus vectors (*e.g.*, rabies virus, VSV), measles virus vector (*e.g.*, MV-Edm), Newcastle disease virus vectors, poxvirus vectors (*e.g.*, VV), measles virus, and picornavirus vectors (*e.g.*, Cocksackievirus).

[00417] In some embodiments, the vector or polycistronic expression cassette comprises one or more additional elements. Additional elements include, but are not limited to, promoters, enhancers, polyadenylation (polyA) sequences, and selection genes.

[00418] In some embodiments, the vector comprises a polynucleotide sequence that encodes for a selectable marker that confers a specific trait on cells in which the selectable marker is expressed enabling artificial selection of those cells. Exemplary selectable markers include, but are not limited to, antibiotic resistance genes, *e.g.*, resistance to kanamycin, ampicillin, or triclosan.

[00419] In some embodiments, the polycistronic expression cassette comprises a transcriptional regulatory element. Exemplary transcriptional regulatory elements include, but are not limited to promoters and enhancers. In some embodiments, the polycistronic expression cassette comprises a promoter sequence 5' of the first 5' cistron. In some embodiments, the promoter comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 150. In some embodiments, the promoter comprises the polynucleotide sequence of SEQ ID NO: 150. In some embodiments, the polynucleotide sequence of the promoter consists of a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 150. In some embodiments, the polynucleotide sequence of the promoter consists of the polynucleotide sequence of SEQ ID NO: 150.

[00420] In some embodiments, the polycistronic expression cassette comprises a polyA sequence 3' of the 3' terminal cistron. In some embodiments, the polyA sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 151. In some embodiments, the polyA sequence comprises the nucleic acid sequence of SEQ ID NO: 151. In some embodiments, the polyA sequence consists of a sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 151. In some embodiments, the polyA sequence consists of the nucleic acid sequence of SEQ ID NO: 151.

[00421] The polynucleotide sequence of exemplary promoters and polyA sequences are provided in Table 9, herein.

Table 9. Polynucleotide sequences of exemplary promoters and polyA sequences.

Description	Nucleic Acid Sequence	SEQ ID NO
hEF-1 α Hybrid Promoter	GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATC GCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACC GGTGCCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCG TGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATAT AAGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCGCAACGGGTTTGCC GCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCAC GCGCCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCG CGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCC GTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGG CGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTG CCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTT CTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGAT	150
BGH polyA sequence	GATCTGCTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCTT TCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTC ATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGA TTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATG G	151

[00422] In some embodiments, the polycistronic expression cassette comprises a polynucleotide sequence that encodes an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence recited in Tables 10A-10C.

Table 10A. Exemplary amino acid sequences encoded by polycistronic expression cassettes.

Description	Sequence	SEQ ID NO:
Cα (murine, degenerate)-fP2A	XIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	160
Cβ (murine, degenerate)-fT2A-mbIL15	EDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGEGRGSLLTCGDVEENPGPMDWTWILFL VAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEK I KEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCPPP SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTP SLKCI RDPALVHQRPAPPSTVTAGVTPQPESLSPSGKEPAASSPSSNNTAA TTAALVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQP PGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKS RQTPPLASVEMEAME ALPVTWGTSSRDEDLNCSHHL X at position 57 is Ser or Cys	161
Cα (murine, degenerate)-fT2A	XIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	162
Cβ (murine, degenerate)-fP2A-mbIL15	EDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILFL LVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEK NI KEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCPPP MSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTP PSLKCI RDPALVHQRPAPPSTVTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAALVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKS RQTPPLASVEMEAM EALPVTWGTSSRDEDLNCSHHL X at position 57 is Ser or Cys	163

Description	Sequence	SEQ ID NO:
C α (murine, degenerate)-fP2A-mbIL15-fT2A	XIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLLLKVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVSNNVVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLSNG NVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSG GGGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPLSKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAATVPGSQLMPKSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHLRAKRSGSGEGRGS LLTCGDVEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	164
C α (murine, degenerate)-fT2A-mbIL15-fP2A	XIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLLLKVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVSNNVVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLSNGN VTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLT ECVLNKATNVAHWTTPLSKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAATVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHLRAKRSGSGATNFSL I.KQAGDVFFENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	165
C β (murine, degenerate)-fP2A	EDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKEPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGATNFSLLKQAGDVEENPGP X at position 57 is Ser or Cys	166
C α (murine, degenerate)-fT2A-mbIL15	XIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLLLKVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVSNNVVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLSNGN VTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLT ECVLNKATNVAHWTTPLSKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAATVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	167

Description	Sequence	SEQ ID NO:
Cβ (murine, degenerate)-fT2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVMMAMVKRKN SRAKRSGSGEGRGSLLTCGDVEENPGP X at position 57 is Ser or Cys	168
Cα (murine, degenerate)-fP2A-mbIL15	XIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDALTLEKSFETDM NLNFQNLXVXXLRILLK VAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLEELQVISLES GDASIHDTVENLII LANNSLS SNG NVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSG GGGSGGGS LQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPSLKCIRDPALVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMP SKSPSTGTTEISSHES SHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	169
Cβ (murine, degenerate)-fP2A-mbIL15-fT2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVMMAMVKRKN SRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILF LVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLEELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEK NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCPPP MSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPALVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAIVPGSQLMP SKSPSTGTTEISSHES SHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYL KSRQTPPLASVEMEAM EALPVTWGTSSRDEDLENC SHHLRAKRSGSGEGRGSLLTCGDVEENPGP X at position 57 is Ser or Cys	170
Cβ (murine, degenerate)-fT2A-mbIL15-fP2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVMMAMVKRKN SRAKRSGSGEGRGSLLTCGDVEENPGPMDWTWILFL VAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLEELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEK NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCPPP MSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPALVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA TTAAIVPGSQLMP SKSPSTGTTEISSHES SHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYL KSRQTPPLASVEMEAM EALPVTWGTSSRDEDLENC SHHLRAKRSGSGATNFSLLKQAGDVEENPGP X at position 57 is Ser or Cys	171
mbIL15-fP2A	MDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPS CKVTAMKCFLEELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGG LQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKA TNVAHWTTPSLKCIRDPALVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAAS SPSSNNTAATTAIVPGSQLMP SKSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYL KSRQTPPL ASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGATNFSLLKQAGDV EENPGP	172

Description	Sequence	SEQ ID NO:
mbIL15-ft2A	MDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPS CKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGG LQITCPPPMMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKA TNVAHWTTPSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAAS SPSSNNTAATTAIVPGSQLMPSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPL ASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGEGRGSLLTCGDVE ENPGP	173

Table 10B. Exemplary amino acid sequences encoded by polycistronic expression cassettes

Description	Sequence	SEQ ID NO:
C α (murine, cysteine- and LIV-substituted)-fP2A	NIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRLIRILLKVGAFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGP	180
C β (murine, cysteine-substituted)-fT2A-mbIL15	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKN SRAKRSGSGEGRGSLLTCGDVEENPGPMDWTWILFL VAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEK NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGGSLQITCPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAA TTAAIVPGSQLMPSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQ PGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDLENC SHHL	181
C α (murine, cysteine- and LIV-substituted)-fT2A	NIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRLIRILLKVGAFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGP	182
C β (murine, cysteine-substituted)-fP2A-mbIL15	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKN SRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILF LVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKC FLELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEK NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGGSLQITCPP MSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAIVPGSQLMPSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAM EALPVTWGTSSRDEDLENC SHHL	183

Description	Sequence	SEQ ID NO:
C α (murine, cysteine- and LIV-substituted)-fP2A-mbIL15-fT2A	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWVNVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNG NVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGGSGGSLQITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPLSKCIRD PALVHQRPA PPTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAATVPGSQLMP SKSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGEGRGS LLTCGDVEENPGP	184
C α (murine, cysteine- and LIV-substituted)-fT2A-mbIL15-fP2A	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWVNVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNGN VTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLT ECVLNKATNVAHWTTPLSKCIRD PALVHQRPA PPTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAATVPGSQLMP SKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGATNFSL LKQAGDVEENPGP	185
C β (murine, cysteine-substituted)-fP2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELS W W V N G K E V HSGVCTDPPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDK WPEGSPKPV TQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNSRAKRSGSGATNFSLLKQAGDVEENPGP	186
C α (murine, cysteine- and LIV-substituted)-fT2A-mbIL15	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWVNVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNGN VTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLT ECVLNKATNVAHWTTPLSKCIRD PALVHQRPA PPTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAATVPGSQLMP SKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	187
C β (murine, cysteine-substituted)-fT2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELS W W V N G K E V HSGVCTDPPQAYKESNYSYCLSSRLRV SATFWHNPRNHFR CQVQFHGLSEEDK WPEGSPKPV TQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNSRAKRSGSGEGRGSLLTCGDVEENPGP	188
C α (murine, cysteine- and LIV-substituted)-fP2A-mbIL15	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWVNVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNG NVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGGSGGSLQITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPLSKCIRD PALVHQRPA PPTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAATVPGSQLMP SKSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	189

Description	Sequence	SEQ ID NO:
Cβ (murine, cysteine-substituted)-fP2A-mbIL15-fT2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVMMAMVKRKNRAKRS GSGATNFSLLKQAGDVEENPGPMDWTWILF LVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKC FLELEQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEK NIKEFLQSFVHIVQMFIN TSSGGGSGGGGSGGGGSGGGGSLQITCPPP MSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCI RDPALVHQRPA PPSVTVTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAIVPGSQLMP SKSPSTGTTEISSHES SHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAV SLLACYLKSRQTPPLASVEMEAM EALPVTWGTSSRDEDL ENC SHHLRAKRS GSGEGRGSL LTCGDVEENPGP	190
Cβ (murine, cysteine-substituted)-fP2A-mbIL15-fP2A	EDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVMMAMVKRKNRAKRS GSGEGRGSL LTCGDVEENPGPMDWTWILF VAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELEQVISLES GDASIHDTVENLIILANNSLSSNGNVTESGCKECEEELEEK NIKEFLQSFVHIVQMFIN TSSGGGSGGGGSGGGGSGGGGSLQITCPPPM SVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCI RDPALVHQRPA PPSVTVTAGVTPQPESLSPSGKEPAASSPSSNNTA TTAAIVPGSQLMP SKSPSTGTTEISSHES SHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAV SLLACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDL ENC SHHLRAKRS GSGATNFSLLKQAGDVEENPGP	191

Table 10C. Exemplary amino acid sequences encoded by polycistronic expression cassettes

Description	Sequence	SEQ ID NO:
Cα (murine, LIV substituted)-fP2A	NIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRLIRILLK VAGFNLLMTLRLWSSRAKRS GSGATNFSLLKQAG DVEENPGP	210
Cα (murine, LIV substituted)-fT2A	NIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRLIRILLK VAGFNLLMTLRLWSSRAKRS GSGEGRGSL LTCGD VEENPGP	212
Cα (murine, LIV substituted)-fP2A-mbIL15-fT2A	NIQNPEPAVYQLKDPRS QDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRLIRILLK VAGFNLLMTLRLWSSRAKRS GSGATNFSLLKQAG DVEENPGPMDWTWILFVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELEQVISLES GDASIHDTVENLIILANNSLSSNG NVTESGCKECEEELEEKNIKEFLQSFVHIVQMFIN TSSGGGSGGGGSGGGGSG GGGSGGGSLQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPSLKCI RDPALVHQRPA PPSVTVTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMP SKSPSTGTTEISSHES SHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAV SLLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDL ENC SHHLRAKRS GSGEGRGSL LTCGDVEENPGP	214

Description	Sequence	SEQ ID NO:
C α (murine, LIV substituted)-fT2A-mbIL15-fP2A	NIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDM NLNFQNLVIVLRLILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNGN VTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGGS LQITC P P P P M S V E H A D I W V K S Y S L Y S R E R Y I C N S G F K R K A G T S S L T ECVLNKATNVAHWTTTPSLKCIRD PALVHQRPA P P S T V T T A G V T P Q P E S L S P S GKEPAASSPSSNNTAATTAATTAIVPGSQLMP SKSPSTGTTEI S S H E S S H G T P S Q TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGATNFS L LKQAGDVEENPGP	215
C α (murine, LIV substituted)-fT2A-mbIL15	NIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDM NLNFQNLVIVLRLILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNGN VTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGGS LQITC P P P P M S V E H A D I W V K S Y S L Y S R E R Y I C N S G F K R K A G T S S L T ECVLNKATNVAHWTTTPSLKCIRD PALVHQRPA P P S T V T T A G V T P Q P E S L S P S GKEPAASSPSSNNTAATTAATTAIVPGSQLMP SKSPSTGTTEI S S H E S S H G T P S Q TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	217
C α (murine, LIV substituted)-fP2A-mbIL15	NIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDM NLNFQNLVIVLRLILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAAATRVHSNWNVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLIILANNSLS SNGN NVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGGSGGGS LQITC P P P P M S V E H A D I W V K S Y S L Y S R E R Y I C N S G F K R K A G T S S L TECVLNKATNVAHWTTTPSLKCIRD PALVHQRPA P P S T V T T A G V T P Q P E S L S P SGKEPAASSPSSNNTAATTAATTAIVPGSQLMP SKSPSTGTTEI S S H E S S H G T P S QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	219

[00423] Tables 11A, B and C below provide exemplary polynucleotide sequences for use in constructing vectors of the present disclosure. As shown in Tables 11A, B and C, vectors of the present disclosure can include one or more of the following sequences: (1) an “AP” sequence which encodes (i) a C α sequence disclosed herein and (ii) a P2A element sequence disclosed herein; (2) a “BT” sequence which encodes (i) a C β sequence disclosed herein and (ii) a T2A element sequence disclosed herein; (3) a “BT15” sequence which encodes (i) a C β sequence disclosed herein, (ii) a T2A element sequence disclosed herein, and (iii) a mbIL15 sequence disclosed herein; (4) an “AT” sequence which encodes (i) a C α sequence disclosed herein and (ii) a T2A element sequence disclosed herein; (5) a “BP” sequence which encodes (i) a C β sequence disclosed herein and (ii) a P2A element sequence disclosed herein; (6) a “BP15” sequence which encodes (i) a C β sequence disclosed herein, (ii) a P2A element sequence disclosed herein, and (iii)

a mbIL15 sequence disclosed herein; (7) an “AP15” sequence which encodes (i) a C α sequence disclosed herein, (ii) a P2A element sequence disclosed herein, and (iii) a mbIL15 sequence disclosed herein; (8) a “15T” sequence which encodes (i) a mbIL15 sequence disclosed herein and (ii) a T2A element sequence disclosed herein; (9) an “AP15T” sequence which encodes (i) a C α sequence disclosed herein, (ii) a P2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a T2A element sequence disclosed herein (10) an “AT15” sequence which encodes (i) a C α sequence disclosed herein, (ii) a T2A element sequence disclosed herein, and (iii) a mbIL15 sequence disclosed herein; (11) a “15P” sequence which encodes (i) a mbIL15 sequence disclosed herein, and (ii) a P2A element sequence disclosed herein; (12) an “AT15P” sequence which encodes (i) a C α sequence disclosed herein, (ii) a T2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a P2A element sequence disclosed herein; (13) an “BP15T” sequence which encodes (i) a C β sequence disclosed herein, (ii) a P2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a T2A element sequence disclosed herein; (14) an “BT15P” sequence which encodes (i) a C β sequence disclosed herein, (ii) a T2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a P2A element sequence disclosed herein.

[00424] The nucleotide sequences provided herein (and their corresponding amino acid sequences) may be used in any appropriate combination. An “appropriate combination” is a combination where desired molecular function(s) are provided by one or more of the sequences disclosed herein. For example, in general, any 2A element sequence provided herein can provide the function of ribosome skipping (via the 2A element) and, optionally, furin-mediated cleavage (via the furin recognition site). Thus, an “AT” sequence in a vector of the present disclosure could, in alternative embodiments, be replaced by an “AP” sequence of the present disclosure. Similarly, “AE” and “AF” sequences, comprising C α region sequences and E2A or F2A element sequences can also be used. “BT,” “BP,” “BE,” and “BF” sequences comprising C β region sequences and 2A element sequences are all also interchangeable. “15T,” “15P,” “15E,” and “15F” sequences comprising mbIL15 sequences and 2A element sequences are all also interchangeable. Additionally, any combination of TCR α , TCR β , and mbIL15 sequences may appear from 5' to 3' on a vector of the present disclosure in any order and may be separated by sequences which provide appropriate 2A element sequence function (e.g., ribosome skipping, furin cleavage).

[00425] Accordingly, sequences of the present disclosure provide ribosome skipping, furin recognition, TCR α function, TCR β function, and mbIL15 function in any appropriate combination

or 5' to 3' order.

Table 11A. Exemplary polynucleotide sequences for use in polycistronic expression cassettes.

Description	Sequence	SEQ ID NO:
AP nucleotide sequence	NNNATCCAGAATCCCAGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTGCCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCAGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	230
BT nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCCCTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCAAAGCCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT NNN at positions 169-171 make up a codon that encodes Ser or Cys	231
BT15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGCTTCTTTCCCGATCACGTGGAGCTGTCCCTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCAAAGCCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGA GATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG	232

Description	Sequence	SEQ ID NO:
	TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCCTGCCCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTGTGCTGGCCTGTACCTGAAGTCTAGACAGACACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 169-171 make up a codon that encodes Ser or Cys	
AT nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTCAACGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCC GGCGAAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCT NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	233
BP nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACT CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCCTGGTGGTTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTCAGCCTG CTGAAGCAGCGGGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 169-171 make up a codon that encodes Ser or Cys	234
BP15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACT CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCCTGGTGGTTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTCAGCCTG CTGAAGCAGCGGGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 169-171 make up a codon that encodes Ser or Cys	235

Description	Sequence	SEQ ID NO:
	CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTG ACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGCAGATGTTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGC GGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAAATGTCTGTGGAGCACGCCGATATTTGGGTG AAGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATGAAGTCCCT GCCCTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCCTGCTGTGT GGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 169-171 make up a codon that encodes Ser or Cys	
AP15 nucleotide sequence	NNNATCCAGAATCCCAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCC GGCGGAAACGCTCTGGAAGCGGAGCGACCAATTTT CAGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATTGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGTCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT	236

Description	Sequence	SEQ ID NO:
	CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
15T nucleotide sequence	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCAC AGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATC CAGAGCATGCACATTGATGCCACCCCTGTACACAGAATCTGATGTGCACCCT AGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATT TCTCTGGAAAGCGAGATGCCCTCTATCCACGACACAGTGGAGAATCTGATC ATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGC TGTAAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAG AGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGA TCTGGAGGAGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGC GGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCC GATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGC AACAGCGGCTTTAAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTG CTGAATAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGC ATTAGAGATCCTGCCCTGGTCCACCAGAGGCCCTGCCCCCTCCATCTACAGTG ACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAA GAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCC GCCATTGTGCCTGGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGC ACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCCTCTACCAGCCTCCAGGA GTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACA GTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAG TCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCC CTGCCTGTGACATGGGGAAACAAGCAGCAGAGATGAAGACCTGGAGAATTGT TCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGT CTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	237
AP15T nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTTCAACCGACTTTGATAGCCAGATCAACGTG CCTAAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCCGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCTGTGTAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA	238

Description	Sequence	SEQ ID NO:
	AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGGCTGCCCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCCGGCG AAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCCGTGAC GTGGAGGAGAATCCCGGCCCT NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Scr, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
AT15 nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCC GGCGGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCTCTGGCCAAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTCAATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTGT GATACAACAGTGGCCATCAGCACATCTACAGTGCCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr;	239

Description	Sequence	SEQ ID NO:
	NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
15P nucleotide sequence	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCAC AGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATC CAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCT AGCTGTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATT TCTCTGGAAAGCGGAGATGCCCTCTATCCACGACACAGTGGAGAATCTGATC ATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGC TGTAAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAG AGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGA TCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGC GGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCC GATATTTGGGTGAAGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGC AACAGCGGCTTTAAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTG CTGAATAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGC ATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTG ACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTCTGGAAAA GAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCGCCACAACAGCC GCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGC ACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGA GTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACA GTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAG TCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGCCATGGAAGCC CTGCCTGTGACATGGGGAAACAAGCAGCAGAGATGAAGACCTGGAGAATTGT TCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTCAGC CTGCTGAAGCAGGCGGGCGSATGTGGAGGAGAACCCTGGCCCA	240
AT15P nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGCACACTGTGCCCTGTTCCACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCCACCTATCCT TCCTCTGACGTGCCATGTGATGCCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCCGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCACTGGAGGCGGAGGATCTGGCGGAGGATCTCTCGAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCCCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGACCCCTGCCCTCCATCTACACTGACAACAGCCCGAGTGCACCT	241

Description	Sequence	SEQ ID NO:
	CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAA CGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCGGGCGAT GTGGAGGAGAACCCTGGCCCA NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
BP15T nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGGAATAAGCAGAAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAGAG GTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGTCTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGTCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTG ACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAAGGATGT GAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGCAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGC GGATCTGGAGGAGGAGGCACTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTG AAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGGTGTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCCCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGTGT GGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG CGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGC GGTGACCTGGAGGAGAATCCCGGCCCT	242

Description	Sequence	SEQ ID NO:
	NNN at positions 169-171 make up a codon that encodes Ser or Cys	
BT15P nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAAATCCCGGCCCTATGGATTGGACCTGG ATTCTGTTTCTGGTGGCGCTGCCACAAGAGTGCACAGCACTCCGAGGAAAT GTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATT GATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACC GCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGA GATGCCCTCTATCCACGACACAGTGGAGAAATCTGATCATCTTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAG GAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGCACTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAG ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGG GCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCG GGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 169-171 make up a codon that encodes Ser or Cys	243

Table 11B. Exemplary polynucleotide sequences for use in polycistronic expression cassette.

Description	Sequence	SEQ ID NO:
AP nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGCACACTGTGCCTGTTCAACGACCTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGCGCGCATCGCTGGTCCATCAG ACATCTTTCACTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTTCATCGTGTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	250
BT nucleotide	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC	251

Description	Sequence	SEQ ID NO:
sequence	AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCCTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAGCGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	
BT15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCCTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAGCGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGG ATTCTGTTTCTGGTGGCCGTGCCACAAGAGTGCACAGCAACTGGGTGAAT GTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATT GATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACC GCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGA GATGCCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAG GAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTTCATCAATACAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGCGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAG ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCCTGCCCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	252
AT nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCAGACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGTGCCTGCTGGAT ATGAAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT	253

Description	Sequence	SEQ ID NO:
	TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCT	
BP nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCCTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGACCCCTAGCTGTAAGTG ACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGG GGATCTGGAGGAGGAGGCACTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAAATGTCTGTGGAGCAGCGCATATTTGGGTG AAGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAGAAGCCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGT GGACTGTCTGCCGTGTCTGTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	254
BP15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCCTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGACCCCTAGCTGTAAGTG ACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGG GGATCTGGAGGAGGAGGCACTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAAATGTCTGTGGAGCAGCGCATATTTGGGTG AAGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAGAAGCCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGT GGACTGTCTGCCGTGTCTGTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	255
AP15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCTGTTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGTGCCTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGTGAGAACTCTG	256

Description	Sequence	SEQ ID NO:
	CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCTTGGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	
AP15T nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCCTGTTACCGACTTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTTCATCACCGACAAGTGCCTGCTGGAT ATGAAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCTTGGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTG	258

Description	Sequence	SEQ ID NO:
	TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	
AT15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCCTGTTACCCGACTTTGATAGCCAGATCAACGTGCCTAAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGTGCCTGCTGGATATGAAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCGGGCGAAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTCTGAGGAGCTGAGGAGAAGAACATCAAGGAGTTTCTGCGAGAGCTTTGTGCACATCGTGAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAAGGAGGCGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAAGGCCGGCACCTCTTCTCTGACAGAGTGGCTGCTGAATAAGGCCACAAATGTGGCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACAGAGGCCCTGCCCTCCATCTACAGTGACAACAGCCGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCCTGGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTCTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	259
AT15P nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCCTGTTACCCGACTTTGATAGCCAGATCAACGTGCCTAAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGTGCCTGCTGGATATGAAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCGGGCGAAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGAGGAGAAGAACATCAAGGAGTTTCTGCGAGAGCTTTGTGCACATCGTGAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA	261

Description	Sequence	SEQ ID NO:
	GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGC'TTTAAGAGAAAAG GCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCTCCT AGCTCTAATAATAACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAA CGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCGGGCGAT GTGGAGGAGAACCCTGGCCCA	
BP15T nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAAGCGACCCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTG CTGAAGCAGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTG ACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGCAGATGTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGC GGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTG AAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGC'TTT AAGAGAAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCC AGCTCTCCTAGCTCTAATAATAACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGT GGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG CGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGC GGTGACGTGGAGGAGAATCCCGGCCCT	262
BT15P nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAAGCGACCCCTGGTGTGCCTGGCGAGG	263

Description	Sequence	SEQ ID NO:
	GGCTTCTTTCCCGATCACGTGGAGCTGTCCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGG ATTCTGTTTCTGGTGGCGCTGCCACAAGAGTGACACAGCAACTGGGTGAAT GTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATT GATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACC GCCATGAAGTGTTTTCTGCTGGAGCTGCAGTGATTTCTCTGGAAAGCGGA GATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAG GAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGCGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAG ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTTGTGCCTGGA TCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGG GCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCCTGCTGAAGCAGGCG GGCGATGTGGAGGAGAACCCTGGCCCA	

Table 11C. Exemplary polynucleotide sequences for use in polycistronic expression cassette.

Description	Sequence	SEQ ID NO:
AP nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGCACACTGTGCCTGTTCAACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAAATCTGCTGGTCATCGTGAAGATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCAGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	270
AT nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGCACACTGTGCCTGTTCAACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT	273

Description	Sequence	SEQ ID NO:
	TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCCGGCCCT	
AP15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGTGGAT ATGAAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCTGTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCTGTACACAGAATCTGATGTGCACCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGACAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCTGTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	276
AP15T nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGTGGAT ATGAAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCTGTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCTGTACACAGAATCTGATGTGCACCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGACAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT	278

Description	Sequence	SEQ ID NO:
	GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGC'TTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCT CCTAGCTCTAATAATAACCGCCGCCACAACAGCCGCCATTGTGCCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGTCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCG AAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGAC GTGGAGGAGAATCCCGGCCCT	
AT15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCCGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCTCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGAG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCC'TGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGTCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	279
AT15P nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCCGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCTCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGAG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCC'TGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGTCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	281

Description	Sequence	SEQ ID NO:
	GACATGAACCTGAATTTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCCGGCTGTGGAGT TCCCCGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCTGTACACAGAATCTGATGTGCACCCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCCCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCCTGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCCGGCGAAA CGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCGGGCGAT GTGGAGGAGAACCCTGGCCCA	

5.7 Transposon and Transposase Systems

[00426] In some embodiments, transgenes of the recombinant vector are introduced into an immune effector cell via synthetic DNA transposable elements, *e.g.*, a DNA transposon/transposase system, *e.g.*, *Sleeping Beauty* (SB). SB belongs to the Tc1/mariner superfamily of DNA transposons. DNA transposons translocate from one DNA site to another in a simple, cut-and-paste manner. Transposition is a precise process in which a defined DNA segment is excised from one DNA molecule and moved to another site in the same or different DNA molecule or genome.

[00427] Exemplary DNA transposon/transposase systems include, but are not limited to, *Sleeping Beauty* (see, *e.g.*, US6489458, US8227432, the contents of each of which are incorporated by reference in their entirety herein), piggyBac transposon system (see *e.g.*, US9228180, Wilson et al, “PiggyBac Transposon-mediated Gene Transfer in Human Cells,” *Molecular Therapy*, 15:139-145 (2007), the contents of each of which are incorporated by reference in their entirety herein), piggyBac transposon system (see *e.g.*, Mitra *et al.*, “Functional

characterization of piggyBac from the bat *Myotis lucifugus* unveils an active mammalian DNA transposon,” *Proc. Natl. Acad. Sci USA* 110:234- 239 (2013), the contents of which are incorporated by reference in their entirety herein), TcBuster (*see e.g.*, Woodard *et al.* “Comparative Analysis of the Recently Discovered hAT Transposon TcBuster in Human Cells,” *PLOS ONE*, 7(11): e42666 (Nov. 2012), the contents of which are incorporated by reference in their entirety herein), and the Tol2 transposon system (*see e.g.*, Kawakami, “Tol2: a versatile gene transfer vector in vertebrates,” *Genome Biol.* 2007; 8(Suppl 1): S7, the contents of each of which are incorporated by reference in their entirety herein). Additional exemplary transposon/transposase systems are provided in US7148203; US8227432; US20110117072; Mates *et al.*, *Nat Genet*, 41(6):753- 61 (2009); and Ivies *et al.*, *Cell*, 91(4):501-10, (1997), the contents of each of which are incorporated by reference in their entirety herein).

[00428] In some embodiments, the transgenes described herein are introduced into an immune effector cell via the SB transposon/transposase system. The SB transposon system comprises a SB a transposase and SB transposon(s). The SB transposon system can comprise a naturally occurring SB transposase or a derivative, variant, and/or fragment that retains activity, and a naturally occurring SB transposon, or a derivative, variant, and/or fragment that retains activity. An exemplary SB system is described in, Hackett *et al.*, “A Transposon and Transposase System for Human Application,” *Mol Ther* 18:674-83, (2010), the entire contents of which are incorporated by reference herein.

[00429] In some embodiments, the vector comprises a Left inverted terminal repeat (ITR), *i.e.*, an ITR that is 5' to an expression cassette, and a Right ITR, *i.e.*, an ITR that is 3' to an expression cassette. The Left ITR and Right ITR flank the polycistronic expression cassette of the vector. In some embodiments, the Left ITR is in reverse orientation relative to the polycistronic expression cassette, and the Right ITR is in the same orientation relative to the polycistronic expression cassette. In some embodiments, the Right ITR is in reverse orientation relative to the polycistronic expression cassette, and the Left ITR is in the same orientation relative to the polycistronic expression cassette.

[00430] In some embodiments, the Left ITR and the Right ITR are ITRs of a DNA transposon selected from the group consisting of a *Sleeping Beauty* transposon, a piggyBac transposon, TcBuster transposon, and a Tol2 transposon. In some embodiments, the Left ITR and the Right ITR are ITRs of the *Sleeping Beauty* DNA transposon.

[00431] In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290 or 291. In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290. In some embodiments, the Left ITR comprises the polynucleotide sequence of SEQ ID NO: 290. In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 291. In some embodiments, the Left ITR comprises the polynucleotide sequence of SEQ ID NO: 291. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292, 293, or 294. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 293. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 294. In some embodiments, the Right ITR comprises the polynucleotide sequence of SEQ ID NO: 292. In some embodiments, the Right ITR comprises the polynucleotide sequence of SEQ ID NO: 293. In some embodiments, the Right ITR comprises the polynucleotide sequence of SEQ ID NO: 294.

[00432] The polynucleotide sequences of exemplary SB ITRs are provided in Table 12, herein.

Table 12. Polynucleotide sequence of exemplary SB ITRs.

Description	Polynucleotide Sequence	SEQ ID NO
Left ITR – A	AGTTGAAGTCGGAAGTTTACATACACTTAAGTTGGAGTCATTAAAA CTCGTTTTTCAACTACTCCACAAATTTCTTGTTAACAAACAATAGT TTTGGCAAGTCAGTTAGGACATCTACTTTGTGCATGACACAAGTCA TTTTTCCAACAATTGTTTACAGACAGATTATTTCACTTATAATTCA CTGTATCACAATTCAGTGGGTCAGAAGTTTACATACACTAA	290
Left ITR – A2	TACAGTTGAAGTCGGAAGTTTACATACACTTAAGTTGGAGTCATTAA AACTCGTTTTTCAACTACTCCACAAATTTCTTGTTAACAAACAAT AGTTTTGGCAAGTCAGTTAGGACATCTACTTTGTGCATGACACAAG TCATTTTTCCAACAATTGTTTACAGACAGATTATTTCACTTATAAT TCACTGTATCACAATTCAGTGGGTCAGAAGTTTACATACACTAA	295
Left ITR – B	ATATCAATTGAGTTGAAGTCGGAAGTTTACATACACTTAAGTTGGA GTCATTAAAACTCGTTTTTCAACTACACCACAAATTTCTTGTTAAC AAACAATAGTTTTTGGCAAGTCAGTTAGGACATCTACTTTGTGCATG	291

Description	Polynucleotide Sequence	SEQ ID NO
	ACACAAGTCATTTTTTCCAACAATTGTTTACAGACAGATTATTTTAC TTATAATTCACCTGTATCACAATTCAGTGGGTGAGAAGTTTACATA CACTAACAATTGATAT	
Right ITR – A	TTGAGTGTATGTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAAATAAAGTGGTGATCCTAACTGACCTAAGACAGGG AATTTTTACTAGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTTT AAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACTG	292
Right ITR – A2	TTGAGTGTATGTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAAATAAAGTGGTGATCCTAACTGACCTAAGACAGGG AATTTTTACTAGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTTT AAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACTGTA	296
Right ITR – B	TTGAGTGTATGTTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAAATAAAGTGGTGATCCTAACTGACCTAAGACAGG GAATCTTTACTCGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTT TAAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACT	293
Right ITR – B2	TTGAGTGTATGTTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAAATAAAGTGGTGATCCTAACTGACCTAAGACAGG GAATCTTTACTCGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTT TAAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACTGT A	297
Right ITR – C	ATATCTCGAGTTGAGTGTATGTTAACTTCTGACCCACTGGGAATGT GATGAAAGAAATAAAAGCTGAAATGAATCATTCTCTCTACTATTAT TCTGATATTTTACATTCTTAAAATAAAGTGGTGATCCTAACTGACC TTAAGACAGGGAATCTTTACTCGGATTAAATGTCAGGAATTGTGAA AAAGTGAGTTTAAATGTATTTGGCTAAGGTGTATGTAACTTCCGA CTTCAACTCTCGAGATAT	294

[00433] In some embodiments, the DNA transposase is a SB transposase. In some embodiments, the SB transposase is selected from the group consisting of SB11, SB100X, hSB110, and hSB81. In some embodiments, the SB transposase is SB11. Exemplary SB transposases are described in US9840696, US20160264949, US9228180, WO2019038197, US10174309, and US10570382, the full contents of each of which is incorporated by reference herein.

[00434] In some embodiments, the DNA transposase comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300. In some embodiments, the DNA transposase comprises the amino acid sequence of SEQ ID NO: 300. In some embodiments, the amino acid sequence of the DNA transposase consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300. In some embodiments, the amino acid sequence of the DNA transposase consists of the amino acid sequence of SEQ ID NO: 300.

[00435] In some embodiments, the DNA transposase comprises an amino acid sequence that

lacks its N-terminal methionine. In some embodiments, the DNA transposase comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300. In some embodiments, the DNA transposase comprises the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300. In some embodiments, the amino acid sequence of the DNA transposase consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300. In some embodiments, the amino acid sequence of the DNA transposase consists of the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300.

[00436] In some embodiments, the DNA transposase is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 301. In some embodiments, the DNA transposase is encoded by the polynucleotide sequence of SEQ ID NO: 301.

[00437] In some embodiments, the DNA transposase is encoded by a polynucleotide that is introduced into a cell. In some embodiments, the polynucleotide encoding the DNA transposase is a DNA vector. In some embodiments, the polynucleotide encoding the DNA transposase is an RNA vector. In some embodiments, the DNA transposase is encoded on a first vector and the transgenes are encoded on a second vector. In some embodiments, the DNA transposase is directly introduced to a population of cells as a polypeptide.

[00438] The amino acid and polynucleotide sequence of an exemplary SB transposase is provided in Table 13, herein.

Table 13. Amino acid and polynucleotide sequence of an exemplary SB transposase.

Description	Sequence	SEQ ID NO
SB11 (exemplary amino acid sequence)	MGKSKEISQDLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKH HGTTQPSYRSGRRRVLSRDERTLVRKVQINPRTTAKDLVKMLEETGT KVSISTVKRVLYRHNLKGRSARKKPLLQNRHKKARLRFARAHGDKDRT FWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSI MLWGCFAAGGTGALHKIDGIMRKENYVDILKQHLKTSVRKLKLGKRWV FQQDNDPKHTSKHVRKWLKDNKVKLEWPSQSPDLNPIENLWAELEKKR VRARRPTNLTQLHQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGN ATKY	300
SB11 (exemplary nucleotide sequence)	ATGGGAAAATCAAAGAAATCAGCCAAGACCTCAGAAAAAAATTGTA GACCTCCACAAGTCTGGTTCATCCTGGGAGCAATTTCAAACGCCTG AAAGTACCACGTTTCATCTGTACAAACAATAGTACGCAAGTATAAACAC CATGGGACCACGCAGCCGTCATACCGCTCAGGAAGGAGACGCGTTCTG	301

Description	Sequence	SEQ ID NO
	TCTCCTAGAGATGAACGTACTTTGGTGCGAAAAGTGCAAATCAATCCC AGAACAACAGCAAAGGACCTTGTGAAGATGCTGGAGGAAACAGGTACA AAAGTATCTATATCCACAGTAAAACGAGTCCTATATCGACATAACCTG AAAGGCCGCTCAGCAAGGAAGAAGCCACTGCTCCAAAACCGACATAAG AAAGCCAGACTACGGTTTGCAAGAGCACATGGGGACAAAGATCGTACT TTTTGGAGAAATGTCCTCTGGTCTGATGAAACAAAAATAGAAGTGT GGCCATAATGACCATCGTTATGTTTGGAGGAAGAAGGGGGAGGCTTGC AAGCCGAAGAACACCATCCCAACCGTGAAGCACGGGGGTGGCAGCATC ATGTTGTGGGGGTGCTTTGCTGCAGGAGGGACTGGTGCACCTTCACAAA ATAGATGGCATCATGAGGAAGGAAAATTATGTGGATATATTGAAGCAA CATCTCAAGACATCAGTCAGGAAGTTAAAGCTTGGTCGCAAATGGGTC TTCCAACAAGACAATGACCCCAAGCATACTTCCAAACACGTGAGAAAA TGGCTTAAGGACAACAAAGTCAAGGTATTGGAGTGGCCATCACAAAGC CCTGACCTCAATCCTATAGAAAATTTGTGGGCAGAACTGAAAAAGCGT GTGCGAGCAAGGAGGCTACAAACCTGACTCAGTTACACCAGCTTGTG CAGGAGGAATGGGCCAAAATTCACCCAACTTATTGTGGGAAGCTTGTG GAAGGCTACCCGAAACGTTTGACCCAAGTTAAACAATTTAAAGGCAAT GCTACCAAATAC	

5.8 Immune Effector Cells and Methods of Engineering

[00439] In one aspect, provided herein are cells, *e.g.*, immune effector cells, comprising a recombinant vector comprising a polycistronic expression cassette (*e.g.*, a vector described herein). In some embodiments, the immune effector cell is a T cell. For example, in certain embodiments, the T cell is selected from the group consisting of a naïve T cell (CD4⁺ or CD8⁺); a killer CD8⁺ T cell; a cytotoxic CD4⁺ T cell; a CD4⁺ T cell corresponding to Th1, Th2, Th9, Th17, Th22, follicular helper (Tfh), regulatory (Treg) lineages; a CD8⁺ cytotoxic T cell, a CD4⁺ cytotoxic T cell; a CD4⁺ helper T cell (*e.g.*, a Th1 or a Th2 cell); a CD4/CD8 double positive T cell; a tumor infiltrating T cell (TIL); a thymocyte; a memory T cell, (*e.g.*, a central memory T cell, an effector memory T cell, a stem cell-like memory T cell, or a stem cell memory T cell), and a natural killer T cell, *e.g.*, an invariant natural killer T cell. In some embodiments, the T cell is a CD39^{neg}CD69^{neg} T cell or a CD8⁺CD39^{neg}CD69^{neg} cell, as described, *e.g.*, in Krishna *et al.*, “Stem-like CD8 T cells mediate response of adoptive cell immunotherapy against human cancer,” 2020 370(6522):1328-1334, which is incorporated by reference herein in its entirety. Precursor cells of the cellular immune system (*e.g.*, precursors of T lymphocytes) are also useful for presenting a TCR disclosed herein because these cells may differentiate, develop, or mature into effector cells. Accordingly, in certain embodiments, the mammalian cell is a pluripotent stem cell (*e.g.*, an embryonic stem cell, an induced pluripotent stem cell), a hematopoietic stem cell, or a lymphocyte progenitor cell. In certain embodiments, the hematopoietic stem cell or lymphocyte progenitor cell is isolated and/or enriched from, *e.g.*, bone marrow, umbilical cord blood, or peripheral blood. In some

embodiments, the immune effector cell is a CD4⁺ T cell. In some embodiments, the immune effector cell is a CD8⁺ T cell. In one aspect, provided herein is a population of immune effector cells comprising a polycistronic vector described herein. In some embodiments, the population of immune effector cells comprises CD4⁺ T cells and CD8⁺ T cells. In some embodiments, the population of immune effector cells are an *ex vivo* culture.

[00440] In one aspect, provided herein are methods of introducing a vector described herein into a plurality of cells, *e.g.*, immune effector cells, to produce a plurality of engineered cells, *e.g.*, immune effector cells. Methods of introducing vectors into a cell are well known in the art. In the context of an expression vector, the vector can be readily introduced into a host cell, *e.g.*, mammalian (*e.g.*, human) cell by any method in the art. For example, the expression vector can be transferred into a host cell by transfection or transduction. Exemplary methods for introducing a vector into a host cell, include, but are not limited to, electroporation (also referred to herein as electro-transfer), sonication, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, mechanical deformation by passage through a microfluidic device, and the like, *see, e.g.*, Sambrook *et al.* Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (2001), the entire contents of which is incorporated by reference herein. In some embodiments, a polycistronic vector is introduced into an immune effector cell or population of immune effector cells via electroporation. Alternative delivery systems include, *e.g.*, colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. In some embodiments, the polycistronic vector is introduced into a population of cells, *e.g.*, immune effector cells, *ex vivo*, *in vitro*, or *in vivo*. In some embodiments, the polycistronic vector is introduced into a population of cells, *e.g.*, immune effector cells, *ex vivo*.

[00441] In some embodiments, co-expression of mbIL-15 with a transgenic TCR in T cells produces a final drug product that contains T stem cell memory cells (Tscm) which are capable of self-renewal and differentiation into other effector T cell subsets. The expression of mbIL-15 on T cells maintains a population of self-renewing T stem cell memory or T stem cell memory like (Tscm-like) cells that are defined by the surface marker phenotype CD45RA⁺CD45RO⁻CD62L⁺CD95⁺ or CD45RA⁺CD45RO⁺CD62L⁺CD95⁺, respectively. In some embodiments, expression of mbIL-15 on T cells is able to maintain Tscm or Tscm-like subsets as defined above in the absence of external growth and survival factors (*i.e.*, cytokines or antigen stimulation).

[00442] In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic

TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% Tscm cells. In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% Tscm-like cells. In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95+ cells. In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95+ cells.

5.8.1 Sources of immune effector cells

[00443] Immune effector cells may be obtained from a subject by any suitable method known in the art. For example, T cells (*e.g.*, CD4+ T cells and CD8+ T cells) can be obtained from several sources, including peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In some embodiments, immune effector cells (*e.g.*, T cells) are obtained from blood collected from a subject using any number of techniques known to the skilled artisan. In some embodiments, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. T cells are isolated from peripheral blood lymphocytes by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a Percoll gradient or by counter flow centrifugal elutriation.

[00444] The cells collected by apheresis can be washed to remove the plasma fraction and to place the cells in an appropriate buffer (*e.g.*, phosphate buffered saline (PBS)) or media for subsequent processing steps. The washing step may be accomplished by methods known to those in the art, such as by using a semi-automated “flow-through” centrifuge. After washing, the cells may be resuspended in a variety of biocompatible buffers, such as, for example, Ca-free, Mg-free PBS, PlasmaLyte A, or other saline solution with or without buffer. Alternatively, the undesirable components of the apheresis sample may be removed and the cells directly resuspended in culture media.

[00445] A specific subpopulation of cells can be further isolated by positive or negative

selection techniques (*e.g.*, antibody coated beads, flow cytometry, etc.). In some embodiments, a specific subpopulation of T cells, such as CD3⁺, CD28⁺, CD4⁺, CD8⁺, CD45RA⁺, and CD45RO⁺T cells, can be further isolated by positive or negative selection techniques (*e.g.*, antibody coated beads, flow cytometry, etc.).

[00446] In certain embodiments, the mammalian cell is a population of cells presenting a TCR disclosed herein on the cell surface. The population of cells can be heterogeneous or homogenous. In certain embodiments, at least 50% (*e.g.*, at least 60%, 70%, 80%, 90%, 95%, 99%, 99.5%, or 99.9%) of the population is a cell as described herein. In certain embodiments, the population is substantially pure, wherein at least 50% (*e.g.*, at least 60%, 70%, 80%, 90%, 95%, 99%, 99.5%, or 99.9%) of the population is homogeneous. In certain embodiments, the population is heterogeneous and comprises a mixed population of cells (*e.g.*, the cells have different cell types, developmental stages, origins, are isolated, purified, or enriched by different methods, are stimulated with different agents, and/or are engineered by different methods). In certain embodiments, the cells are a population of peripheral blood mononuclear cells (PBMC) (*e.g.*, human PBMCs).

[00447] Populations of cells can be enriched or purified, as needed. In certain embodiments, regulatory T cells (*e.g.*, CD25⁺ T cells) are depleted from the population, *e.g.*, by using an anti-CD25 antibody conjugated to a surface such as a bead, particle, or cell. In certain embodiments, an anti-CD25 antibody is conjugated to a fluorescent dye (*e.g.*, for use in fluorescence-activated cell sorting). In certain embodiments, cells expressing checkpoint receptors (*e.g.*, CTLA-4, PD-1, TIM-3, LAG-3, TIGIT, VISTA, BTLA, TIGIT, CD137, or CEACAM1) are depleted from the population, *e.g.*, by using an antibody that binds specifically to a checkpoint receptor conjugated to a surface such as a bead, particle, or cell. In certain embodiments, a T cell population can be selected so that it expresses one or more of IFN- γ , TNF α , IL-17A, IL-2, IL-3, IL-4, GM-CSF, IL-13, granzyme (*e.g.*, granzyme B), and perforin, or other appropriate molecules, *e.g.*, other cytokines. Methods for determining such expression are described, for example, in PCT Publication No.: WO 2013/126712, which is incorporated by reference herein in its entirety.

5.8.2 Methods of Manufacture

[00448] Engineered cells described herein can be manufactured by any method known in the art. Exemplary methods are shown in U.S. Patent Publication No. 2020/0347350 and International Publication No. WO 2019/067242, incorporated by reference in their entireties.

5.9 Pharmaceutical Compositions

[00449] Provided herein are pharmaceutical compositions comprising a population of engineered immune effector cells disclosed herein having the desired degree of purity in a physiologically acceptable carrier, excipient or stabilizer (see, *e.g.*, Remington's Pharmaceutical Sciences (1990) Mack Publishing Co., Easton, PA). Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol, alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONIC™ or polyethylene glycol (PEG).

[00450] Pharmaceutical compositions described herein can be useful in inducing an immune response in a subject and treating a condition, such as cancer. In one embodiment, the present disclosure provides a pharmaceutical composition comprising a population of engineered immune effector cells described herein for use as a medicament. In another embodiment, the disclosure provides a pharmaceutical composition for use in a method for the treatment of cancer. In some embodiments, pharmaceutical compositions comprise a population of engineered immune effector cells disclosed herein, and optionally one or more additional prophylactic or therapeutic agents, in a pharmaceutically acceptable carrier.

[00451] A pharmaceutical composition may be formulated for any route of administration to a subject. Specific examples of routes of administration include parenteral administration (*e.g.*, intravenous, subcutaneous, intramuscular). In some embodiments, the pharmaceutical composition is formulated for intravenous administration. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions. The injectables can contain one or more excipients. Exemplary excipients include, for example, water, saline, dextrose, glycerol or ethanol. In addition, if desired, the pharmaceutical compositions to be administered can also contain minor

amounts of non-toxic auxiliary substances such as wetting or emulsifying agents, pH buffering agents, stabilizers, solubility enhancers, and other such agents, such as for example, sodium acetate, sorbitan monolaurate, triethanolamine oleate and cyclodextrins.

[00452] In some embodiments, the pharmaceutical composition is formulated for intravenous administration. Suitable carriers for intravenous administration include physiological saline or phosphate buffered saline (PBS), and solutions containing thickening and solubilizing agents, such as glucose, polyethylene glycol, and polypropylene glycol and mixtures thereof.

[00453] The compositions to be used for *in vivo* administration can be sterile. This is readily accomplished by filtration through, *e.g.*, sterile filtration membranes.

[00454] Pharmaceutically acceptable carriers used in parenteral preparations include for example, aqueous vehicles, nonaqueous vehicles, antimicrobial agents, isotonic agents, buffers, antioxidants, local anesthetics, suspending and dispersing agents, emulsifying agents, sequestering or chelating agents and other pharmaceutically acceptable substances. Examples of aqueous vehicles include sodium chloride injection, Ringer's injection, isotonic dextrose injection, sterile water injection, dextrose and lactated Ringer's injection. Nonaqueous parenteral vehicles include fixed oils of vegetable origin, cottonseed oil, corn oil, sesame oil and peanut oil. Antimicrobial agents in bacteriostatic or fungistatic concentrations can be added to parenteral preparations packaged in multiple-dose containers which include phenols or cresols, mercurials, benzyl alcohol, chlorobutanol, methyl and propyl p-hydroxybenzoic acid esters, thimerosal, benzalkonium chloride and benzethonium chloride. Isotonic agents include sodium chloride and dextrose. Buffers include phosphate and citrate. Antioxidants include sodium bisulfate. Local anesthetics include procaine hydrochloride. Suspending and dispersing agents include sodium carboxymethylcellulose, hydroxypropyl methylcellulose and polyvinylpyrrolidone. Emulsifying agents include Polysorbate 80 (TWEEN[®] 80). A sequestering or chelating agent of metal ions includes EDTA. Pharmaceutical carriers also include ethyl alcohol, polyethylene glycol and propylene glycol for water miscible vehicles; and sodium hydroxide, hydrochloric acid, citric acid or lactic acid for pH adjustment.

The precise dose to be employed in a pharmaceutical composition will also depend on the route of administration, and the seriousness of the condition caused by it, and should be decided according to the judgment of the practitioner and each subject's circumstances. For example, effective doses may also vary depending upon means of administration, target site, physiological state of the subject (including age, body weight, and health), other medications administered, or whether treatment is prophylactic or therapeutic. Treatment dosages are optimally titrated to optimize

safety and efficacy.

5.10 Kits

[00455] In one aspect, provided herein are kits comprising one or more pharmaceutical composition, population of engineered effector cells (*e.g.*, recombinant cells), polynucleotide, or vector described herein and instructions for use. Such kits may include, *e.g.*, a carrier, package, or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like. Suitable containers include, for example, bottles, vials, syringes, and test tubes. In one embodiment, the containers are formed from a variety of materials such as glass or plastic.

[00456] In a specific embodiment, provided herein is a pharmaceutical kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions described herein, population of engineered immune effector cells, polynucleotides, or vectors provided herein. In one embodiment, the kit comprises a pharmaceutical composition comprising a population of engineered immune effector cells described herein. In one embodiment, the kit comprises a pharmaceutical composition comprising a population of immune effector cells engineered according to a method described herein. In some embodiments, the kit contains a pharmaceutical composition described herein and a prophylactic or therapeutic agent. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

6. EXAMPLES

[00457] The examples of the present disclosure are offered by way of illustration and explanation, and are not intended to limit the scope of the present disclosure.

6.1 Example 1: Construction of Transposon Plasmids

[00458] To improve homogeneity of multigene co-expression and product manufacturability, recombinant nucleic acid SB transposon plasmids comprising polycistronic expression cassettes were constructed. The polycistronic expression cassettes each include a transcriptional regulatory element operably linked to a polycistronic polynucleotide that encodes the TCR α chain of TCR001 (referred to herein as “TCR α ” or “A”), the TCR β chain of TCR001 (referred to herein as “TCR β ” or “B”), and membrane-bound IL-15/IL-15R α fusion protein (referred to herein as “mbIL15” or “15”), each separated by a furin recognition site and either a P2A element or a T2A element that mediates ribosome skipping to enable expression of separate polypeptide chains.

[00459] The TCR used in this Example, TCR001, is a chimeric TCR with murine-derived constant regions and with human V α and V β regions specific for the R175H mutation of the p53 protein (in which position 175 of the p53 protein is mutated from Arg to His) in the context of HLA-A*02:01.

[00460] Briefly, TCR α was generated by fusing a human V α region, including its N-terminal signal sequence (SEQ ID NO: 1006) with a glutamic acid at position 2, to a murine C α region modified by substituting a cysteine at amino acid position 48, a leucine at amino acid position 112, an isoleucine at amino acid position 114, and a valine at amino acid position 115 (SEQ ID NO: 41). TCR β was generated by fusing a human V β region, including its N-terminal signal sequence (SEQ ID NO: 2006) with an alanine at position 2, to a murine C β modified by substituting a cysteine at amino acid position 57 (SEQ ID NO: 51). mbIL15 was constructed by joining human IL-15 (SEQ ID NO: 76) to human IL-15R α (SEQ ID NO: 78) via a Gly-Ser-rich linker peptide (SEQ ID NO: 81), with an IgE signal sequence (SEQ ID NO: 83) N-terminal to the human IL-15. Schematics of each of these three polypeptide constructs are shown in **FIG. 1**, from N terminus (left) to C terminus (right) for each construct.

[00461] To explore the effect of gene/element order on expression and function, eight tricistronic polynucleotide expression cassettes were generated with polynucleotides encoding each of TCR α , TCR β , and mbIL15. In each expression cassette, these three elements were fused pairwise with a) a polynucleotide encoding a furin recognition site joined to a P2A element (SEQ ID NO: 11) (referred to herein as “fP2A” or “P”) and b) a polynucleotide encoding a furin recognition site joined to a T2A element (SEQ ID NO: 13) (referred to herein as “fT2A” or “T”). The resulting tricistronic expression cassettes, including suitable transcriptional regulatory elements, were inserted between the ITRs of *Sleeping Beauty* (SB) transposon plasmids. The 5' to 3' order of elements in the open reading frame (ORF) of each expression cassette and SB Plasmid is shown in **Table E1**, and schematics of the ORFs of these eight expression cassettes are shown in **FIG. 2A**.

Table E1. Tricistronic SB transposon plasmids.

Plasmid Name	Cassette Name	Order of Elements (5' to 3')
Plasmid APBT15	Cassette APBT15	TCR α -fP2A-TCR β -fT2A-mbIL15
Plasmid ATBP15	Cassette ATBP15	TCR α -fT2A-TCR β -fP2A-mbIL15
Plasmid AP15TB	Cassette AP15TB	TCR α -fP2A- mbIL15-fT2A-TCR β
Plasmid AT15PB	Cassette AT15PB	TCR α -fT2A- mbIL15-fP2A-TCR β
Plasmid BPAT15	Cassette BPAT15	TCR β -fP2A-TCR α -fT2A-mbIL15
Plasmid BTAP15	Cassette BTAP15	TCR β -fT2A-TCR α -fP2A-mbIL15

Plasmid Name	Cassette Name	Order of Elements (5' to 3')
Plasmid BP15TA	Cassette BP15TA	TCR β -fP2A- mbIL15-fT2A-TCR α
Plasmid BT15PA	Cassette BT15PA	TCR β -fT2A- mbIL15-fP2A-TCR α

[00462] The polynucleotide sequences of the ORFs of these transposon plasmids is shown in **Table E2**.

Table E2. Polynucleotide sequences of SB plasmid ORFs.

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
Plasmid APBT15	ATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATTTCCCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGCTGTTTCTGCTGCTGATTCTGGGAGAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACCACTGAAGCAGTCTCTGTTTCACATCACAGCGTCTCAGCC AGCGGACAGCGGACCTACCTGTGCGCGTGGACATCTACCCCTCAGGATATGAGATTCGGC GCGGGCACAAAGGCTGACCGTGAAACCAAACATCCAGAATCCCGAGCCTGCGGTGTACCAGC TGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGAT CAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTACCT GCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCCTGTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGC TGTGGAGTTCCCGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCA GGCGGGCGATGTGGAGGAGAACCTGGCCCAATGGCGACAAGACTGCTGTGCTGGCGGGCG CTGTGCCTGCTGGGAGCGGAAGTGAAGCGGGGGTTCGCGCAGAGCCCTCGATACAAAA TCATTGAGAAGCGGCAGTCTGTGGCGTCTGCTGCAACCCAATCAGCGGACACGCGACCCCT GTACTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATTCAAGTCCAGAACAAAT GGCGTGGTGGACGATAGCCAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCG TGGACTCTACACTGAAAATTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGC GAGCTCCCTGGACCCAGGCGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACA GTGCTGGAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTCGAGCCATCCAAGG CGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGA TCACGTGGAGCTGTCTGTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGTGCACAGAC CCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCG CGACCTTTTGGCACAAACCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTG CGAGGAGGATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAG GCGTGGGGAAGAGCGGACTGTGGCATTACAGCGCGTCTTATCAGCAGGGCGTGTCTCCG CGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCAC CCTGGTGGTGTGCGGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGA GAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGGCCCTATGGATT GGACCTGGATTCTGTTCTGGTGGCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGT GATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCCTG TACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTGCTGCTGG AGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCCTCTATCCACGACACAGTGGAGATCT GATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAG GAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCG TGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGG AGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATG TCTGTGGAGCACGCCGATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACA TCTGCAACAGCGGCTTTAAGAGAAAAGCGCGCACCTCTTCTCTGACAGAGTGCCTGCTGAA TAAGGCCACAAATGTGGCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCTTGCC CTGGTCCACCAGAGGCCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGC CTGAATCTCTGAGCCCTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATAC	320

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	CGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGC ACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCAGGGAACACCTTCTCAGACCACCG CCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGG CCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTGCTGTGTGGACTGTCTGCC GTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGA TGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGA GAATTGTTCTCACCACCTG	
Plasmid ATBP15	ATGGAGTCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTGAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATTTCCCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGCTGTTTCTGCTGCTGATTCCGGGAGAAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTCACATCACAGCGTCTCAGCC AGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCTCAGCATATGAGATTCGGC GCGGGCACAAGGCTGACCCTGAAACCAAACATCCAGAATCCCGAGCCTGCGGTGTACCAGC TGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGAT CAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCACGACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCTGGTCCAATCAGACATCTTTTCACT GCCAGGATATCTTCAAGGAGACAAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGC TGTGGAGTTTCCCGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATG CGGTGACGTGGAGGAGAATCCCGGCCCTATGGCGACAAGACTGCTGTGCTGGGCGGCGCTG TGCTGCTGGGAGCGGAACTGACTGAAGCGGGGGTTCGCGCAGAGCCCTCGATACAAAATCA TTGAGAAGCGGCGAGTCTGTGGCGTTCTGGTGCAACCCAATCAGCGGACACGCGACCCGTGA CTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATTGAGTTCAGAACAAATGGC GTGGTGGACGATAGCCAGCTGCCAAAAGATAGATTTCGCGGAGAGGCTGAAGGCGTGG ACTCTACACTGAAAATTGAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAG TCTCCTGAGCCAGGCGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTG CTGGAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGG AGATCGCGAATAAGCAGAAAAGCGACCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCA CGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTGCACCTCTGGCGTGTGCACAGACCCCT CAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGA CCTTTTGGCACAACCCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGA GGAGGATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCG TGGGGAAGACCGGACTGTGGCATTAACAAGCGCTCCTATCAGCAGGCGCTGCTGTCCGCGA CCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCT GGTGGTCATGGCGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCG ACCAATTTGAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATT GGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGT GATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTTGATGCCACCCCTG TACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGG AGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCT GATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAG GAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCG TGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGG AGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATG TCTGTGGAGCACGCCGATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACA TCTGCAACAGCGGCTTTAAGAGAAAAGCCGGCACCTCTTCTCTGACAGATGCGTGCTGAA TAAGGCCACAATGTGGCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGGCC CTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGC CTGAATCTCTGAGCCCTCTGGAAAAAGAACCTGCCGCCAGCTCTCTAGCTCTAATAATAC CGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGC ACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCAGGGAACACCTTCTCAGACCACCG CCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGG CCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTGCTGTGTGGACTGTCTGCC	321

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
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Plasmid AP15TB	ATGGAGTCTCTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATTCCTCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGTGTTTCTGCTGCTGATTCTGGGAGAAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTCACATCACAGCGTCTCAGCC AGCGGACAGCGGACCTACCTGTGCGCGCTGGACATCTACCCTCACGATATGAGATTCTGGC GCGGGCACAAGGCTGACCGTGAAACCAAACATCCAGAATCCCGAGCCTGCGGTGTACCAGC TGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCCTGTTACCGACTTTGATAGCCAGAT CAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGGCTGCTGGATATG AAAGCGTAGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACACTTTTCACCT GCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGC TGTGGAGTTCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCA GGCGGGCGATGTGGAGGAGAAACCTGGCCCAATGGATTGGACCTGGATTCTGTTTCTGGTG GCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCG AGGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCC TAGCTGTAAGTGACCGCCATGAAGTGTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAA AGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCACAATAGCC TGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAA GAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGC TCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTG GCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTG GGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCCTCTTCTCTGACAGAGTGGCTGCTGAATAAGGCCACAAATTTGGCCCACT GGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCTGCCCC TCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGA AAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTG TGCTTGATCTCAGCTGATGCCCTAGCAAATCTCCTAGCACAGGCACAACAGAGATCAGCAG CCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAAGAAATGGGAGCTGACAGCC TCTGCCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCA TAGCAGCATCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGCTGTTTCTG GAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCT GTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGG CGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGA GAATCCCGGCCCTATGGCGACAAGACTGCTGTGCTGGCGGGCGCTGTGCCCTGCTGGGAGCG GAAGTGAAGCGGGGGTTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGT CTGTGGCGTCTGGTGCAACCCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGAT CCTGGGCCAGGGCCCTAAGCTGCTGATTCTAGTTCAGAACAAATGGCGTGGTGGACGATAGC CAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAA TTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGG CGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGTGGAGGACCTGAGG AACGTGACCCACCTAAAGTGAGCCTGTTTCAGGCCATCCAAGGCGGAGATCGCGAATAAGC AGAAAGCGACCCCTGGTGTGCCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTG GTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGTGCACAGACCCCTCAGGCGTACAAGGAG AGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGGACCTTTTGGCACAAC CCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAATGGCC TGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGAC TGTGGCATTACAAGCGCGTCTTATCAGCAGGGCGTGTGTCCGCGACCATCCTGTACGAGA TTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGAT GGTGAAGAGGAAAACTCT	322
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Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
AT15PB	CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATTTCCCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGCTGTTTCTGCTGCTGATTCTGGGAGAAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACCACTGAAGCAGTCTCTGTTTCACATCACAGCGTCTCAGCC AGCGGACAGCGGACCTACCTGTGCGCGCTGGACATCTACCTCACGATATGAGATTGGC GCGGGCACAAAGGCTGACCGTGAAACCAAACATCCAGAATCCCGAGCCTGCGGTGTACCAGC TGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGAT CAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTACCT GCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGC TGTCAGGATTTCCCGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCAACATG CGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCC GCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGG ATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAG CTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCTGGCCAACAATAGCCTGA GCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAA CATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCT GGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCG GAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGT GAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGA CAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCTCC ATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAA GAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCT CTGGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCA CGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCT GCCTCTCACCAGCCTCCAGGAGTGATCTCCTCAGGGCCACTCTGATACAACAGTGGCCATCA GCACATCTACAGTGCTGCTGTGTGGACTGCTGCGCTGTCTCTGCTGGCCTGTTACCTGAA GTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTG ACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGA AACGCTGTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGA GAACCTGTGGCCCAATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGTGGGAGCG GAACTGACTGAAGCGGGGGTCTGCGCGAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGT CTGTGGCGTTCTGGTGCAACCCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGAT CCTGGGCCAGGGCCCTAAGCTGCTGATTGATTCAGTTCCAGAACAATGGCGTGGTGGACGATAGC CAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAA TTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGG CGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGCTGGAGGACCTGAGG AACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGC AGAAAGCGACCCCTGCTGTGCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGT GTGGGTGAACGGCAAGAGGTGCACTCTGGCGTGTGCACAGACCCCTCAGGCGTACAAGGAG AGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACC CCCGGAATCACTTCCGCTGCCAGGTGCACTTTACGCGCTGTCCGAGGAGGATAAATGGCC TGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGAC TGTGGCATTACAAGCGCGTCTTATCAGCAGGGCGTGTGTCCGCGACCATCCTGTACGAGA TTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCCTGGTGGTTCATGGCGAT GGTGAAGAGGAAAAACTCT	
Plasmid BPAT15	ATGGCGACAAGACTGCTGTGCTGGGCGGGCGCTGTGCCTGCTGGGAGCGGAACCTGACTGAAG CGGGGGTCTGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTG GTGCAACCCAATCAGCGGACACGCCACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGC CCTAAGCTGCTGATTGATTCAGTTCCAGAACAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAG ATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAATTCAGCCTGCGAA	324

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
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Plasmid BTAP15	ATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAACTGACTGAAGCGGGGCTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTGTGGCAACATCAGCGGACACGCGACCCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATTCAGTTCCAGAACAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAATTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGGCGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGCTGGAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCCTGGTGGGTGAACGGC	325

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	AAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCGGAATCACTT CCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCA AAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAA GCGCGTCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAA GGCGACACTGTATGCGGTGCTGGTGTCACCCCTGGTGGTCATGGCGATGGTGAAGAGGAAA AACTCTCGGGCGAAAACGCTCTGGAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTG ACGTGGAGGAGAATCCCGGCCCTATGGAGTCCCTTTCTGGGCGGCGTGCTGCTGATCCTGTG GCTGCAGGTGGACTGGGTGAAATCCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATT CAGGAGGGCAAGACCGCGACACTGACCTGCAACTACACAAATTATTCCCCAGCGTACCTGC AGTGGTATAGGCAGGACCCAGGCAGGGGACCCGTGTTTCTGCTGCTGATTCTGGGAGAATGA GAAGGAGAAAAAGAAAGGAGAGGCTGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTG TTTCACACTCAGCGCTCTCAGCCAGCGGACAGCGCGACCTACCTGTGCGCTGGACATCTG ACCCTCACGATATGAGATTCGGCGCGGGCACAAGGCTGACCGTGAACCCAAACATCCAGAA TCCCAGCGCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTG TTCACCGACTTTGATAGCCAGATCAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCA CCGACAAGTGCGTGCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTG GTCCAATCAGACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACC TGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTT TAATCTGCTGATGACACTGCGGCTGTGGAGTTCCTGGGCGAAAACGCTCTGGAAGCGGAGCG ACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATT GGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGT GATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTG TACACAGAATCTGATGTGCACCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGG AGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCT GATCATCTGGCCACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAAG GAGTGTGAGGAGCTGGAGGAGAAAGACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCG TGCAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGG AGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATG TCTGTGGAGCACGCCGATATTTGGGTGAAGTCCCTACAGCCTGTACAGCAGAGAGAGATACA TCTGCAACAGCGGCTTTAAGAGAAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAA TAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGC CTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATAC CGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGC ACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCG CCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGG CCTCTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTGCTGTGTGGACTGTCTGCC GTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGA TGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGA GAATTGTTCTCACCACCTG	
Plasmid BP15TA	ATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAAGTGAAG CGGGGGTTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTG GTGCAACCCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGC CCTAAGCTGCTGATTAGTTCCAGAACAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAG ATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAATTTCAGCCTGCGAA GCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGGCGATACCGGAGAG CTGTTCTTTGGAGAGGGCAGCCGGTGACAGTGTGGAGGACCTGAGGAACGTGACCCAC CTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCT GGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGC AAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCGGAATCACTT CCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCA AAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAA	326

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	CGCGTCTCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAA GGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCAATGGCGATGGTGAAGAGGAAA AACTCTCGGGCGAAACGCTCTGGAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGG GCGATGTGGAGGAGAACCTGGCCCAATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGC TGCCACAAGAGTGACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGAT CTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCT GTAAAGTGACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGG AGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGC AGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACA TCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGG CGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGA GGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGA AGTCTCAGAGCCTGTACAGCAGAGAGATACATCTGCAACAGCGGCTTTGAGCAAGAGGCA CGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGACA ACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCCTGCCCTCCAT CTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGA ACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACG AATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGC CTCTCACCAGCCTCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGC ACATCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGT CTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGAC ATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAA CGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATC CCGGCCCTATGGAGTCTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTG GGTGAAATCCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTGAGGAGGGCAAGACC CGACACTGACCTGCAACTACACAAATTATTTCCCGAGCGTACCTGCAGTGGTATAGGCGAGG ACCCAGGCGAGGGGACCCGTGTTTCTGCTGCTGATTGCGGAGAAATGAGAAGGAGAAAAGAAA GGAGAGGCTGAAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTACATCACAGCG TCTCAGCCAGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCTCAGCATATGA GATTGCGGCGGGGACAAGGCTGACCGTGAACCAAACATCCAGAATCCCAGGCCTGCGGT GTACCAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCCGACTTTGAT AGCCAGATCAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGC TGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGGATCGCGTGGTCCCAATCAGACATC TTTCACTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCA TGTGATGCGACACTGACCGAGAAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATC TGCTGGTCACTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGAC ACTGCGGCTGTGGAGTTCC	
Plasmid BT15PA	ATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAACCTGACTGAAG CGGGGGTTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTCTG GTGCAACCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGATCCTGGGCGAGGGC CCTAAGCTGCTGATTGAGTTCCAGAACAAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAG ATAGATTTTCCGCGGAGAGGCTGAAAGGCGTGGACTCTACACTGAAAATTCAGCCTGCGAA GCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGGCGATACCGGAGAG CTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGTGGAGGACCTGAGGAACGTGACCCAC CTAAAGTGAGCCTGTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCT GGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGC AAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTAGCAGACTGAGGGTGAGCGGACCTTTTGGACAACCCCGGAATCACTT CCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCA AAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTAACA GCGCGTCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAA GGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCAATGGCGATGGTGAAGAGGAAA AACTCTCGGGCGAAACGCTCTGGAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTG ACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGC	327

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	CACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTG ATCCAGAGCATGCACATTGATGCCACCTGTACACAGAACTCTGATGTGCACCTAGCTGTA AAGTGACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGA TGCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGC AATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAATCA AGGAGTTTCTGCAGAGCTTTGTGCACATCCTGCAGATGTTTCATCAATACAAGCTCTGGCGG AGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGA TCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGT CCTACAGCCTGTACAGCAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGG CACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACA CCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCCTGCCCTCCATCTA CAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACC TGCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTTGTGGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAAT CTTCTACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTC TCACCAGCCTCCAGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACA TCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTA GACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATG GGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAACGC TCTGGAAGCGGAGCGACCAATTTTACGCTGTCTGAAGCAGGCGGGCGATGTGGAGGAGAACC CTGGCCCAATGGAGTCCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTG GGTGAAATCCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACC GCGACACTGACCTGCAACTACACAAATTATTCCCCAGCGTACCTGCAGTGGTATAGGCAGG ACCCAGGCAGGGGACCCGCTGTTTCTGCTGCTGATTCTGGGAGAATGAGAAGGAGAAAAGAAA GGAGAGGCTGAAAGTGACCTTCGATACCACTGAAGCAGTCTCTGTTTCACATCACAGCG TCTCAGCCAGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCTCACGATATGA GATTCTGCGCGCGGGCACAAGGCTGACCGTGAAACCAAACATCCAGAATCCCAGACCTGCGGT GTACCAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCGACTTTGAT AGCCAGATCAACGTGCCTAAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGC TGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATC TTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCA TGTGATGCGACACTGACCAGAGAGGCTTCGAGACAGACATGAACCTGAATTTTCAGAATC TGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGAC ACTGCGGCTGTGGAGTTCC	

[00463] The corresponding theoretical polypeptide translation product resulting from each ORF, not accounting for N-terminal signal sequence cleavage or ribosomal skipping at each P2A and T2A site, is shown in **Table E3**.

Table E3. Polypeptide sequences encoded by SB plasmid ORFs.

Plasmid	Amino Acid Translation of ORF	SEQ ID NO:
Plasmid APBT15	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRKERLKVTFDRTLKQSLFHITASQPADSATYLCALDIYPHDMRFG AGTRLTVKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAGDVEENPGPMATRLLCWAA LCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNN GVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLT VLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTD PQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN SRAKRSGSG EGRGSLLTTCGDVEENPGPMDWTWILFLVAAAATRVHSNWNVVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLEELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFIN TSSGGSGGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTTPSLKCI RDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTA AIVPGSQLMPSPKSPS TGTTEISSHESHGTPSQTTAKNWE LTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	330
Plasmid ATBP15	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRKERLKVTFDRTLKQSLFHITASQPADSATYLCALDIYPHDMRFG AGTRLTVKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTTCGDVEENPGPMATRLLCWAA LCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNN VVDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTV LEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDP QAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE WGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN SRAKRSGSGA VNSYLLKQAGDVEENPGPMDWTWILFLVAAAATRVHSNWNVVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLEELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFIN TSSGGSGGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTTPSLKCI RDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTA AIVPGSQLMPSPKSPS TGTTEISSHESHGTPSQTTAKNWE LTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	331
Plasmid AP15TB	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRKERLKVTFDRTLKQSLFHITASQPADSATYLCALDIYPHDMRFG AGTRLTVKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILFLV AAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLEELQVISLE SGDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFIN T SGGGSGGGSGGGSGGGSGGGSGGGSLQITCPPMSVEHADIWVKSYSLSRERYICNSGFKR KAGTSSLTECVLNKATNVAHWTTTPSLKCI RDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSG KEPAASSPSSNNTAATTA AIVPGSQLMPSPKSPSTGTTEISSHESHGTPSQTTAKNWE LT SASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAMEALP VTWGTSSRDEDLENC SHHLRAKRSGSGEGRGSLLTTCGDVEENPGPMATRLLCWAALCLLGA ELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNNGVVDD SQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLR NVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKE SNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	332
Plasmid AT15PB	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRKERLKVTFDRTLKQSLFHITASQPADSATYLCALDIYPHDMRFG	333

Plasmid	Amino Acid Translation of ORF	SEQ ID NO:
	AGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGDVEENPGPMDWTWILFLVA AATRVHSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSS GGSGGGSGGGSGGGSGGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRK AGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGK EPAASSPSSNNTAATTAATTAIVPGSQLMPKSPSTGTTEISSHESHHGTSPSTTAKNWELTAS ASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAMEALPV TWGTSSRDEDLENC SHHLRAKRSGSGATNFSLLKQAGDVEENPGPMATRLLCWAALCCLLGA ELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSD QLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRSLTVLEDLR NVTPPKVSLEFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKES SNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	
Plasmid BPAT15	MATRLLCWAALCCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQG PKLLIQFQNNGVVDDSDQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRSLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSP KPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN NSRAKRSGSGATNFSLLKQAGDVEENPGPMESFLGGVLLI LWLQVDWVKSQKIEQNSEALN IQEGKTATLT CNYTNYS PAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFD TTKQS LFHITASQPADSATYLCALDIYPHDMRFAGATRLTVKPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATY PSSDVPCDATLTEKSFETDMNLNFQNLIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSG EGRGSLLTCGDVEENPGPMDWTWILFLVAAAATRVHSNWVNVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCK NCEELEEKNIKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSLQITCPPPMS VEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAATTAIVPGSQLMPKSPS TGTTEISSHESHHGTSPSTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLACYLKSRQTPPLASVEMEAMEALPV TWGTSSRDEDLENC SHHL	334
Plasmid BTAP15	MATRLLCWAALCCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQG PKLLIQFQNNGVVDDSDQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRSLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSP KPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN NSRAKRSGSGEGRGSLLTCGDVEENPGPMESFLGGVLLI LWLQVDWVKSQKIEQNSEALNI QEGKTATLT CNYTNYS PAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFD TTKQSL FHITASQPADSATYLCALDIYPHDMRFAGATRLTVKPNIQNPEPAVYQLKDPRSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYP SSDVPCDATLTEKSFETDMNLNFQNLIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGA TNFSLLKQAGDVEENPGPMDWTWILFLVAAAATRVHSNWVNVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSLQITCPPPMS VEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAATTAIVPGSQLMPKSPS TGTTEISSHESHHGTSPSTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLACYLKSRQTPPLASVEMEAMEALPV TWGTSSRDEDLENC SHHL	335
Plasmid BP15TA	MATRLLCWAALCCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQG PKLLIQFQNNGVVDDSDQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRSLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSP KPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN NSRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILFLVAAAATRVHSNWVNVISDLKKIED	336

Plasmid	Amino Acid Translation of ORF	SEQ ID NO:
	LIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVLSLES GDASIHDTVENLIILANNSLS SNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGG GSLQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHW TTPSLKCI RDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAI VPGSOLMPKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAIS TSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAK RSGSGEGRGSLLTCTGDVEENPGPMESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKT ATLTCNYTNYS PAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITA SQPADSATYLCALDIYPHDMRFAGTRLTVPKPNIQNPEPAVYQLKDPQSQDSTLCCLFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPS SDVP CDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	
Plasmid BT15PA	MATRLLCWAALCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPISGHATLYWYQQILGQG PKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRQNTVLEDLRNVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELS WVVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSP KPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NSRAKRS GSGEGRGSLLTCTGDVEENPGPMDWTWILFLVAAATRVHSNWNVNISDLKKIEDL IQSMHIDATLYTESDVHPSCKVTAMKCFLELQVLSLES GDASIHDTVENLIILANNSLS SNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGG SLQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCI RDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAI VPGSOLMPKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAIST STVLLCGLSAVSLACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAK SGSGATNFSLLKQAGDVEENPGPMESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKT ATLTCNYTNYS PAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITA SQPADSATYLCALDIYPHDMRFAGTRLTVPKPNIQNPEPAVYQLKDPQSQDSTLCCLFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPS SDVP CDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	337

[00464] For control purposes, three additional SB transposon plasmids were prepared. Plasmid 15 contains a monocistronic expression cassette, Cassette 15, encoding mbIL15. Plasmid APB contains a bicistronic expression cassette, Cassette APB, encoding TCR α (5') and TCR β (3') with an intervening fP2A element. Plasmid BPA contains a bicistronic expression cassette, Cassette BPA, encoding TCR β (5') and TCR α (3') with an intervening fP2A element. These expression cassettes, including suitable transcriptional regulatory elements, were inserted between the ITRs of SB transposon plasmids. The 5' to 3' order of elements in the ORF of each control expression cassette and SB Plasmid is shown in **Table E4**, and schematics of the ORFs of these three expression cassettes are shown in **FIG. 2B**.

Table E4. Control SB transposon plasmids.

Plasmid Name	Cassette Name	Order of Elements (5' to 3')
Plasmid 15	Cassette 15	mbIL15
Plasmid APB	Cassette APB	TCR α -fP2A-TCR β
Plasmid BPA	Cassette BPA	TCR β -fP2A-TCR α

[00465] A plasmid encoding SB11 transposase, Plasmid TA, was also constructed.

6.2 Example 2: Generation and Evaluation of T Cells

[00466] This Example describes the generation and evaluation of T cells co-expressing TCR α , TCR β , and mbIL15 from the plasmids described in Example 1. A schematic of the gene transfer process for both double transposition (using separate plasmids encoding TCR α /TCR β and mbIL15) and single transposition (using a tricistronic plasmid encoding TCR α /TCR β and mbIL15 together) is shown in **FIG. 3**.

[00467] Briefly, peripheral blood mononuclear cells (PBMCs) were enriched from leukapheresis product obtained from a normal donor (Discovery Life Sciences, Austin, TX). The resulting PBMCs were collected, cryopreserved, and stored in the vapor phase of a liquid nitrogen tank.

[00468] To generate the TCR-T cells described in this Example 2, the plasmids described in Example 1 were electroporated into the enriched PBMCs. Briefly, cryopreserved PBMCs were thawed, resuspended in supplemented media, and incubated in a 37°C/5% CO₂ incubator for one hour. The PBMC test articles listed in **Table E5** were then prepared.

Table E5. PBMC test articles.

Group	Name	Description
1	NT cells	Non-transposed PBMCs
2	mbIL15 cells	PBMCs transposed with Plasmid 15 and Plasmid TA
3	APB cells	PBMCs transposed with Plasmid APB and Plasmid TA
4	BPA cells	PBMCs transposed with Plasmid BPA and Plasmid TA
5	APB+15 cells	PBMCs transposed with Plasmid APB, Plasmid 15, and Plasmid TA
6	BPA+15 cells	PBMCs transposed with Plasmid BPA, Plasmid 15, and Plasmid TA
7	APBT15 cells	PBMCs transposed with Plasmid APBT15 and Plasmid TA
8	ATBP15 cells	PBMCs transposed with Plasmid ATBP15 and Plasmid TA
9	AP15TB cells	PBMCs transposed with Plasmid AP15TB and Plasmid TA
10	AT15PB cells	PBMCs transposed with Plasmid AT15PB and Plasmid TA
11	BPAT15 cells	PBMCs transposed with Plasmid BPAT15 and Plasmid TA
12	BTAP15 cells	PBMCs transposed with Plasmid BTAP15 and Plasmid TA
13	BP15TA cells	PBMCs transposed with Plasmid BP15TA and Plasmid TA
14	BT15PA cells	PBMCs transposed with Plasmid BT15PA and Plasmid TA

[00469] Test articles were prepared as follows:

[00470] Group 1: Rested cells were harvested, spun down, resuspended in supplemented media, and incubated in a 37°C/5% CO₂ incubator overnight.

[00471] Groups 2-14: Rested cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E5**, and electroporated. Following

electroporation, cell suspensions were collected, transferred to supplemented media, and incubated in a 37°C/5% CO₂ incubator overnight.

[00472] Within 24 hours post-electroporation (Day 1), the cells were harvested from culture, counted, and sampled by flow cytometry to determine mbIL15 and TCR transgene expression. Briefly, up to 1×10^6 cells of each test article were stained with human Fc Block (BD Biosciences 564220) first to reduce background staining for 10 minutes at room temperature. Cell suspensions were further stained with fluorochrome conjugated antibodies (listed in **Table 1**) diluted in Brilliant Stain Buffer (BD Biosciences 566349) for 30 minutes at 4°C. TCR expression was detected using PerCP-Cy5.5 conjugated anti-mouse TCR β antibody specific for the murine constant region of TCR β . Other fluorescently conjugated antibodies used included: CD3 (Clone OKT-3), IL-15 (34559), CD8 (Clone RPA-T8), and Invitrogen violet live/Dead dye (**Table E6**).

Table E6. Fluorescently Conjugated Antibodies.

Antibody Target	Clone	Fluorophore	Company & Cat #
Live/Dead		Pacific Blue	Invitrogen L34955A
Human CD3	OKT3	BV510	Biolegend 317332
Human CD8	RPA-T8	PE-Cy7	BD Biosciences 557746
Human IL-15	34559	PE	R&D Systems IC2471P
Mouse TCR	H57-597	PerCP-Cy5.5	BD Biosciences 560657

[00473] Cells were washed with FACS buffer (PBS, 2% FBS, 0.1% sodium azide). Data were acquired using an NovoCyte Quanteon flow cytometer system (Agilent) and analyzed with FlowJo software (version 10.7.1; TreeStar, Ashland, OR) to determine the percentage of each transgenic subpopulation (mbIL15⁺mTCR⁺, mbIL15^{neg}mTCR⁺, mbIL15⁺mTCR^{neg}, mbIL15^{neg}mTCR^{neg}) present in each test article. Unless described otherwise, transgene expression was assessed on gated cell events, singlets, viable events, and CD3⁺ cells.

[00474] Results of flow cytometry are shown in **FIG. 4** and **Table E7**.

Table E7. Day 1 post-electroporation specifications and transgene expression of genetically modified T cells.

Group	Name	Viability (%)	mbIL15 ⁺ (% CD3 ⁺)	mTCR ⁺ (% CD3 ⁺)	mbIL15 ⁺ mTCR ⁺ (% CD3 ⁺)
1	NT cells	97.5	N/A	N/A	N/A
2	mbIL15 cells	83.9	33.4	N/A	N/A
3	APB cells	68.3	N/A	18.6	N/A
4	BPA cells	75.4	N/A	26.1	N/A
5	APB+15 cells	65.7	11.5	9.99	5.07
6	BPA+15 cells	78.5	20.7	23.0	15.2
7	APBT15 cells	78.0	9.91	21.9	7.60

Group	Name	Viability (%)	mbIL15 ⁺ (% CD3 ⁺)	mTCR ⁺ (% CD3 ⁺)	mbIL15 ⁺ mTCR ⁺ (% CD3 ⁺)
8	ATBP15 cells	82.7	13.9	29.1	11.1
9	AP15TB cells	84.1	9.45	20.6	6.05
10	AT15PB cells	81.6	12.6	23.2	8.58
11	BPAT15 cells	64.3	3.41	8.88	2.11
12	BTAP15 cells	73.8	8.66	20.9	5.47
13	BP15TA cells	83.7	13.3	29.9	9.52
14	BT15PA cells	74.5	6.68	12.9	3.12

6.3 Example 3: Generation and Evaluation of Expanded T Cells

[00475] This Example describes the generation and evaluation of T cells co-expressing TCR α , TCR β , and mbIL15 from the plasmids described in Example 1. TCR-T cells described in this Example 3 were generated similarly to those described in Example 2 except as indicated below.

[00476] Briefly, cryopreserved PBMCs were thawed, resuspended in supplemented media (IL-7 + IL-15), and incubated in a 37°C/5% CO₂ incubator for one hour.

[00477] Test articles as listed above in **Table E5** were then prepared as follows:

[00478] Group 1: Rested cells were harvested, spun down, resuspended in recovery media (50:50 media containing IL-7 + IL-15 + n-acetylcysteine (NAC)), and incubated in a 37°C/5% CO₂ incubator overnight.

[00479] Groups 2-14: Rested cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E5**, and electroporated. Following electroporation, cell suspensions were collected, transferred to recovery media (50:50 media containing IL-7 + IL-15 + NAC), and incubated in a 37°C/5% CO₂ incubator overnight.

[00480] Groups 3-14: Within 24 hours post-electroporation (Day 1), mTCR positive (mTCR⁺) cells were isolated using mTCR antibody and MACS® Cell Separation system (Miltenyi Biotec). Live cells from groups 1 & 2 and live TCR⁺ enriched cells from groups 3-14 were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a first expansion media (50:50 media containing IL-21 + IL-7) with irradiated allogeneic feeder cells and OKT3 antibody. Cells were fed regularly with cytokines. After 13 days of first phase expansion, cells were harvested, and expression of mTCR and mbIL15 was detected on CD3⁺ gated population with mouse TCR beta antibody and IL-15 antibody as described in Example 2. Cell count and viability was accessed with a NC3000 cell counter. Unless described otherwise, transgene expression was assessed on gated cell events, singlets, viable events, and CD3⁺ cells.

[00481] Expression of mTCR and mbIL15 and cell viability was assessed for each test article at two separate time points: 1) after electroporation (Day 1), and 2) after first expansion phase (Day 13).

[00482] TCR expression after electroporation (Day 1) is shown in **FIG. 5A-5B**. **FIG. 5A** provides representative TCR expression data from each test article. **FIG. 5B** provides TCR expression data from three donors presented as % mTCR+ cells out of CD3+ cells.

[00483] TCR and mbIL15 expression after first phase expansion (Day 13) is shown in **FIG. 6A-6C**. **FIG. 6A** provides representative TCR and mbIL15 expression data from each test article. **FIG. 6B** provides TCR expression data from three donors presented as % mTCR+ cells out of CD3+ cells and **FIG. 6C** provides % TCR+mbIL15+ cells out of CD3+ cells.

[00484] TCR+ and TCR+mbIL15+ cell number was also assessed after first phase expansion (Day 13) as shown in **FIG. 7A-7B**. **FIG. 7A** provides TCR expression data from three donors presented as total number of mTCR+ T cells and **FIG. 7B** provides total number of TCR+mbIL15+ T cells.

[00485] Cell viability after electroporation (Day 1) and after first phase expansion (Day 13) is shown in **FIG. 8A & 8B**, respectively.

[00486] The transgene expression data and cell count data demonstrate that BP15TA and AP15TB are the most potent candidates to have mbIL15+TCR+ T cells with the highest level of TCR and mbIL15 expression. Viability data demonstrated that despite of the size of the tricistronic mbIL15+TCR vectors (Groups 7-14), the viability is similar to the two-vector co-transfection system (Groups 5 & 6).

[00487] Functionality of the TCR-T cells was also measured following first phase expansion (Day 13) as described below.

[00488] Activation of TCR-T cells generated by electroporation with different polycistronic plasmids was assessed. After 13 days of first phase expansion, cells were co-cultured with wild-type or mutant neoantigen peptide pulsed T2 cells which have endogenous expression of HLA-A*02:01. After overnight incubation, cells were harvested and induction of 4-1BB molecule on CD3+CD8+ cells was detected with 4-1BB antibody. Results are shown in **FIG. 9A-9B** demonstrating that mbIL15/TCR-T cells were highly avid and specific to the target neoantigen as measured by upregulation of 4-1BB co-stimulatory receptor with negligible recognition of wild type sequence. There was no significant difference in function between the mbIL15/TCR-T cells generated using different polycistronic plasmids.

[00489] The level of phosphorylated STAT5 was also assessed for TCR-T cells electroporated with different polycistronic plasmids. After 13 days of first phase expansion, cells were washed and incubated in cytokine-free 50:50 media overnight to stabilize the phosphorylation of STAT5. Phosphorylation of STAT5 was detected the following day on CD3+ cells using pSTAT5 (pY694). Results are shown in **FIG. 10** demonstrating that the expressed mbIL15 is functional. IL15 signaling was activated, inducing phosphorylation of STAT5 (downstream of IL15 receptor). Phosphorylation of STAT5 in mbIL15 TCR-T cells generated with different polycistronic plasmids was not significantly different between plasmids but was increased in all mbIL15 containing plasmids relative to TCR only conditions that lacked mbIL15.

[00490] The level of apoptosis after 9 days of activation was assessed for TCR-T cells electroporated with different polycistronic plasmids. After 13 days of first phase expansion, cells were washed and activated with CD3/CD28 Dynabeads® (ThermoFisher) for 9 days. After activation, apoptosis of CD3+TCR+ cells was monitored with AnnexinV/7ADD kit (Biolegend). Results are shown in **FIG. 11** demonstrating that expression of mbIL15 on CD3+TCR+ cells inhibited AICD (activation-induced cell death) as measured by fewer cells stained for AnnexinV and/or PI. This inhibition of AICD was not significantly different between the different polycistronic plasmids tested, nor was it different from two-vector systems (APB+mbIL15 and BPA+mbIL15).

[00491] A second expansion phase was performed as described below and vector copy number (VCN) following the second expansion phase was assessed. Briefly, T cells from Groups 3-14 were isolated by MACS using mTCR antibodies. T cells from Groups 2-14 were then incubated with a second expansion media (50:50 media containing IL-21) and irradiated feeder cells and OKT3 antibody. Cells were fed regularly with cytokines. After 15 days second phase expansion, cells were harvested and VCN was detected using qPCR as average number of *Sleeping Beauty* transgene DNA copy per cell in a sample. Results are shown in **Table E8** demonstrating that low levels of vector were detected in TCR-T cells and mbIL15/TCR-T cells after two rounds of expansion.

Table E8. Vector Copy Number (VCN) after second expansion phase.

Group	Name	VCN
2	mbIL15 cells	0.3
3	APB cells	0.4
4	BPA cells	1.4
5	APB+15 cells	2.6

Group	Name	VCN
6	BPA+15 cells	2.1
7	APBT15 cells	4.7
8	ATBP15 cells	4.5
9	AP15TB cells	5.3
10	AT15PB cells	3.9
11	BPAT15 cells	1.5
12	BTAP15 cells	2.1
13	BP15TA cells	2.3
14	BT15PA cells	2.9

[00492] **Conclusion:** The series of data described in this example illustrate that BP15TA and AP15TB are the most potent candidates to generate mbIL15 TCR-T cell with the highest level of TCR and mbIL15 expression. All plasmids evaluated expressing mbIL15 increased phosphorylation of STAT5 indicating the mbIL15 expressed at sufficient levels in T cells to elicit downstream signaling. Moreover, co-expression of mbIL15 with a transgenic TCR, reduces AICD following T cell activation. Furthermore, all tricistronic mbIL15/TCR plasmids tested resulted in acceptable VCN values.

6.4 Example 4: Evaluation of polycistronic TCR constructs with different murine constant regions.

[00493] This Example evaluates the effect of different murine constant regions on the TCR constructs described above in Examples 1-3.

[00494] Briefly, the amino acid sequences of the TCR α chain and TCR β chain examined here are identical to the TCR α chain and TCR β chain described in Examples 1-3 except that the constant region of each chain is not cysteine-substituted. Specifically, the TCR α chain was generated by fusing a human V α region, including its N-terminal signal sequence (SEQ ID NO: 1006) with a glutamic acid at position 2, to a murine C α region modified by substituting a leucine at amino acid position 112, an isoleucine at amino acid position 114, and a valine at amino acid position 115 (SEQ ID NO: 42). The TCR β chain was generated by fusing a human V β region, including its N-terminal signal sequence (SEQ ID NO: 2006) with an alanine at position 2, to a murine wild-type C β (SEQ ID NO: 52). The constructs containing the cysteine-substituted constant domains, as described in Examples 1-3, are referred to below as the “S version” and the newly-generated constructs containing the non-cysteine-substituted constant domains are referred to below as the “N version”. A schematic of these constructs is provided in **FIG. 12**.

[00495] The unified plasmids, “NU version” referred to below, vary in the nucleotide sequence of the TCR constant regions compared to the “N version”. All “NU versions” contain the same nucleotide sequences encoding the TCR constant regions (C α and C β); however, the amino acid sequences of the TCR constant regions encoded by the “NU version” are identical to those of the “N version.” No other differences exist between the “N version” and “NU version.”

[00496] To generate the TCR-T cells described in this Example 4, the plasmids described above were electroporated into the enriched PBMCs. Briefly, cryopreserved PBMCs were thawed, exchanged into 50:50 media and electroporated. The PBMC test articles listed in **Table E9** were then prepared. Where it is indicated that cells were transposed, cells were co-electroporated with the indicated plasmid and plasmid TA.

Table E9. PBMC test articles.

Group	Name	Description
2.1	NT cells	Non-transposed PBMCs
2.2	BPA cells	PBMCs transposed with Plasmid BPA
2.3	BPA-N cells	PBMCs transposed with N version of Plasmid BPA
2.4	AP15TB cells	PBMCs transposed with Plasmid AP15TB
2.5	BP15TA cells	PBMCs transposed with Plasmid BP15TA
2.6	AP15TB-N cells	PBMCs transposed with N version of Plasmid AP15TB
2.7	BP15TA-N cells	PBMCs transposed with N version of Plasmid BP15TA
2.8	AP15TB-NU cells	PBMCs transposed with unified N version of Plasmid AP15TB
2.9	BP15TA-NU cells	PBMCs transposed with unified N version of Plasmid BP15TB

[00497] Test articles were prepared as follows:

[00498] Group 2.1: Cells were harvested, spun down, resuspended in recovery media (50:50 media containing IL-7 + IL-15 + n-acetylcysteine (NAC)), and incubated in a 37°C/5% CO₂ incubator overnight.

[00499] Groups 2.2-2.9: Cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E9**, and electroporated. Following electroporation, cell suspensions were collected, transferred to recovery media (50:50 media containing IL-7 + IL-15 + NAC), and incubated in a 37°C/5% CO₂ incubator overnight.

[00500] Within 24 hours post-electroporation (Day 1), live cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a first expansion media (50:50 media containing IL-21 + IL-7 + IL-12 + T Cell TransAct™). Cells were fed regularly with cytokines. After 11 days of first phase expansion, TCR+ cells were isolated with mTCR antibody.

The isolated TCR⁺ T cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a second expansion media (50:50 media containing 3000 IU/ml of IL-2 + T Cell TransAct™). Cells were fed regularly with cytokines. After 11 or 16 days of second phase expansion, cells were harvested, and the various assays described below were performed.

[00501] Transgene expression was assessed for T cells electroporated with different polycistronic plasmids. On Day 1 (post-electroporation), Day 11 pre-enrichment (post-1st phase expansion), Day 11 post-enrichment, and Day 22 (post-2nd phase expansion), cells were harvested and the expression of mTCR and mbIL15 was detected on CD3⁺ gated population with mouse TCR beta antibody and IL-15R α antibody. On Day 1 after electroporation the level of TCR expression was similar between the different versions of polycistronic plasmids (**FIG. 13A**). Prior to enrichment on Day 11, TCR expression trended lower in mbIL15/TCR T cells compared to TCR only; however, TCR expression was comparable post-enrichment on Day 11 (**FIG. 13B**). On Day 22, when the cells were harvested, TCR expression was comparable with no notable difference between “S” and “N” versions of the polycistronic plasmids. Co-expression of TCR and mbIL15 was found to be similar between the different versions of polycistronic plasmids throughout the process (**FIGS. 14-15**).

[00502] Fold expansion of total cell count (**FIG. 16A-16B**) and mTCR⁺ cell count (**FIG. 17A-17B**) was assessed for T cells electroporated with different polycistronic plasmids. Fold expansion value was calculated as: Cell number on Day 11/ Cell number on Day 1 (**FIG. 16A**) and Cell number on Day 22/ Cell number on Day 11 (**FIG. 16B**). Cells transposed with mbIL15/TCR tricistronic plasmids tended to expand less than cells transposed with TCR only bicistronic plasmids during both first and second phase expansion. However, significant degrees of expansion were achieved in all groups and no difference was seen between the different versions of the polycistronic plasmids. mTCR⁺ cell number was calculated as: Total cell number X CD3 population (%) X mTCR population (%).

[00503] The above transgene expression and cell growth data demonstrate that cells generated using N version and NU versions of the polycistronic plasmids were not phenotypically different from cells generated using the S version of the polycistronic plasmids.

[00504] To carry out the pSTAT5 assay, the 4-1BB induction assay, and IFN- γ assay described below, the second expansion phase was extended to 16 days (due to the logistic load). Phosphorylation of STAT5 in T cells at Day 27 was detected on CD3⁺ cells with pSTAT5

(pY694). The pSTAT5 data shown in **FIG. 18** demonstrated that the expressed mbIL15 is functional. IL15 signaling was activated, inducing phosphorylation of STAT5 (downstream of IL15 receptor). Phosphorylation of STAT5 in mbIL15 TCR-T cells generated with the different versions of polycistronic plasmids was not significantly different. The levels of phosphorylated STAT5 trended higher in cells co-expressing mbIL15 and TCR compared to those expressing TCR alone.

[00505] To assess antigen-specific activation of the generated TCR-T cells, overnight co-culture of the generated TCR-T cells with wild-type or mutant neoantigen pulsed DCs (HLA matched) was performed after 16 days of second phase expansion and 4-1BB induction and IFN- γ secretion were measured. Induction of 4-1BB on CD3+CD8+ cells was detected with 4-1BB antibody. Secretion of IFN- γ measured by ELISA (Clone 2G1 and B133.5, Thermo Fisher). The 4-1BB induction results shown in **FIG. 19A**, and IFN- γ secretion results shown in **FIG. 19B** demonstrate that the function of mbIL15 TCR-T cells generated with different versions of the polycistronic plasmids was not significantly different.

[00506] The long-term withdrawal (LTWD) assay was performed to examine the transgene expression, survival and activation of T cells cultured under cytokine-free conditions. The LTWD assay was performed as follows. The engineered T cells at Day 22 (post-first and second phase expansion) were transferred to T25 flask and cultured for 4 weeks in cytokine-free media (50:50). 50% of media was exchanged every week. For the control groups (groups 2.2 & 2.3, **Table E9**), cells were treated with 300U/ml IL-2 twice a week while exchanging the 50% of media. Flow data were acquired using an NovoCyte Quanteon flow cytometer system (Agilent) and analyzed with FlowJo software (version 10.7.1; TreeStar, Ashland, OR). (Data n = 4, pooled from 2 independent experiments)

[00507] After 4 weeks LTWD incubation, the expression of mTCR was detected on CD3+ gated population with mouse TCR beta antibody (**FIG. 20A**) and cell count and viability were accessed (**FIG. 20B**). This mTCR expression and cell count data demonstrated no significant difference between mbIL15 TCR-T cells generated with different versions of the polycistronic plasmids. The number of viable cells decreased after long-term cytokine withdrawal in all groups, but cells from the groups co-expressing mbIL15 and TCR survived 5~6 fold more compared to cells from the TCR only groups.

[00508] The activation of TCR-T cells after LTWD culture was assessed by 4-1BB induction and IFN- γ secretion after overnight co-culture with wild-type or mutant neoantigen (10 μ g/mL)

pulsed DCs (HLA matched). As described above, induction of 4-1BB on CD8⁺ T cells was detected with 4-1BB antibody (**FIG. 21A-21B**) and IFN- γ secretion was measured by ELISA (**FIG. 22A-22B**). These data demonstrate that mbIL15 TCR-T cells which survived LTWD culture retained their specific function and demonstrated more potent activation than T cells from control TCR only groups (IL-2 treated); however, the function of mbIL15 TCR-T cells generated with different versions of the polycistronic plasmids was not significantly different.

[00509] Memory phenotype of TCR-T cells electroporated with different polycistronic vectors was also assessed. T cell memory subsets are defined as: CD45RA⁺CD45RO⁺CD62L⁺CD95⁺ = stem cell memory-like (Tscm-like); CD45RA⁺CD45RO⁻CD62L⁺CD95⁺ = stem cell memory (Tscm); CD45RA⁻CD45RO⁺CD62L⁺CD95⁺ = central memory (Tcm); CD45RA⁻CD45RO⁺CD62L⁻CD95⁺ = effector memory (Tem). T cell effector (Teff) are defined as CD45RA⁺CD45RO⁺CD62L⁻CD95⁺. The pie charts in **FIG. 23A-23C** show the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-first phase expansion (**FIG. 23A**), day 22 post-second phase expansion (**FIG. 23B**), and after 4 weeks of LTWD culture (**FIG. 23C**) in cells transposed with the tested plasmids.

[00510] Memory phenotype data shows the kinetics of TCR-T memory and effector differentiation. At days 11 and 22 post-expansion, there is no difference between the different polycistronic TCR plasmids (**FIG. 23A-23B**). There were more Tscm and Teff cells and fewer Tcm cells in the TCR-T cells expressing mbIL15 relative to TCR-T cells without mbIL15. After 4 weeks of culture in absence or presence of IL-2, TCR-T cells predominantly differentiated into Teff cells (over 85%). TCR-T cells expressing mbIL15 cultured for 4 weeks in the absence of cytokines differentiated into 3 main subsets: Teff, Tscm-like and Tscm cells (**FIG. 23C**). These results suggest that mbIL15 is sufficient to support the Tscm phenotype.

[00511] **Conclusions:** The mbIL15 TCR-T cells generated from different versions of the polycistronic plasmids showed comparable features including TCR expression, memory phenotype, specificity, and IFN- γ secretion. This data supports that removal of cysteine-substitutions in the mouse constant domains used in the first-generation vectors and use of unified mouse constant regions will not produce any significant changes in the mbIL15 TCR-T cell product.

6.5 Example 5: Generation and Evaluation of T cells generated using various tricistronic TCR/mbIL15 vectors

[00512] This Example describes the evaluation of T cells expressing mbIL15 in combination with different TCR α /TCR β chains generated using tricistronic vectors as described below. Similar to the vectors described in Example 4, the tricistronic expression cassettes used in this Example each include a transcriptional regulatory element operably linked to a polycistronic polynucleotide that encodes a TCR α chain (referred to herein as “TCR α ” or “A”), a TCR β chain (referred to herein as “TCR β ” or “B”), and membrane-bound IL-15/IL-15R α fusion protein (referred to herein as “mbIL15” or “15”), each separated by a furin recognition site and either a P2A element or a T2A element that mediates ribosome skipping to enable expression of separate polypeptide chains.

[00513] The nine TCRs used in this Example are each directed against a different target as shown in **Table E10**. The V α amino acid sequences and V β amino acid sequences for each of the nine TCRs listed correspond to the sequences provided in **Table 6**. Each TCR α chain was generated by fusing the V α sequence to a murine C α region modified by substituting a leucine at amino acid position 112, an isoleucine at amino acid position 114, and a valine at amino acid position 115 (SEQ ID NO: 42). Each TCR β chain was generated by fusing the V β sequence to a murine wild-type C β (SEQ ID NO: 52).

Table E10. TCR Targets.

Target Protein	Mutation	HLA Type	TCR
TP53	R175H	A*02:01	TCR001
		DRB1*13:01	TCR009
	R248W	A*68:01	TCR057
	Y220C	DRB3*02:02	TCR016
KRAS	G12D	A*11:01	TCR022
		C*08:02	TCR064
	G12V	A*11:01	TCR075
		C*01:02	TCR055
EGFR	E746-A750del	DPA1*02:01/DPB1*01:01	TCR077

[00514] For each of the TCRs above, three vectors were constructed and evaluated: 1) TCR only (BA); 2) A15B; and 3) B15A. The TCR only (BA) vectors contain a bicistronic expression cassette encoding TCR β chain and TCR α chain separated by a furin recognition site and a P2A element in the following orientation from 5' to 3': TCR β -TCR α . The AP15TB vectors contain a tricistronic expression cassette encoding TCR α chain, TCR β chain, and mbIL15 in the following orientation from 5' to 3': TCR α -mbIL15-TCR β . The BP15TA vectors contain a tricistronic

expression cassette encoding TCR α chain, TCR β chain, and mbIL15 in the following orientation from 5' to 3': TCR β -mbIL15-TCR α .

[00515] TCR-T cells described in this Example were generated similarly to those described in Examples 2-4 except as indicated below. Where it is indicated that cells were transposed, cells were co-electroporated with the indicated plasmid as well as plasmid TA or similar Transposase expression plasmid unless otherwise stated.

[00516] Briefly, cryopreserved PBMCs were thawed, resuspended in 50:50 media and placed in a 37°C/5% CO₂ incubator before electroporation.

[00517] Test articles as listed in **Table E11** were then prepared.

Table E11. PBMC test articles.

Group	TCR	Name	Description
3.1	None	NT	Non-transposed PBMCs
3.2	TCR001	BPA-N ¹	PBMCs transposed with TCR001 BPA-N
3.3	TCR001	AP15TB-NU ²	PBMCs transposed with TCR001 AP15TB-NU
3.4	TCR001	BP15TA-NU ³	PBMCs transposed with TCR001 BP15TA-NU
3.5	TCR057	BPA-N	PBMCs transposed with TCR057 BPA-N
3.6	TCR057	AP15TB-NU	PBMCs transposed with TCR057 AP15TB-NU
3.7	TCR057	BP15TA-NU	PBMCs transposed with TCR057 BP15TA-NU
3.8	TCR009	BPA-N	PBMCs transposed with TCR009 BPA-N
3.9	TCR009	AP15TB-NU	PBMCs transposed with TCR009 AP15TB-NU
3.10	TCR009	BP15TA-NU	PBMCs transposed with TCR009 BP15TA-NU
3.11	TCR016	BPA-N	PBMCs transposed with TCR016 BPA-N
3.12	TCR016	AP15TB-NU	PBMCs transposed with TCR016 AP15TB-NU
3.13	TCR016	BP15TA-NU	PBMCs transposed with TCR016 BP15TA-NU
3.14	None	NT	Non-transposed PBMCs
3.15	TCR022	BPA-N	PBMCs transposed with TCR022 BPA-N
3.16	TCR022	AP15TB-NU	PBMCs transposed with TCR022 AP15TB-NU
3.17	TCR022	BP15TA-NU	PBMCs transposed with TCR022 BP15TA-NU
3.18	TCR075	BPA-N	PBMCs transposed with TCR075 BPA-N
3.19	TCR075	AP15TB-NU	PBMCs transposed with TCR075 AP15TB-NU
3.20	TCR075	BP15TA-NU	PBMCs transposed with TCR075 BP15TA-NU
3.21	TCR055	BPA-N	PBMCs transposed with TCR055 BPA-N
3.22	TCR055	AP15TB-NU	PBMCs transposed with TCR055 AP15TB-NU
3.23	TCR055	BP15TA-NU	PBMCs transposed with TCR055 BP15TA-NU
3.24	TCR064	BPA-N	PBMCs transposed with TCR064 BPA-N
3.25	TCR064	AP15TB-NU	PBMCs transposed with TCR064 AP15TB-NU
3.26	TCR064	BP15TA-NU	PBMCs transposed with TCR064 BP15TA-NU
3.27	None	NT	Non-transposed PBMCs
3.28	TCR077	BPA-N	PBMCs transposed with TCR077 BPA-N
3.29	TCR077	AP15TB-NU	PBMCs transposed with TCR077 AP15TB-NU
3.30	TCR077	BP15TA-NU	PBMCs transposed with TCR077 BP15TA-NU

¹ Generated using the same plasmid as BPA-N group in Example 4.

² Generated using the same plasmid as AP15TB-NU group in Example 4.

³ Generated using the same plasmid as BP15TA-NU group in Example 4.

[00518] Test articles were prepared in three batches (Batch 1 = Groups 3.1-3.13; Batch 2 = Groups 3.14-3.26; Batch 3 = Groups 3.27-3.30) as follows:

[00519] Groups 3.1, 3.14, & 3.27: Cells were harvested, spun down, resuspended in recovery media (50:50 media containing IL-7 + IL-15 + n-acetylcysteine (NAC)), and incubated in a 37°C/5% CO₂ incubator overnight.

[00520] Groups 3.2-3.13, 3.15-3.26, & 3.28-3.30: Cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E10**, and electroporated. Following electroporation, cell suspensions were collected, transferred to recovery media (50:50 media containing IL-7 + IL-15 + NAC), and incubated in a 37°C/5% CO₂ incubator overnight.

[00521] Within 24 hours post-electroporation (Day 1), live cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a first expansion media (50:50 media containing IL-21 + IL-7 + IL-12 + T Cell TransAct™). Cells were fed regularly with cytokines. After 11 days of first phase expansion, TCR+ cells were isolated with mTCR antibody. The isolated TCR+ T cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a second expansion media (50:50 media containing 3000U/ml of IL-2 + T Cell TransAct™). During this second expansion phase, cells were fed regularly with cytokines. After 11 or 16 days of second phase expansion, cells were harvested, and the various assays described below were performed.

[00522] Transgene expression was assessed for T cells electroporated with different polycistronic plasmids. On Day 1 (post-electroporation), Day 11 (post-1st phase expansion) and Day 22 (post-2nd phase expansion), cells were harvested and the expression of mTCR and mbIL15 was detected on CD3+ gated population with mouse TCR beta antibody and IL-15Rα antibody. The results are shown in **FIGS. 24-28**.

[00523] Fold expansion of total cell count and mTCR+ cell count was assessed for T cells electroporated with different polycistronic plasmids. Fold expansion value was calculated as: Cell number on Day 11/ Cell number on Day 1 and Cell number on Day 22/ Cell number on Day 11. mTCR+ cell number was calculated as: Total cell number X CD3 population (%) X mTCR population (%). The results are shown in **Table E12**.

Table E12. Fold expansion of total cells and mTCR+ cell count during first and second expansion phases.

Group		Fold Expansion (FE)							
		Total Cell				mTCR+ Cell			
		First expansion		Second expansion		First expansion		Second expansion	
		Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
1	TCR001-BPA-N	83.86	19.60	121.97	11.81	6.11	2.09	171.56	9.57
	TCR001-AP15TB-NU	66.89	13.09	107.01	20.38	18.38	9.60	101.00	17.14
	TCR001-BP15TA-NU	62.93	17.70	108.50	20.15	19.04	7.72	104.08	16.79
2	TCR057-BPA-N	98.21	36.03	110.40	7.05	8.16	4.73	146.17	13.45
	TCR057-AP15TB-NU	58.90	16.21	107.38	16.76	17.34	9.77	104.42	16.05
	TCR057-BP15TA-NU	58.78	16.21	108.69	3.91	14.19	6.44	104.04	3.64
3	TCR009-BPA-N	104.97	30.03	142.34	25.63	11.62	4.92	154.58	28.38
	TCR009-AP15TB-NU	51.68	13.48	95.38	13.31	24.76	12.75	83.83	16.19
	TCR009-BP15TA-NU	49.99	4.70	75.43	10.92	7.03	3.49	77.03	17.45
4	TCR016-BPA-N	87.13	9.63	127.79	25.67	17.38	5.29	142.91	26.78
	TCR016-AP15TB-NU	61.46	12.58	95.42	16.34	26.02	18.67	82.78	10.34
	TCR016-BP15TA-NU	66.33	15.42	93.38	14.09	23.39	15.51	83.30	14.44
5	TCR022-BPA-N	85.99	6.51	169.56	16.12	8.39	1.15	202.20	37.63
	TCR022-AP15TB-NU	59.11	5.90	95.36	12.47	12.21	1.59	102.12	22.10
	TCR022-BP15TA-NU	63.98	5.28	120.10	17.30	11.70	1.79	161.60	69.66
6	TCR075-BPA-N	89.45	6.14	182.86	15.27	9.12	0.75	207.74	21.54
	TCR075-AP15TB-NU	63.30	7.06	106.07	14.15	12.71	2.11	102.37	32.40
	TCR075-BP15TA-NU	59.06	5.91	107.40	20.65	10.57	2.47	114.25	43.15
7	TCR055-BPA-N	78.21	3.52	165.43	25.40	6.05	1.34	198.11	98.27
	TCR055-AP15TB-NU	58.84	1.25	95.98	18.09	10.28	1.79	67.59	20.05
	TCR055-BP15TA-NU	59.15	6.69	87.57	13.96	8.76	2.03	78.66	25.73
8	TCR064-BPA-N	86.10	10.54	177.48	15.01	8.47	1.48	212.18	55.16
	TCR064-AP15TB-NU	55.46	5.95	120.98	12.99	12.61	1.78	162.44	67.74
	TCR064-BP15TA-NU	59.66	4.38	110.54	16.75	9.78	1.98	137.63	59.08
9	TCR077-BPA-N	91.68	6.43	217.14	17.84	12.72	5.26	332.66	29.27
	TCR077-AP15TB-NU	57.10	5.54	97.22	13.45	16.66	7.28	75.79	4.98
	TCR077-BP15TA-NU	63.14	3.27	94.38	19.73	13.41	3.60	75.86	14.16

[00524] Cells generated using the polycistronic plasmids containing different TCR sequences were not phenotypically different from each other as demonstrated by transgene expression and cell growth data.

[00525] To assess activation of the generated TCR-T cells, overnight co-culture of the generated TCR-T cells with wild-type or mutant neoantigen pulsed DCs (HLA matched) was performed after 16 days second phase expansion and 4-1BB induction and IFN- γ secretion were measured. Induction of 4-1BB on CD3+CD8+ cells was detected with 4-1BB antibody. Secretion of IFN- γ measured with the ELISA antibody pair. The 4-1BB induction results are shown in **FIG. 29A-29I**

and IFN- γ secretion results are shown in **FIG. 30A-30I**. The results demonstrate that when challenged with their cognate neoantigen, mbIL-15 TCR-T cells were highly avid and specific to the target neoantigens as measured by upregulation of 4-1BB co-stimulatory receptor and secretion of IFN- γ with negligible recognition of wild type sequences.

[00526] All data from electroporation to the second expansion phase of TCR vetting demonstrated that tricistronic system, expressing TCR α , TCR β and mbIL15 with one plasmid successfully generated mbIL15 TCR-T cells and the features of the generated mbIL15 TCR-T cells are comparable to TCR-T cells in terms of transgene expression, cell growth, and functional specificity (4-1BB induction and IFN- γ secretion).

[00527] Cytolytic activity of TCR-T cells was assessed for T cells electroporated with polycistronic plasmids encoding TCR001 +/- mbIL15 generated as described above (overnight recovery + 11 days first phase expansion + 11 days second phase expansion) and then harvested and frozen on Day 22. On experimental day, frozen Day 22 TCR-T cells were thawed and recovered for 3 days in media containing 3000U/ml of IL-2. Then, the recovered TCR-T cells were incubated with AU565 (Mut+HLA^{neg}) or Tyk-nu (Mut+HLA⁺) cells. After overnight incubation, the remaining T cells were extensively washed, and the extent of viable cells left in the culture after TCR-specific cytolysis was measured using the CellTiter Glo luminescence-based assay. The results are shown in **FIG. 31**.

[00528] Specific lysis was calculated from background subtracted values as:

$$= \left[\frac{("Tumor \& TCR-T" \text{ value} - ("TCR-T" \text{ Value} + \text{Mean "Tumor" Value}))}{("TCR-T" \text{ Value} - ("TCR-T" \text{ Value} + \text{Mean "Tumor" Value}))} \right] \times 100$$

[00529] Cytolytic activity of TCR-T cells was also assessed for T cells electroporated with polycistronic plasmids encoding TCR022 +/-mbIL15 or TCR075 +/- mbIL15 generated as described above (overnight recovery + 11 days first phase expansion + 11 days expansion) and then harvested and frozen on Day 22. On experimental day, frozen Day 22 TCR-T cells were thawed and recovered for 3 days in media containing 3000U/ml of IL-2. Meantime, Saos-2 cells were plated in 96 well plate. After overnight incubation, HLA*11:01 plasmid was transfected into the Saos-2 cells and on the following day, WT or MUT neoantigenic peptides (1ug/ml) were loaded on the transfected Saos-2 cells for 2 hours. Then, the recovered TCR-T cells were incubated with the resulting Saos-2 cells overnight. After the overnight incubation, the remaining T cells were extensively washed, and the extent of viable cells left in the culture after TCR-specific cytolysis was measured using the CellTiter Glo luminescence-based assay. The results are shown in **FIG.**

32A-32B.

[00530] Specific lysis was calculated from background subtracted values as:

$$= \left[\frac{("Peptide loaded tumor \& TCR-T" value - ("TCR-T" Value + Mean "Peptide loaded Tumor" Value))}{"TCR-T" Value - ("TCR-T" Value - Mean "Peptide loaded tumor" Value)} \right] \times 100$$

The cytolytic activity data demonstrated that mbIL15 TCR-T cells generated using the tricistronic system exhibited specific lytic activity against target tumor cells.

[00531] The long-term withdrawal (LTWD) assay was performed to examine the transgene expression, survival and activation of T cells cultured under cytokine-free conditions. The LTWD assay was performed as follows. The engineered T cells at Day 22 (post first phase and second phase expansion) were transferred to T25 flask and cultured for 4 weeks in cytokine-free media (50:50). 50% of media was exchanged every week. For the control TCR only (BA) groups, cells were treated with 300U/ml IL-2 twice a week while exchanging the 50% of media. Flow data were acquired using an NovoCyte Quanteon flow cytometer system (Agilent) and analyzed with FlowJo software (version 10.7.1; TreeStar, Ashland, OR). (Data n = 4, pooled from 2 independent experiments)

[00532] After 4 weeks LTWD incubation, the expression of mTCR was detected on CD3+ gated population with mouse TCR beta antibody (**FIG. 33**) and cell count and viability were accessed (**FIG. 34A-34C**). This mTCR expression and cell count data demonstrated no significant difference between mbIL15 TCR-T cells generated with the different polycistronic plasmids. The number of viable cells decreased after long-term cytokine withdrawal in all groups, but cells from the groups co-expressing mbIL15 and TCR survived 5-6 fold more compared to cells from the TCR only groups.

[00533] The activation of TCR-T cells after LTWD culture was assessed by 4-1BB induction and IFN- γ secretion after overnight co-culture with wild-type or mutant neoantigen pulsed DCs (HLA matched). As described above, induction of 4-1BB on CD3+CD8+ cells was detected with 4-1BB antibody (**FIG. 35A-35I**) and IFN- γ secretion was measured with the ELISA antibody pair (**FIG. 36A-36C**). A comparison of 4-1BB induction assessed for T cells harvested at Day 27 and after LTWD is shown in **FIG. 37A-37I**. These data demonstrate that mbIL15 TCR-T cells which survived LTWD culture are still functional and were more strongly activated than cells from TCR only groups. The data also demonstrate that after 4 week of cytokine withdrawal (LTWD), mbIL15 TCR-T cells showed even more potent induction of 4-1BB compared to those cells after the second expansion phase.

[00534] Memory phenotype of TCR-T cells electroporated with different polycistronic vectors was also assessed. T cell memory subsets are defined as: CD45RA+CD45RO+CD62L+CD95+ = stem cell memory-like (Tscm-like); CD45RA+CD45RO-CD62L+CD95+ = stem cell memory (Tscm); CD45RA-CD45RO+CD62L+CD95+ = central memory (Tcm); CD45RA-CD45RO+CD62L-CD95+ = effector memory (Tem). T cell effector (Teff) are defined as CD45RA+CD45RO+CD62L-CD95+. The data in **Tables E13** and **E14** and representative pie charts in **FIGS. 38-40** show the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-expansion (**Table E13 & FIG. 38**), day 22 post-expansion (**Table E14 & FIG. 39**), and after 4 weeks of LTWD culture (**FIGS. 40A-40E**) in cells transposed with the tested plasmids.

Table E13. Memory phenotype of engineered T cells at D11.

Plasmid		%Tscm-like	% Tscm	%Teff	% Tcm	% Tem
1	TCR001-BPA-N	35.8	0.5	10.3	36.5	16.9
	TCR001-AP15TB-NU	34.1	0.2	7.3	43.3	15.1
	TCR001-BP15TA-NU	29.0	nd	6.7	46.9	17.2
2	TCR057-BPA-N	37.1	0.4	12.3	31.6	18.6
	TCR057-AP15TB-NU	33.7	0.1	7.7	43.5	15.0
	TCR057-BP15TA-NU	31.4	0.2	6.8	45.5	16.1
3	TCR009-BPA-N	38.3	0.6	11.8	29.9	19.4
	TCR009-AP15TB-NU	34.8	0.1	7.1	44.0	14.0
	TCR009-BP15TA-NU	28.5	0.2	6.3	47.7	17.3
4	TCR016-BPA-N	40.2	0.6	12.6	30.0	16.6
	TCR016-AP15TB-NU	32.8	0.4	6.8	44.8	15.2
	TCR016-BP15TA-NU	32.1	0.3	7.0	45.1	15.5
5	TCR022-BPA-N	58.1	2.9	7.5	25.6	5.9
	TCR022-AP15TB-NU	55.1	0.8	2.4	38.7	3.0
	TCR022-BP15TA-NU	56.9	0.7	2.3	37.4	2.7
6	TCR075-BPA-N	59.7	2.8	8.5	23.9	5.1
	TCR075-AP15TB-NU	53.5	0.7	2.1	40.6	3.1
	TCR075-BP15TA-NU	56.8	0.8	2.5	37.2	2.7
7	TCR055-BPA-N	55.6	2.5	8.2	27.8	5.9
	TCR055-AP15TB-NU	56.0	0.9	2.5	38.1	2.5
	TCR055-BP15TA-NU	56.6	0.8	2.5	37.3	2.8
8	TCR064-BPA-N	57.3	3.3	8.2	25.5	5.7
	TCR064-AP15TB-NU	53.3	0.8	2.5	40.1	3.3
	TCR064-BP15TA-NU	54.0	0.6	2.4	39.6	3.4
9	TCR077-BPA-N	63.8	3.0	5.3	22.0	5.8
	TCR077-AP15TB-NU	50.7	0.2	3.7	41.2	4.2
	TCR077-BP15TA-NU	50.7	0.2	4.3	40.4	4.4

Table E14. Memory phenotype of engineered T cells at D22.

Plasmid		%Tscm-like	% Tscm	%Teff	% Tcm	% Tem
1	TCR001-BPA-N	28.8	0.2	23.0	22.8	25.2
	TCR001-AP15TB-NU	33.6	0.9	29.8	15.3	20.4
	TCR001-BP15TA-NU	31.2	0.7	28.4	16.9	22.8
2	TCR057-BPA-N	31.2	0.2	22.7	23.1	22.8
	TCR057-AP15TB-NU	33.5	0.4	28.1	18.0	20.0
	TCR057-BP15TA-NU	34.4	0.7	28.5	16.5	19.9
3	TCR009-BPA-N	26.3	0.1	19.0	27.7	26.9
	TCR009-AP15TB-NU	34.7	0.2	29.4	15.3	19.4
	TCR009-BP15TA-NU	27.5	0.8	32.9	12.7	26.1
4	TCR016-BPA-N	30.7	0.1	22.1	23.3	23.8
	TCR016-AP15TB-NU	35.3	0.8	29.6	14.1	20.2
	TCR016-BP15TA-NU	33.4	0.8	28.9	14.7	22.2
5	TCR022-BPA-N	28.7	0.1	15.3	31.8	24.1
	TCR022-AP15TB-NU	32.3	0.7	22.1	25.1	19.8
	TCR022-BP15TA-NU	30.4	0.5	22.8	24.1	22.2
6	TCR075-BPA-N	26.9	0.2	15.6	33.4	23.9
	TCR075-AP15TB-NU	31.7	0.7	22.6	22.3	22.7
	TCR075-BP15TA-NU	31.4	0.5	23.9	22.2	22.0
7	TCR055-BPA-N	22.9	0.2	14.9	35.1	26.9
	TCR055-AP15TB-NU	28.8	0.5	27.5	19.7	23.5
	TCR055-BP15TA-NU	28.8	0.4	25.7	20.2	24.9
8	TCR064-BPA-N	24.1	0.1	13.9	34.3	27.6
	TCR064-AP15TB-NU	28.7	0.3	21.1	25.8	24.1
	TCR064-BP15TA-NU	28.8	0.6	22.5	23.6	24.5
9	TCR077-BPA-N	34.3	0.3	27.8	19.2	18.4
	TCR077-AP15TB-NU	37.8	2.2	34.8	10.7	14.6
	TCR077-BP15TA-NU	37.8	1.9	36.4	10.1	13.8

[00535] Memory phenotype data shows the kinetics of TCR-T memory and effector differentiation. The addition of mbIL15 to TCR-T cells resulted in changes to the memory phenotype in the expanded product to contain fewer central memory cells (Tcm) and more effector (Teff) and stem cell memory (Tscm) populations relative to conventional TCR-T cells. After 4 weeks of culture in presence of IL-2, TCR-T cells predominantly differentiated into Teff cells. TCR-T cells expressing mbIL15 cultured for 4 weeks in the absence of cytokines differentiated into 3 main subsets: Teff, Tscm-like and Tscm cells. These results suggest that mbIL15 is sufficient to guide T cell differentiation to the Tscm phenotype.

[00536] **Conclusions:** mbIL15 TCR-T cells were successfully generated using 18 different constructs (2 different orientations; AP15TB and BP15TA X 9 TCRs). The addition of mbIL15 to TCR-T cells resulted in changes to the memory phenotype in the expanded product to contain fewer central memory cells (T_{cm}) and more effector (T_{eff}) and stem cell memory (T_{scm}) populations relative to conventional TCR-T cells. Furthermore, long-term withdrawal of cytokine support (LTWD) demonstrated survival of a fraction of mbIL15 TCR-T cells which was significantly higher than survival of TCR-T cells lacking mbIL15. Functional and phenotypic evaluation of the persistent mbIL15 TCR-T cells revealed that they retained their functional neoantigen specificity and potency while displaying a preponderance of T_{scm} TCR-T cells capable of regenerating TCR-T cell effector pools. This suggested that mbIL15 TCR-T cells could likely establish long-lived tumor-specific TCR-T cells that potentially overcome suppression by the tumor microenvironment or other negative regulators. This non-clinical data supports clinical application of mbIL15 TCR-T cell platform and provides evidence that this strategy could result in improved efficacy for cancer treatment.

* * *

[00537] The invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[00538] All references (*e.g.*, publications or patents or patent applications) cited herein are incorporated herein by reference in their entireties and for all purposes to the same extent as if each individual reference (*e.g.*, publication or patent or patent application) was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

Other embodiments are within the following claims.

WHAT IS CLAIMED:

1. A recombinant vector comprising a polycistronic expression cassette, wherein the polycistronic expression cassette comprises a transcriptional regulatory element operably linked to a polycistronic polynucleotide that comprises:
 - a. a first polynucleotide sequence that encodes a T cell receptor (TCR) alpha chain comprising an alpha chain variable ($V\alpha$) region and an alpha chain constant ($C\alpha$) region;
 - b. a second polynucleotide sequence that comprises a first 2A element;
 - c. a third polynucleotide sequence that encodes a TCR beta chain comprising a beta chain variable ($V\beta$) region and a beta chain constant ($C\beta$) region;
 - d. a fourth polynucleotide sequence that comprises a second 2A element; and
 - e. a fifth polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof.
2. The recombinant vector of claim 1, wherein either or both of the first 2A element and the second 2A element, independently, is a P2A element, a T2A element, an F2A element, or an E2A element.
3. The recombinant vector of claim 1, wherein the first 2A element is a P2A element.
4. The recombinant vector of claim 2 or 3, wherein the P2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 18 or 20, or the amino acid sequence of SEQ ID NO: 18 or 20 comprising 1, 2, or 3 amino acid modifications.
5. The recombinant vector of claim 2 or 3, wherein the P2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 19 or 21.
6. The recombinant vector of any one of claims 1 or 3-5, wherein the second 2A element is a T2A element.
7. The recombinant vector of claim 2 or 6, wherein the T2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 22 or 24, or the amino acid sequence of SEQ ID NO: 22 or 24 comprising 1, 2, or 3 amino acid modifications.

8. The recombinant vector of claim 2 or 6, wherein the T2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 23 or 25.
9. The recombinant vector of any one of claims 1-8, wherein either or both of the second polynucleotide sequence and the fourth polynucleotide sequence, independently, encode a furin recognition site.
10. The recombinant vector of claim 9, wherein the furin recognition site comprises the amino acid sequence of SEQ ID NO: 2 or 4, or the amino acid sequence of SEQ ID NO: 2 or 4 comprising 1, 2, or 3 amino acid modifications.
11. The recombinant vector of claim 9, wherein the furin recognition site is encoded by the polynucleotide sequence of SEQ ID NO: 3 or 5 or the polynucleotide sequence of SEQ ID NO: 3 or 5 comprising 1, 2, or 3 nucleotide modifications.
12. The recombinant vector of any one of claims 1-11, wherein the second polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 10, or the amino acid sequence of SEQ ID NO: 10 comprising 1, 2, or 3 amino acid modifications.
13. The recombinant vector of any one of claims 1-11, wherein the second polynucleotide sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 11.
14. The recombinant vector of any one of claims 1-13, wherein the fourth polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 12, or the amino acid sequence of SEQ ID NO: 12 comprising 1, 2, or 3 amino acid modifications.
15. The recombinant vector of any one of claims 1-13, wherein the fourth polynucleotide sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 13.
16. The recombinant vector of any one of claims 1-15, wherein the IL-15, or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 76.
17. The recombinant vector of any one of claims 1-15, wherein the IL-15, or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least

- 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 77.
18. The recombinant vector of any one of claims 1-15, wherein the IL-15R α , or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 78.
 19. The recombinant vector of any one of claims 1-15, wherein the IL-15R α , or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 79.
 20. The recombinant vector of any one of claims 1-19, wherein the IL-15, or functional fragment or functional variant thereof, is operably linked to the IL-15R α , or functional fragment or functional variant thereof, via a peptide linker.
 21. The recombinant vector of claim 20, wherein the peptide linker comprises the amino acid sequence of SEQ ID NO: 81, or the amino acid sequence of SEQ ID NO: 81 comprising 1, 2, or 3 amino acid modifications.
 22. The recombinant vector of claim 20, wherein the peptide linker is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 82.
 23. The recombinant vector of any one of claims 1-22, wherein the fusion protein is membrane bound.
 24. The recombinant vector of any one of claims 1-23, wherein the fusion protein comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 70 or 73.
 25. The recombinant vector of any one of claims 1-22, wherein the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 71 or 74.
 26. The recombinant vector of any one of claims 1-24, wherein the C α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 40-49.

27. The recombinant vector of any one of claims 1-24, wherein the C α region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 55, 57, or 58.
28. The recombinant vector of any one of claims 1-26, wherein the C β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 50-54 or 60.
29. The recombinant vector of any one of claims 1-26, wherein the C β region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 56 or 59.
30. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.
31. The recombinant vector of claim 30, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.
32. The recombinant vector of claim 31, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.
33. The recombinant vector of claim 30, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.

34. The recombinant vector of claim 30, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 181.
35. The recombinant vector of claim 33, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.
36. The recombinant vector of claim 35, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 252.
37. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.
38. The recombinant vector of claim 37, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.
39. The recombinant vector of claim 38, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.

40. The recombinant vector of claim 37, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; and the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.
41. The recombinant vector of claim 37, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; and the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 183.
42. The recombinant vector of claim 40, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.
43. The recombinant vector of claim 41, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 255.
44. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.
45. The recombinant vector of claim 44, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of

- SEQ ID NO: 173; or the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164.
46. The recombinant vector of claim 45, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; or the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238.
47. The recombinant vector of claim 44, wherein the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
48. The recombinant vector of claim 44, wherein the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 184 or 214; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
49. The recombinant vector of claim 47, wherein the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
50. The recombinant vector of claim 48, wherein the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 258 or 278; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.
51. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.
52. The recombinant vector of claim 51, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide

sequence that encodes the amino acid sequence of SEQ ID NO: 162; the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165.

53. The recombinant vector of claim 52, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241.
54. The recombinant vector of claim 51, wherein the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
55. The recombinant vector of claim 51, wherein the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 185 or 215; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
56. The recombinant vector of claim 54, wherein the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
57. The recombinant vector of claim 55, wherein the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 261 or 281; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

58. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.
59. The recombinant vector of claim 58, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.
60. The recombinant vector of claim 59, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.
61. The recombinant vector of claim 58, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.
62. The recombinant vector of claim 58, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 187 or 217.
63. The recombinant vector of claim 61, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; and the tenth

- combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.
64. The recombinant vector of claim 62, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; and the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 259 or 279.
65. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.
66. The recombinant vector of claim 65, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.
67. The recombinant vector of claim 66, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.
68. The recombinant vector of claim 65, wherein the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; and the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.
69. The recombinant vector of claim 65, wherein the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; and the first

- polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 189 or 219.
70. The recombinant vector of claim 68, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.
71. The recombinant vector of claim 69, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 256 or 276.
72. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.
73. The recombinant vector of claim 72, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; or the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170.
74. The recombinant vector of claim 73, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235; the eighth combination polynucleotide sequence comprises the polynucleotide

- sequence of SEQ ID NO: 237; or the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242.
75. The recombinant vector of claim 72, wherein the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
76. The recombinant vector of claim 72, wherein the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 190; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.
77. The recombinant vector of claim 75, wherein the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
78. The recombinant vector of claim 76, wherein the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 262; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
79. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.
80. The recombinant vector of claim 79, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth

polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171.

81. The recombinant vector of claim 80, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243.
82. The recombinant vector of claim 79, wherein the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
83. The recombinant vector of claim 79, wherein the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 191; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.
84. The recombinant vector of claim 82, wherein the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
85. The recombinant vector of claim 83, wherein the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 263; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
86. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.
87. The recombinant vector of claim 86, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide

sequence that encodes the amino acid sequence of SEQ ID NO: 162; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.

88. The recombinant vector of claim 87, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.
89. The recombinant vector of claim 86, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
90. The recombinant vector of claim 86, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
91. The recombinant vector of claim 89, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
92. The recombinant vector of claim 90, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

93. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.
94. The recombinant vector of claim 93, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.
95. The recombinant vector of claim 94, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; or the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237.
96. The recombinant vector of claim 93, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
97. The recombinant vector of claim 93, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
98. The recombinant vector of claim 96, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID

- NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
99. The recombinant vector of claim 97, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.
100. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.
101. The recombinant vector of claim 100, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.
102. The recombinant vector of claim 101, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.
103. The recombinant vector of claim 100, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
104. The recombinant vector of claim 100, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an

eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

105. The recombinant vector of claim 103, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
106. The recombinant vector of claim 104, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
107. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.
108. The recombinant vector of claim 107, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.
109. The recombinant vector of claim 108, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237.
110. The recombinant vector of claim 107, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of

- SEQ ID NO: 173; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
111. The recombinant vector of claim 107, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.
112. The recombinant vector of claim 110, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
113. The recombinant vector of claim 111, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
114. The recombinant vector of any one of claims 1-113, wherein the polycistronic polynucleotide further comprises
- f. a sixth polynucleotide sequence that comprises a third 2A element; and
 - g. a seventh polynucleotide sequence that comprises a marker protein.
115. The recombinant vector of claim 114, wherein the third 2A element is a P2A element, a T2A element, an F2A element, or an E2A element.
116. The recombinant vector of any one of claims 114 or 115, wherein the marker protein comprises: domain III of HER1, or a functional fragment or functional variant thereof; an N-terminal portion of domain IV of HER1; and a transmembrane domain of CD28, or a functional fragment or functional variant thereof.
117. The recombinant vector of claim 116, wherein the domain III of HER1, or a functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%,

- 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 104.
118. The recombinant vector of claim 116, wherein the N-terminal portion of domain IV of HER1 comprises amino acids 1-40, 1-39, 1-38, 1-37, 1-36, 1-35, 1-34, 1-33, 1-32, 1-31, 1-30, 1-29, 1-28, 1-27, 1-26, 1-25, 1-24, 1-23, 1-22, 1-21, 1-20, 1-19, 1-18, 1-17, 1-16, 1-15, 1-14, 1-13, 1-12, 1-11, or 1-10 of SEQ ID NO: 105.
119. The recombinant vector of claim 116, wherein the N-terminal portion of domain IV of HER1 comprises amino acids 1-21 of SEQ ID NO: 105.
120. The recombinant vector of claim 116, wherein the N-terminal portion of domain IV of HER1 comprises the amino acid sequence of SEQ ID NO: 106, or the amino acid sequence of SEQ ID NO: 106, comprising 1, 2, or 3 amino acid modifications.
121. The recombinant vector of any one of claims 114-120, wherein the transmembrane region of CD28 comprises the amino acid sequence of SEQ ID NO: 107, or the amino acid sequence of SEQ ID NO: 107, comprising 1, 2, or 3 amino acid modifications.
122. The recombinant vector of any one of claims 114-121, wherein the marker protein comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, or 112.
123. The recombinant vector of any one of claims 1-122, wherein the V α region comprises complementarity determining region 1 α (CDR1 α), CDR2 α , and CDR3 α , comprising the amino acid sequences of SEQ ID NO: 1001 + 10n, 1002 + 10n, and 1003 + 10n, respectively, wherein n is an integer from 0 to 79.
124. The recombinant vector of any one of claims 1-123, wherein the V β region comprises CDR1 β , CDR2 β , and CDR3 β , comprising the amino acid sequences of SEQ ID NO: 2001 + 10n, 2002 + 10n, and 2003 + 10n, respectively, wherein n is an integer from 0 to 79.
125. The recombinant vector of any one of claims 1-124, wherein the V α region comprises the CDR1 α , CDR2 α , and CDR3 α from a V α region comprising the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79.
126. The recombinant vector of any one of claims 1-125, wherein the V β region comprises the CDR1 β , CDR2 β , and CDR3 β from a V β region comprising the amino acid sequence of

- SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79.
127. The recombinant vector of any one of claims 1-126, wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79.
128. The recombinant vector of any one of claims 1-127, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79.
129. The recombinant vector of any one of claims 1-128, wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2004 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1005 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2005 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1006 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2006 + 10n, and wherein n is an integer from 0 to 79; or wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1007 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2007 + 10n, and wherein n is an integer from 0 to 79.
130. The recombinant vector of any one of claims 1-129, wherein the TCR alpha chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100%

- identical to the amino acid sequence of SEQ ID NO: 1008 + 10n, wherein n is an integer from 0 to 79.
131. The recombinant vector of any one of claims 1-129, wherein the TCR alpha chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1009 + 10n, wherein n is an integer from 0 to 79.
132. The recombinant vector of any one of claims 1-129, wherein the TCR alpha chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1010 + 10n, wherein n is an integer from 0 to 79.
133. The recombinant vector of any one of claims 1-132, wherein the TCR beta chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2008 + 10n, wherein n is an integer from 0 to 79.
134. The recombinant vector of any one of claims 1-132, wherein the TCR beta chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2009 + 10n, wherein n is an integer from 0 to 79.
135. The recombinant vector of any one of claims 1-132, wherein the TCR beta chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2010 + 10n, wherein n is an integer from 0 to 79.
136. The recombinant vector of any one of claims 1-135, wherein the transcriptional regulatory element comprises a promoter.
137. The recombinant vector of claim 136, wherein the promoter is a human elongation factor 1-alpha (hEF-1 α) hybrid promoter.
138. The recombinant vector of claim 136 or 137, wherein the promoter comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 150.
139. The recombinant vector of any one of claims 1-138, further comprising a polyA sequence at the 3' end of the polycistronic expression cassette.

140. The recombinant vector of claim 139, wherein the polyA sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:151.
141. The recombinant vector of any one of claims 1-140, further comprising a Left inverted terminal repeat (ITR) and a Right ITR, wherein the Left ITR and the Right ITR flank the polycistronic expression cassette.
142. The recombinant vector of claim 141, which comprises, in order from 5' to 3':
- i. the Left ITR;
 - ii. the transcriptional regulatory element;
 - iii. the first polynucleotide sequence;
 - iv. the second polynucleotide sequence;
 - v. the third polynucleotide sequence;
 - vi. the fourth polynucleotide sequence;
 - vii. the fifth polynucleotide sequence; and
 - viii. the Right ITR.
143. The recombinant vector of any one of claims 1-142, wherein the recombinant vector is a non-viral vector.
144. The recombinant vector of claim 143, wherein the non-viral vector is a plasmid.
145. The recombinant vector of any one of claims 1-142, wherein the recombinant vector is a viral vector.
146. The recombinant vector of any one of claims 1-145, wherein the recombinant vector is a polynucleotide.
147. A polynucleotide encoding an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 161, 163, 164, 165, 167, 169, 170, and 171.
148. A polynucleotide comprising a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 232, 235, 236, 238, 239, 241, 242, and 243.
149. A population of cells that comprise the recombinant vector of any one of claims 1-146 or the polynucleotide of claim 147 or 148.
150. The population of cells of claim 149, wherein the recombinant vector or the polynucleotide is integrated into the genome of the population of cells.

151. The population of cells of claims 149 or 150, wherein the cells are immune effector cells.
152. The population of cells of claim 151, wherein the immune effector cells are selected from the group consisting of T cells, natural killer (NK) cells, B cells, mast cells, and myeloid-derived phagocytes.
153. The population of cells of claim 152, wherein the immune effector cells are one or more T cells selected from the group consisting of naïve T cells (CD4⁺ or CD8⁺); killer CD8⁺ T cells; cytotoxic CD4⁺ T cells; helper CD4⁺ T cells; CD4⁺ T cells corresponding to Th1, Th2, Th9, Th17, Th22, follicular helper (Tfh), regulatory (Treg) lineages; tumor infiltrating lymphocytes (TILs); and memory T cells (central memory, effector memory, stem cell memory, stem cell-like memory).
154. The population of cells of claim 152, comprising alpha/beta T cells, gamma/delta T cells, or natural killer T (NKT) cells.
155. The population of cells of claim 152, comprising CD4⁺ T cells, CD8⁺ T cells, or both CD4⁺ T cells and CD8⁺ T cells.
156. The population of cells of any one of claims 149-155, wherein the cells are *ex vivo*.
157. The population of cells of any one of claims 149-156, wherein the cells are human.
158. The population of cells of any one of claims 149-157, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95⁺ cells.
159. The population of cells of any one of claims 149-157, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95⁺ cells.
160. A population of cells comprising a polycistronic expression cassette comprising
 - a. a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof;
 - b. a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and
 - c. a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region,
 wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95⁺ cells.

161. A population of cells comprising a polycistronic expression cassette comprising
- a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof;
 - a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and
 - a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region,
- wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95+ cells.
162. A method of producing a population of engineered cells, comprising:
- introducing into a population of cells the recombinant vector of claim 141 or 142, and a DNA transposase or a polynucleotide encoding a DNA transposase; and
- culturing the population of cells under conditions wherein the transposase integrates the polycistronic expression cassette into the genome of the population of cells, thereby producing the population of engineered cells.
163. The method of claim 162, wherein the Left ITR and the Right ITR are ITRs of a DNA transposon selected from the group consisting of a *Sleeping Beauty* transposon, a piggyBac transposon, a TcBuster transposon, and a Tol2 transposon.
164. The method of claim 163, wherein the DNA transposon is the *Sleeping Beauty* transposon.
165. The method of any one of claims 162-164, wherein the transposase is a *Sleeping Beauty* transposase.
166. The method of claim 165, wherein the *Sleeping Beauty* transposase is selected from the group consisting of SB11, SB10, SB100X, hSB110, and hSB81.
167. The method of claim 166, wherein the *Sleeping Beauty* transposase is SB11.
168. The method of claim 167, wherein the SB11 comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 300.
169. The method of claim 167, wherein the SB11 is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 301.

170. The method of any one of claims 162-169, wherein the polynucleotide encoding the DNA transposase is a DNA vector or an RNA vector.
171. The method of any one of claims 162-170, wherein the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290 or 291; and the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292, 293 or 294.
172. The method of any one of claims 162-171, wherein the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation, sonication, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, mechanical deformation by passage through a microfluidic device, or a colloidal dispersion system.
173. The method of claim 172, wherein the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation.
174. The method of any one of claims 162-173, wherein the method is completed within 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.
175. The method of any one of claims 162-173, wherein the method is completed in less than 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.
176. The method of any one of claims 162-175, wherein the population of cells is cryopreserved and thawed before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.
177. The method of any one of claims 162-176, wherein the population of cells is rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.
178. The method of any one of claims 162-177, wherein the population of cells is not rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

179. The method of any one of claims 162-178, wherein the population of cells comprises expanded human *ex vivo* cells.
180. The method of any one of claims 162-179, wherein the population of cells is not activated *ex vivo*.
181. The method of any one of claims 162-180, wherein the population of cells comprises T cells.
182. A method of treating cancer in a subject in need thereof comprising administering to the subject a therapeutically effective amount of the population of cells of any one of claims 149-161, thereby treating the cancer.
183. The method of claim 182, wherein the cancer is selected from lung, cholangiocarcinoma, pancreatic, colorectal, gynecological and ovarian cancer.
184. A method of treating an autoimmune disease or disorder in a subject in need thereof comprising administering to the subject a therapeutically effective amount of the population of cells of any one of claims 149-161, thereby treating the autoimmune disease or disorder.

Polypeptide Schematics

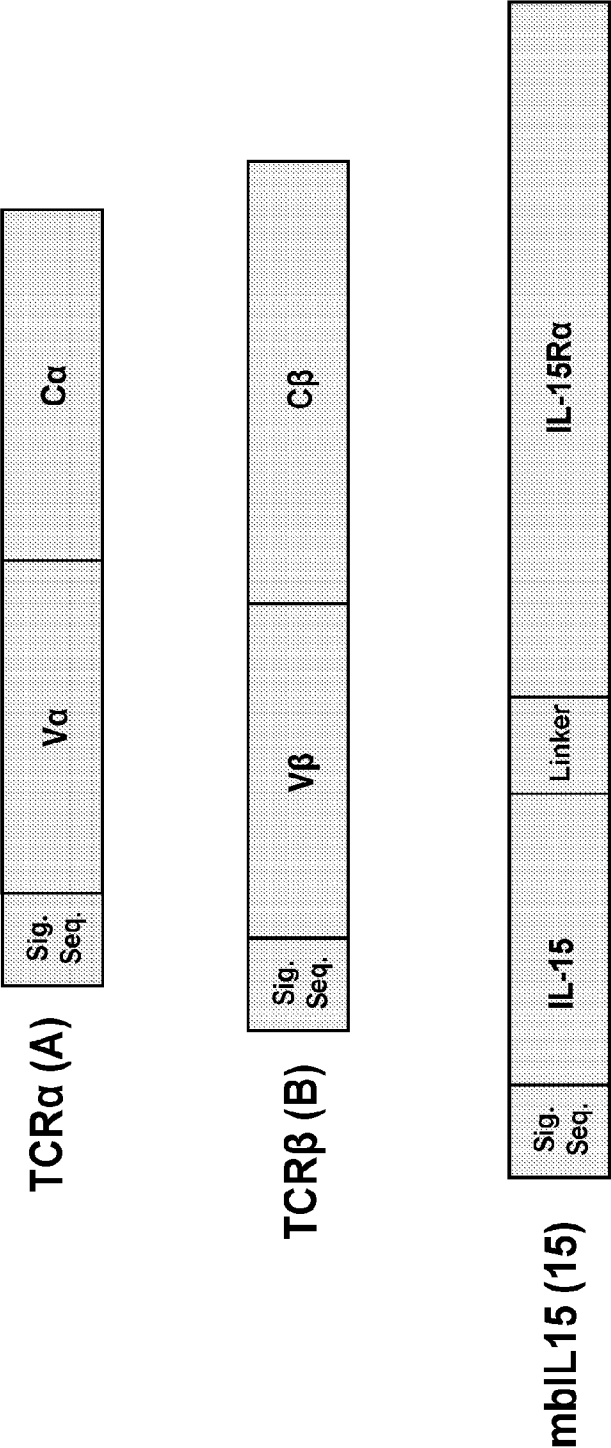


FIG. 1

Tricistronic Cassette ORF Schematics

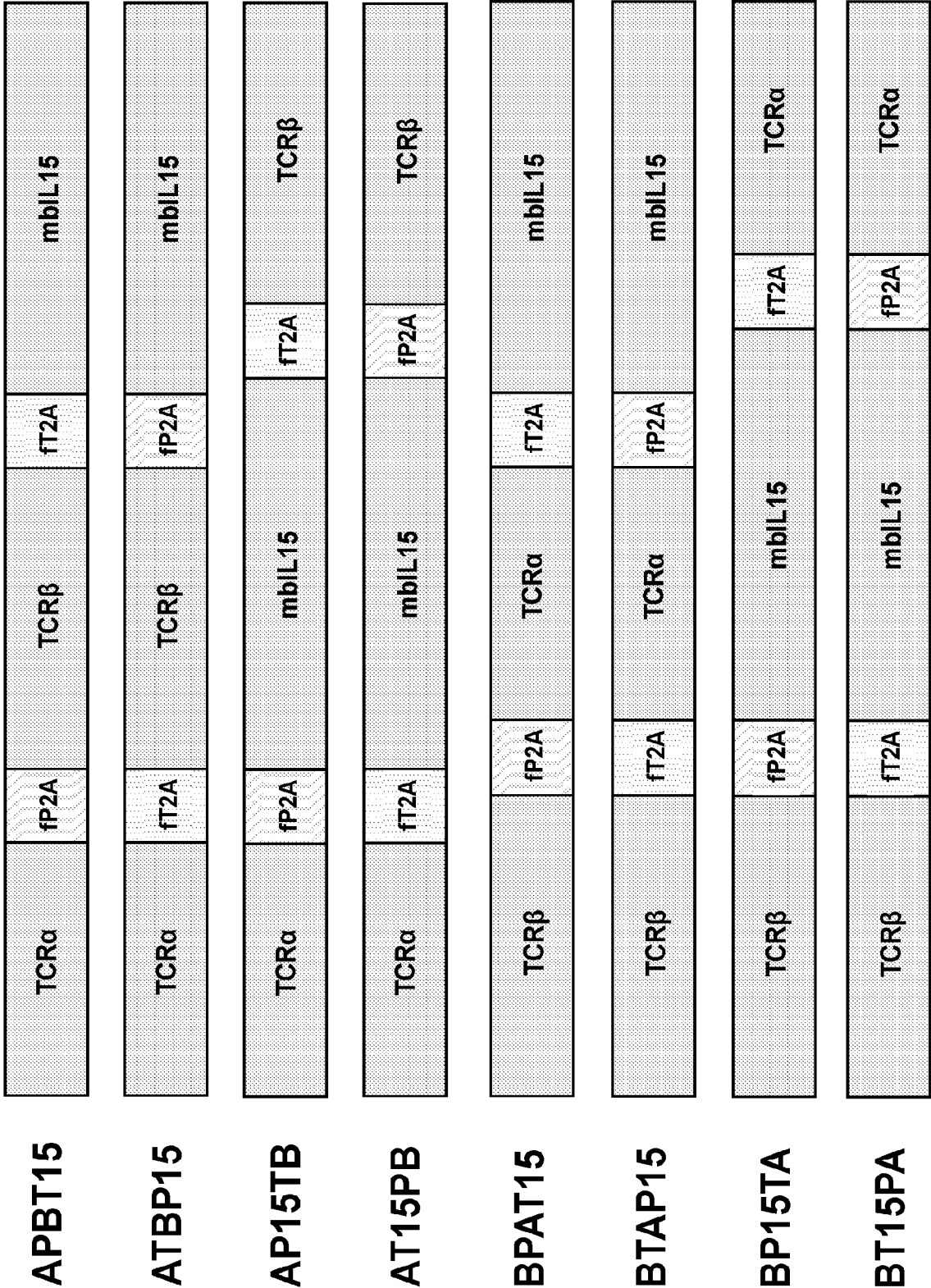


FIG. 2A

Control Cassette ORF Schematics

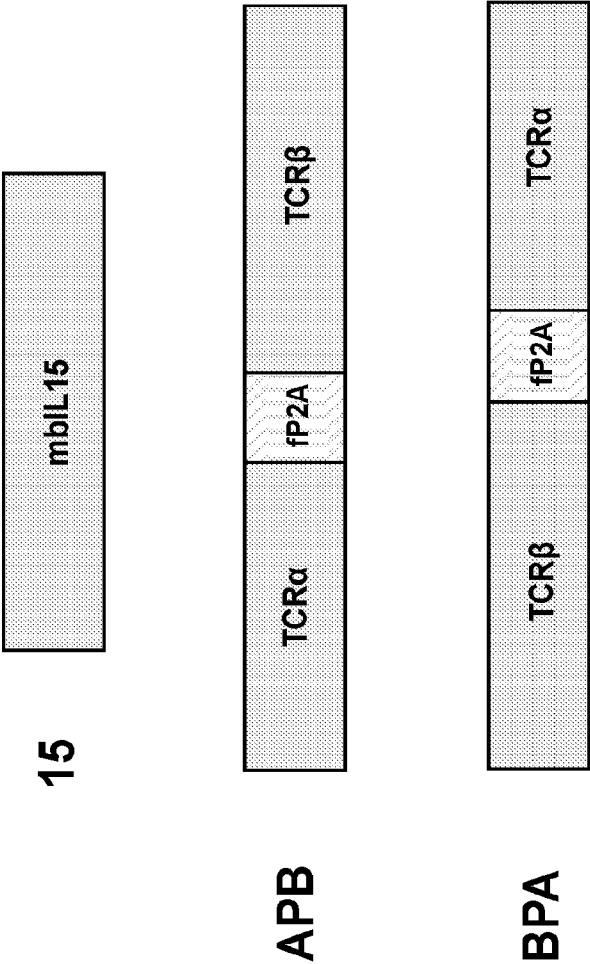


FIG. 2B

Genetic Modification Using Sleeping Beauty
Generate TCR-mbIL15 T Cells

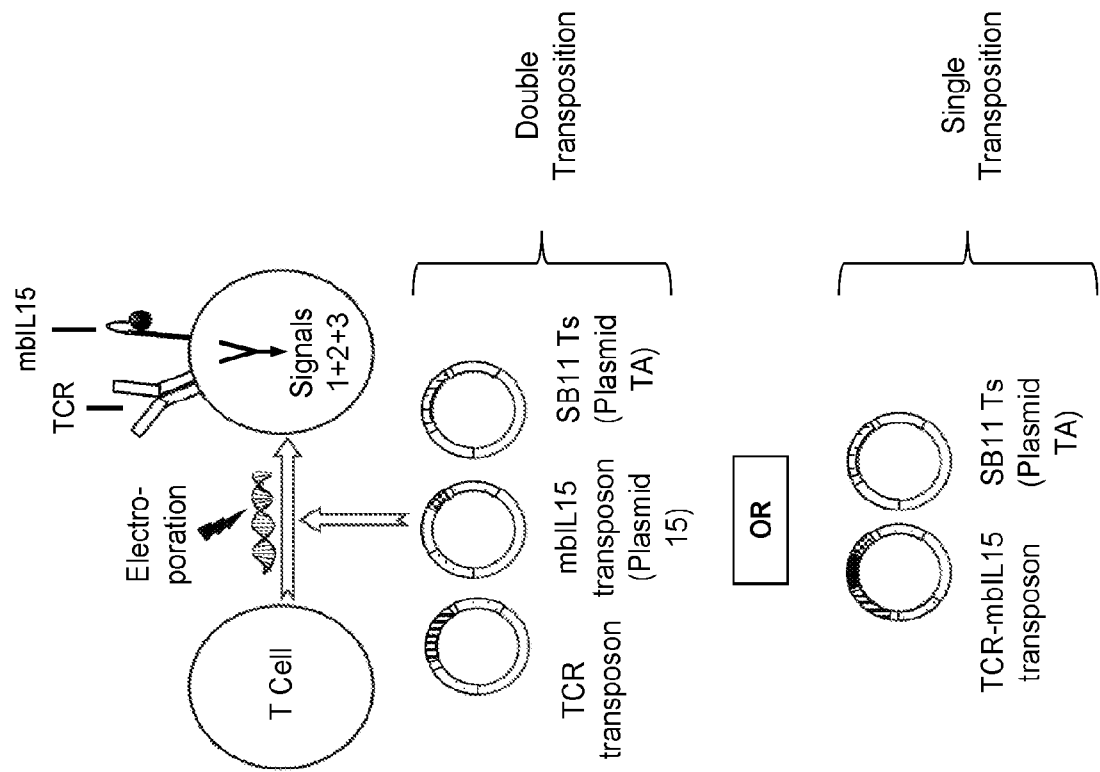


FIG. 3

Transgene Co-Expression by Flow Cytometry

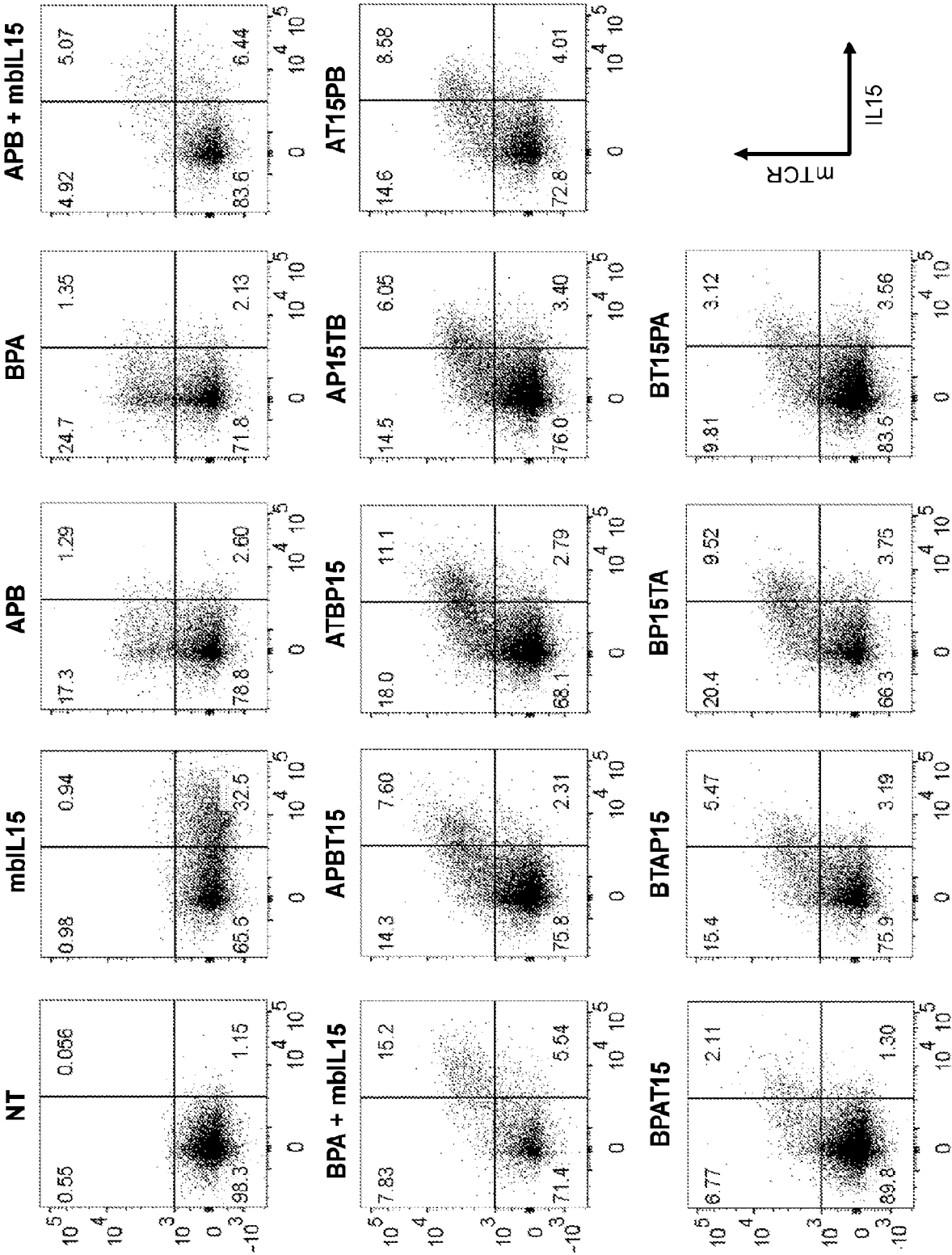


FIG. 4

TCR Expression by Flow Cytometry

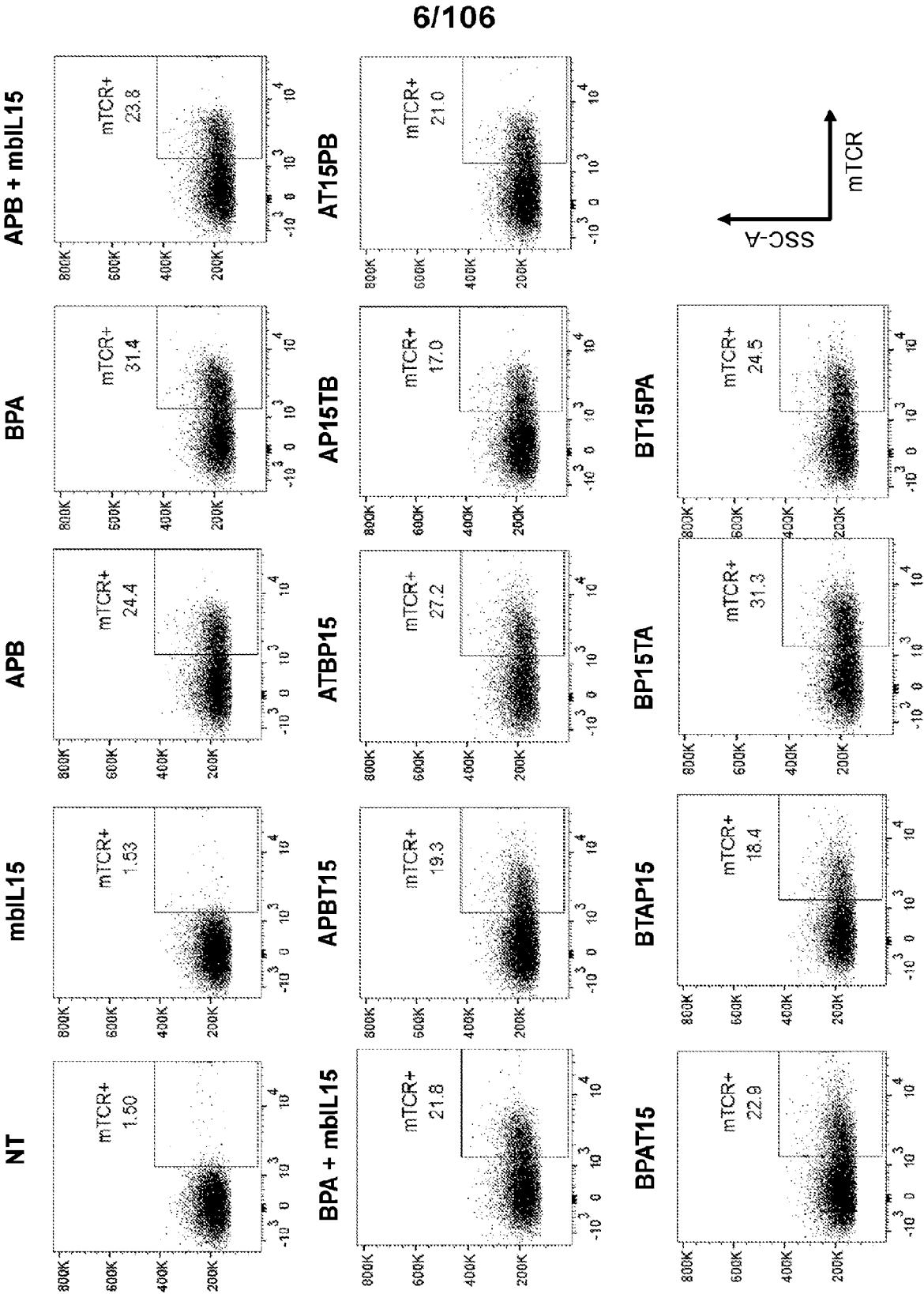
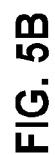


FIG. 5A

TCR Expression after Electroporation



Transgene Co-Expression after Expansion

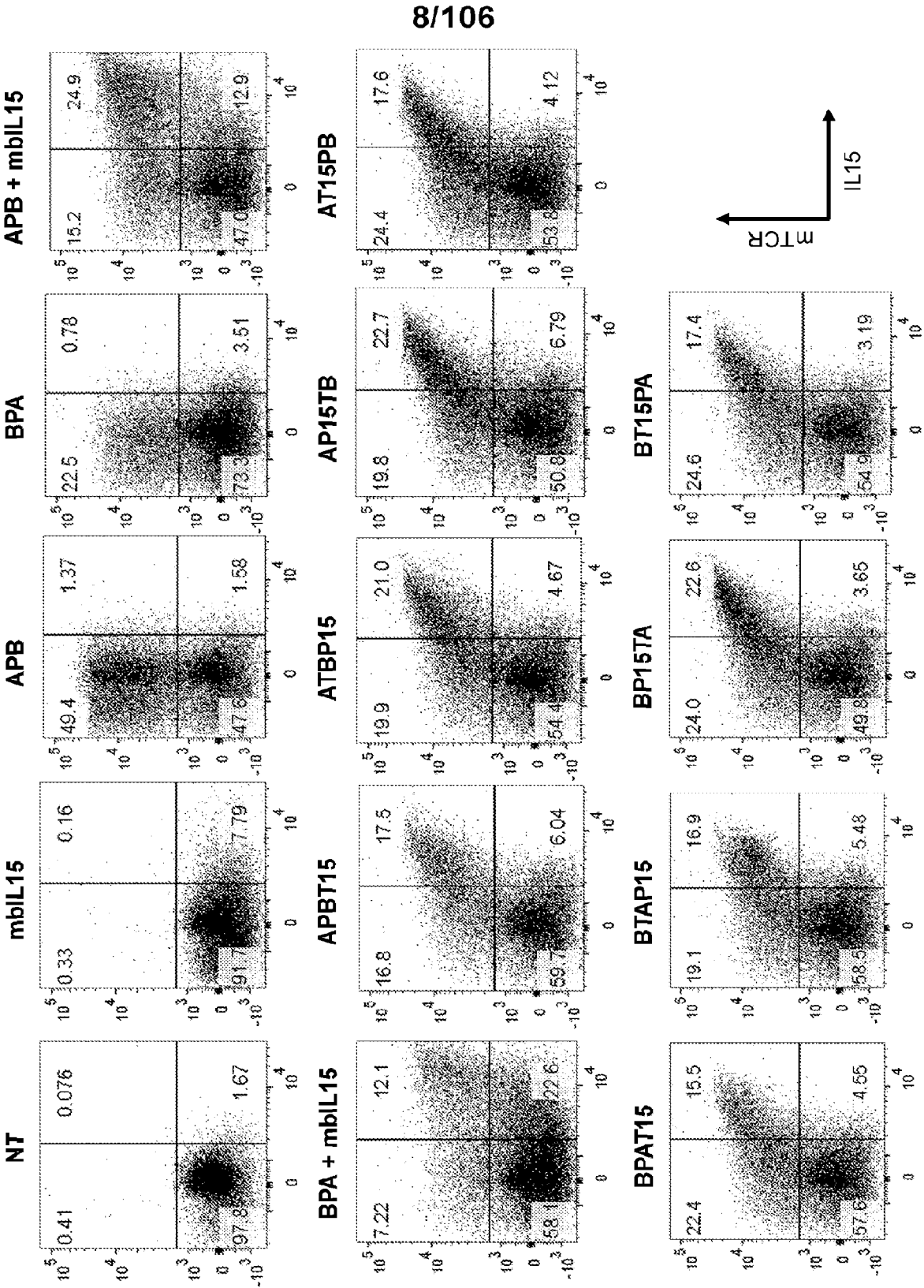


FIG. 6A

TCR Expression after Expansion

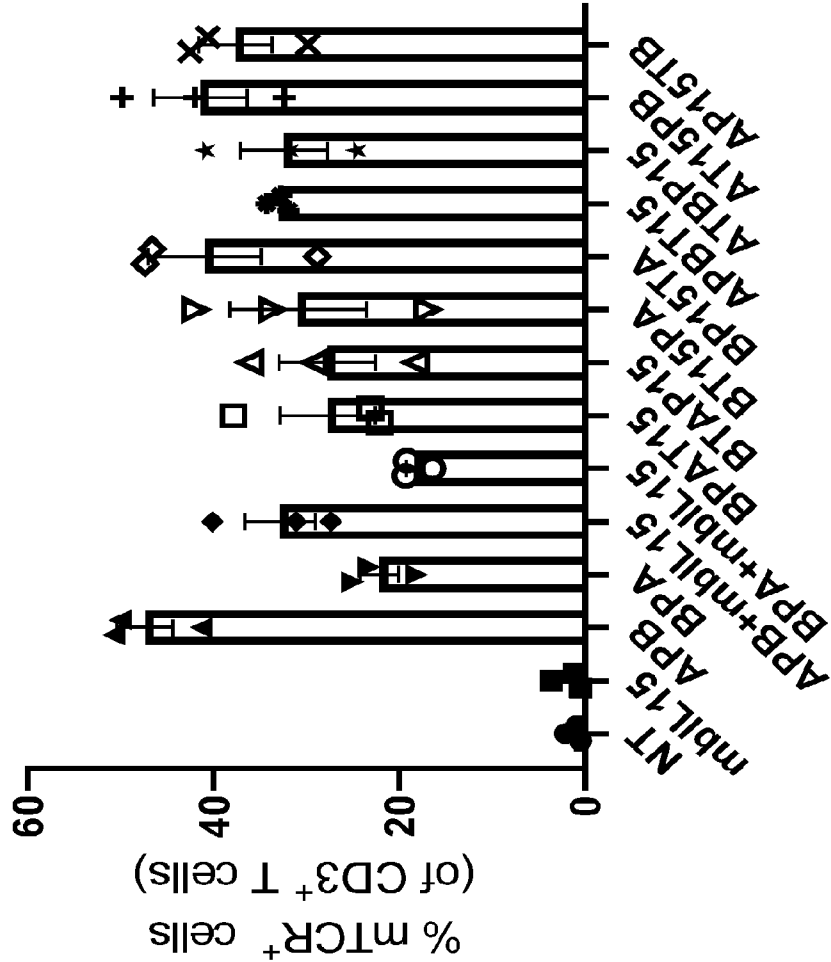


FIG. 6B

TCR+/mbIL15+ Expression after Expansion

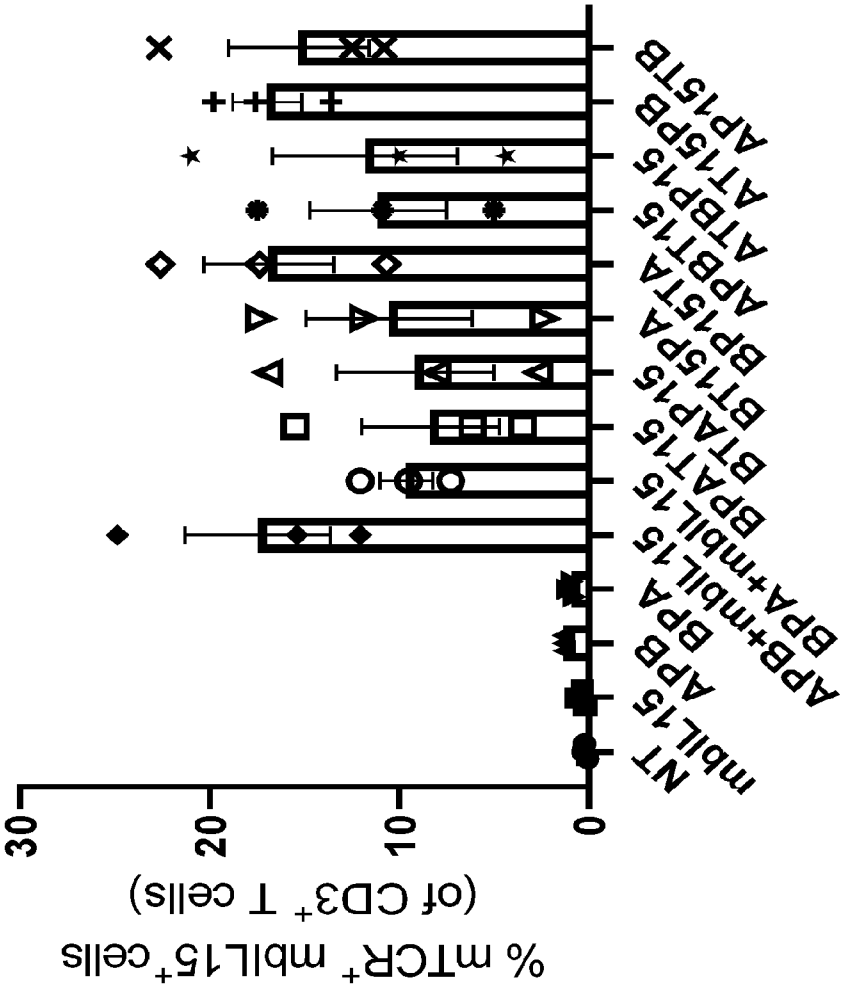


FIG. 6C

TCR+ Cell Number after Expansion

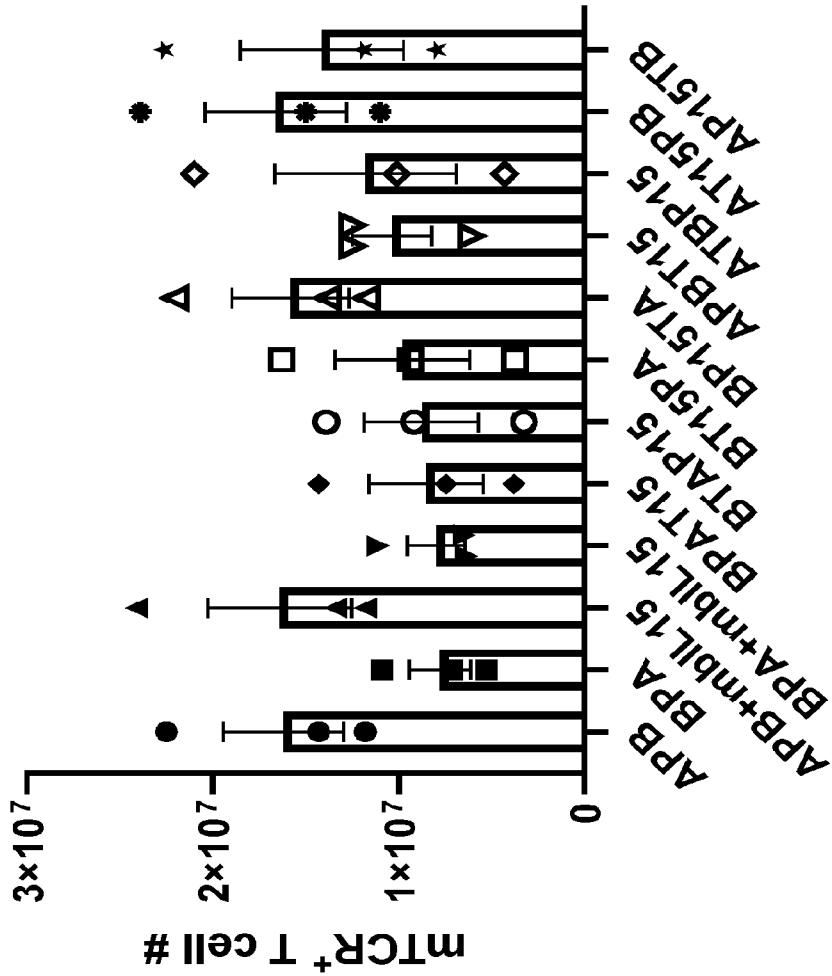


FIG. 7A

TCR+/mbIL15+ Cell Number after Expansion

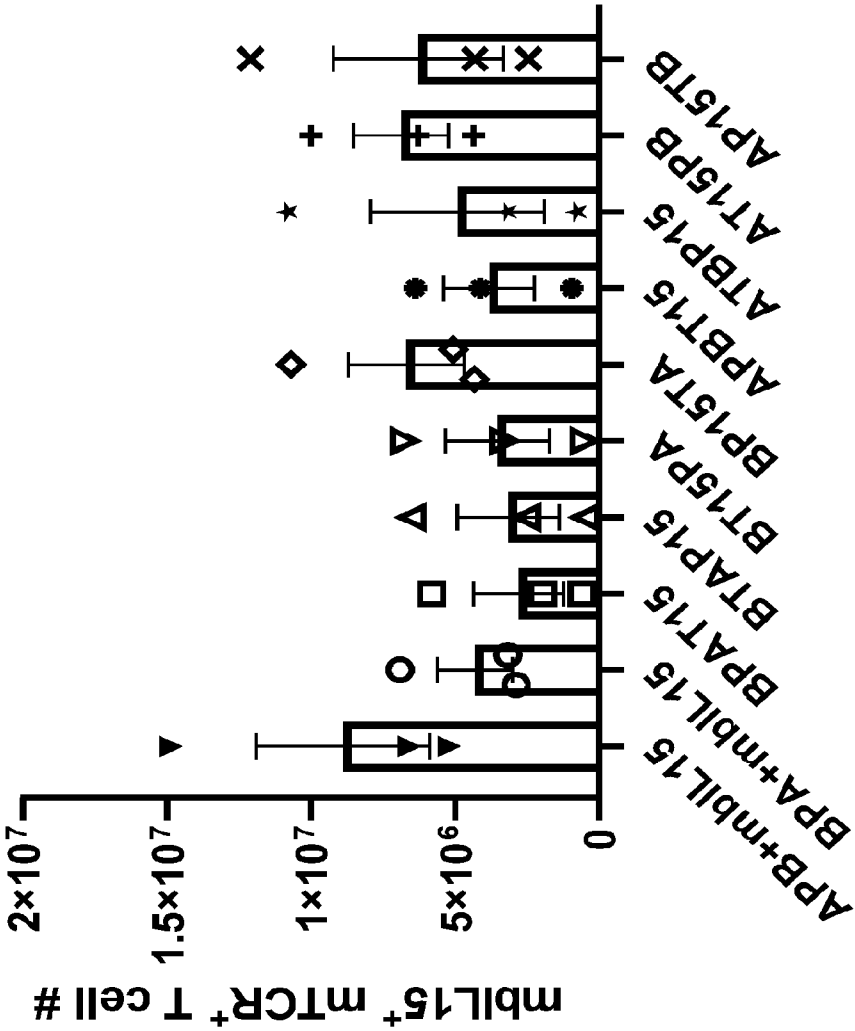


FIG. 7B

Cell Viability after Electroporation

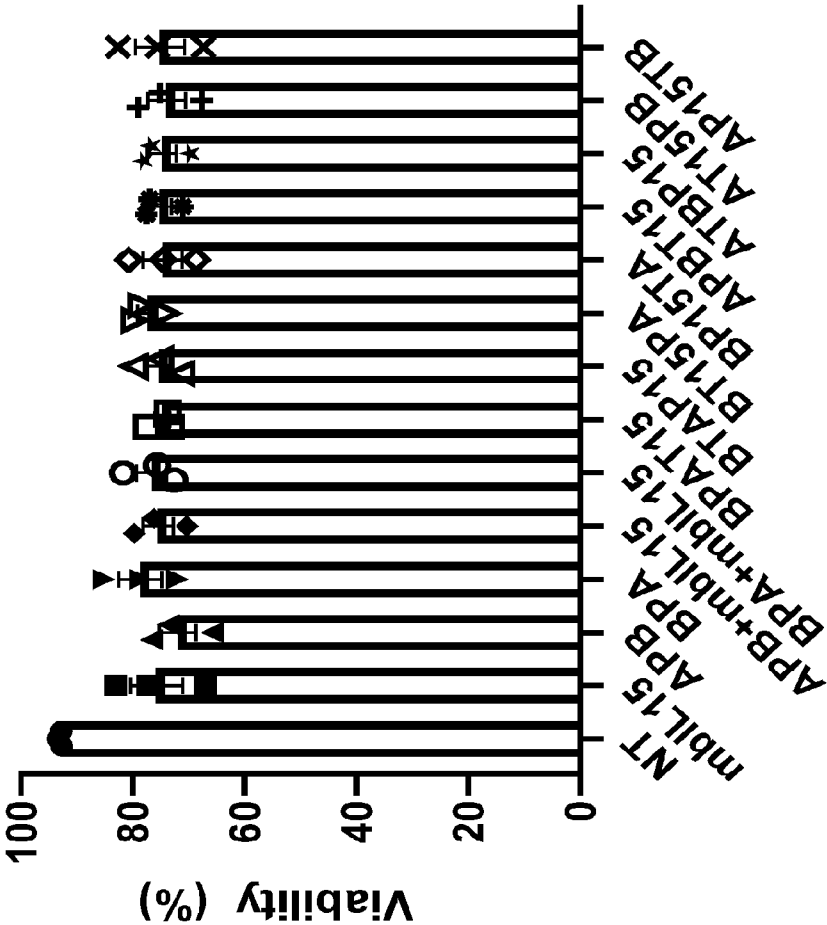
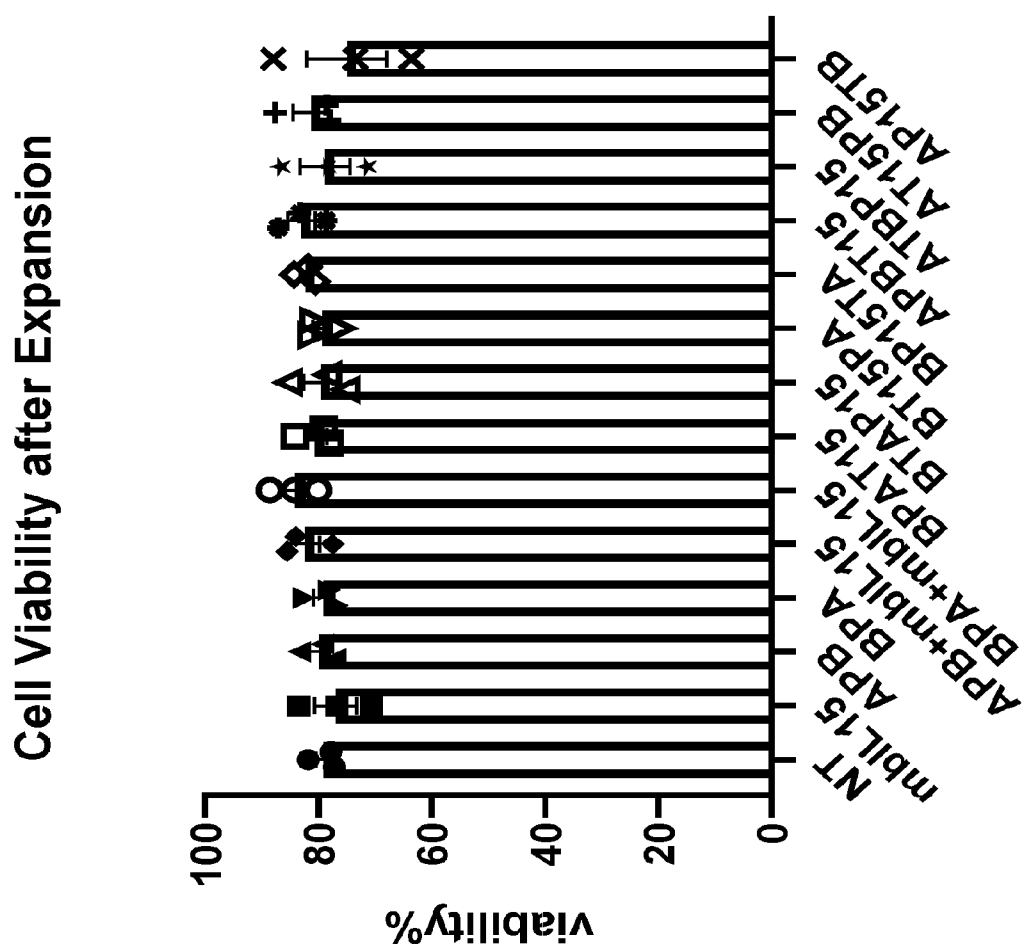


FIG. 8A



Induction of 4-1BB after Expansion

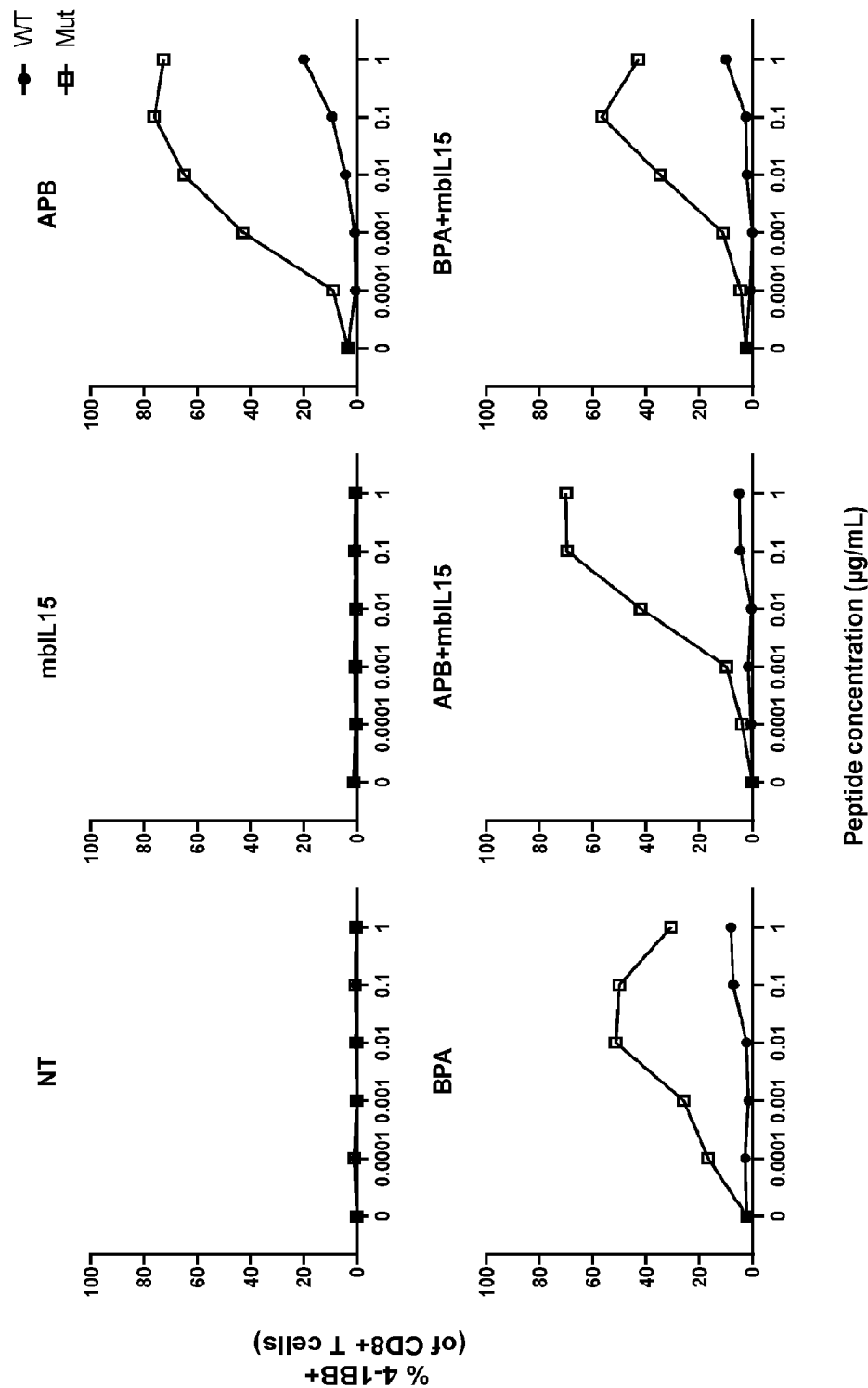


FIG. 9A

Induction of 4-1BB after Expansion

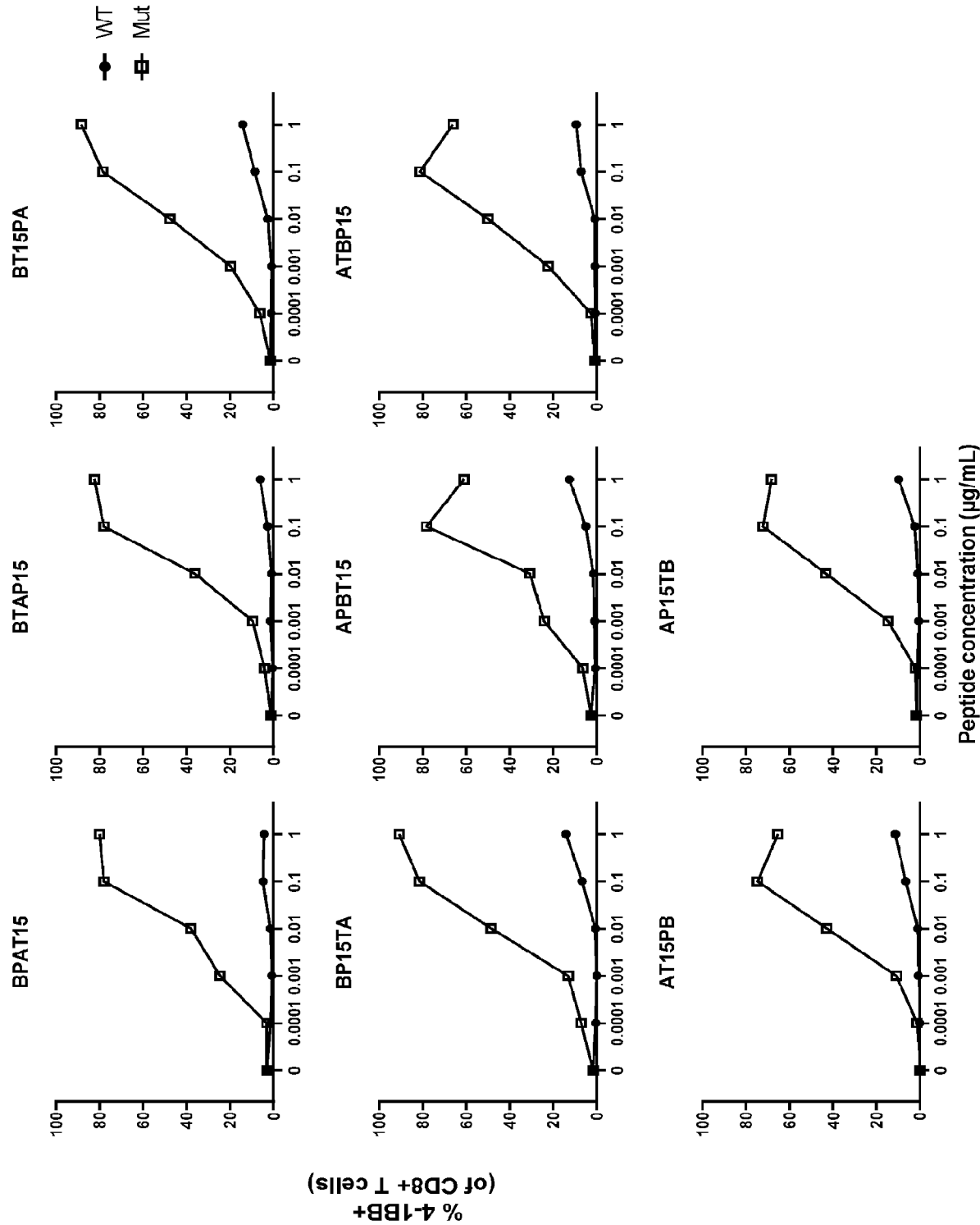


FIG. 9B

Phosphorylation of STAT5 after Expansion

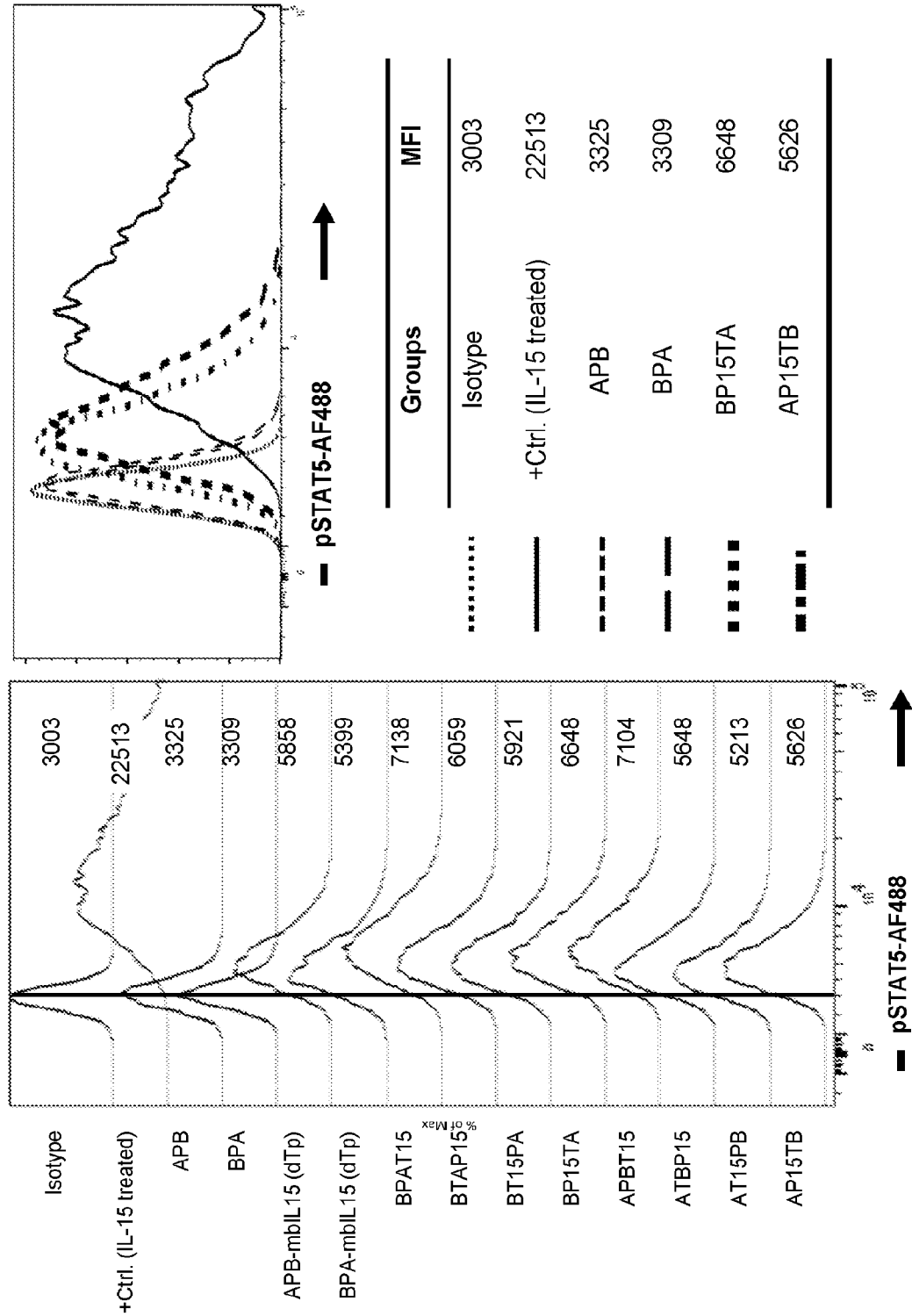


FIG. 10

Apoptosis of Transduced Cells after Activation

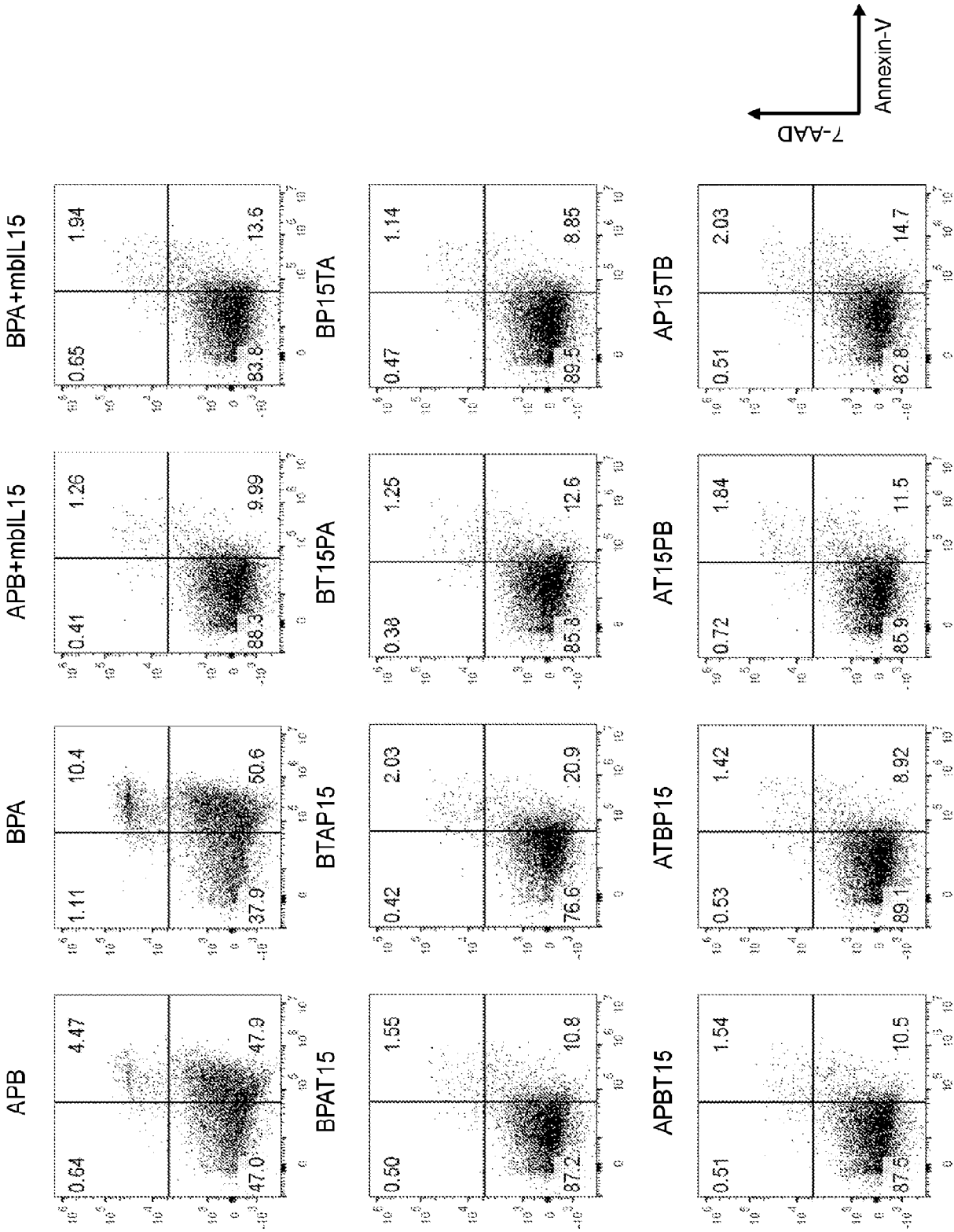


FIG. 11

Cassette ORF Schematic

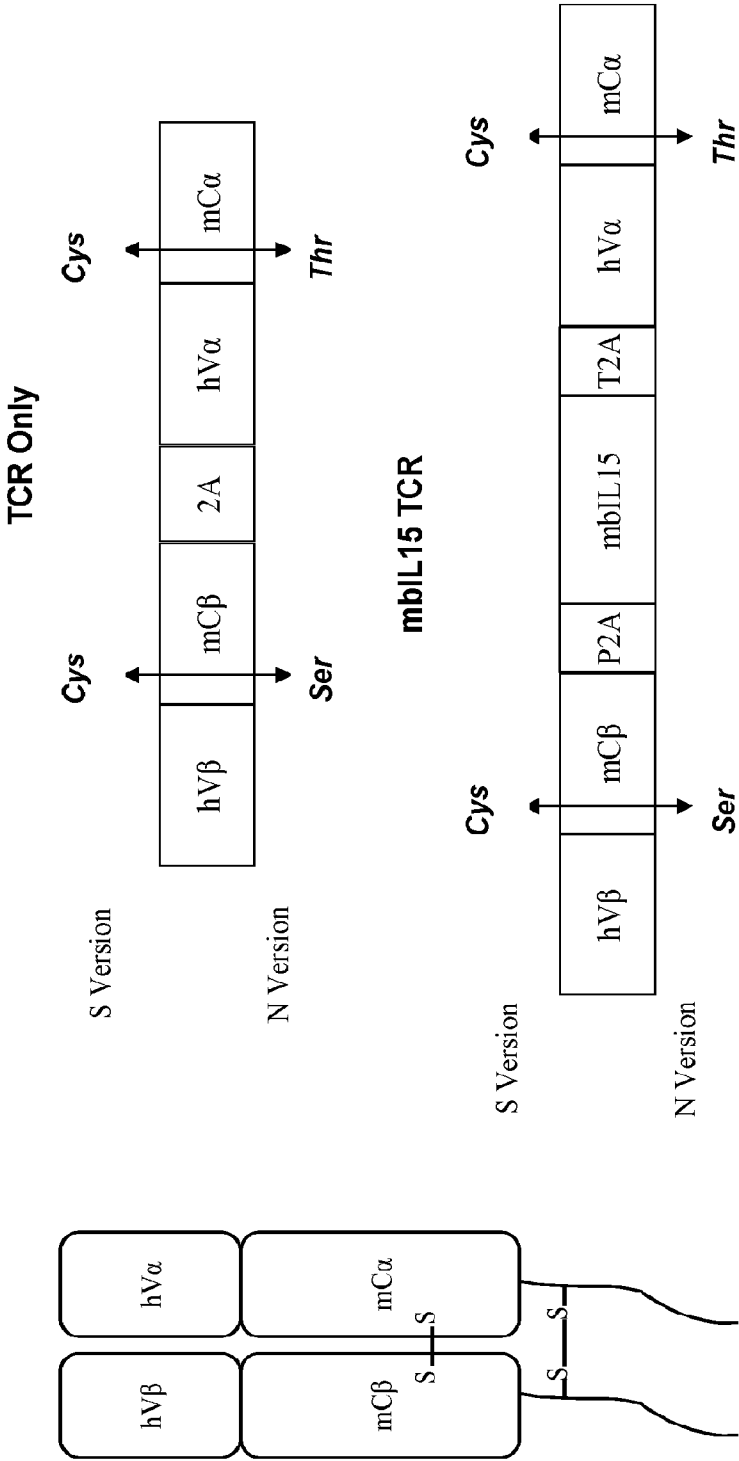


FIG. 12

TCR Expression at D1 (after EP) and D11 (Pre-enrichment)

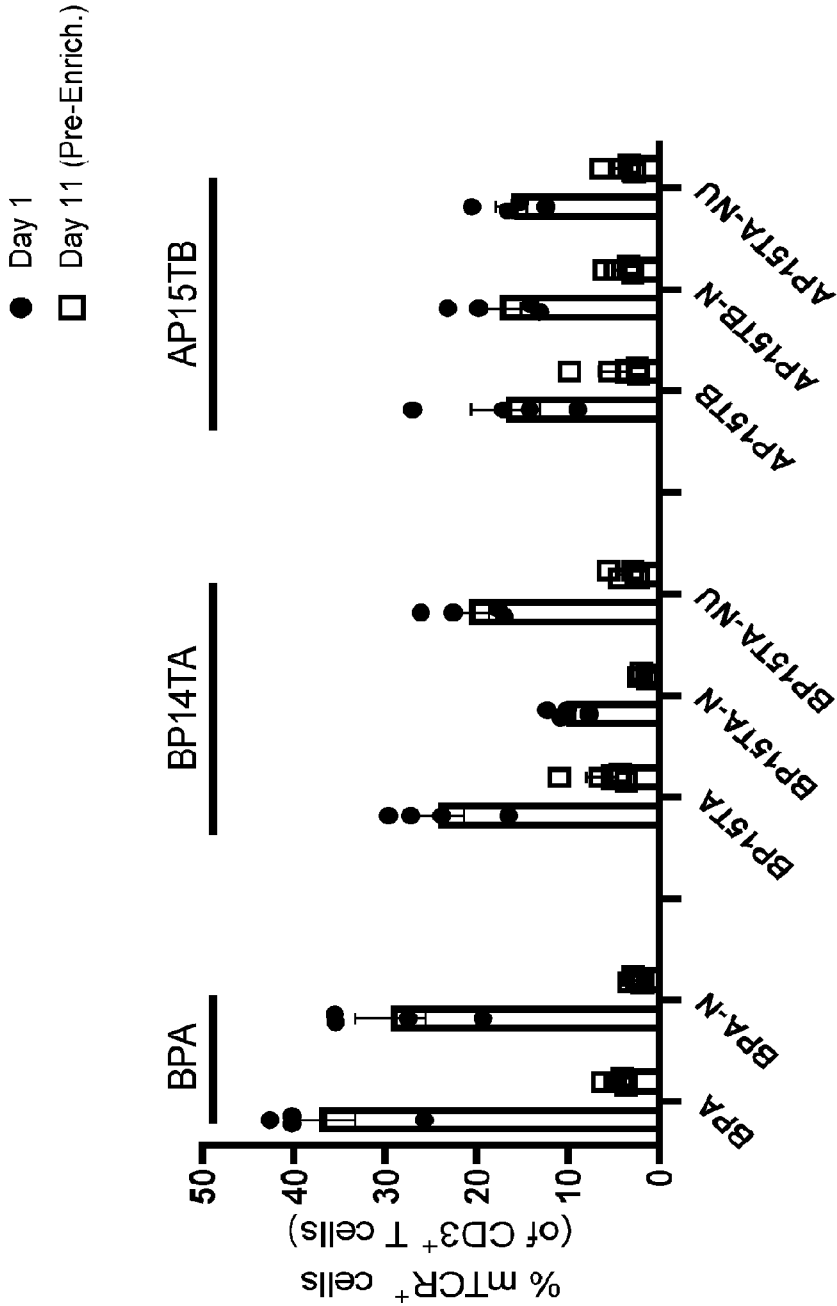


FIG. 13A

TCR Expression at D11 (Post-Enrichment) and D22 (after the Second Expansion Phase)

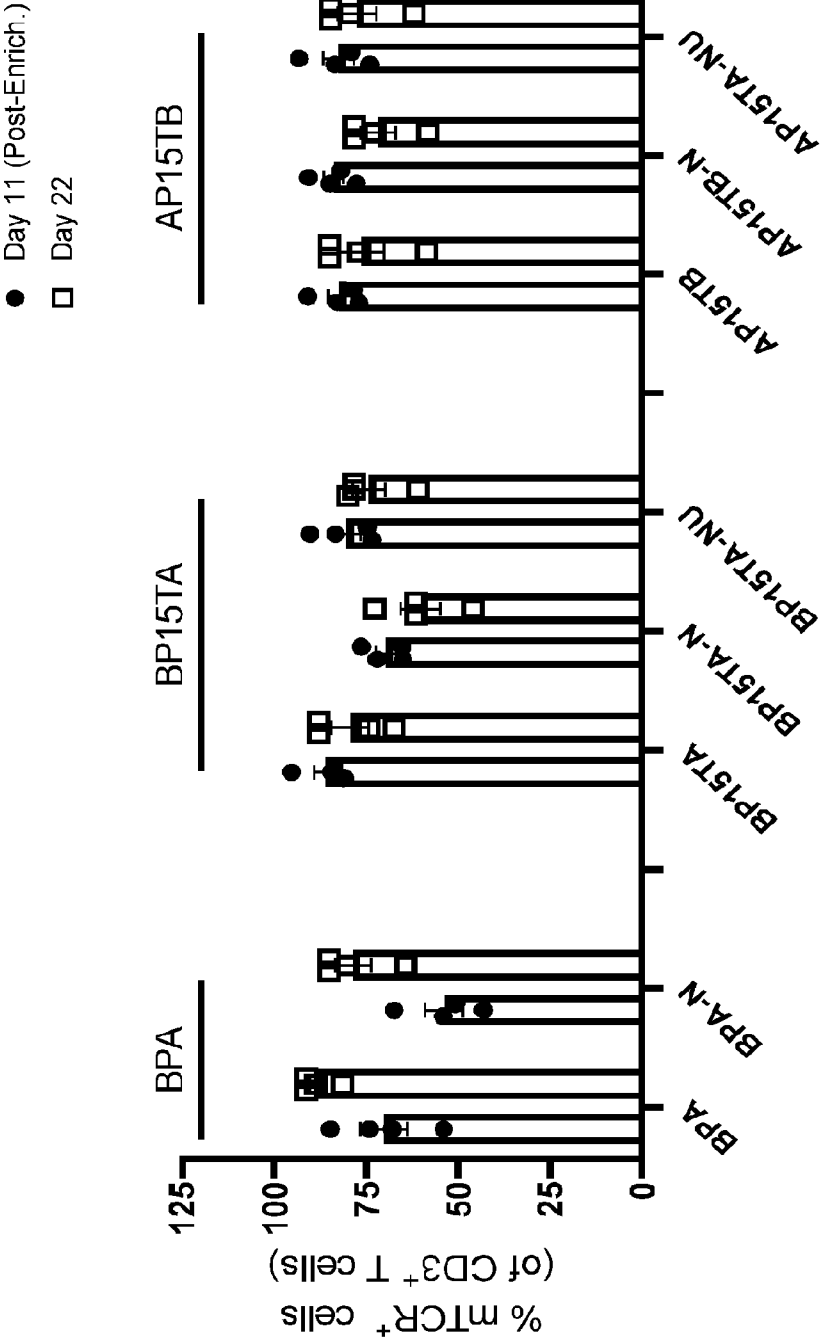


FIG. 13B

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TCR+/mbIL15+ Expression at D1 (after EP) and D11 (Pre-enrichment)

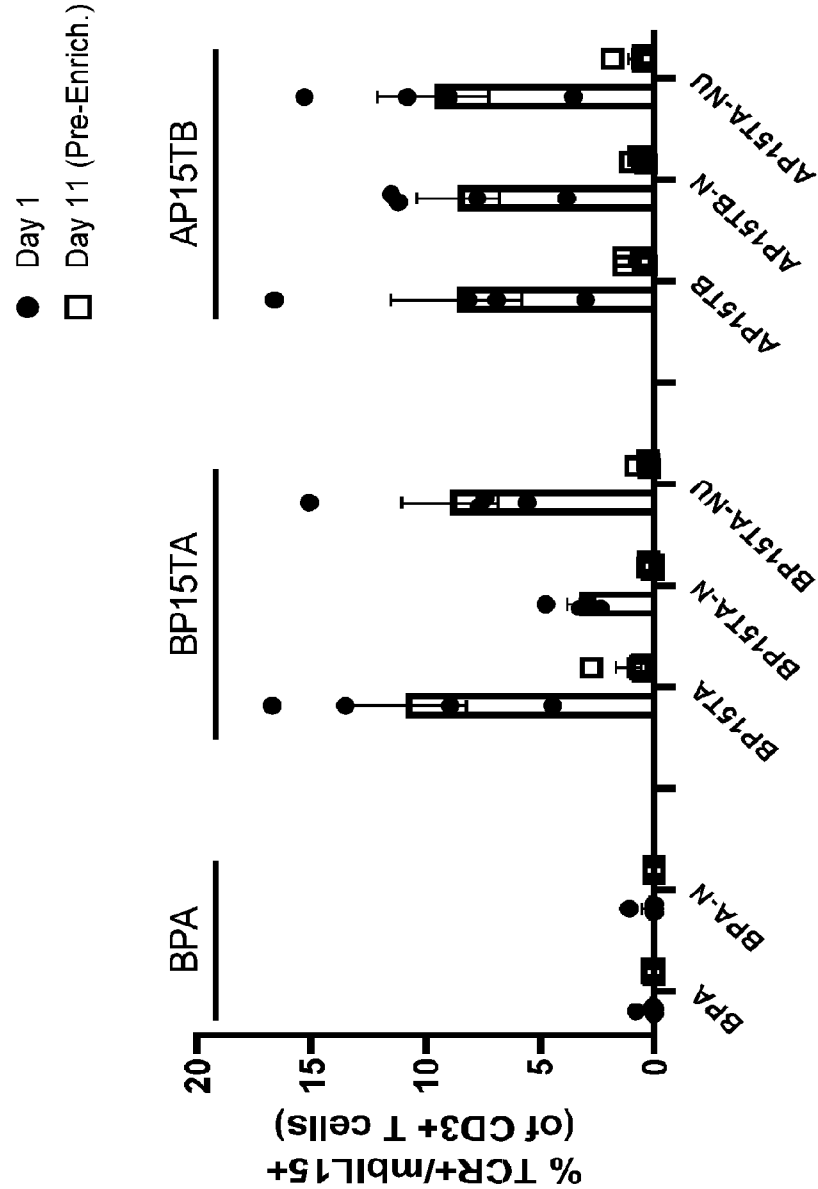


FIG. 14A

TCR+/mbIL15+ Expression at D11 (Post-Enrichment) and D22
(after the Second Expansion Phase)

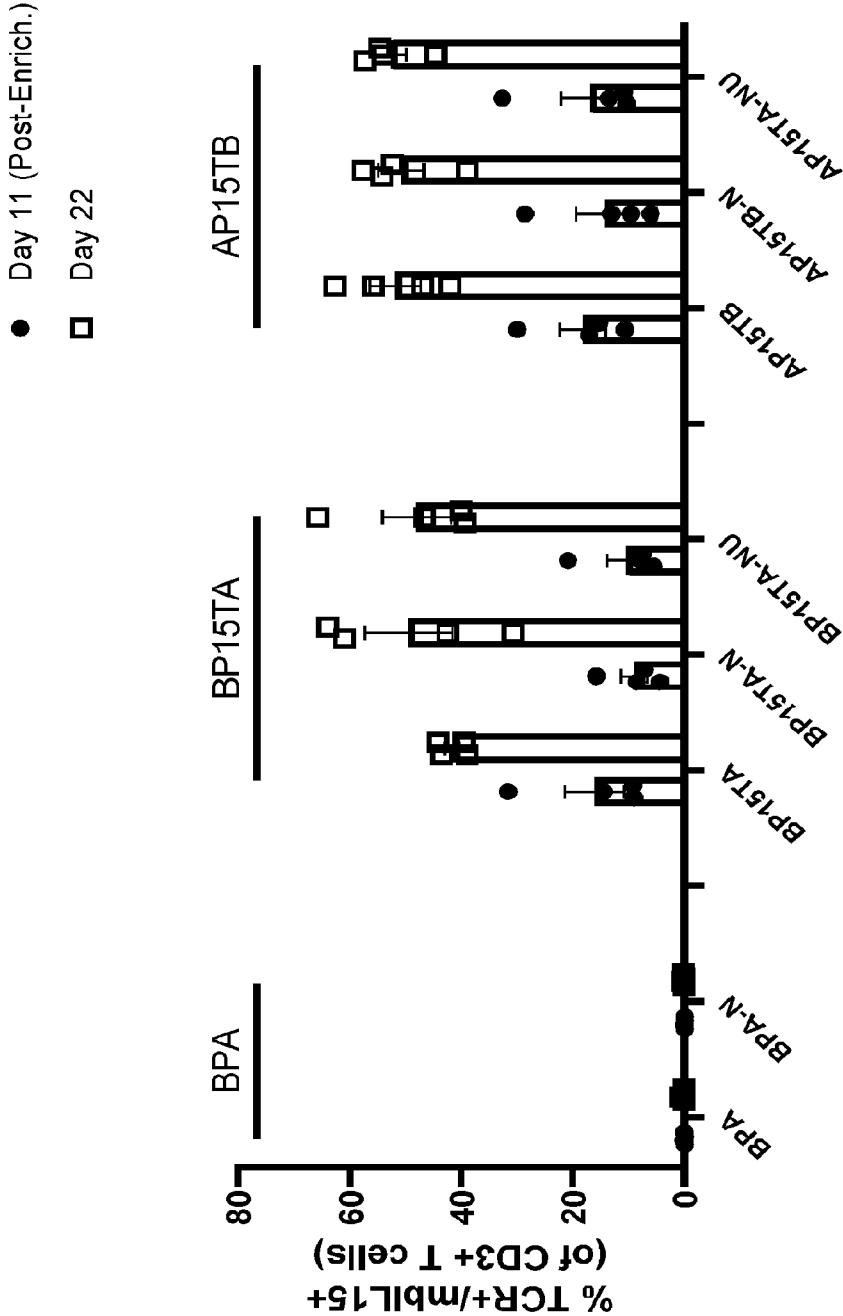


FIG. 14B

TCR and mblL15 Expression after Second Expansion Phase

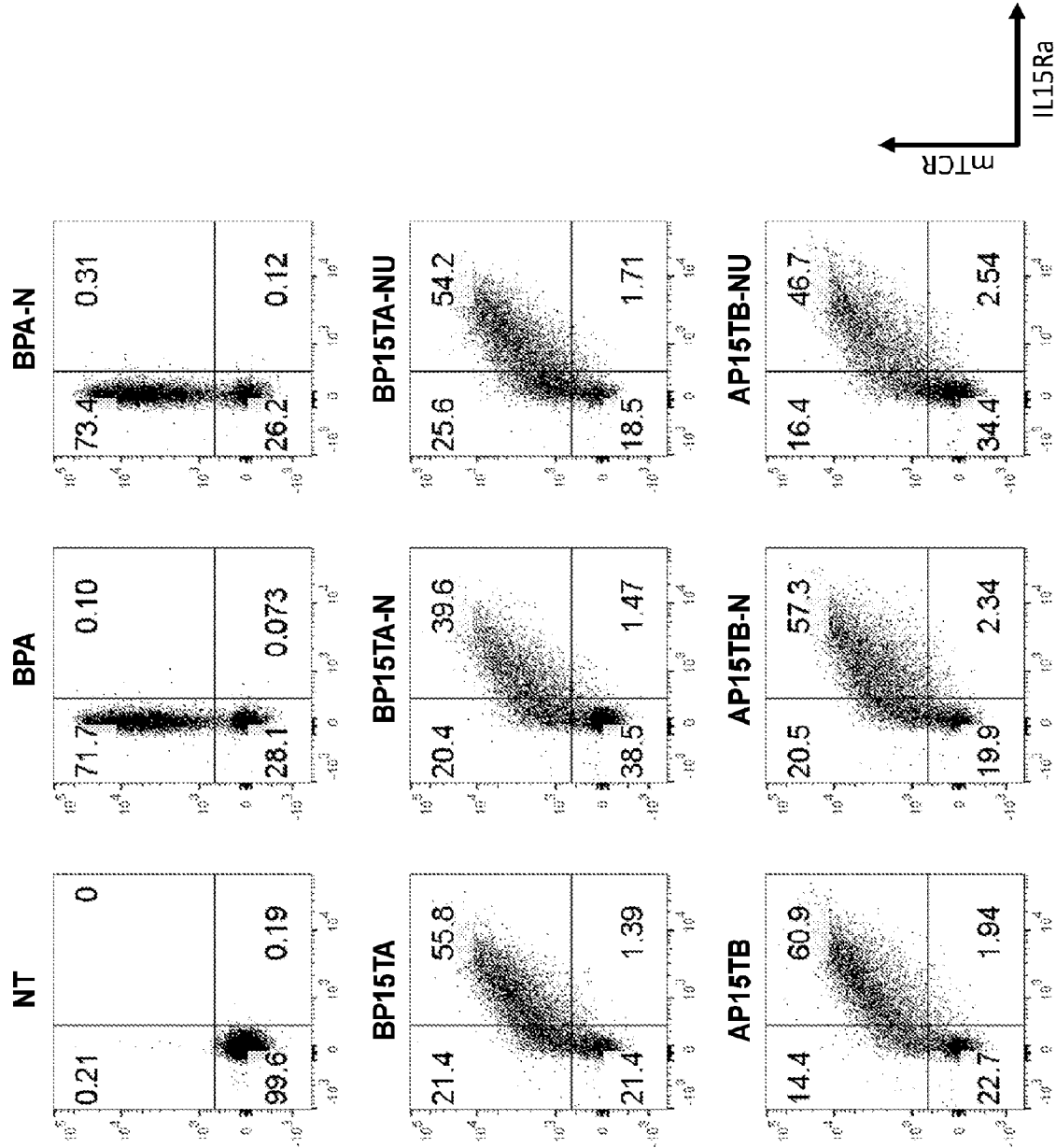


FIG. 15

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Fold Expansion of Cells after First Expansion Phase

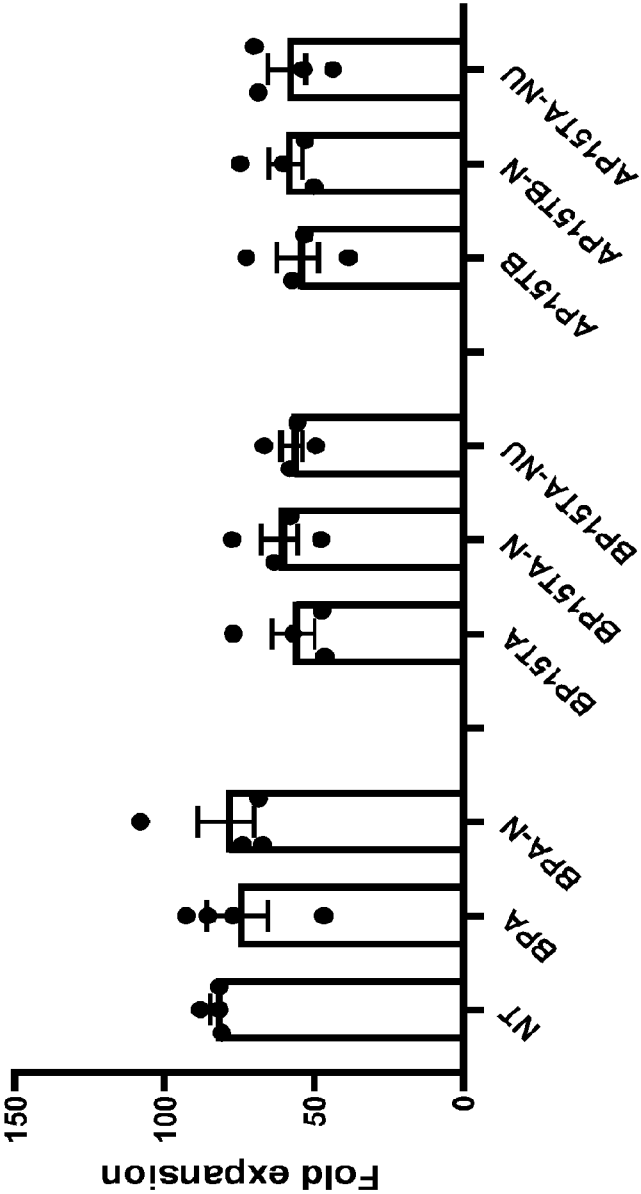


FIG. 16A

Fold Expansion of Cells after Second Expansion Phase

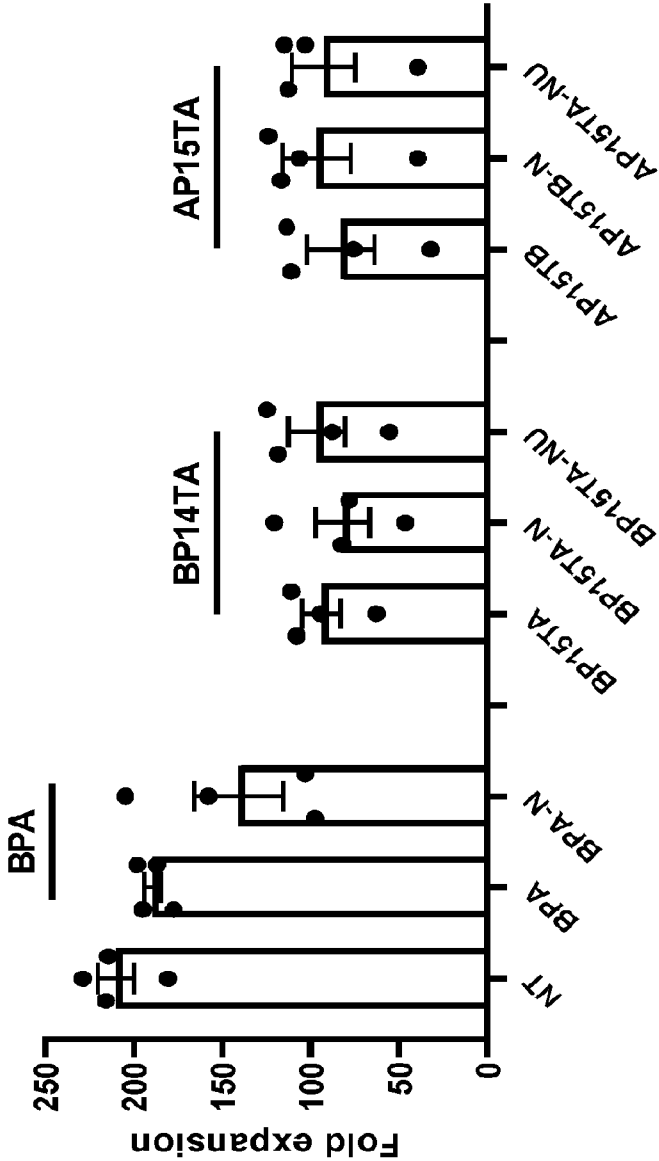


FIG. 16B

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Absolute TCR+ Cell Numbers during First Expansion Phase

- Day 1
- Day 11 (Pre-Enrich.)

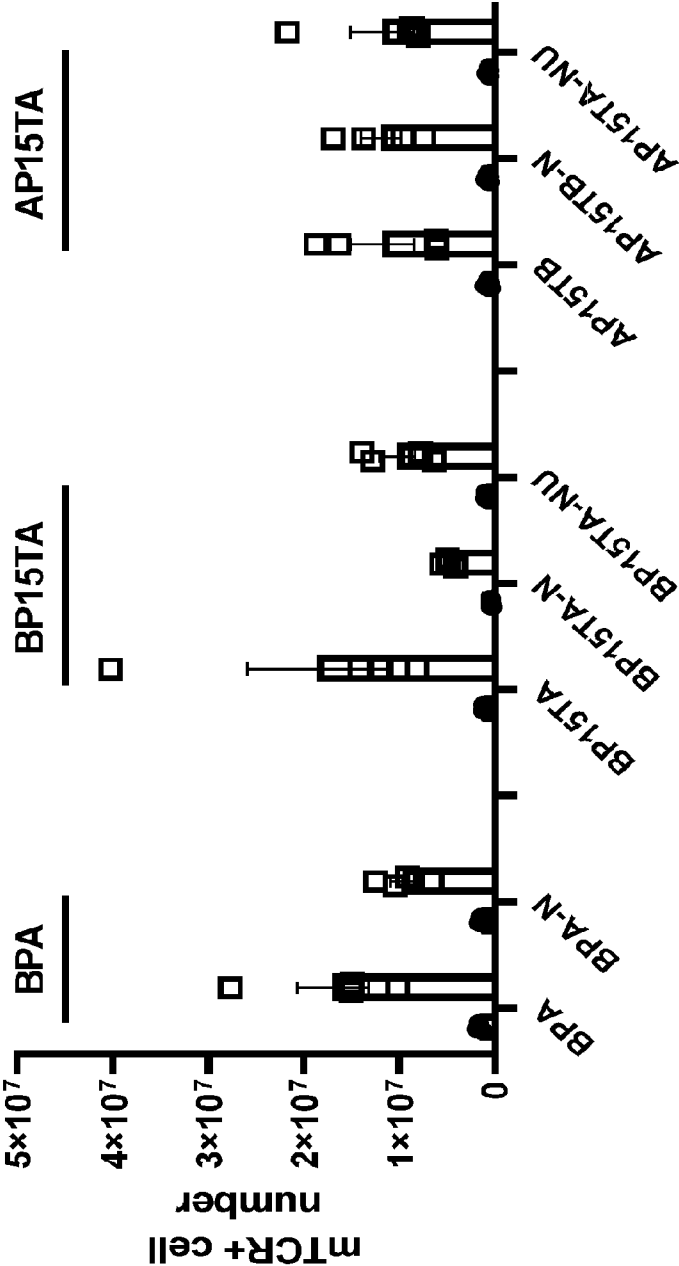


FIG. 17A

Absolute TCR+ Cell Numbers during Second Expansion Phase

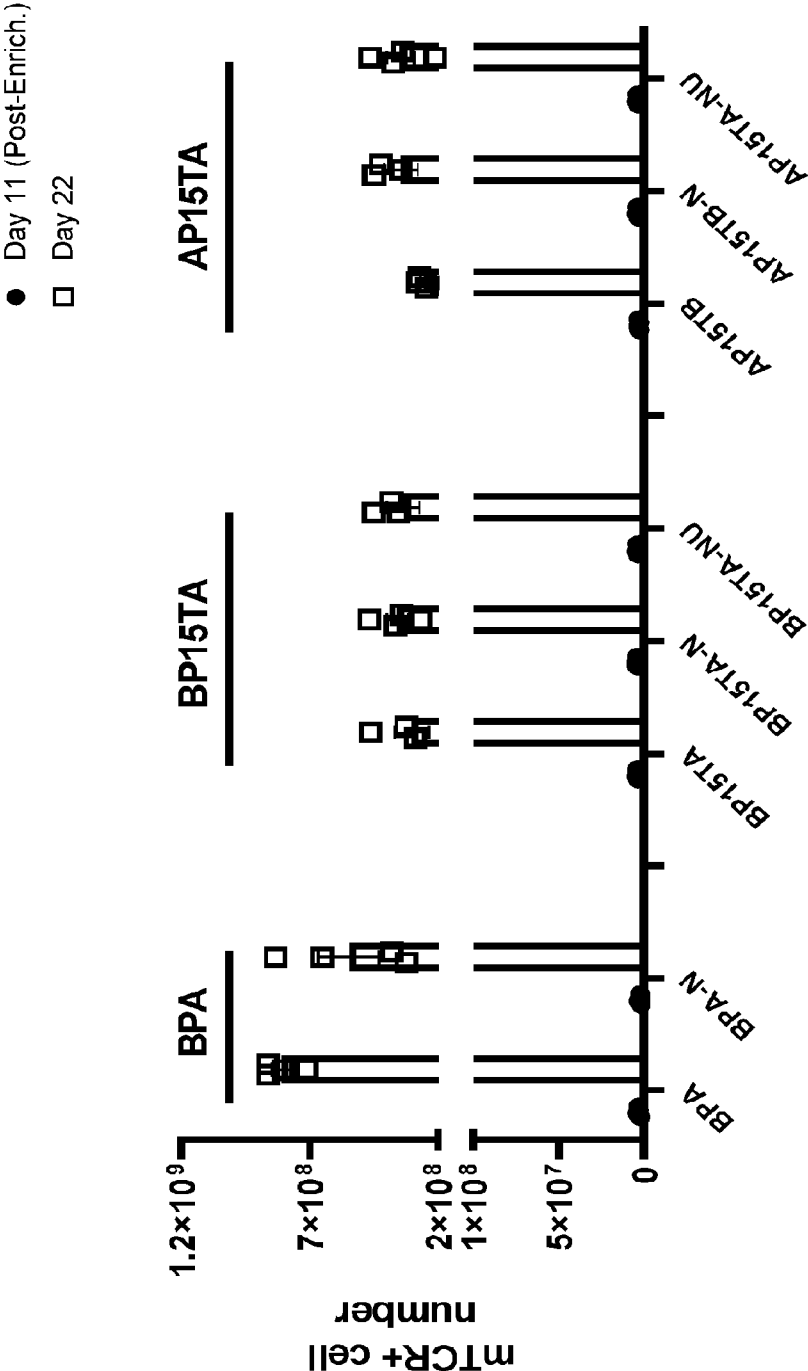


FIG. 17B

Phosphorylation of STAT5 at D27 after Second Phase Expansion

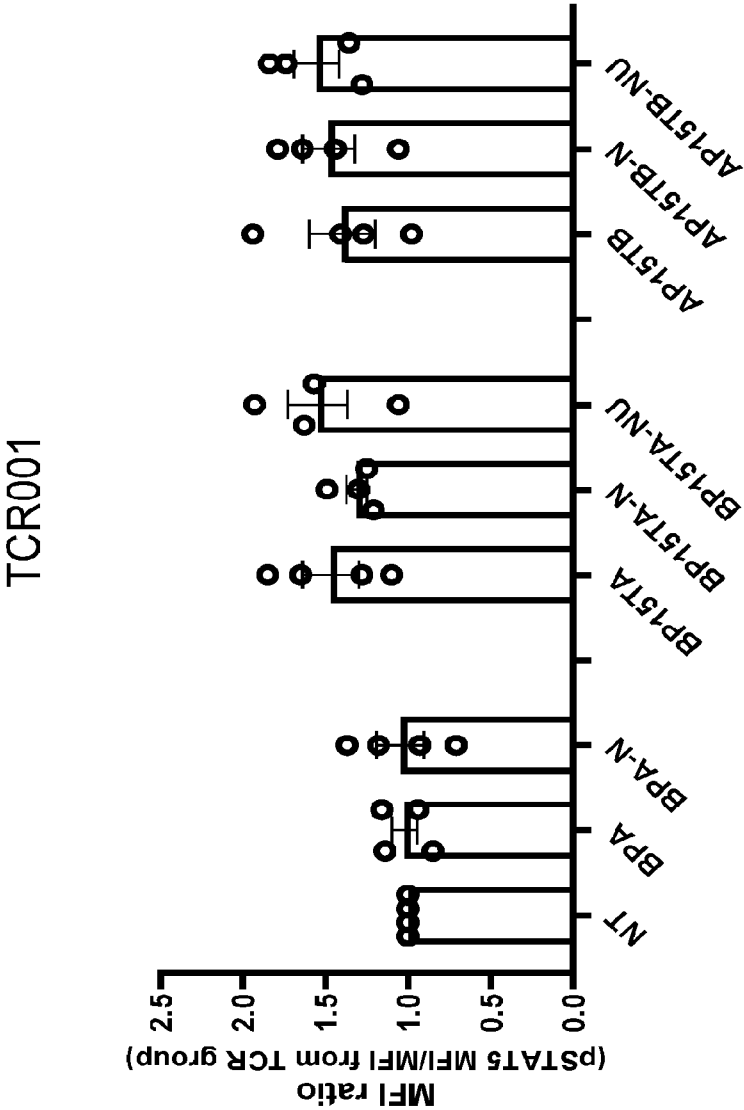


FIG. 18

Antigen-Specific Induction of 4-1BB at D27 after Expansion

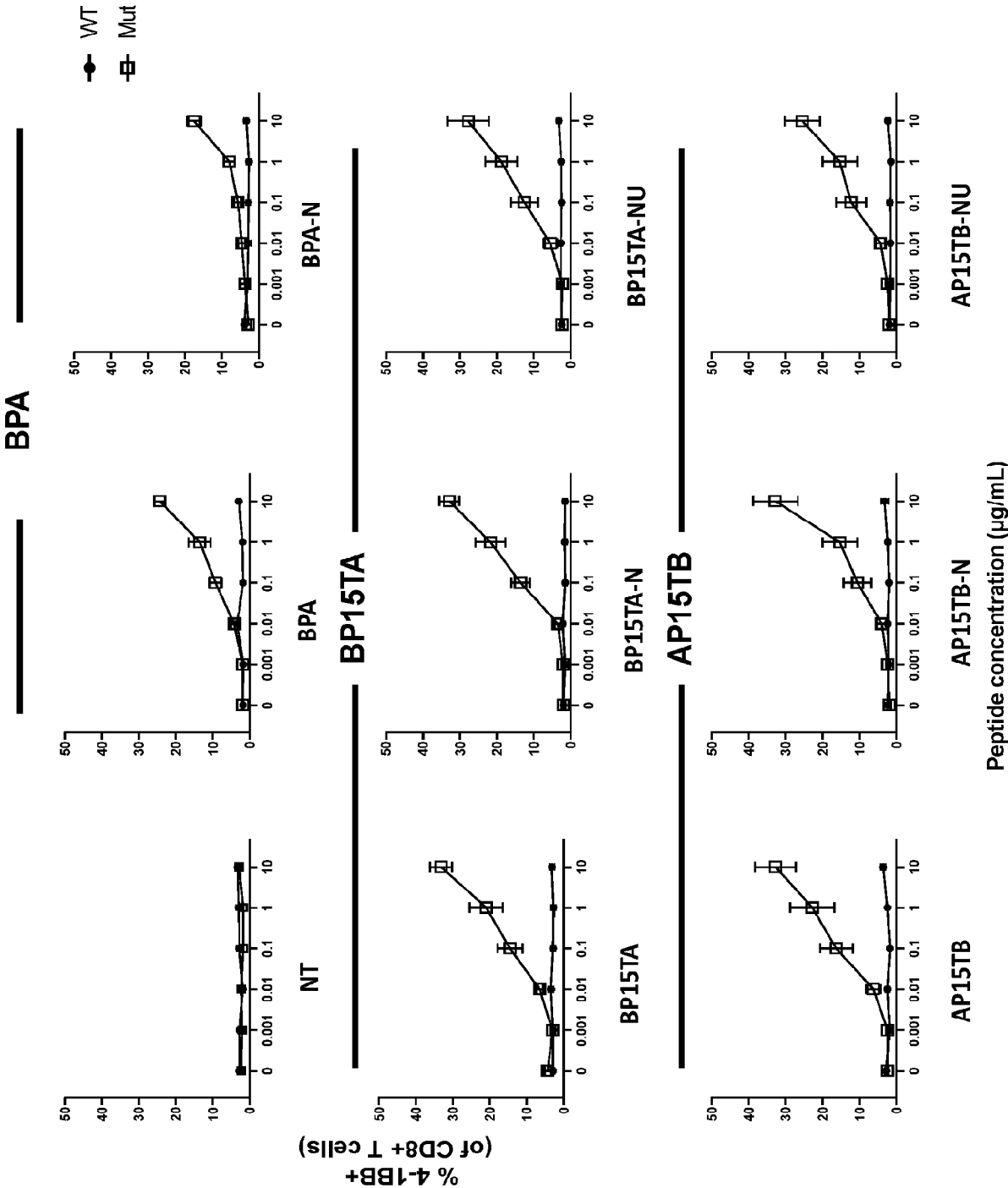
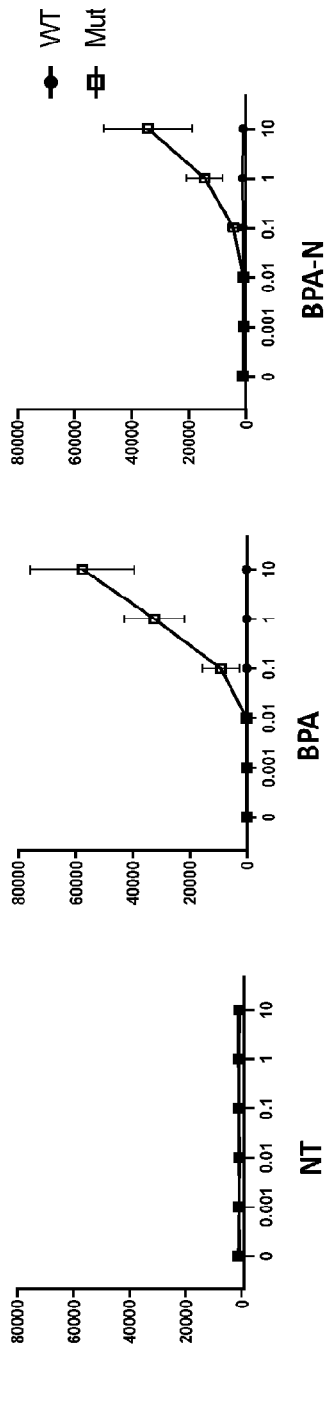


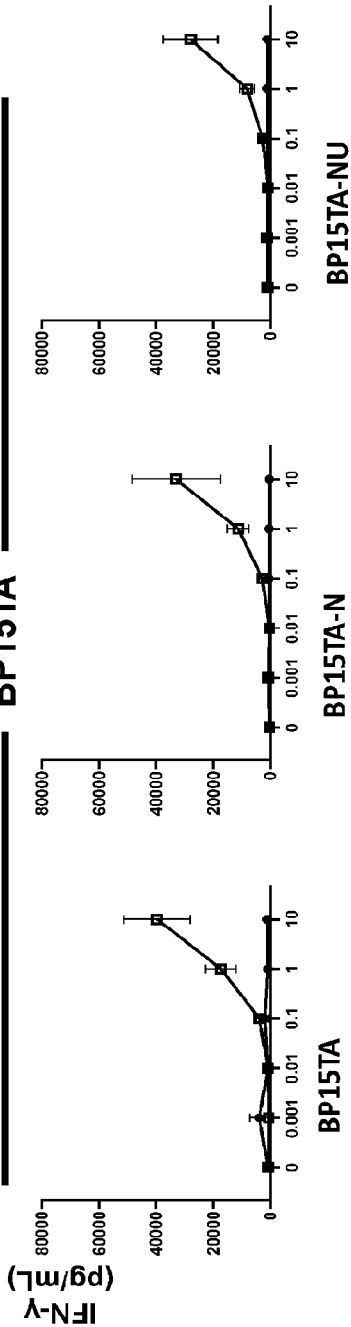
FIG. 19A

IFN- γ Secretion after Expansion

BPA



BP15TA



AP15TB

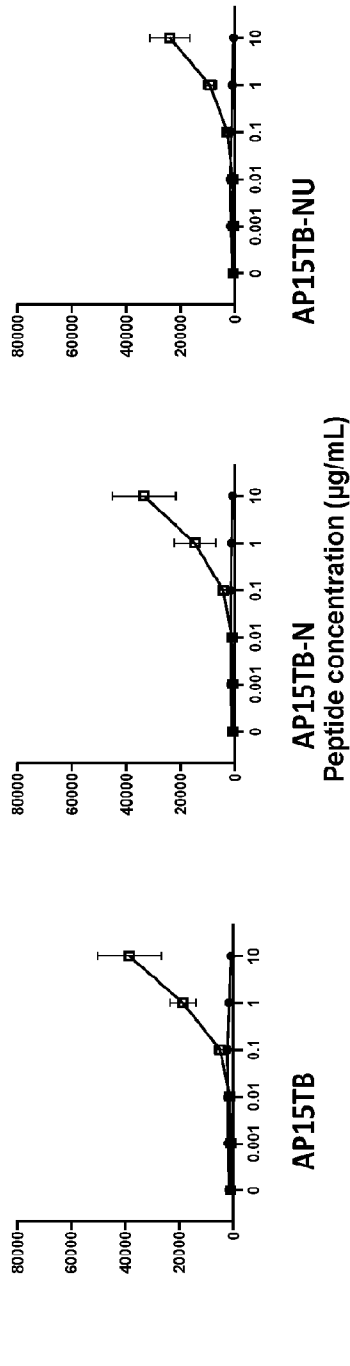


FIG. 19B

TCR+ population after LTWD culture

TCR001

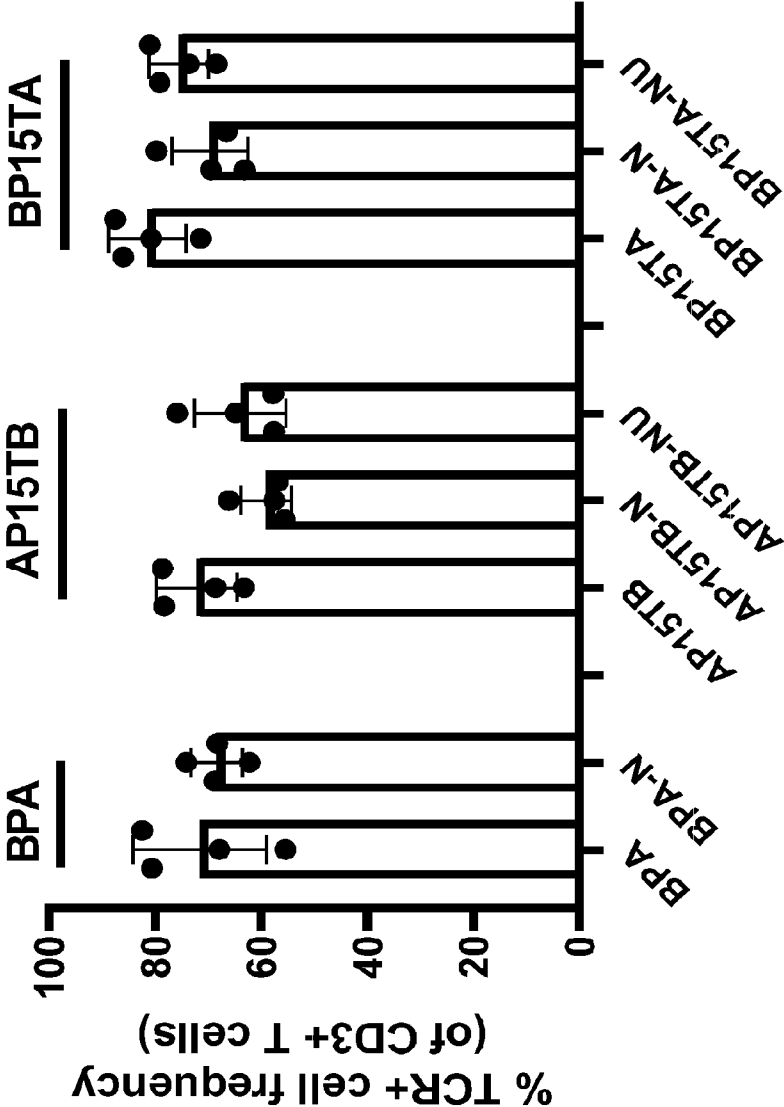


FIG. 20A

Cell Survival after LTWD culture

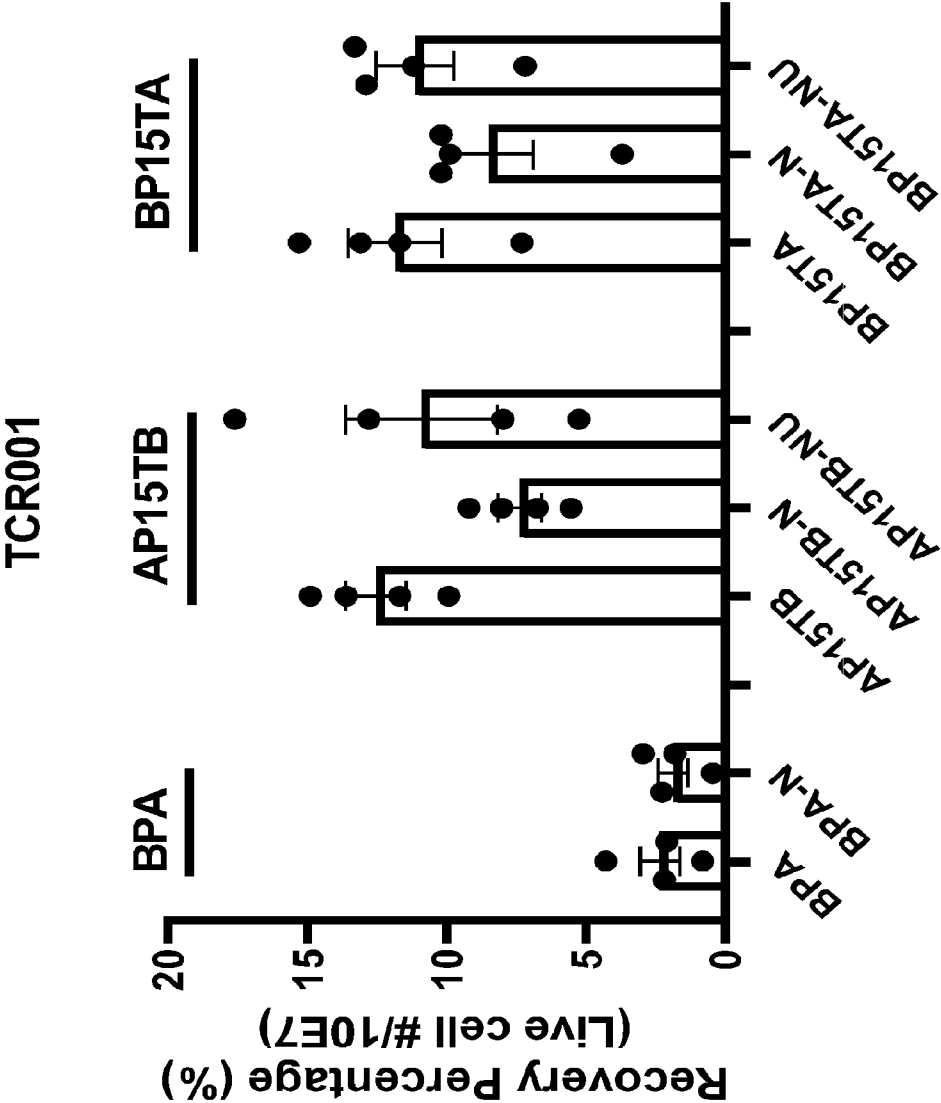


FIG. 20B

4-1BB Induction after LTWD culture

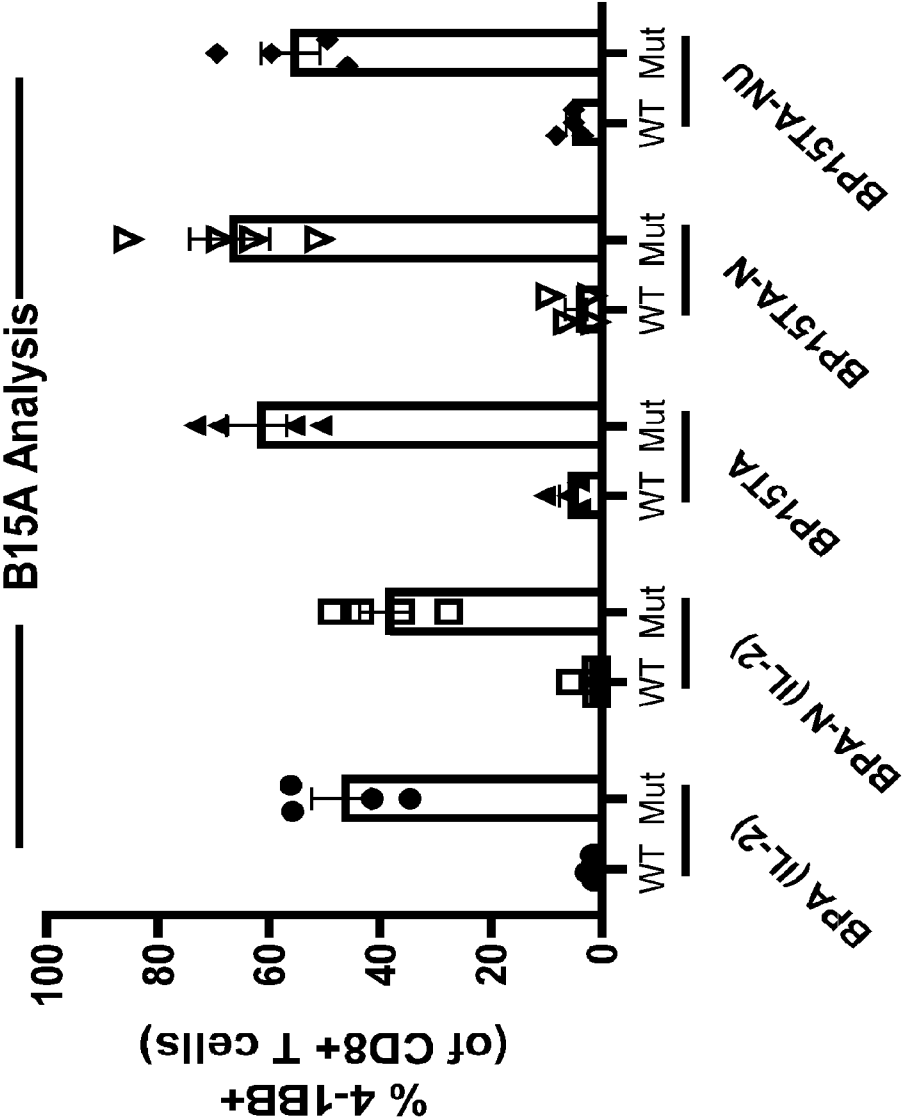


FIG. 21A

4-1BB Induction after LTWD culture

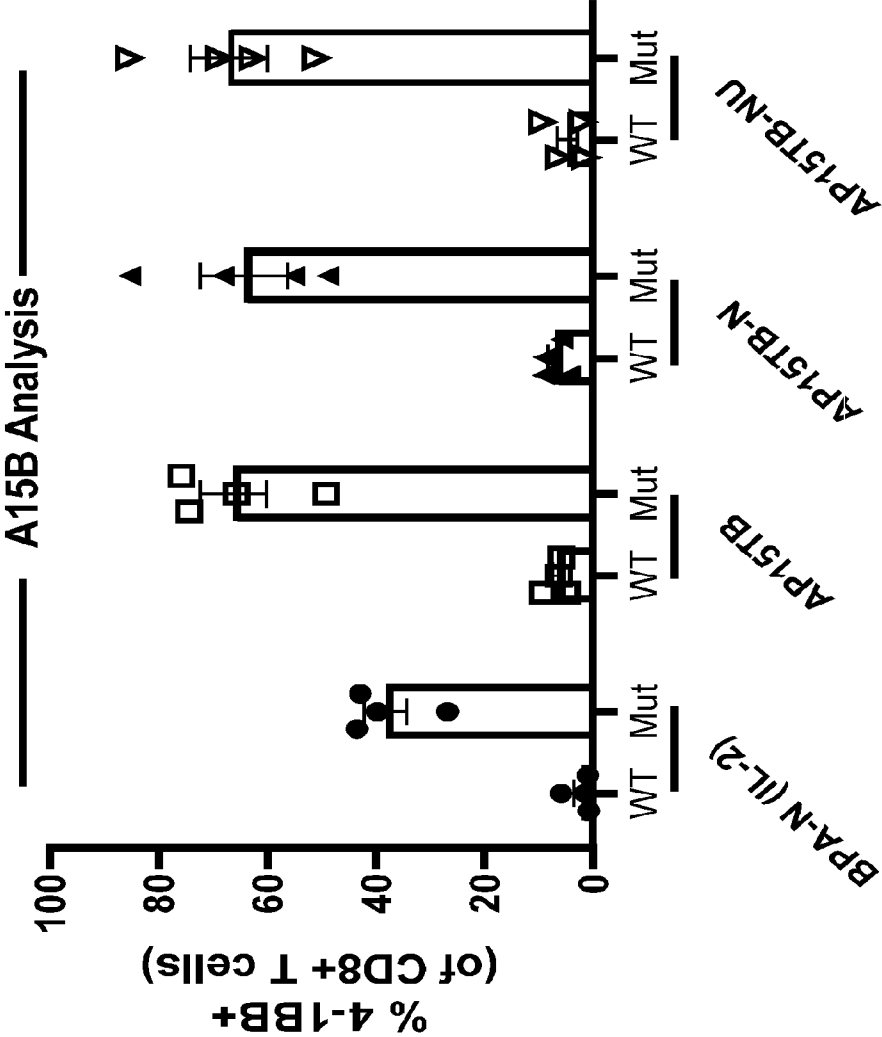


FIG. 21B

IFN- γ Secretion after LTWD culture

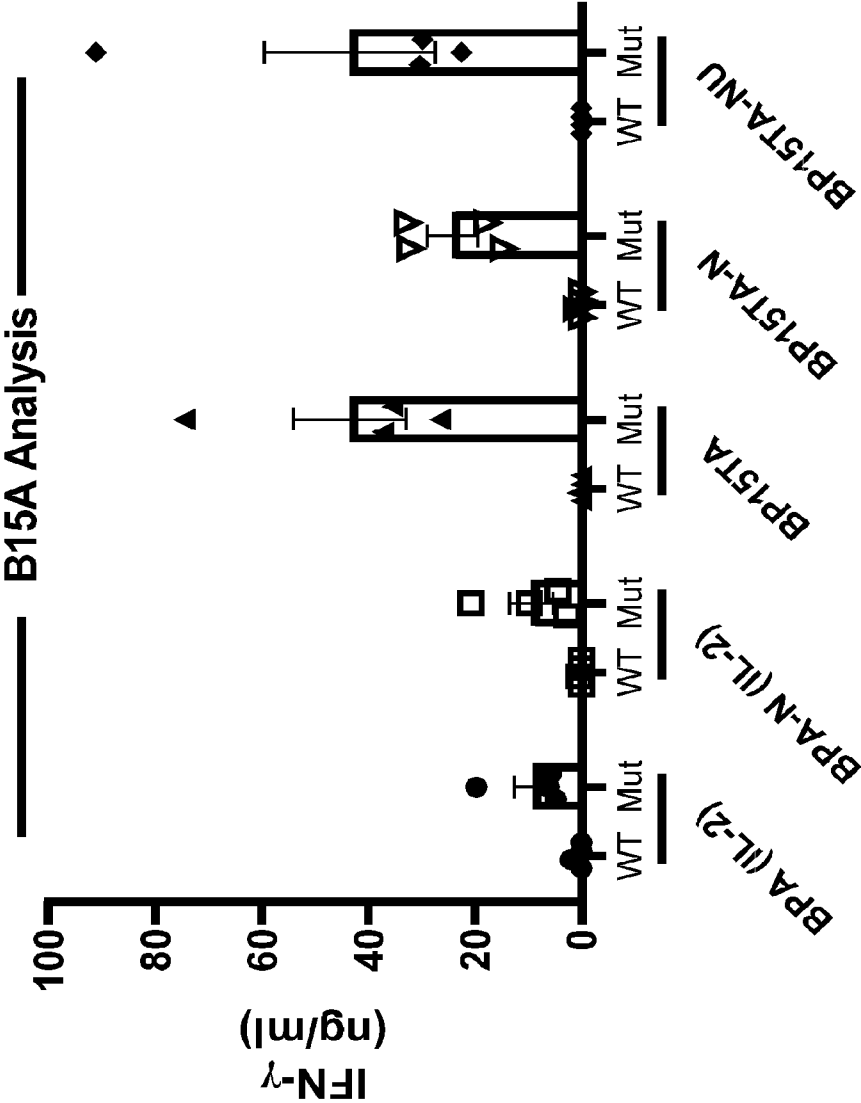


FIG. 22A

IFN- γ Secretion after LTWD culture

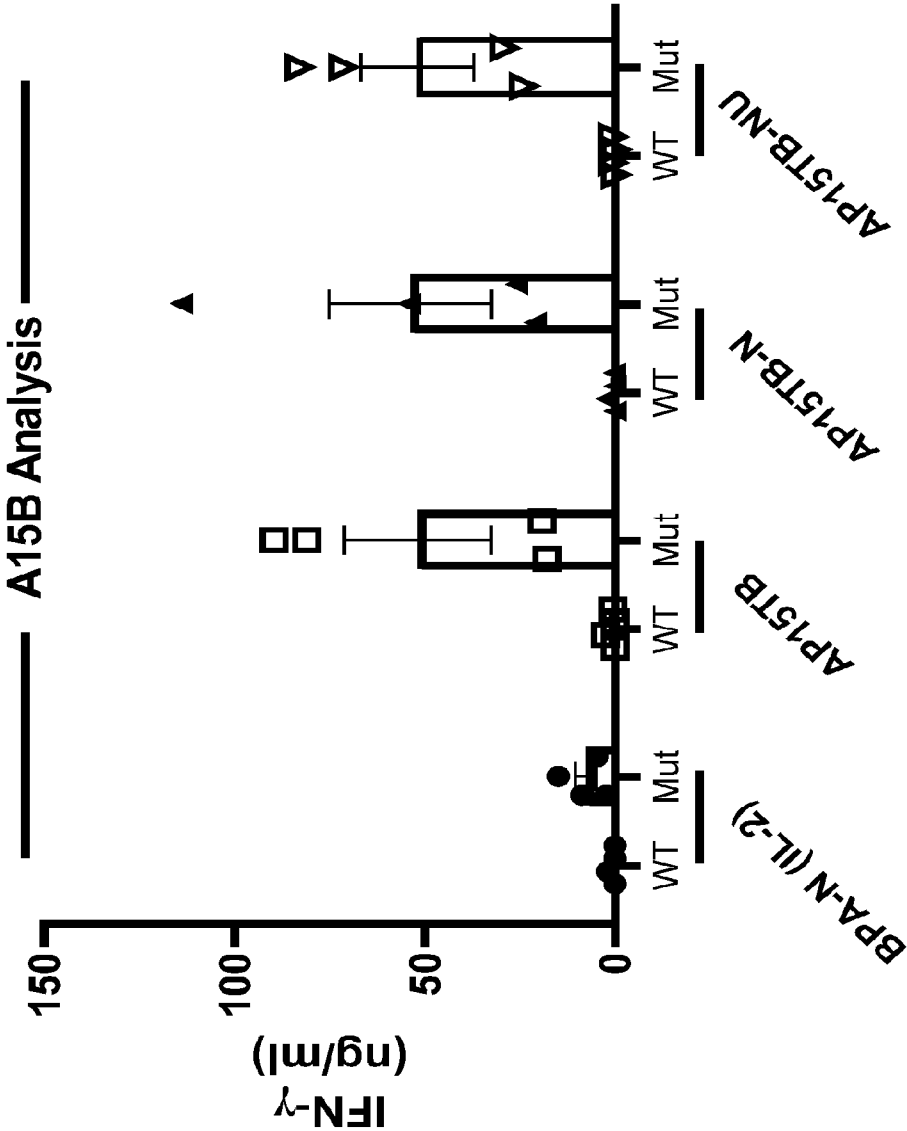
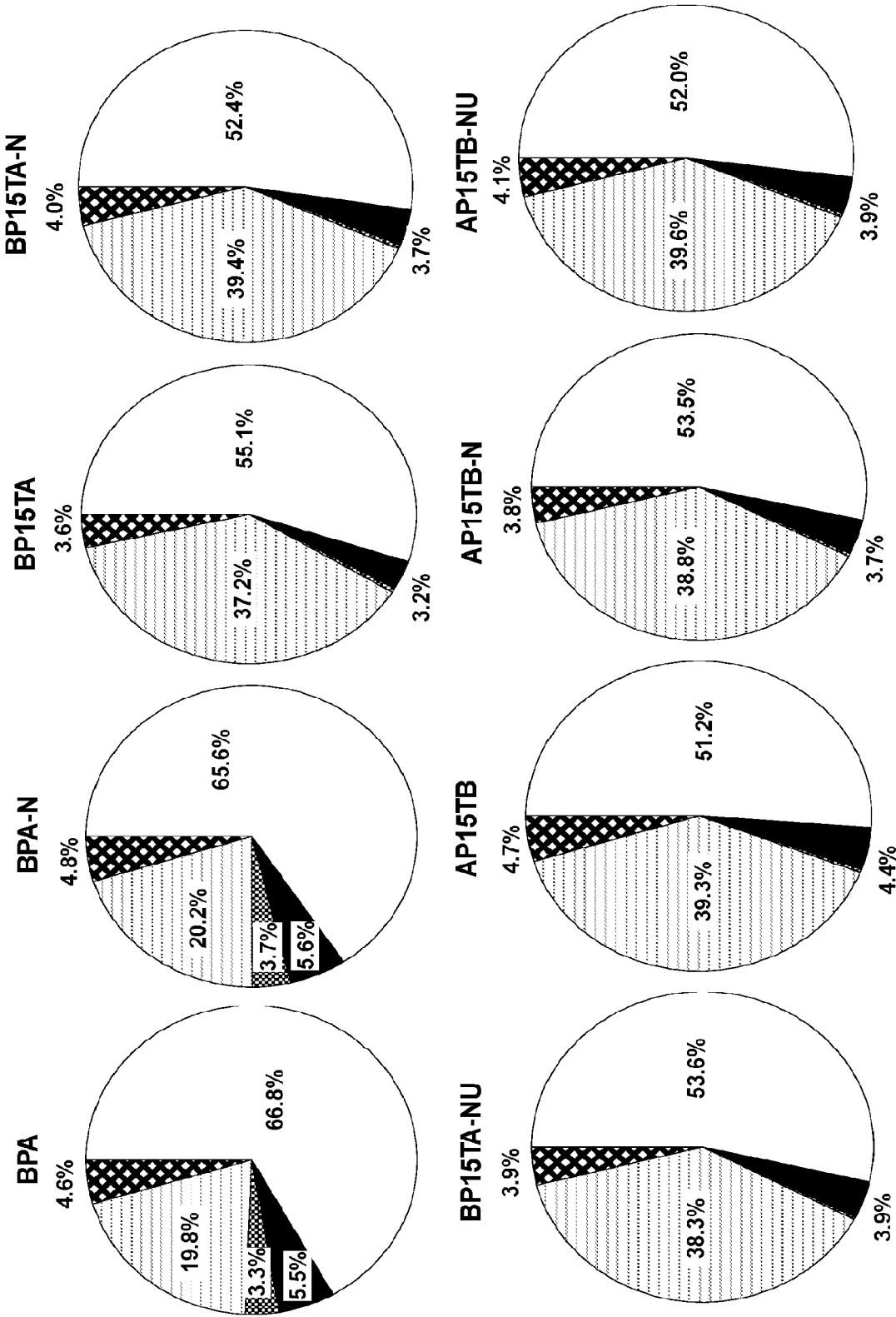


FIG. 22B

Memory Phenotype of Engineered T cells at D11



	CD45RA	CD45RO	CD62L	CD95
Tscm-like	+	+	+	+
Tscm	+	-	+	+
Teff	+	+	-	+
Tcm	-	+	+	+
Tem	-	+	-	+

FIG. 23A

Memory Phenotype of Engineered T cells at D22

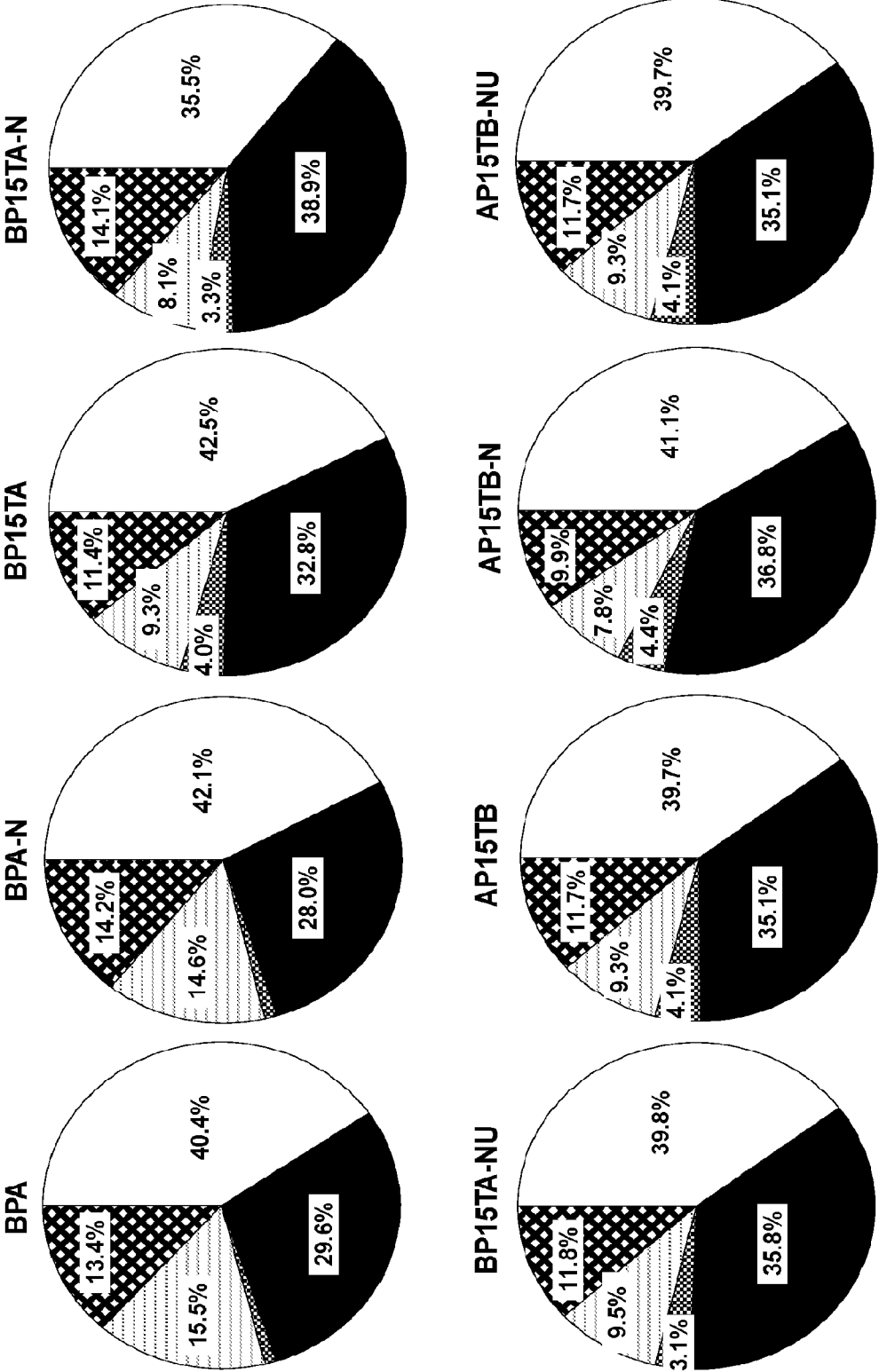


FIG. 23B

	CD45RA	CD45RO	CD62L	CD95
Tscm-like	+	+	+	+
Tscm	+	-	+	+
Teff	+	+	-	+
Tcm	-	+	+	+
Tem	-	+	-	+

Memory Phenotype of Engineered T cells after LTWD Culture

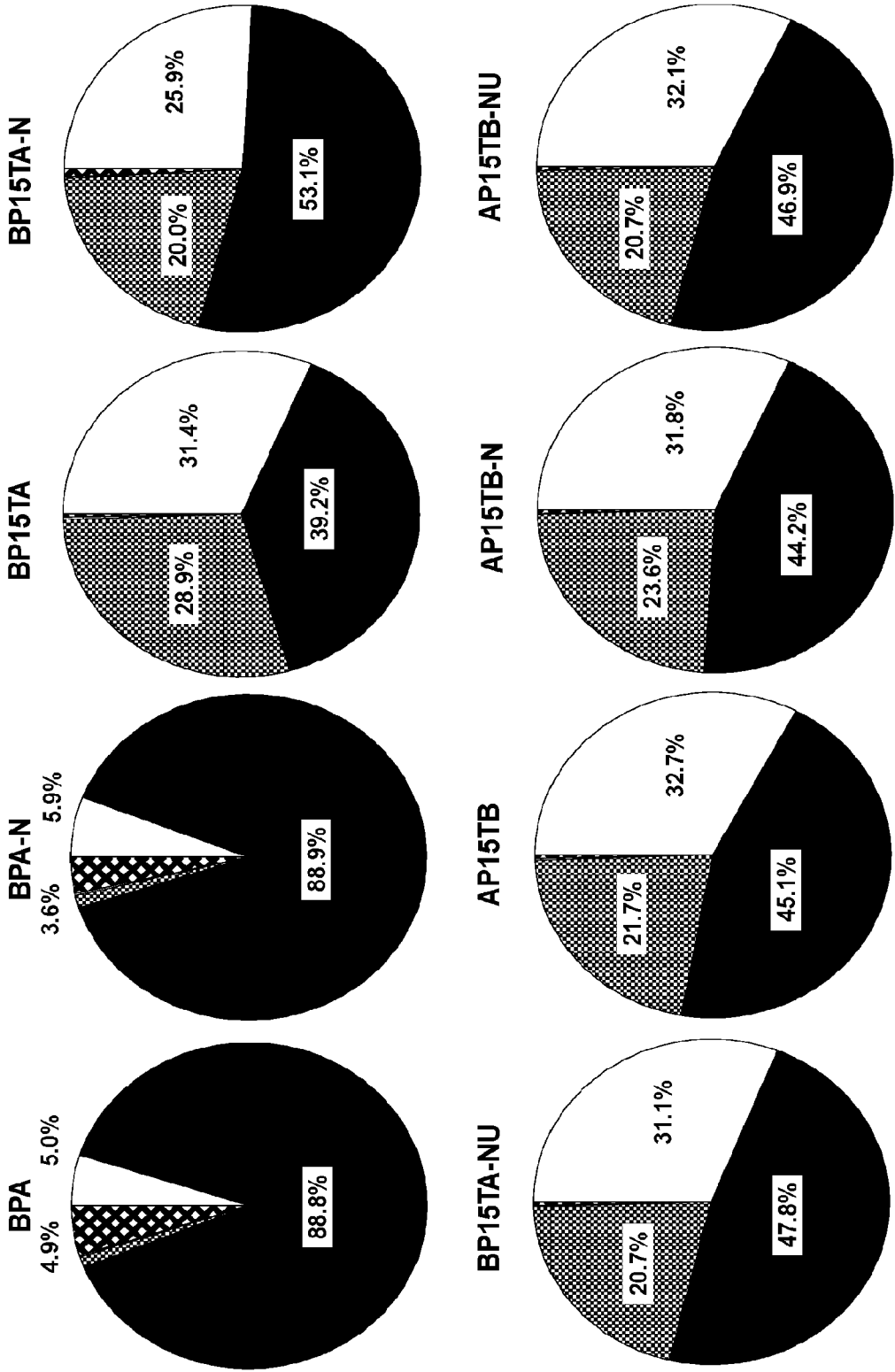


FIG. 23C

	CD45RA	CD45RO	CD62L	CD95
Tscm-like	+	+	+	+
Tscm	+	-	+	+
Teff	+	+	-	+
Tcm	-	+	+	+
xxx Tem	-	+	-	+

TCR & mIL15 Expression During First and Second Expansion Phases

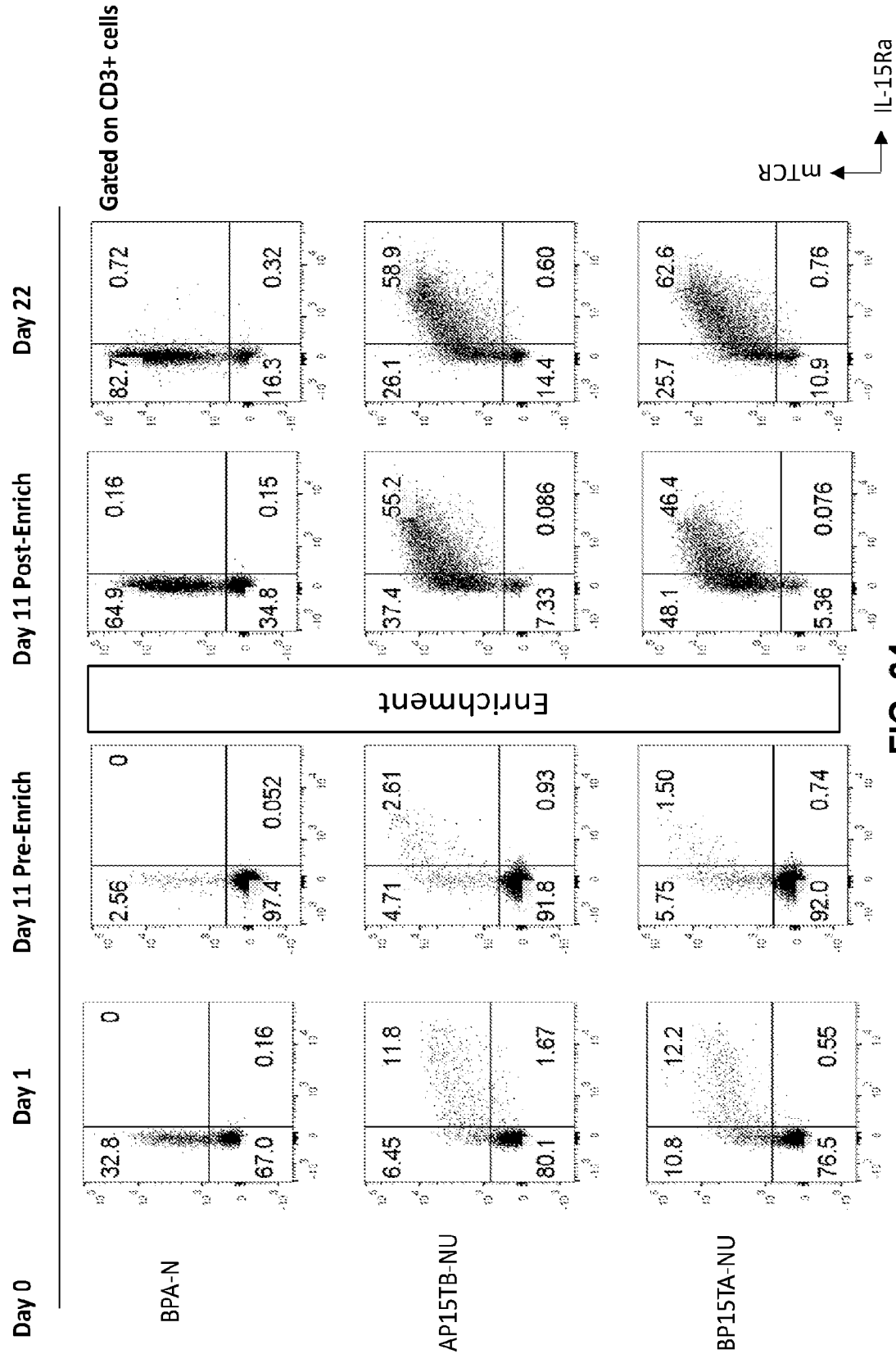


FIG. 24

TCR+ Population Changes During First Expansion Phase

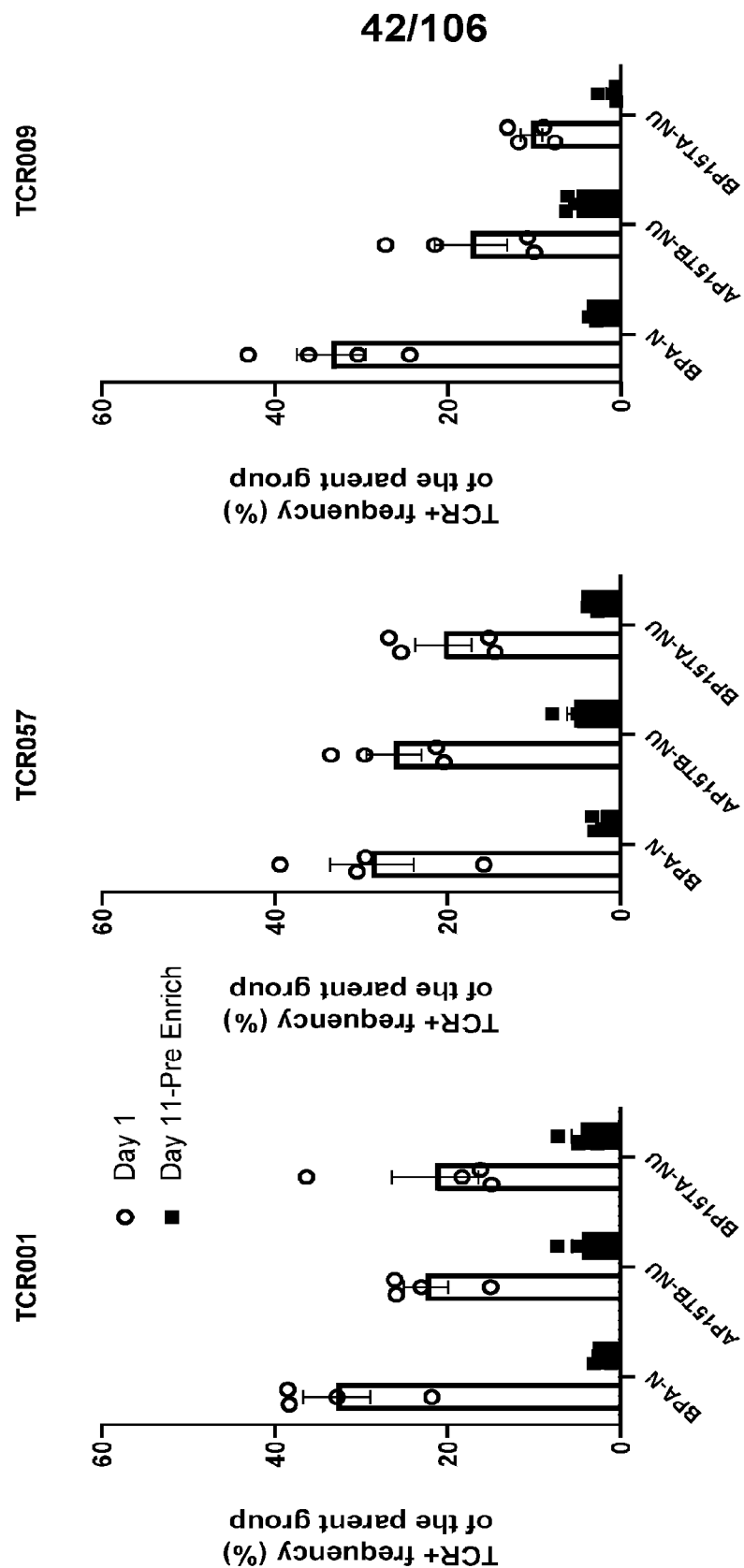


FIG. 25A

TCR+ Population Changes During First Expansion Phase

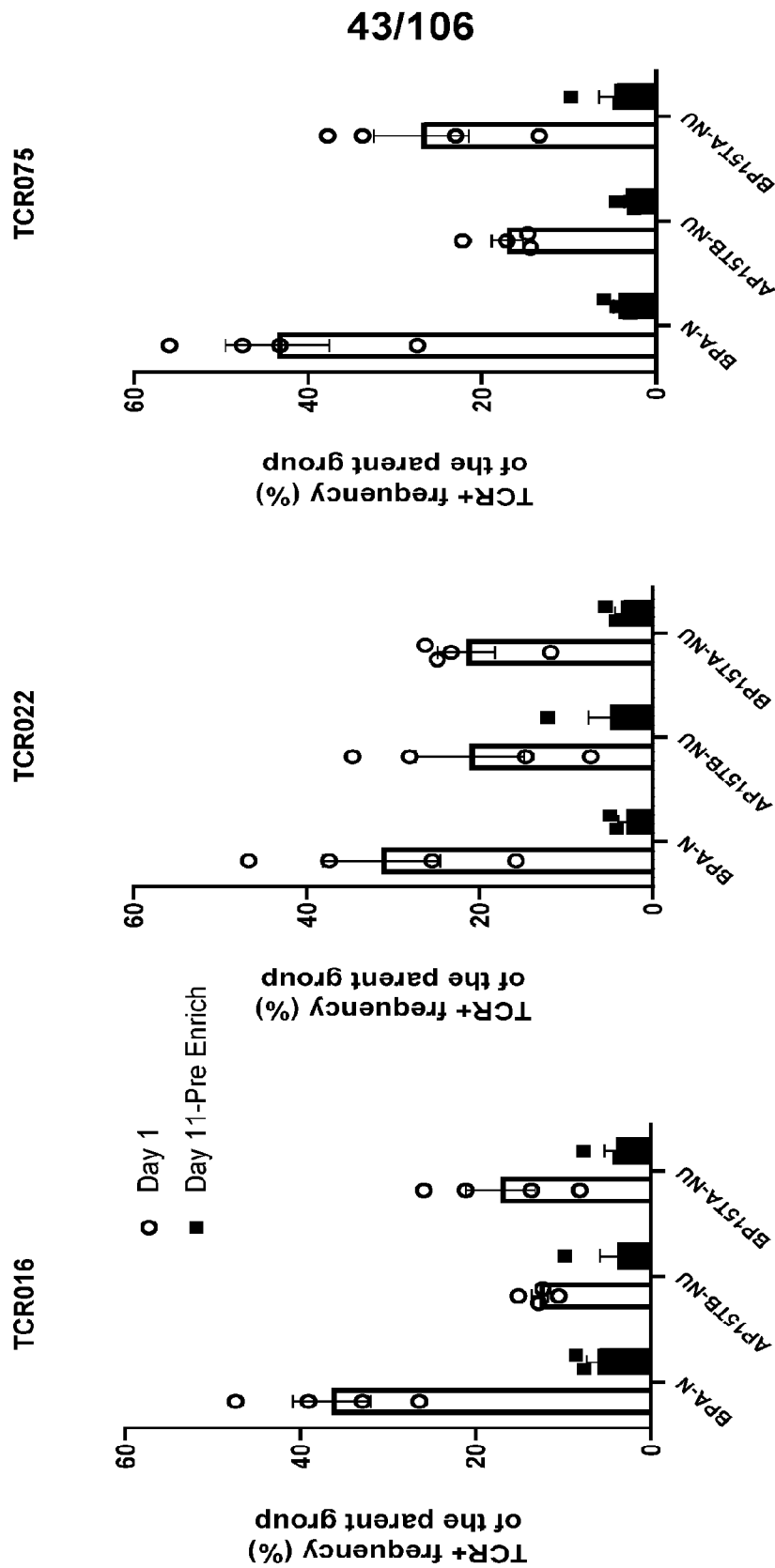


FIG. 25B

TCR+ Population Changes During First Expansion Phase

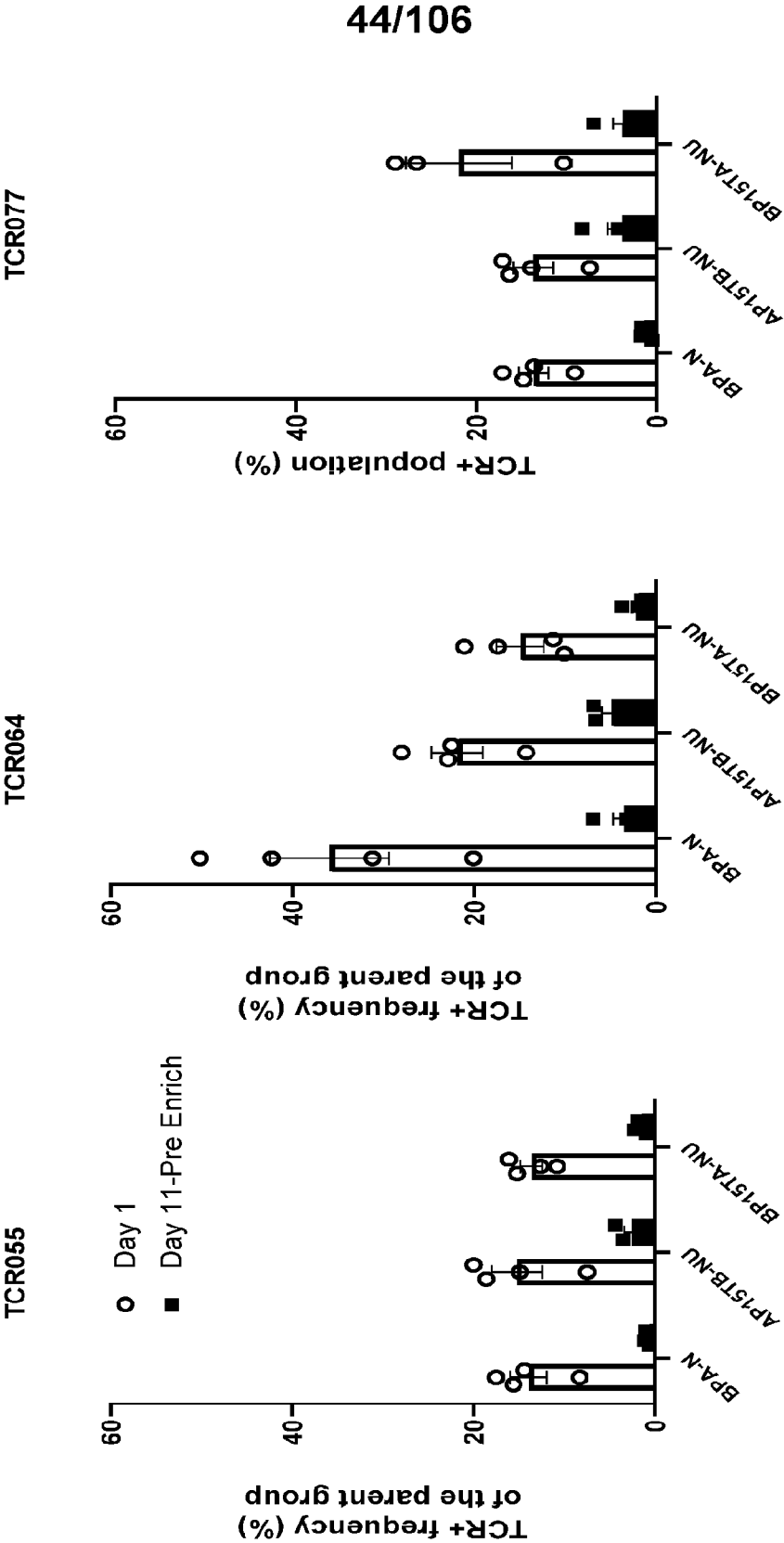


FIG. 25C

Figure 2 displays the TCR frequency of the parent group for three TCRs (TCR001, TCR057, and TCR009) across three groups: BP15TA-NU, AP15TB-NU, and BP15TA-NU. The data is presented as bar charts showing the percentage of TCR+ frequency (%) for each group at Day 11-Post-Enrich (open circles) and Day 22 (filled squares). The y-axis represents the percentage of TCR+ frequency (%) from 0 to 100. The x-axis lists the groups: BP15TA-NU, AP15TB-NU, and BP15TA-NU. The legend indicates that open circles represent Day 11-Post-Enrich and filled squares represent Day 22. Error bars are shown for each data point.

TCR001

Group	Day 11-Post-Enrich (%)	Day 22 (%)
BP15TA-NU	~85	~85
AP15TB-NU	~85	~85
BP15TA-NU	~85	~85

TCR057

Group	Day 11-Post-Enrich (%)	Day 22 (%)
BP15TA-NU	~85	~85
AP15TB-NU	~85	~85
BP15TA-NU	~85	~85

TCR009

Group	Day 11-Post-Enrich (%)	Day 22 (%)
BP15TA-NU	~85	~85
AP15TB-NU	~85	~85
BP15TA-NU	~85	~85

FIG. 26A

TCR+ Population Changes During Second Expansion Phase

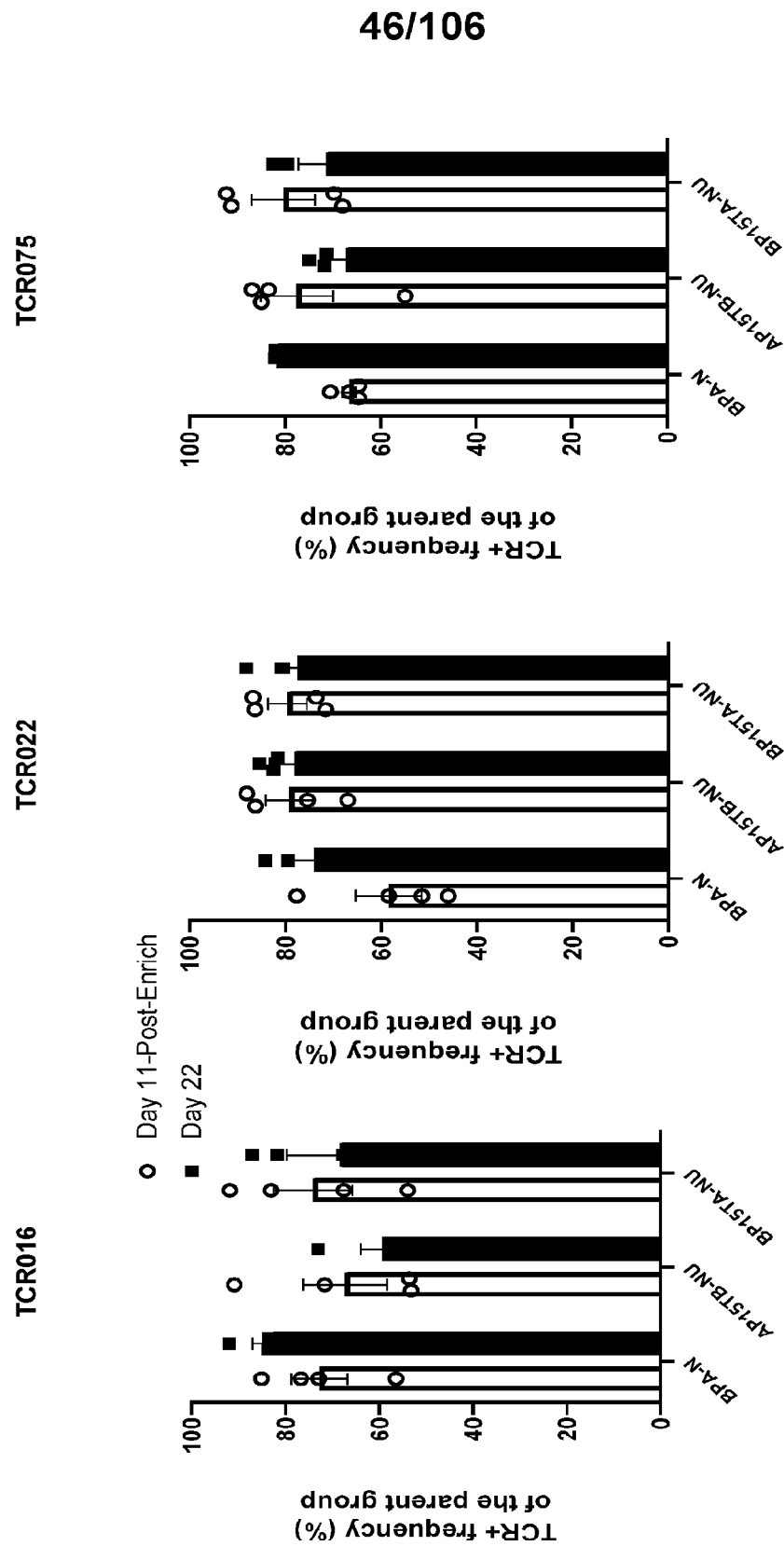


FIG. 26B

TCR+ Population Changes During Second Expansion Phase

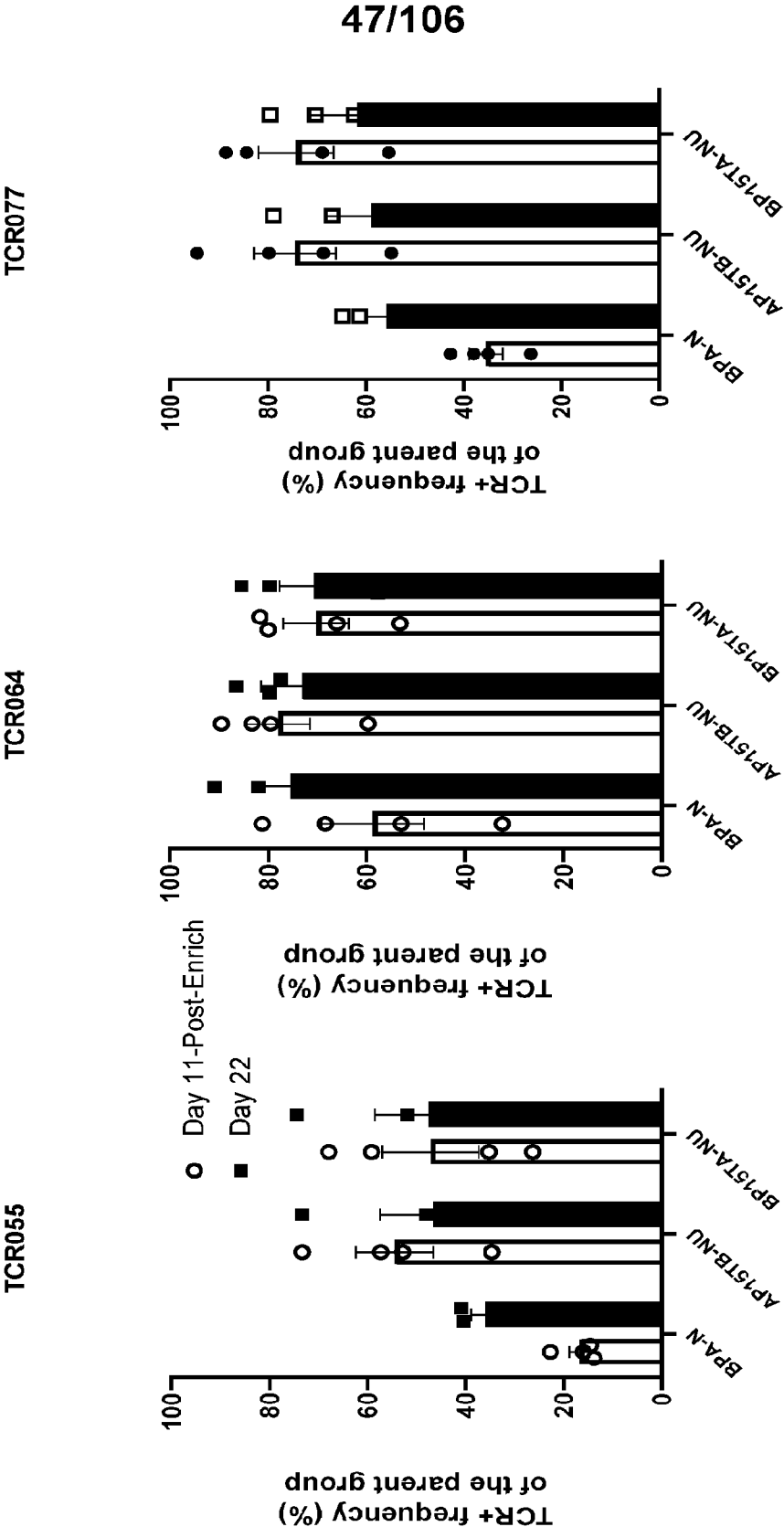


FIG. 26C

TCR+/mblL15+ Population Changes During First Expansion Phase

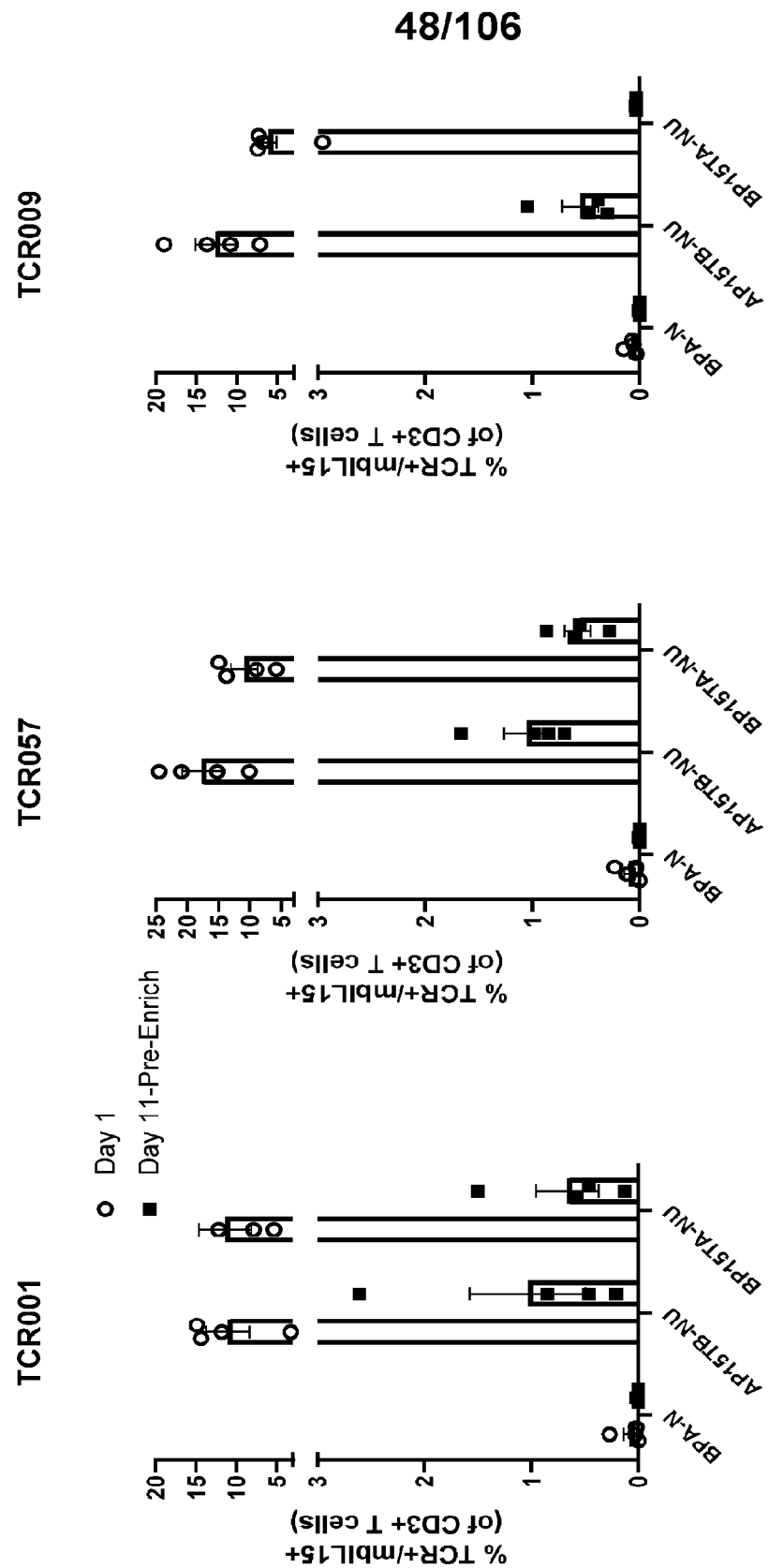


FIG. 27A

TCR+/mblL15+ Population Changes During First Expansion Phase

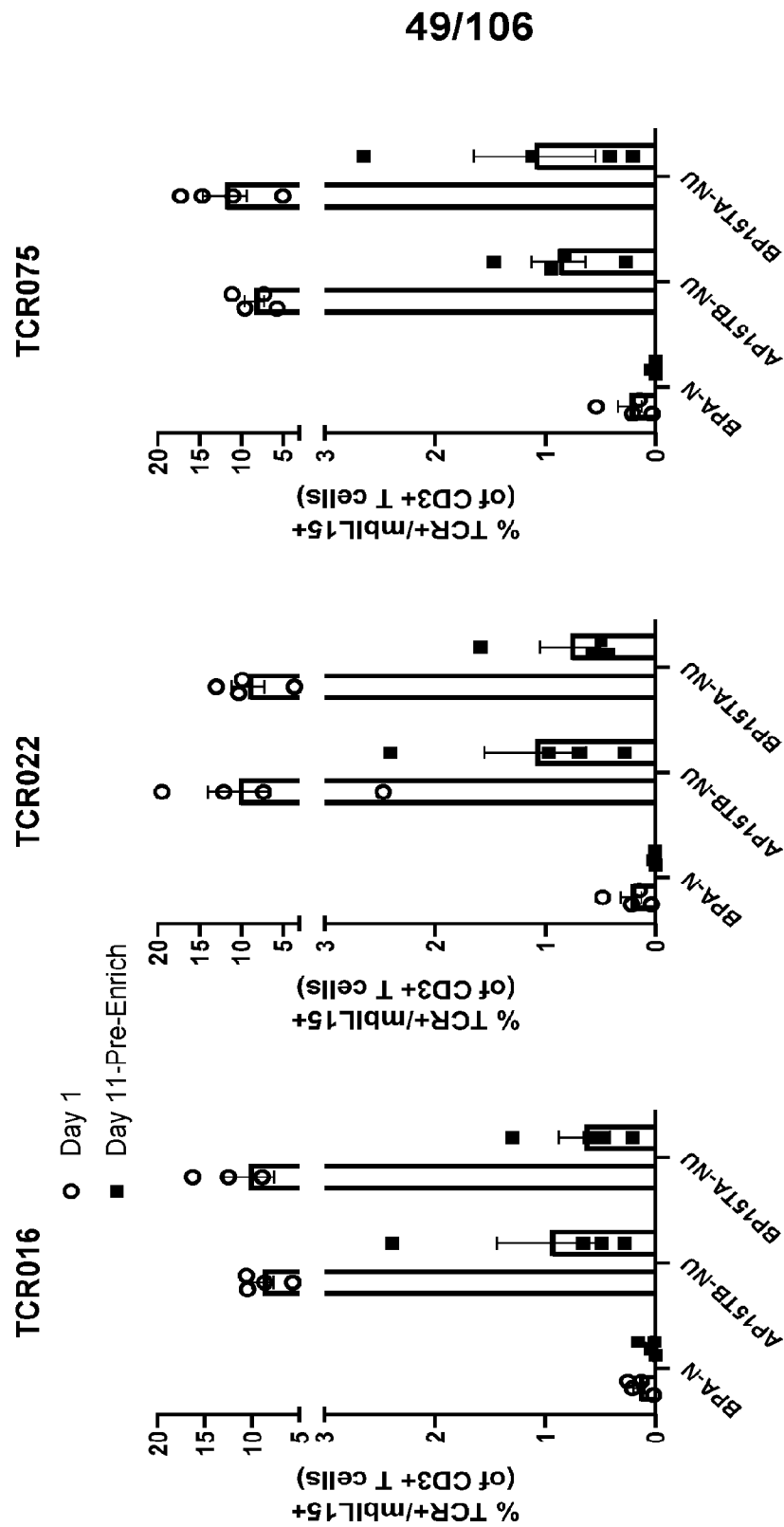


FIG. 27B

TCR+/mbIL15+ Population Changes During First Expansion Phase

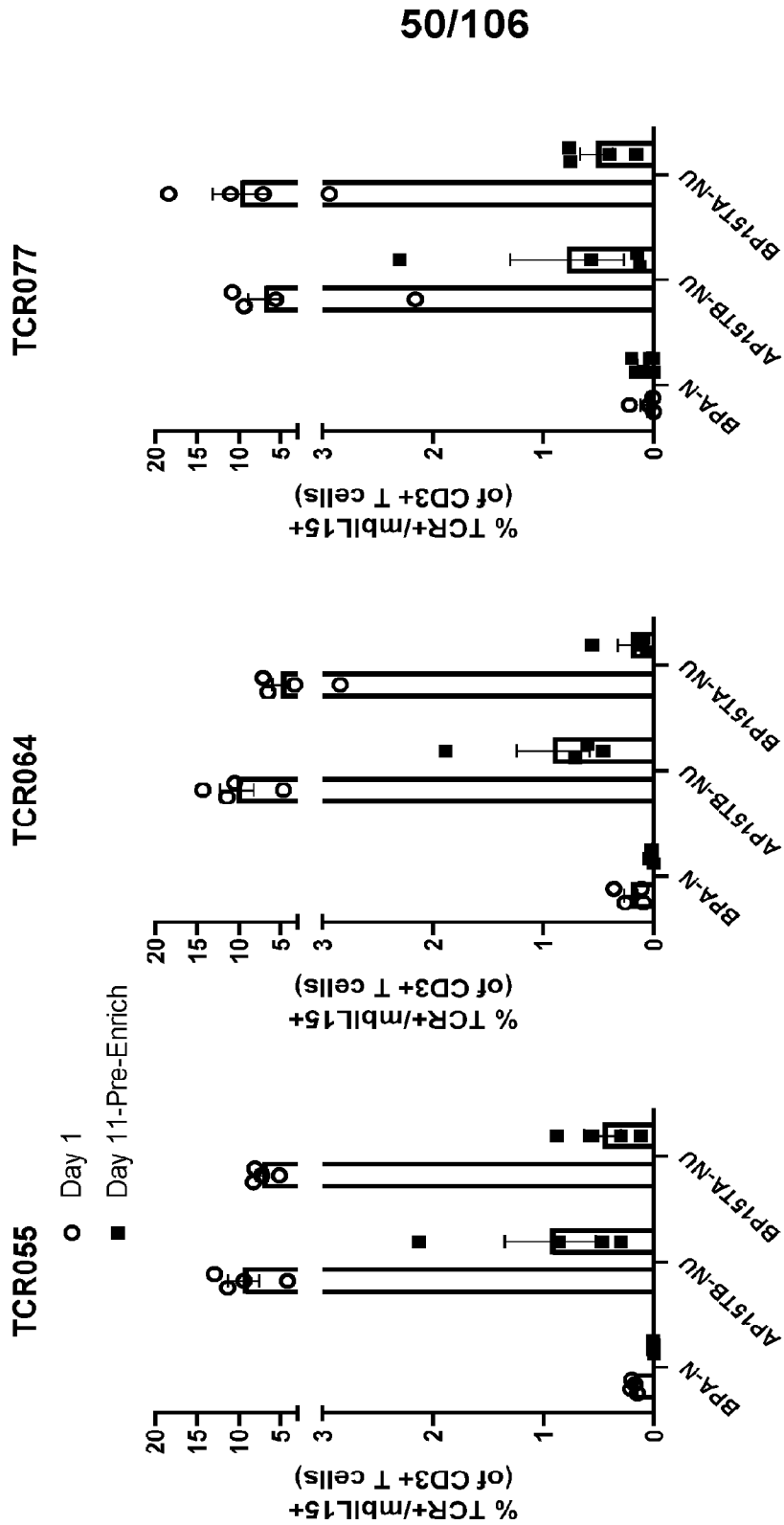


FIG. 27C

TCR+/mbIL15+ Population Changes During Second Expansion Phase

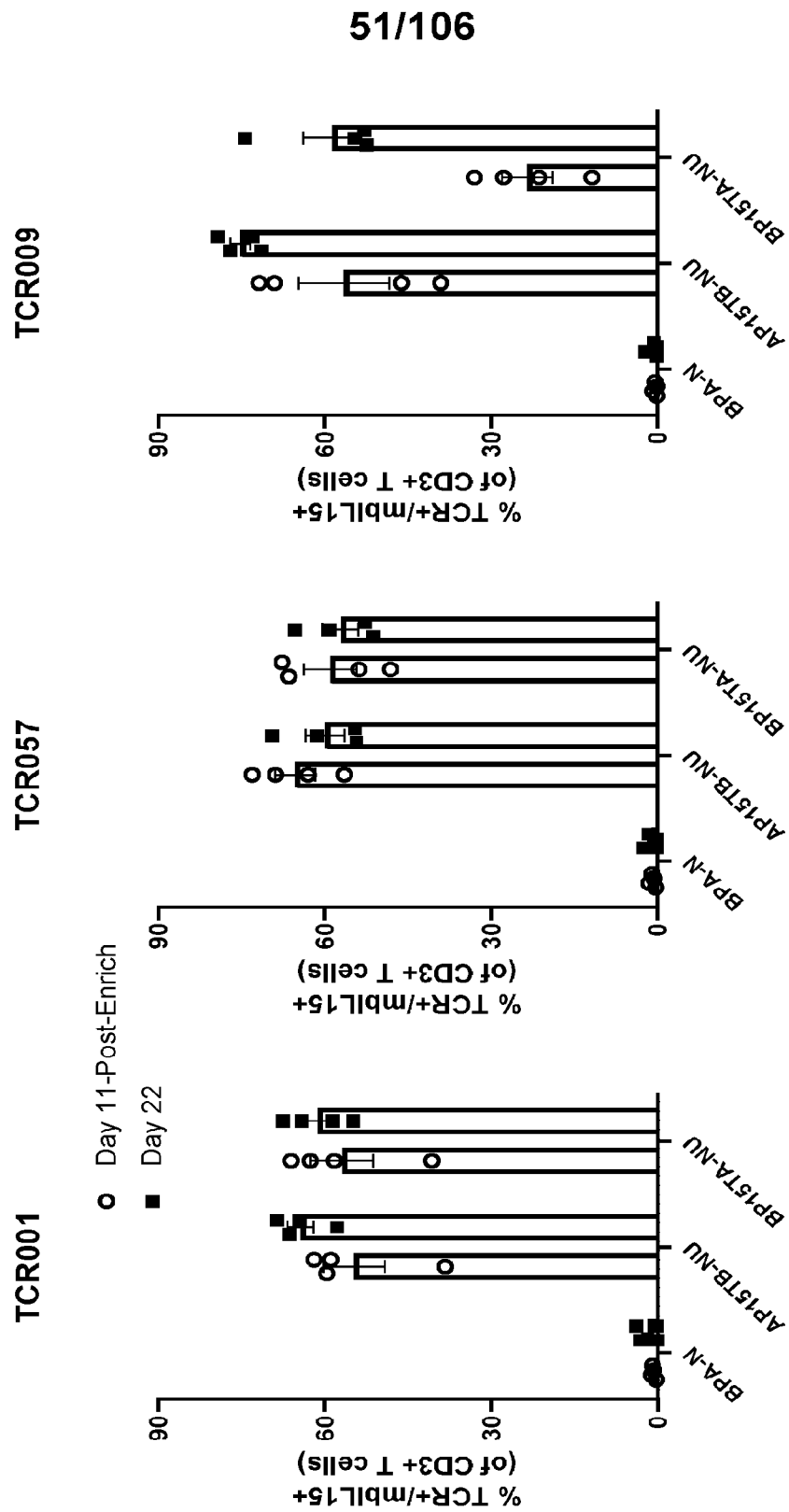


FIG. 28A

TCR+/mbIL15+ Population Changes During Second Expansion Phase

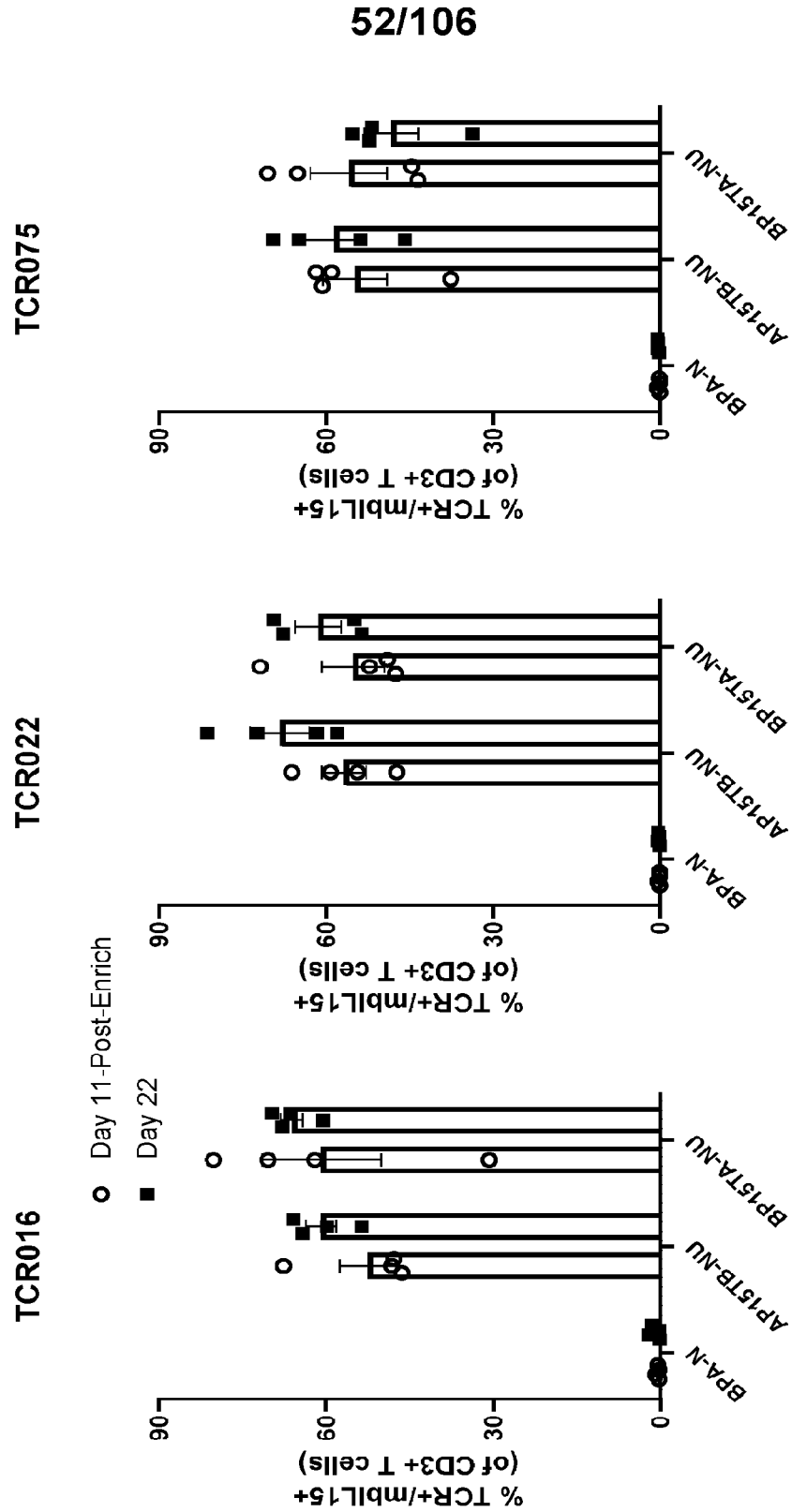


FIG. 28B

TCR+/mbIL15+ Population Changes During Second Expansion Phase

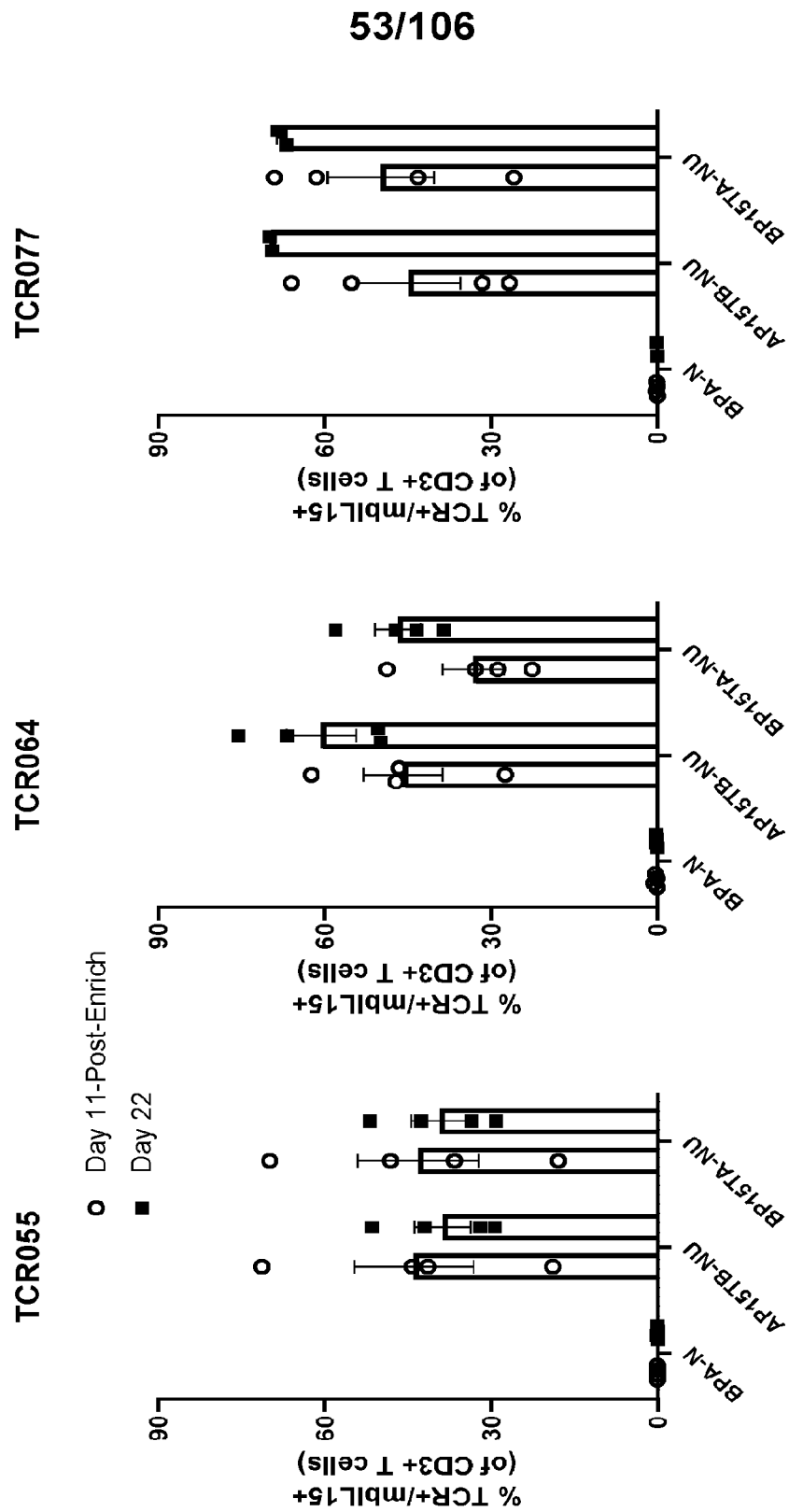


FIG. 28C

4-1BB Induction after Second Phase Expansion

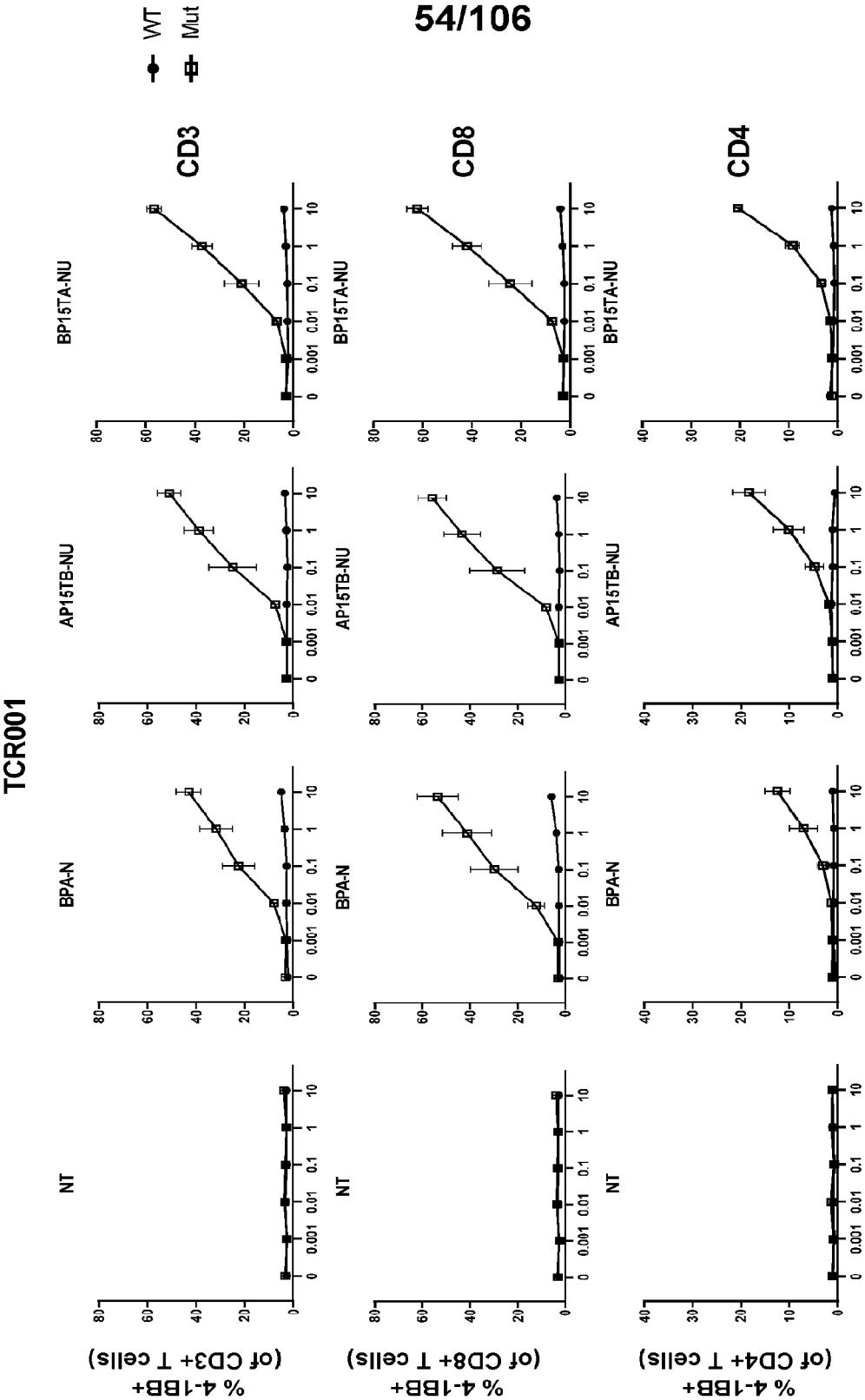


FIG. 29A

4-1BB Induction after Second Phase Expansion

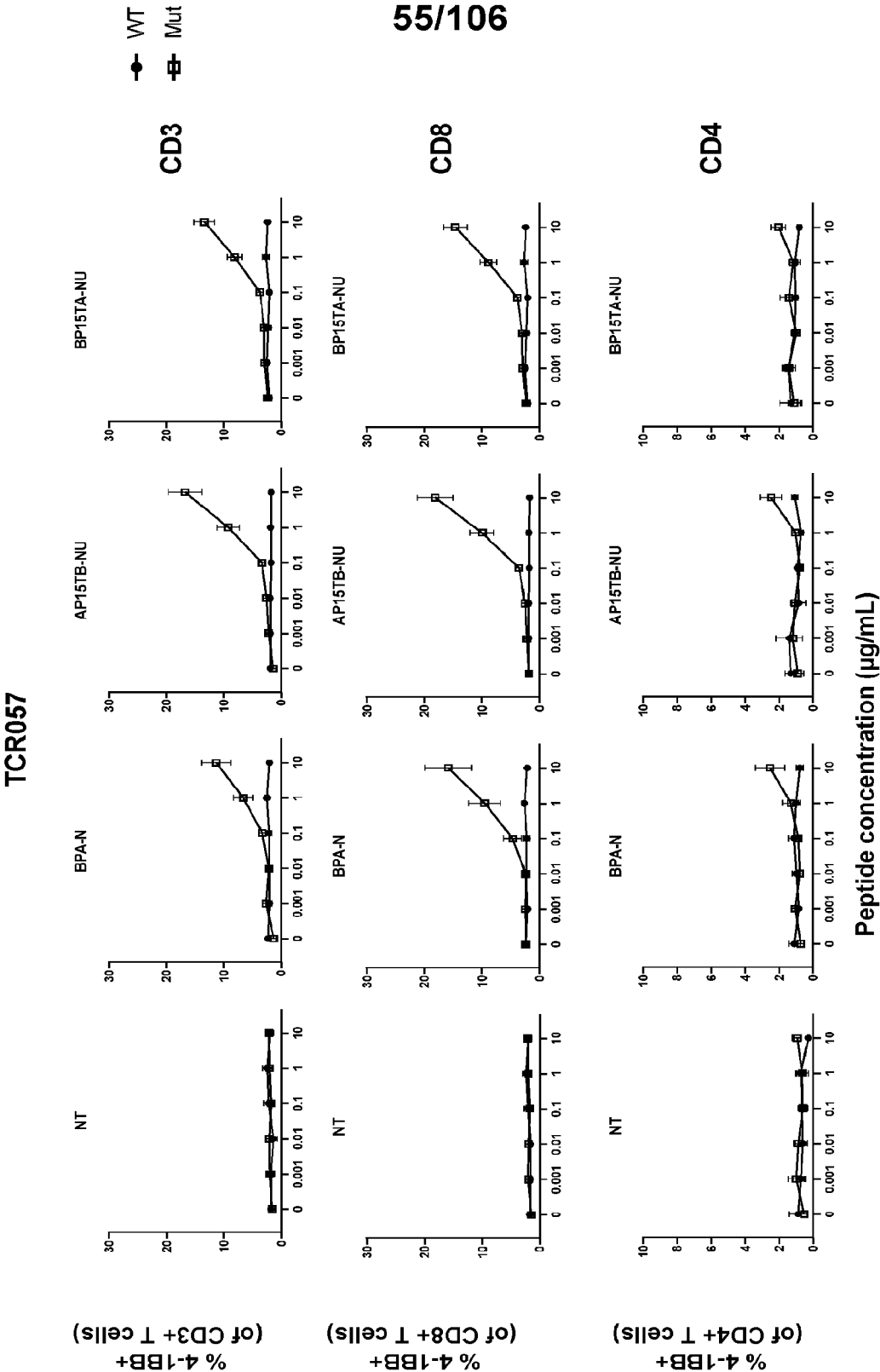


FIG. 29B

4-1BB Induction after Second Phase Expansion

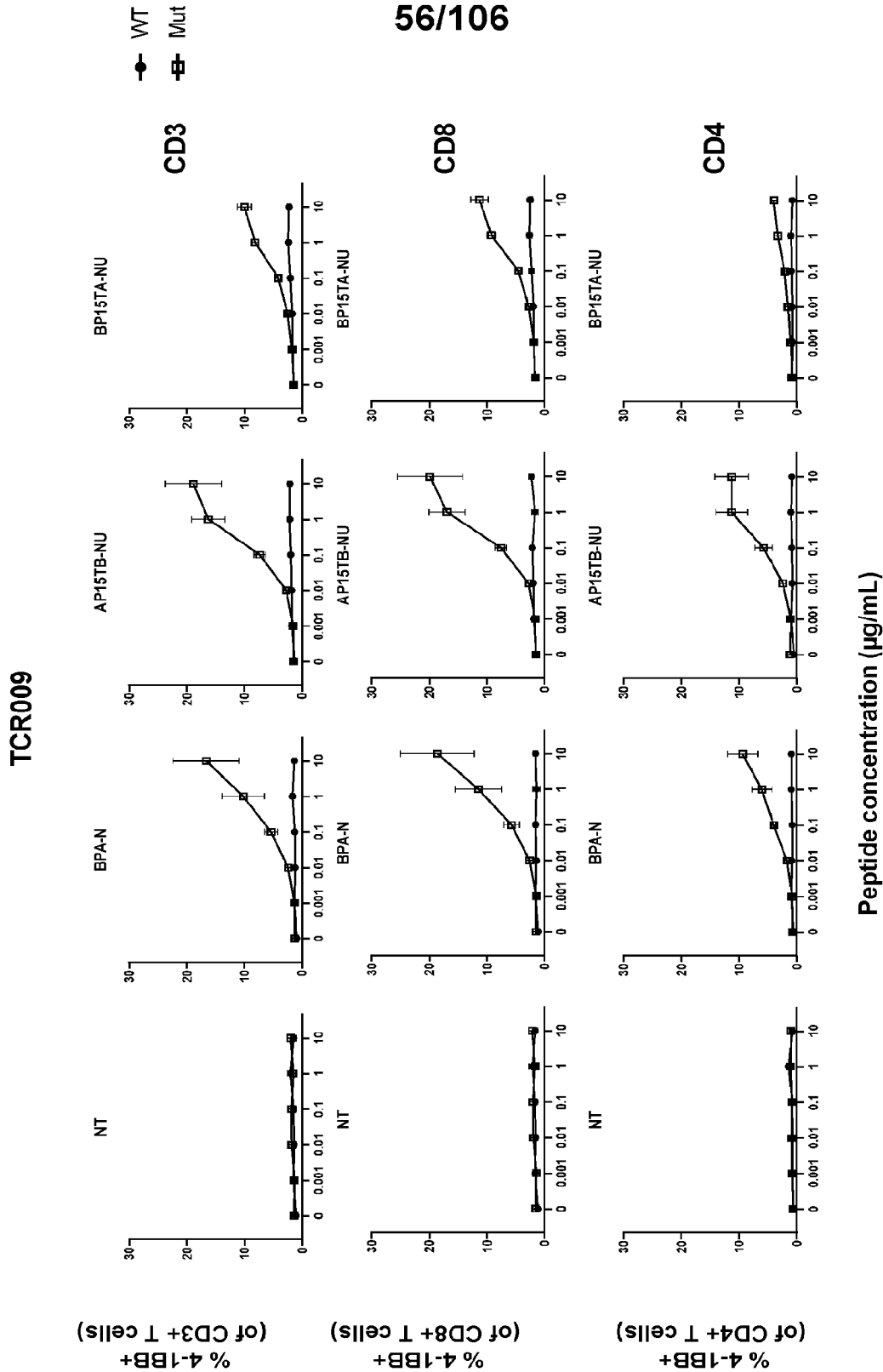


FIG. 29C

4-1BB Induction after Second Phase Expansion

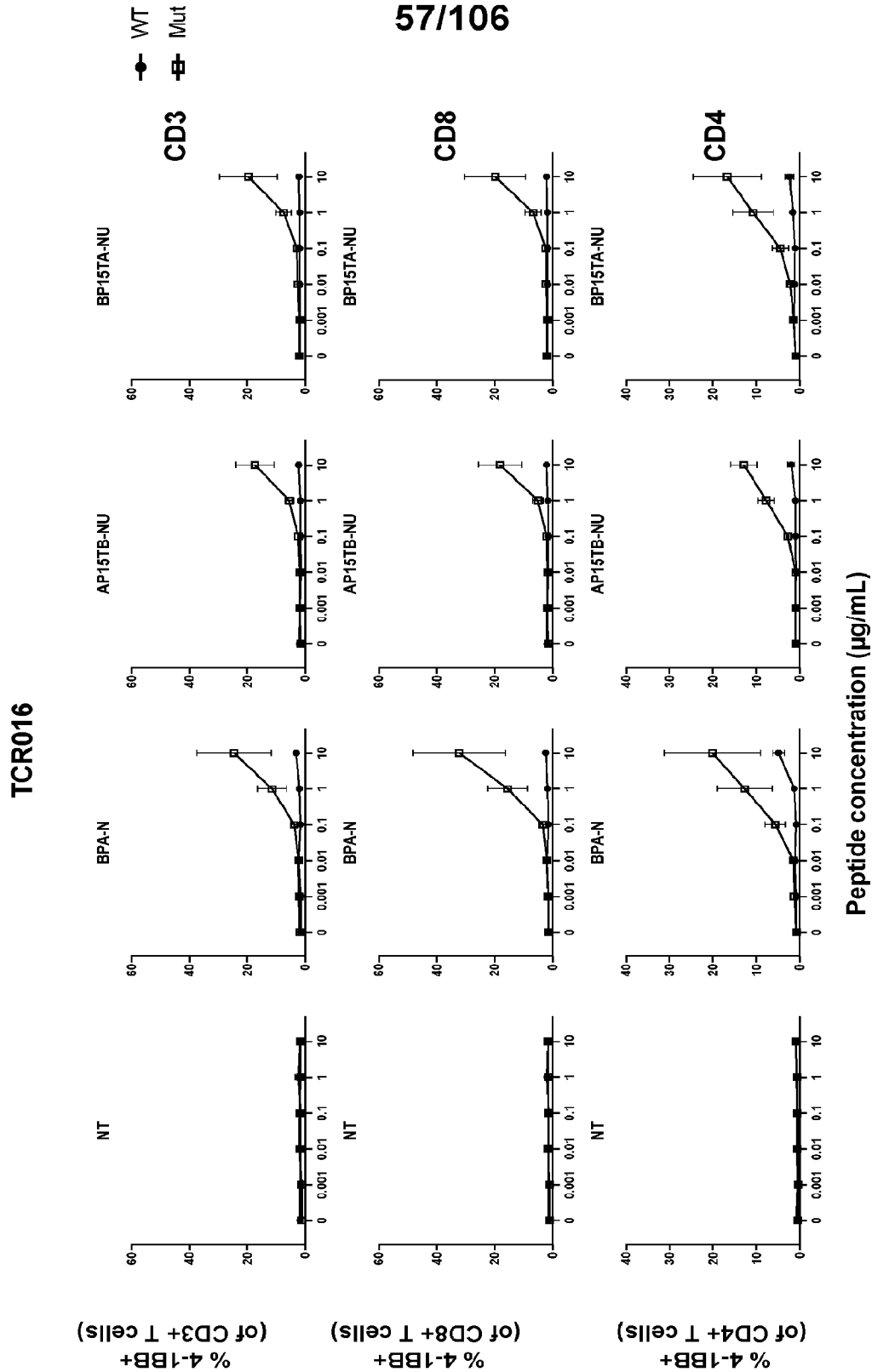


FIG. 29D

4-1BB Induction after Second Phase Expansion

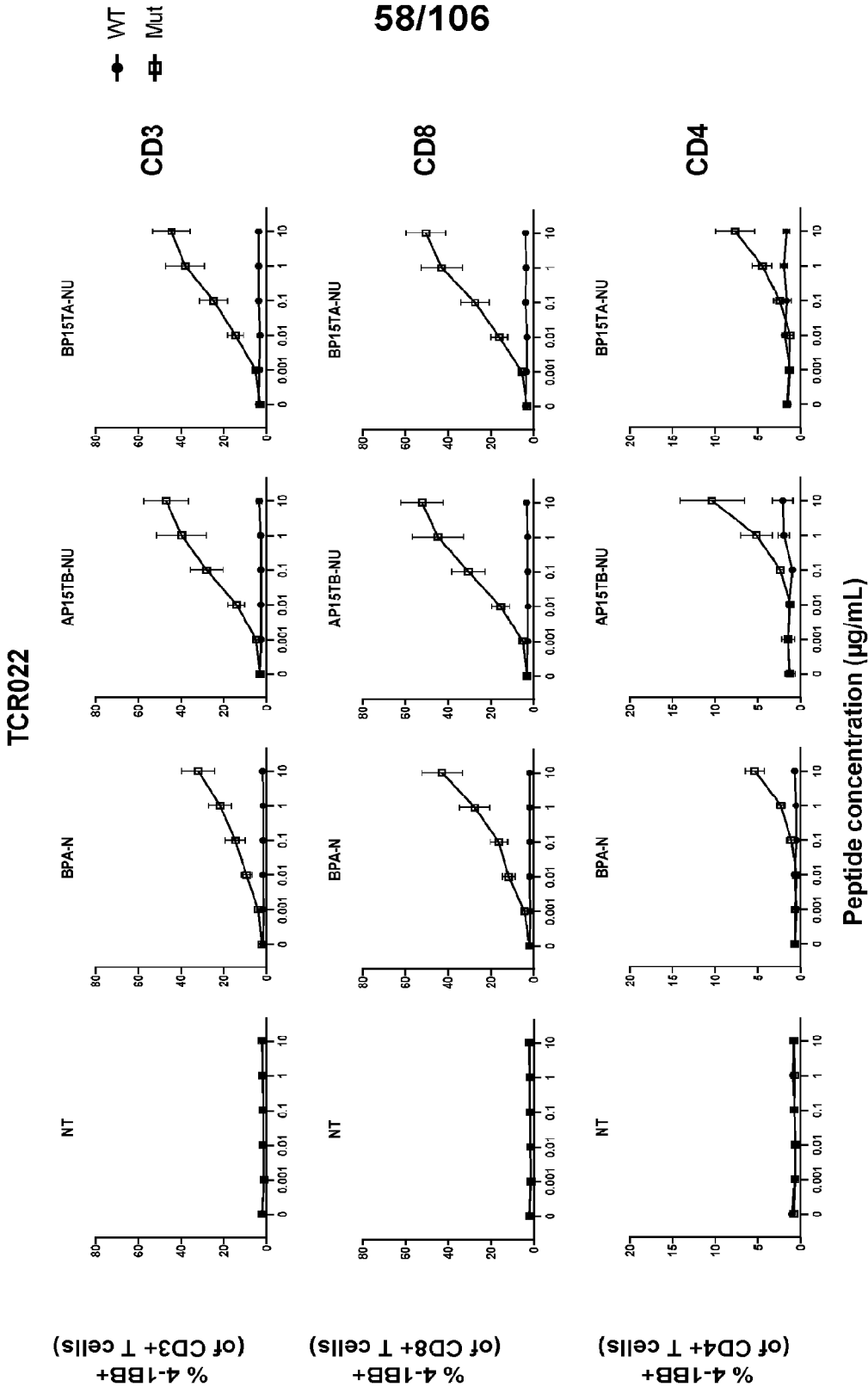


FIG. 29E

4-1BB Induction after Second Phase Expansion

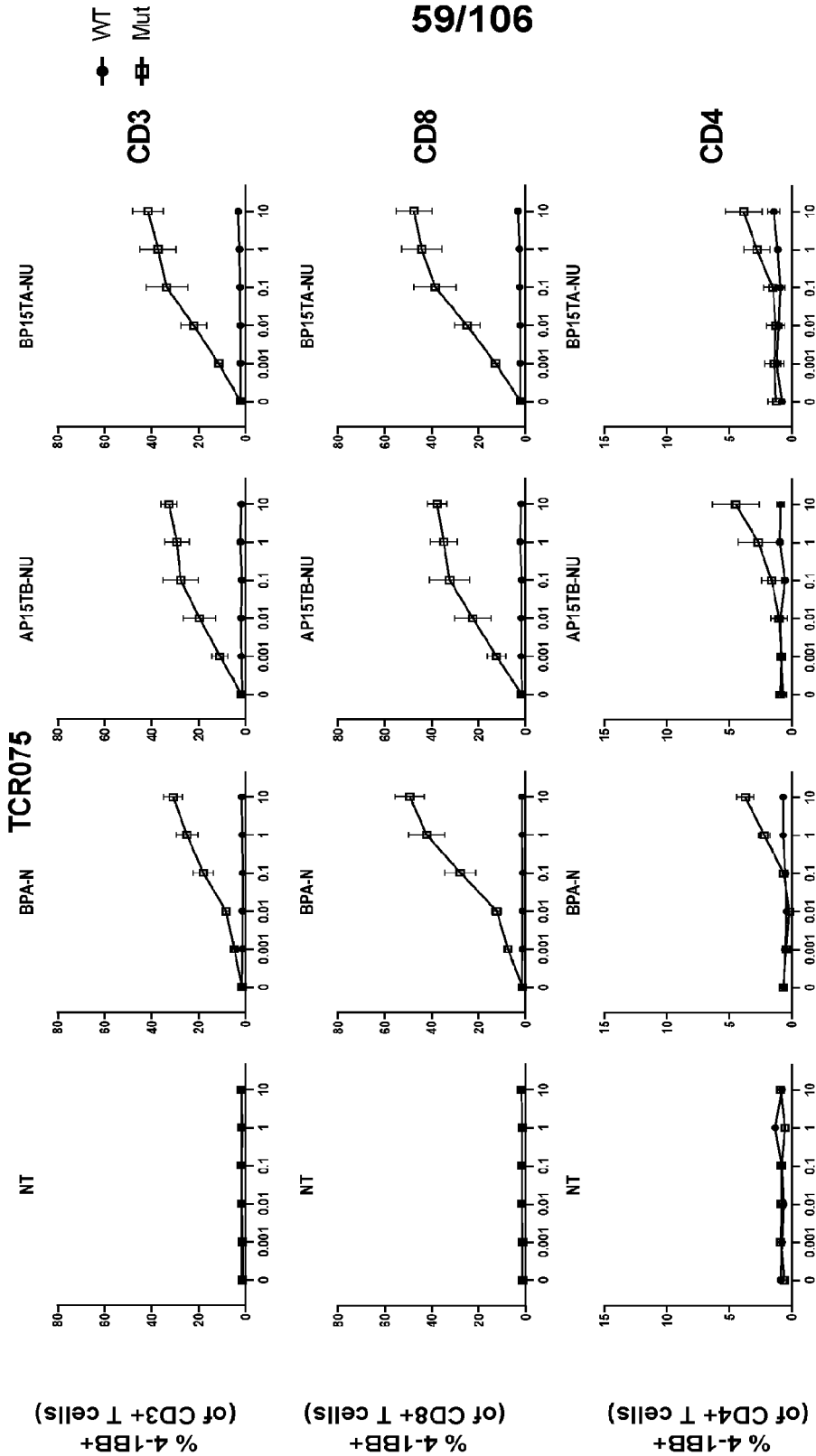


FIG. 29F

4-1BB Induction after Second Phase Expansion

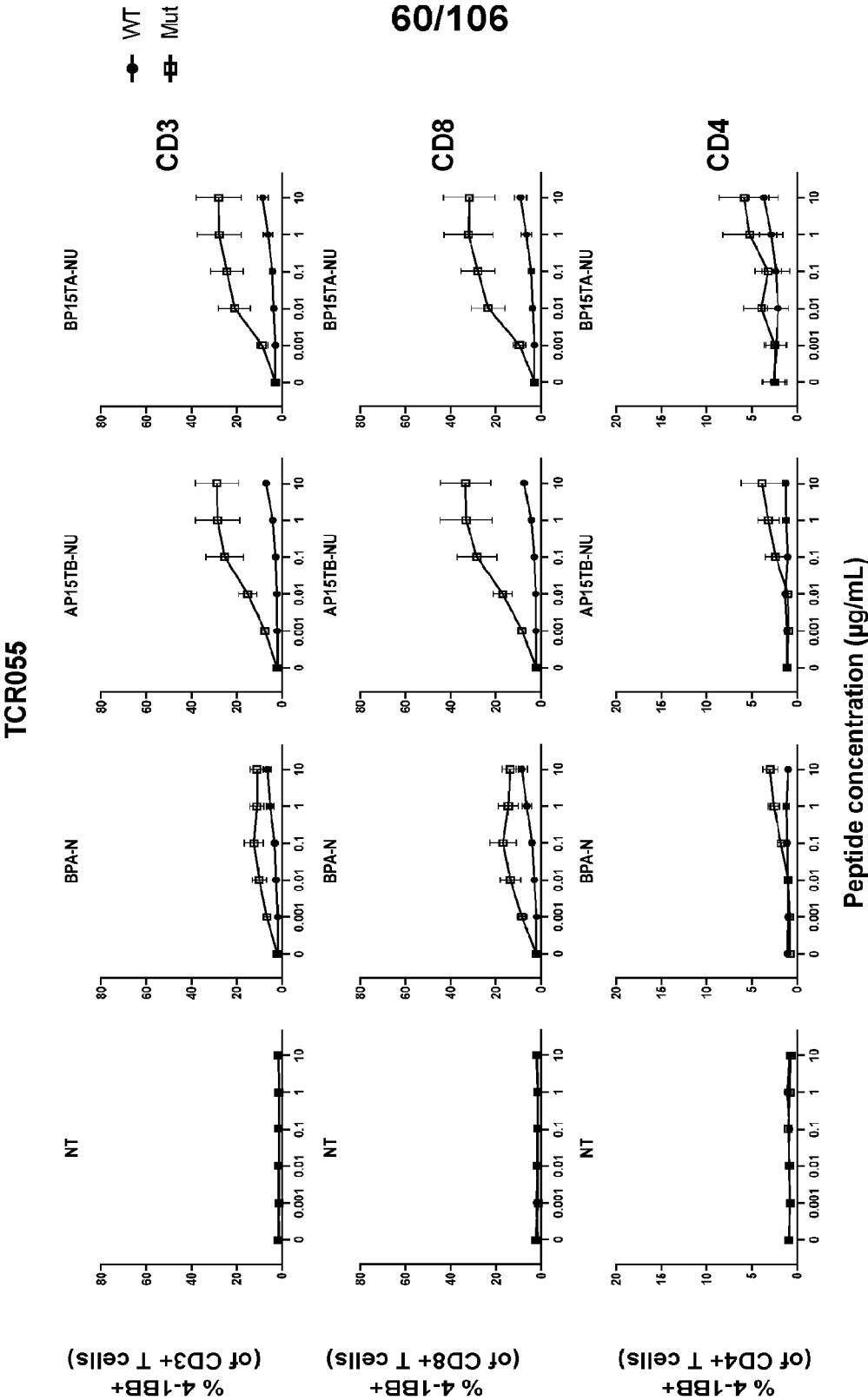


FIG. 29G

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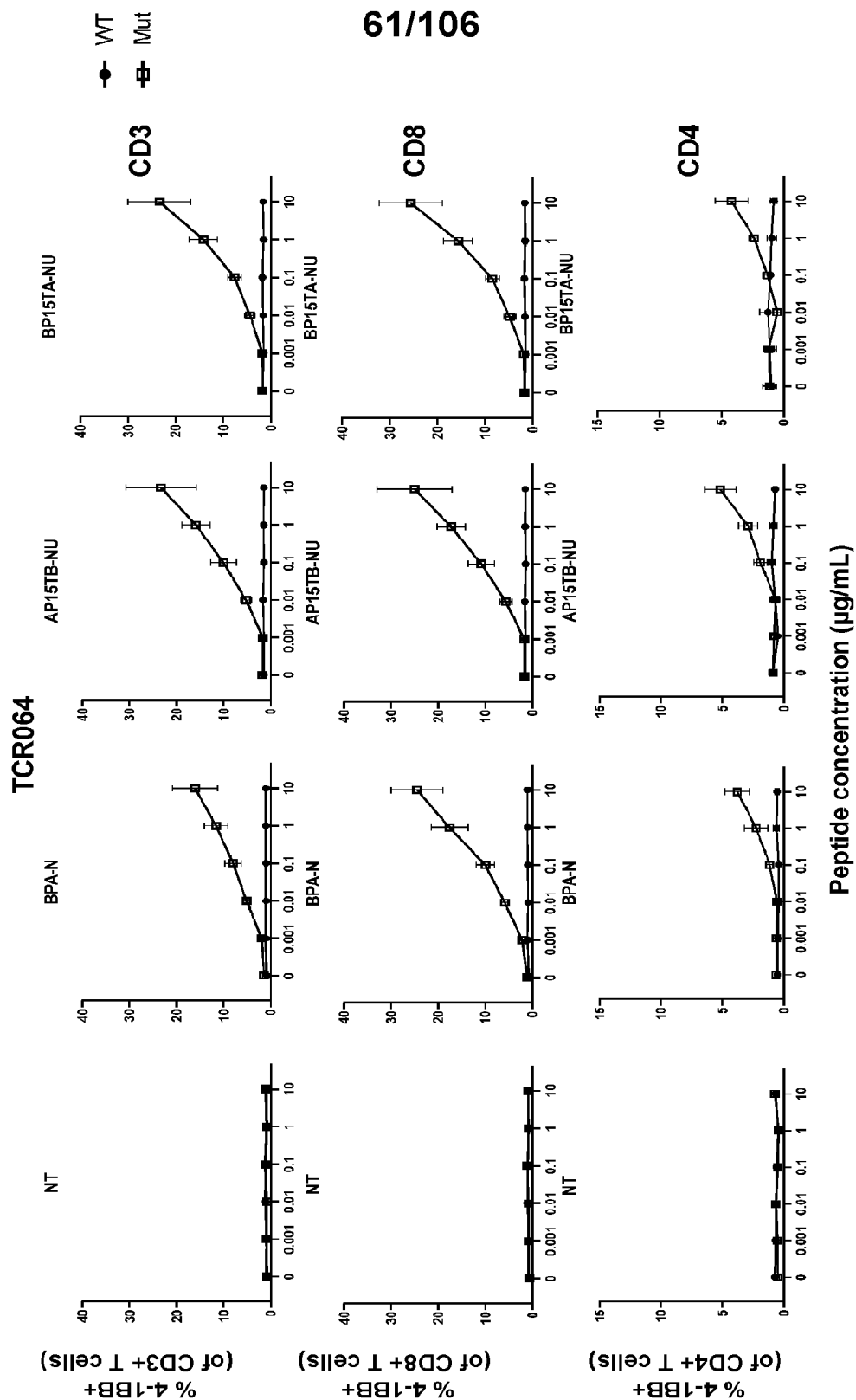


FIG. 29H

4-1BB Induction after Second Phase Expansion

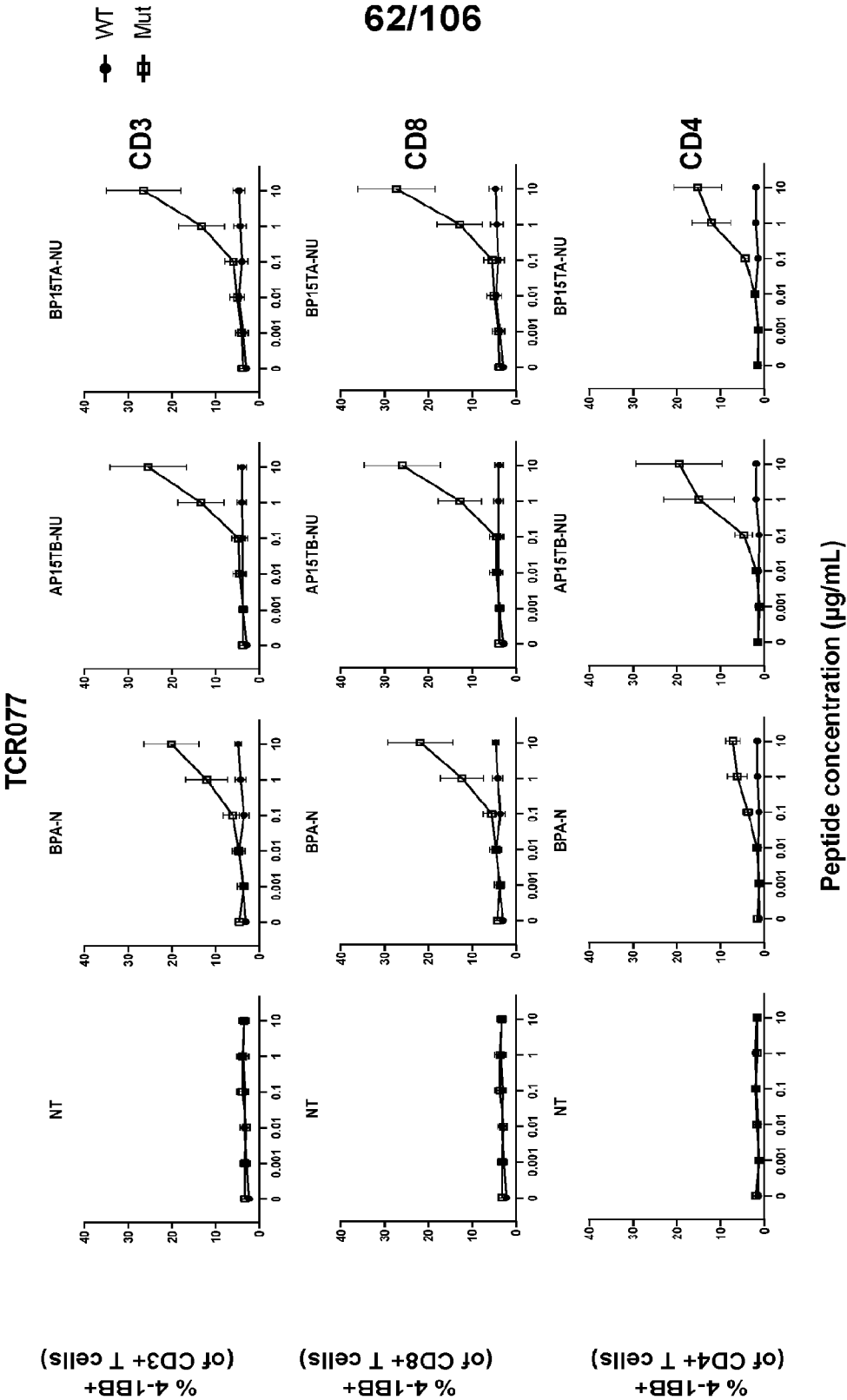


FIG. 29I

IFN-γ Secretion after Second Phase Expansion

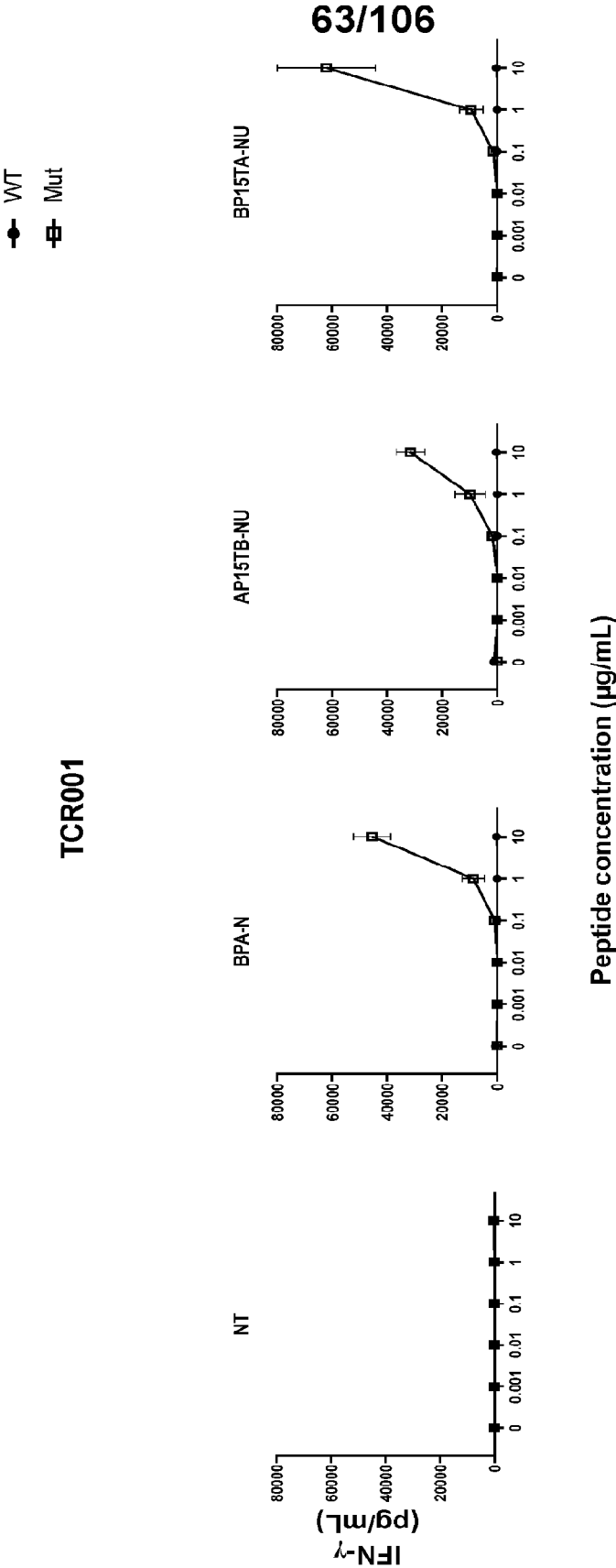


FIG. 30A

IFN-γ Secretion after Second Phase Expansion

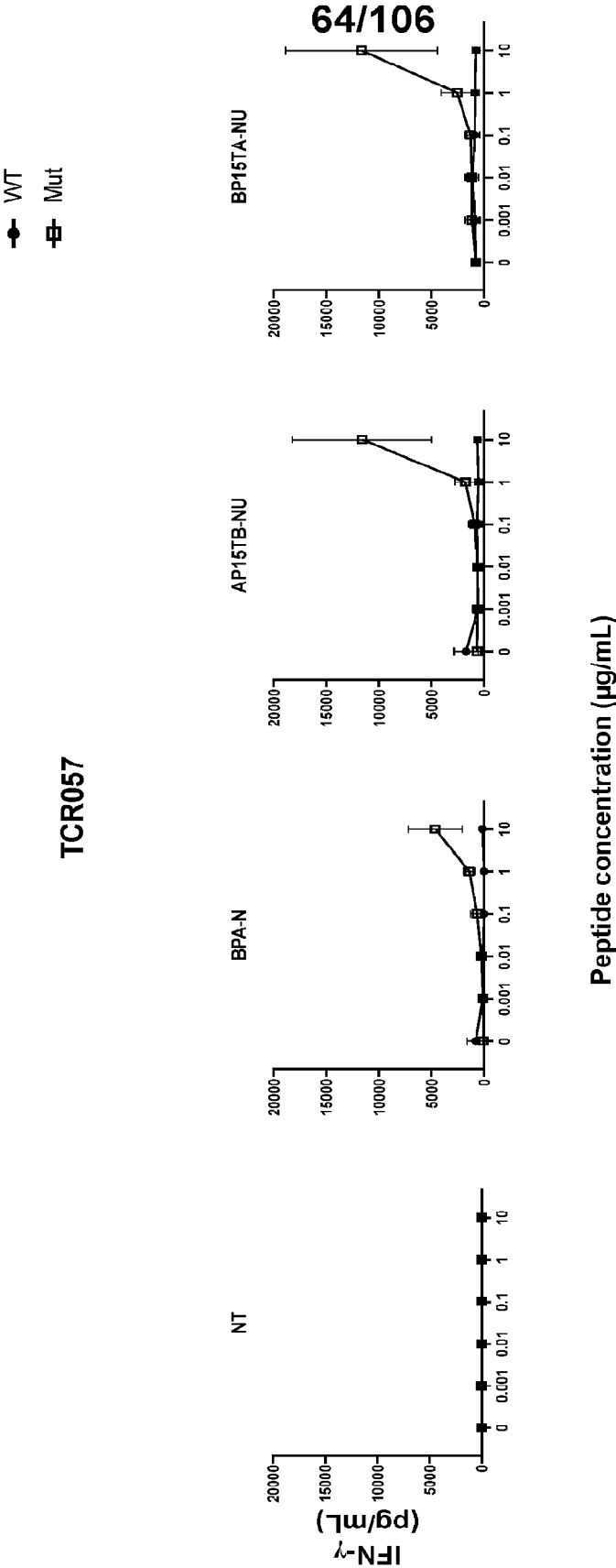


FIG. 30B

IFN-γ Secretion after Second Phase Expansion

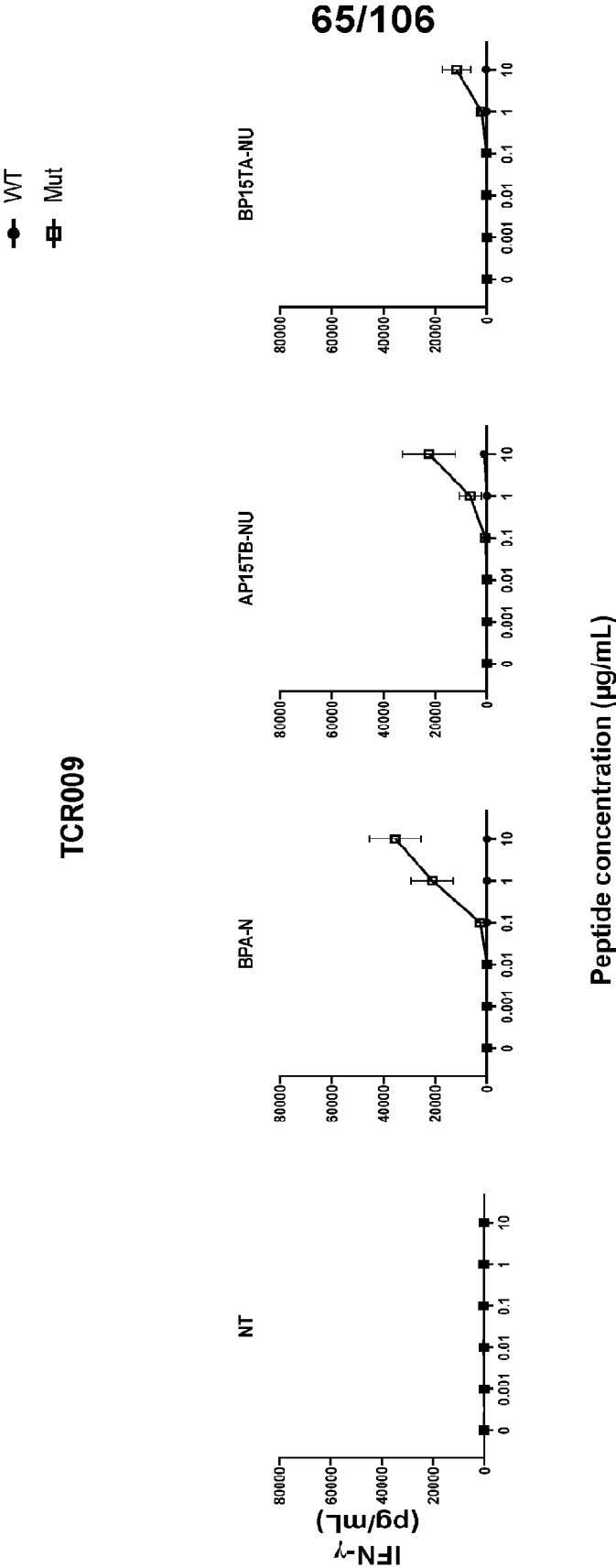


FIG. 30C

IFN-γ Secretion after Second Phase Expansion

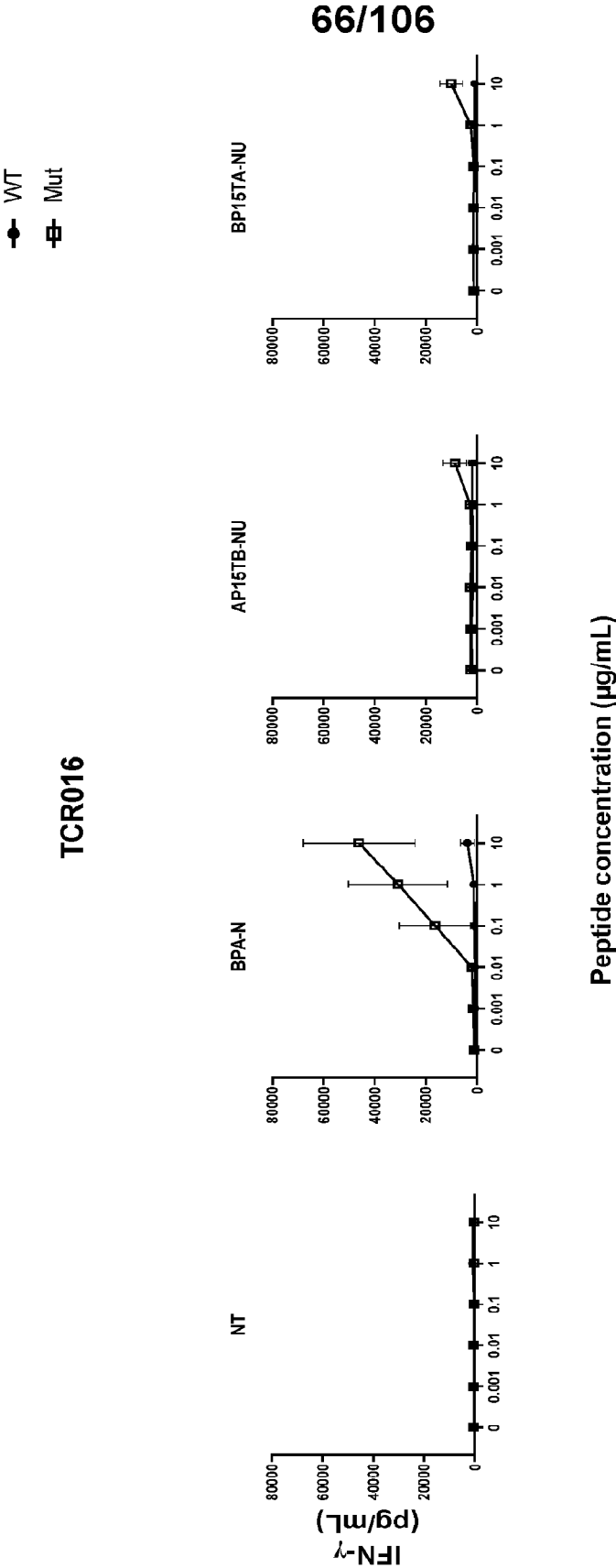


FIG. 30D

IFN- γ Secretion after Second Phase Expansion

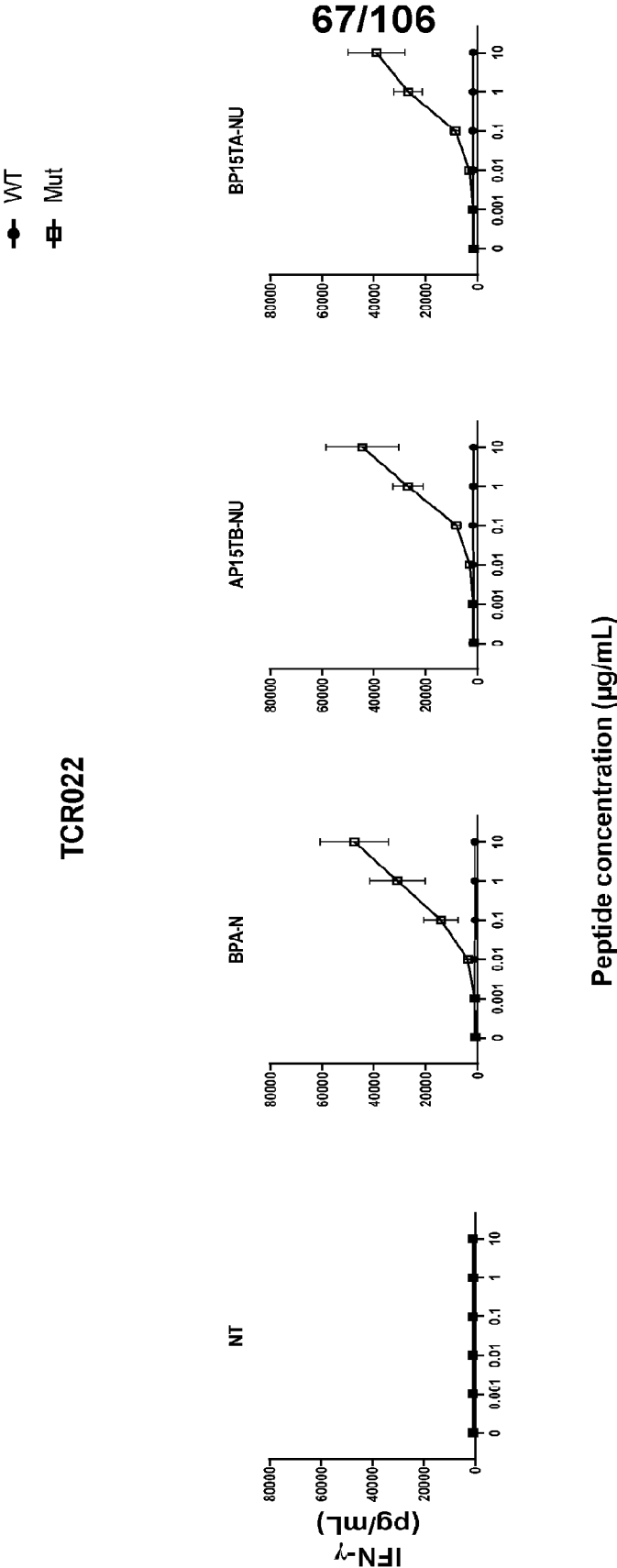


FIG. 30E

IFN- γ Secretion after Second Phase Expansion

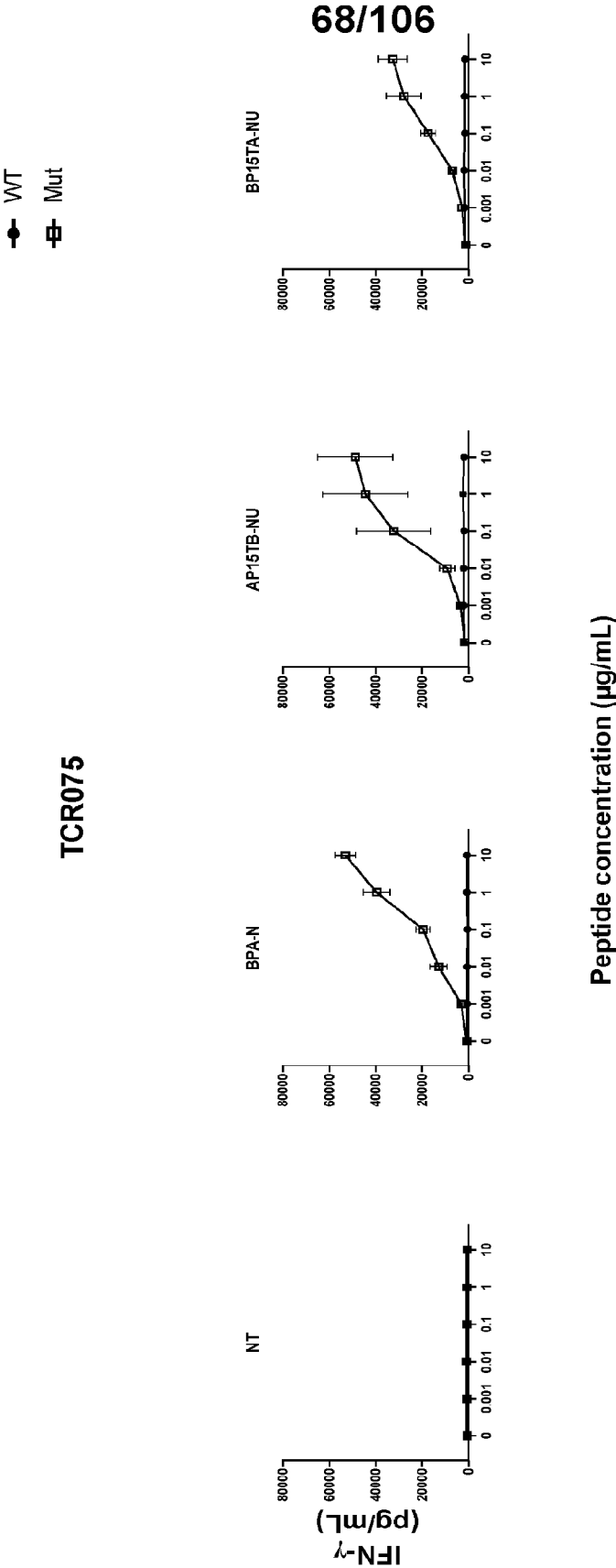


FIG. 30F

IFN- γ Secretion after Second Phase Expansion

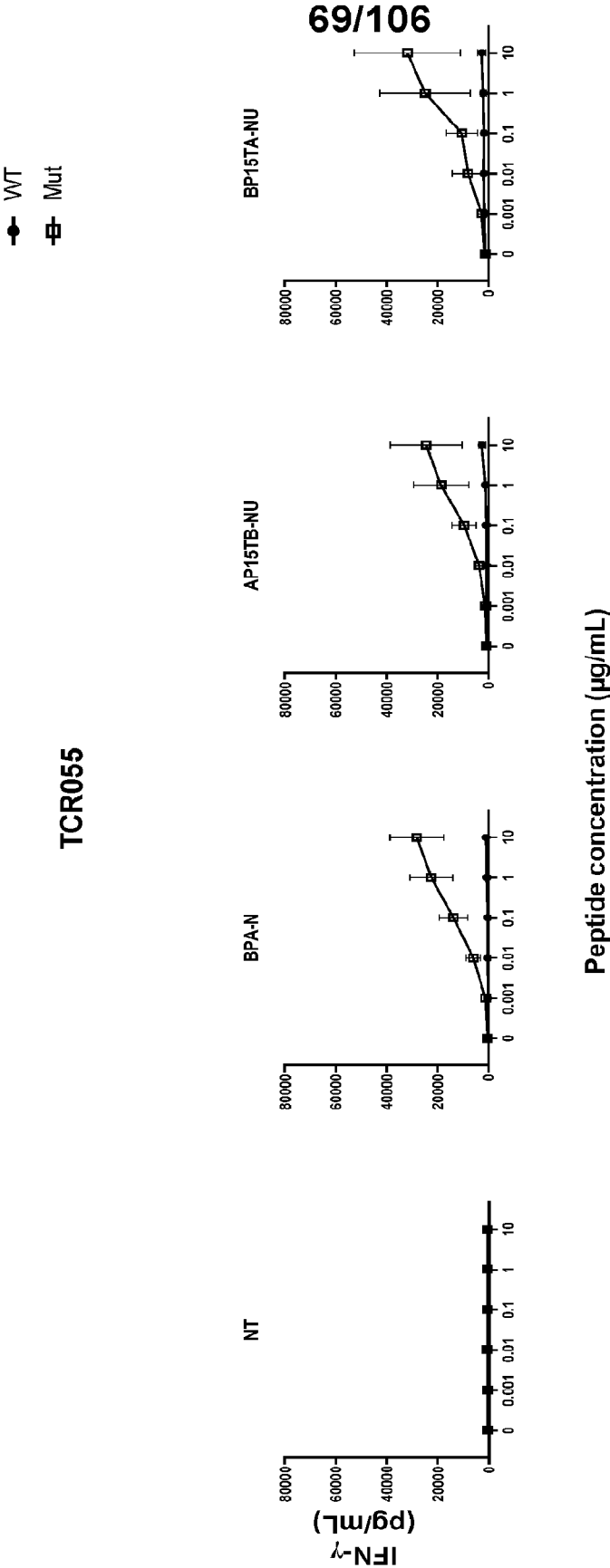


FIG. 30G

IFN- γ Secretion after Second Phase Expansion

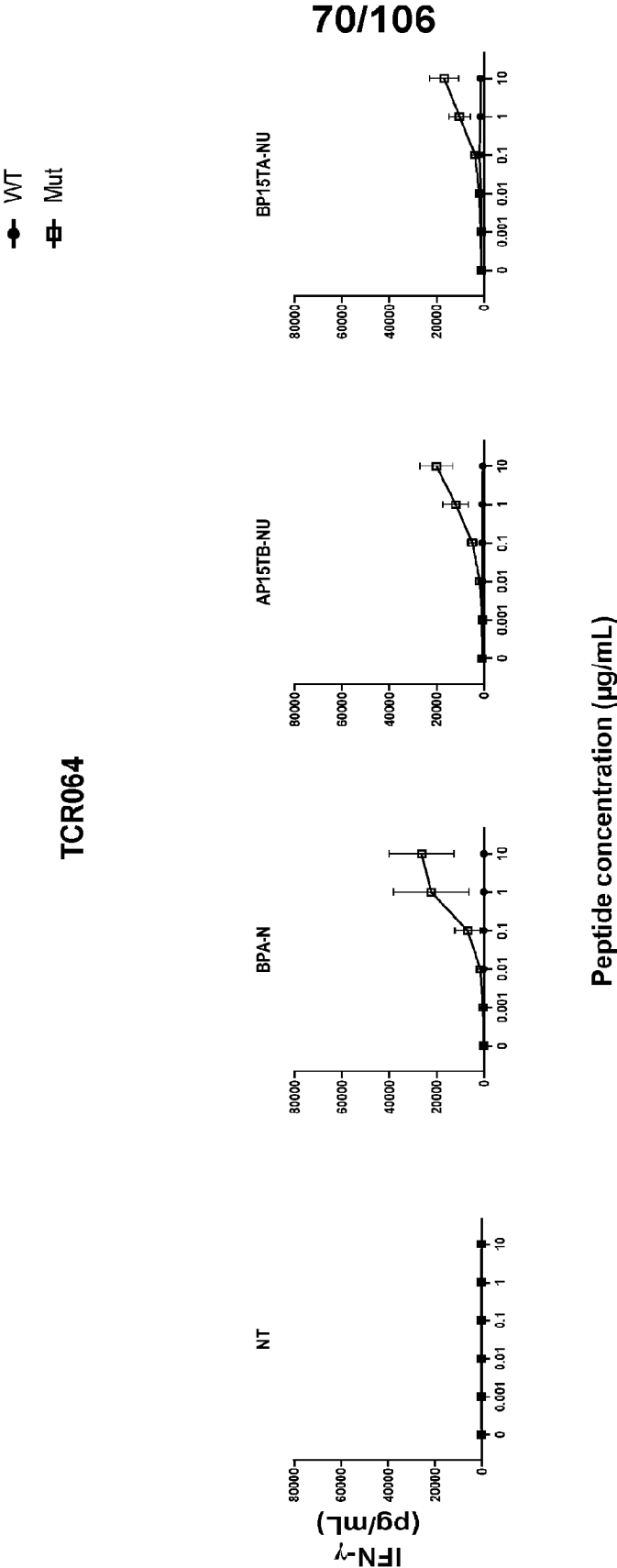


FIG. 30H

IFN-γ Secretion after Second Phase Expansion

WT
Mut

TCR077

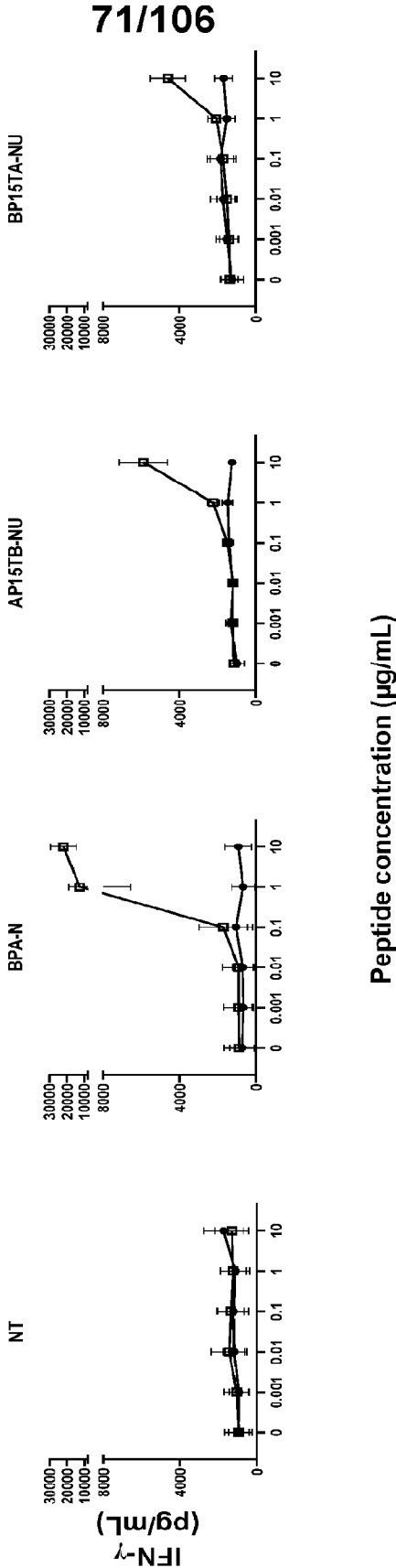


FIG. 30I

Cytolytic Activity of TCR001 TCR-T cells

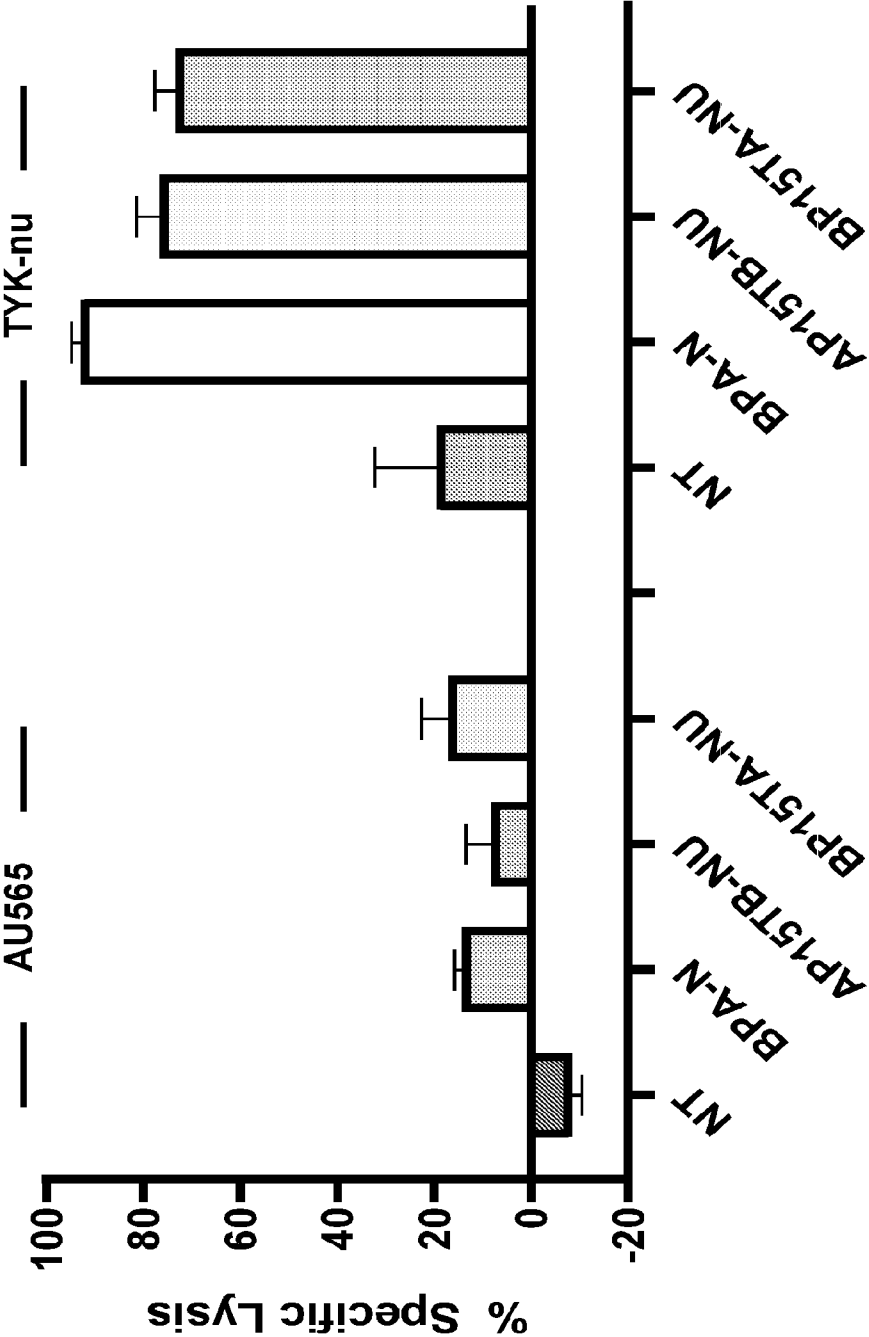


FIG. 31

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Cytolytic Activity of TCR022 TCR-T cells

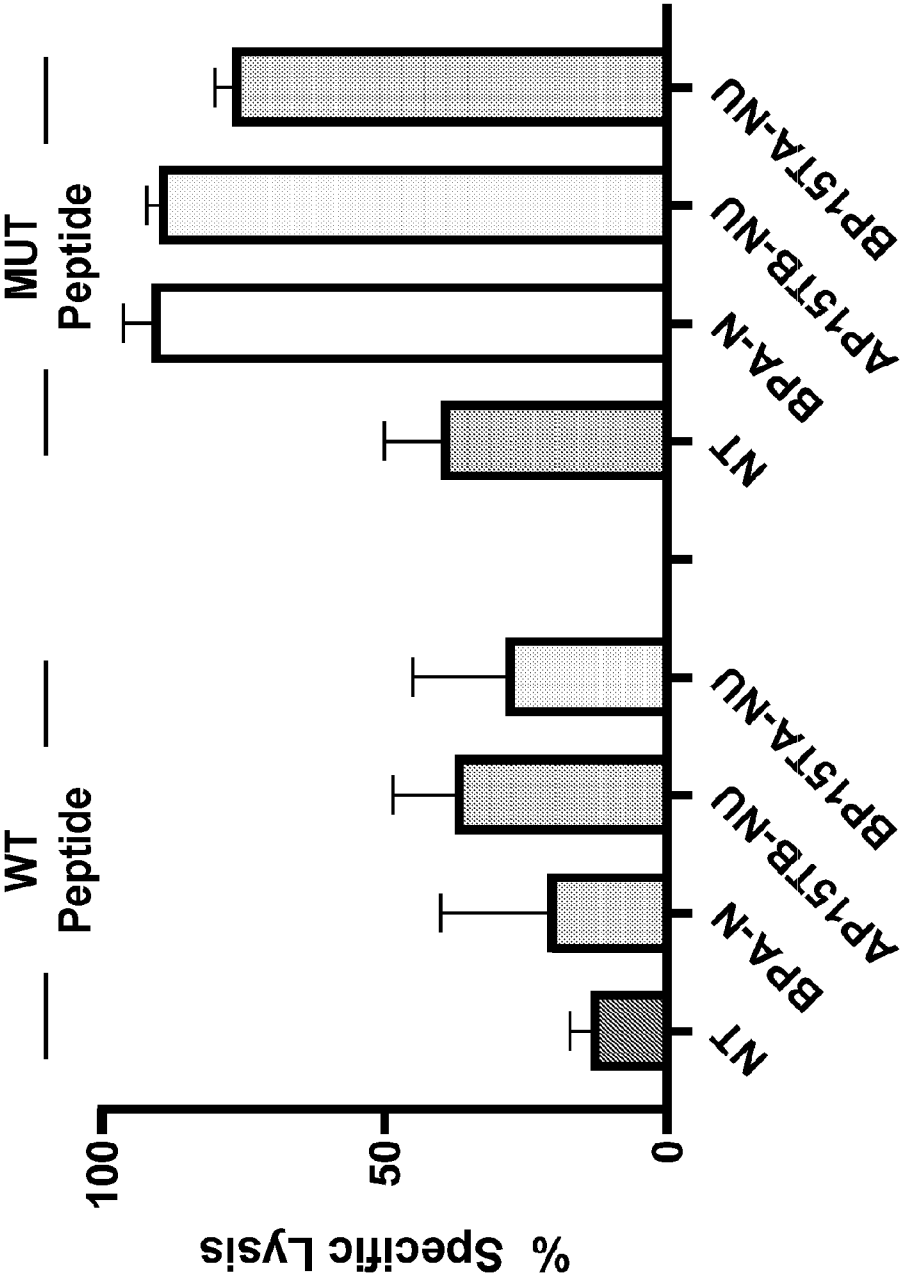


FIG. 32A

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Cytolytic Activity of TCR075 TCR-T cells

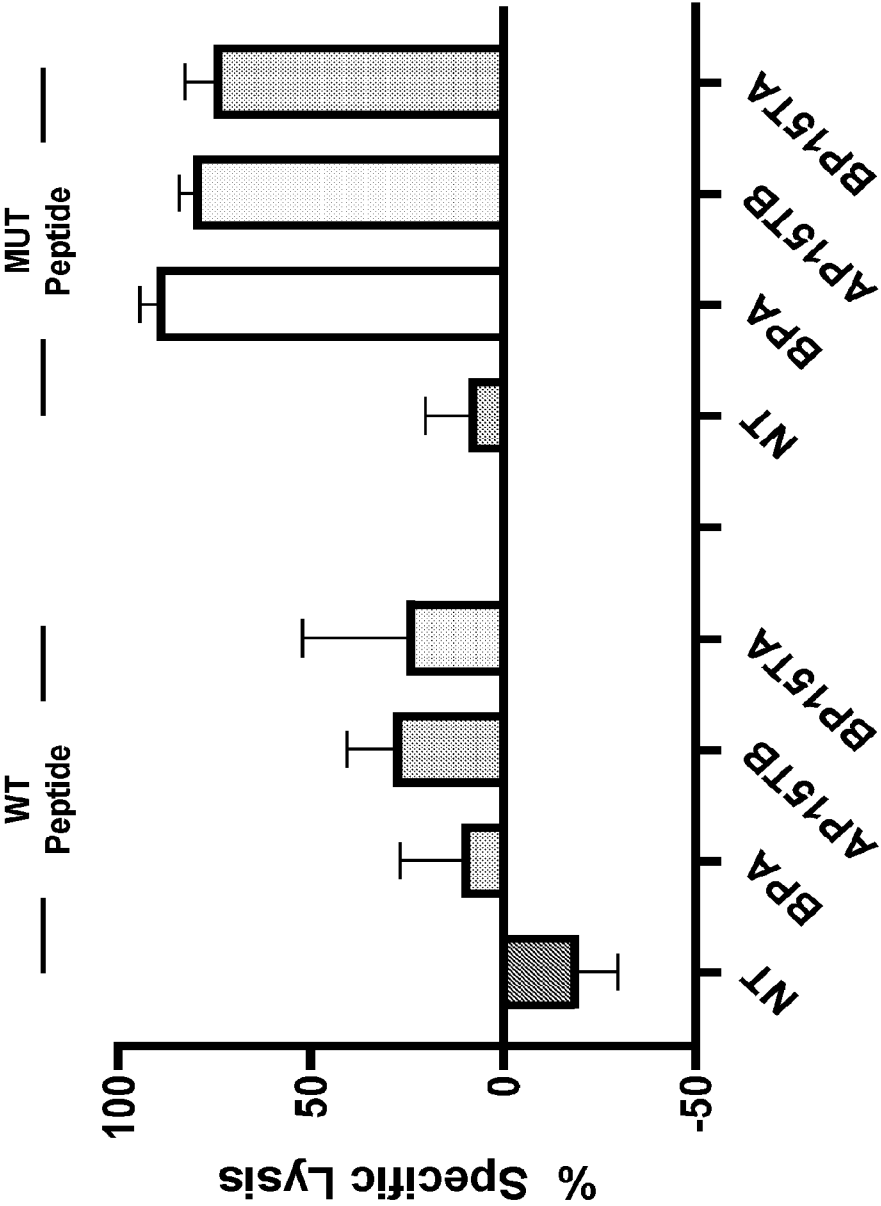


FIG. 32B

TCR+ population after LTWD culture

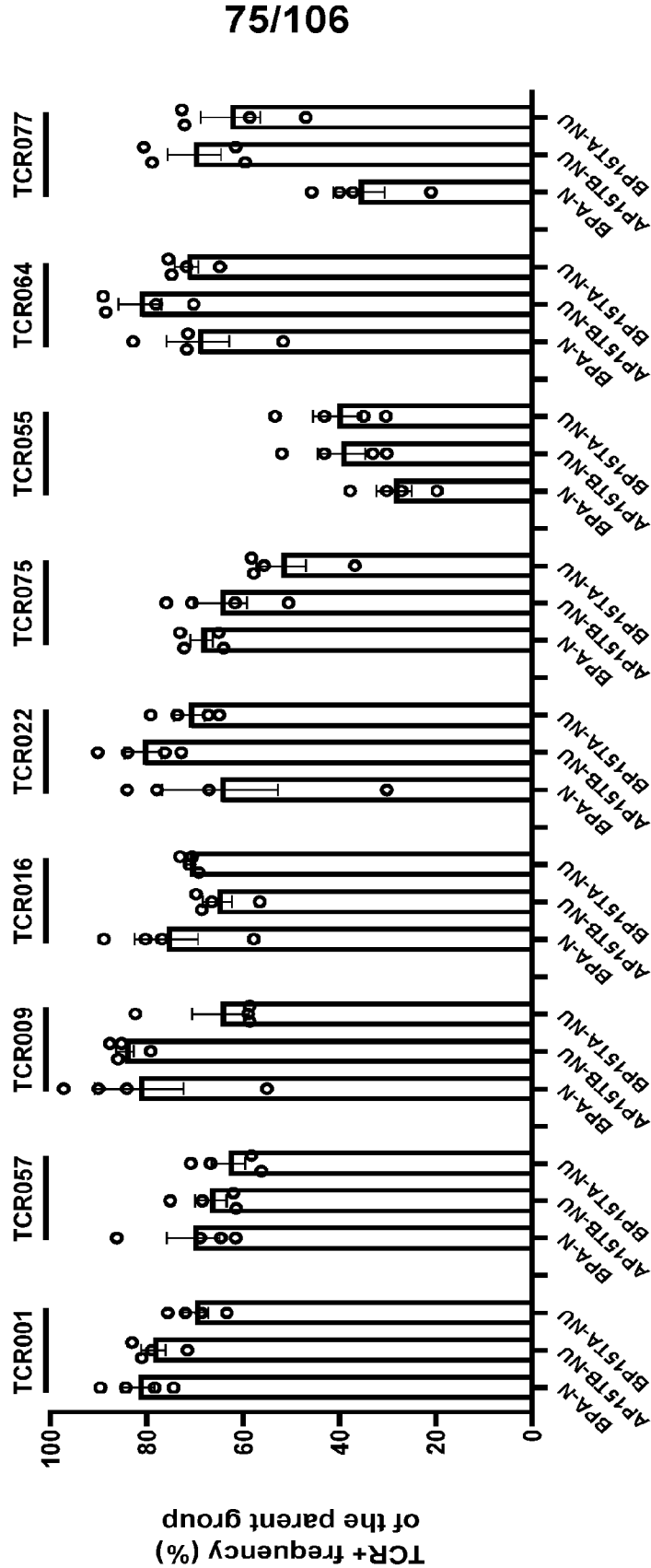


FIG. 33

Cell Survival after LTWD culture

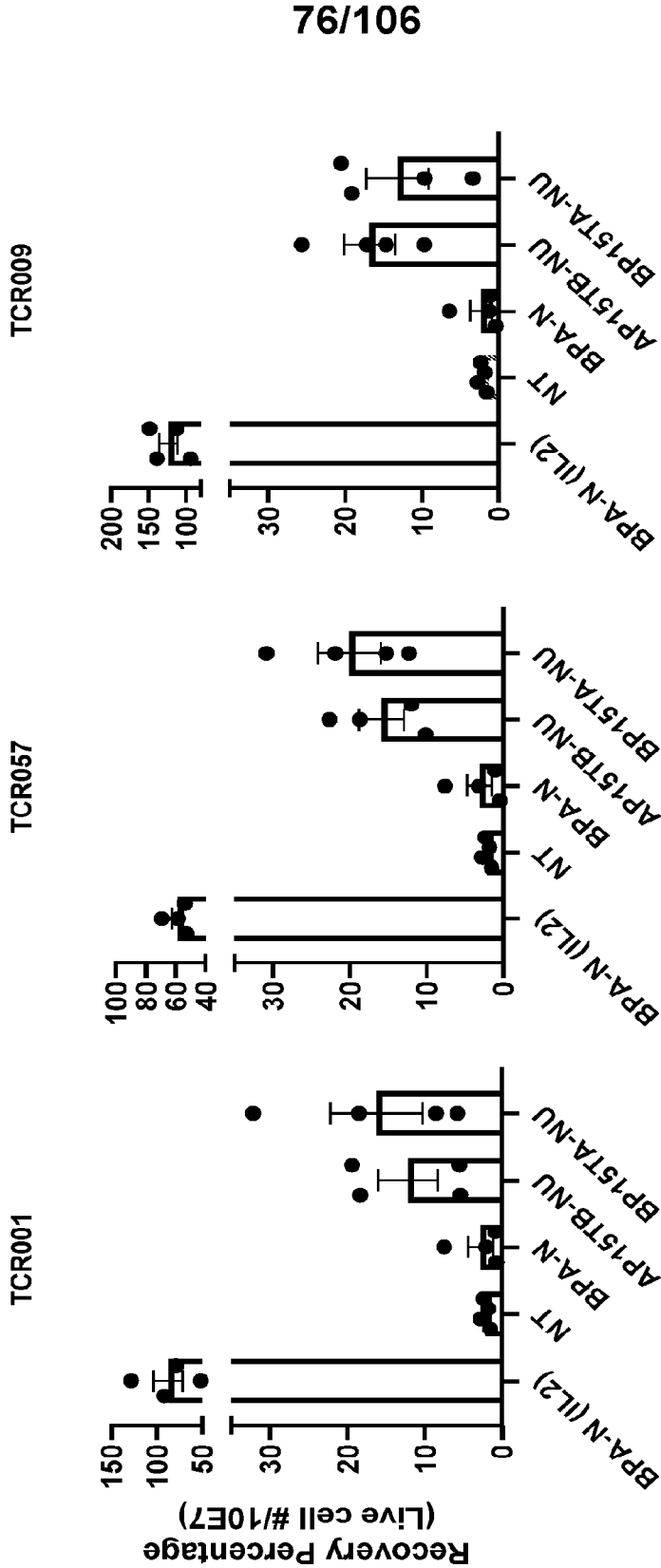


FIG. 34A

Cell Survival after LTWD culture

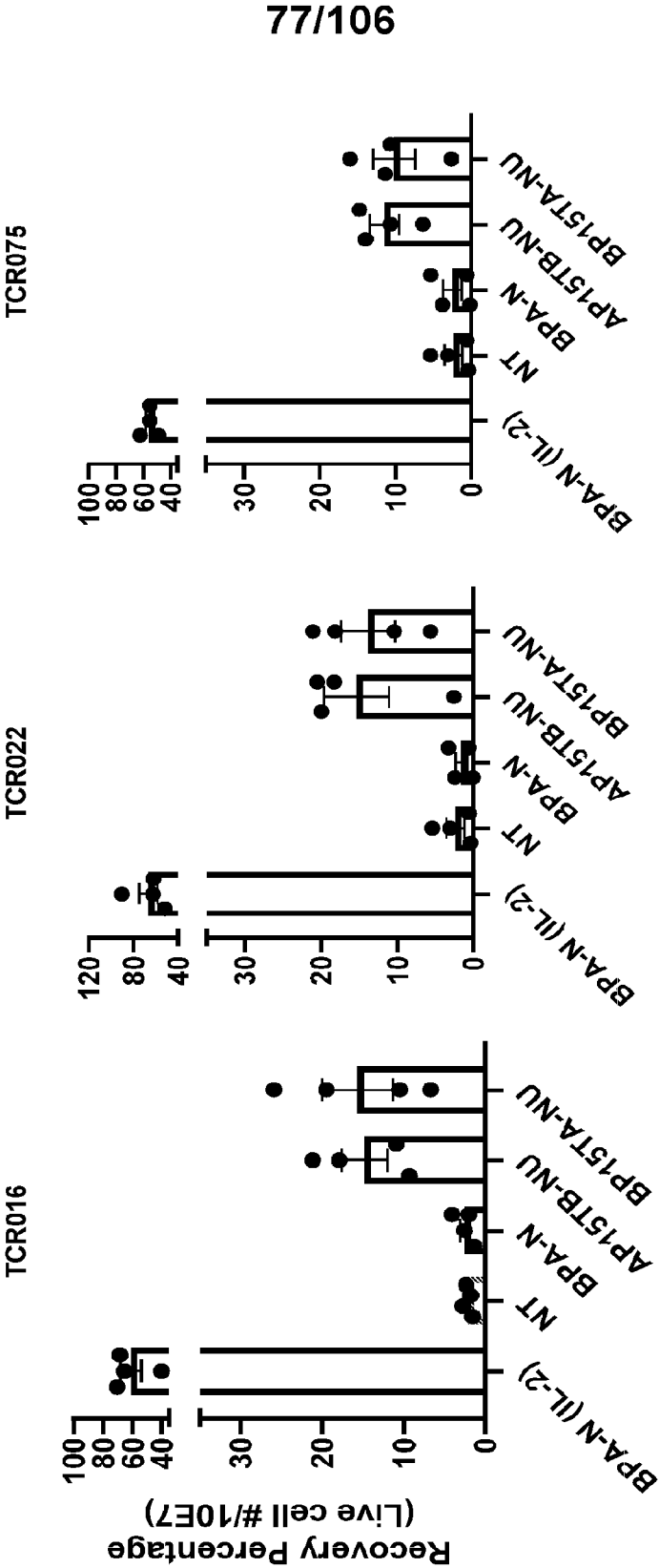


FIG. 34B

Cell Survival after LTWD culture

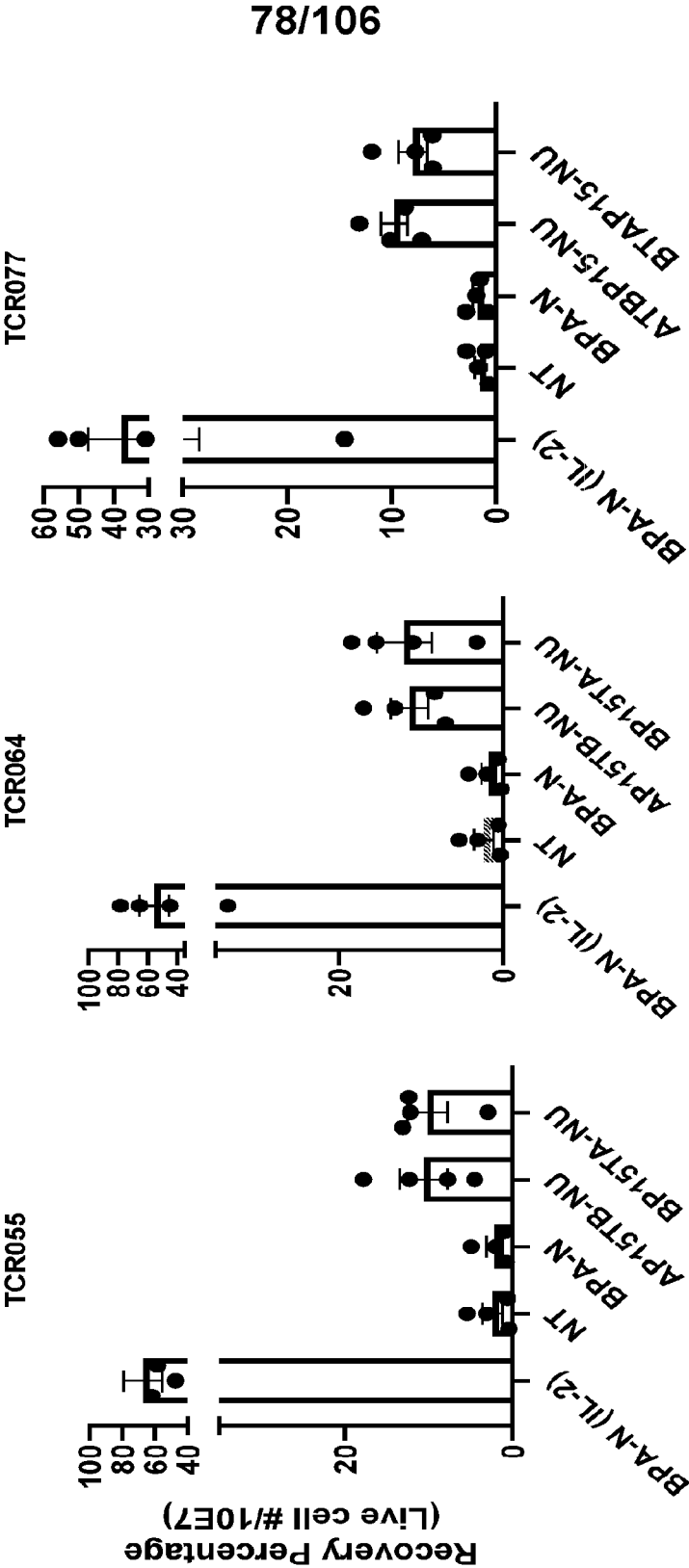


FIG. 34C

4-1BB Induction after LTWD culture

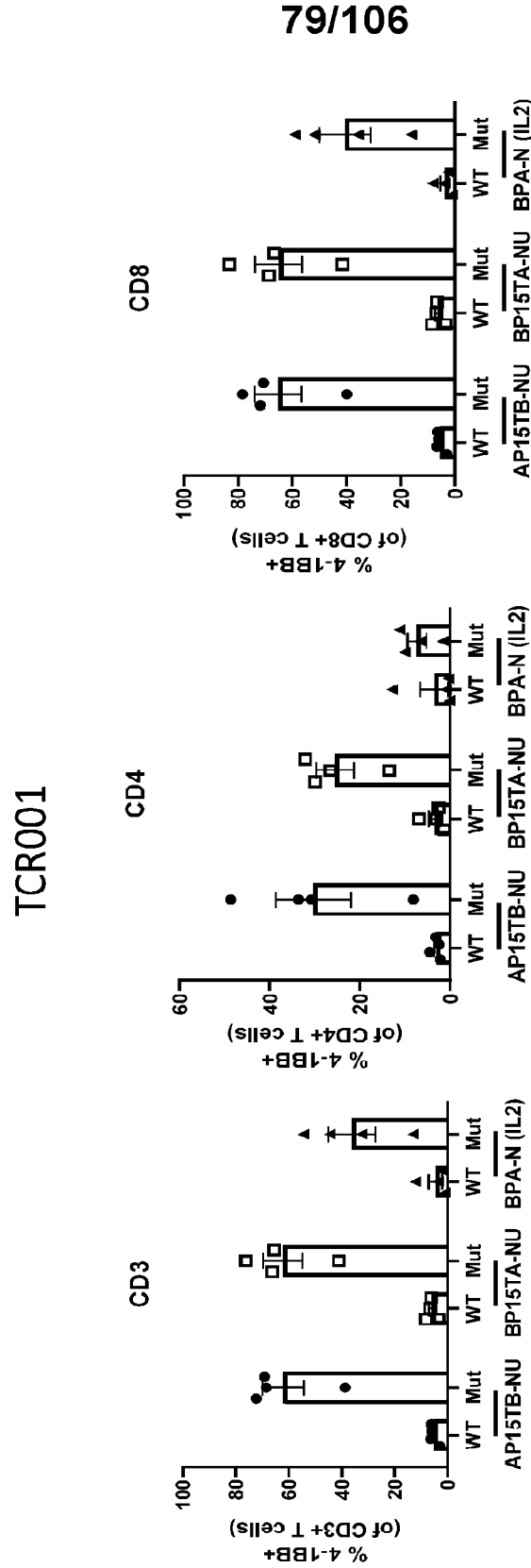


FIG. 35A

4-1BB Induction after LTWD culture

TCR057

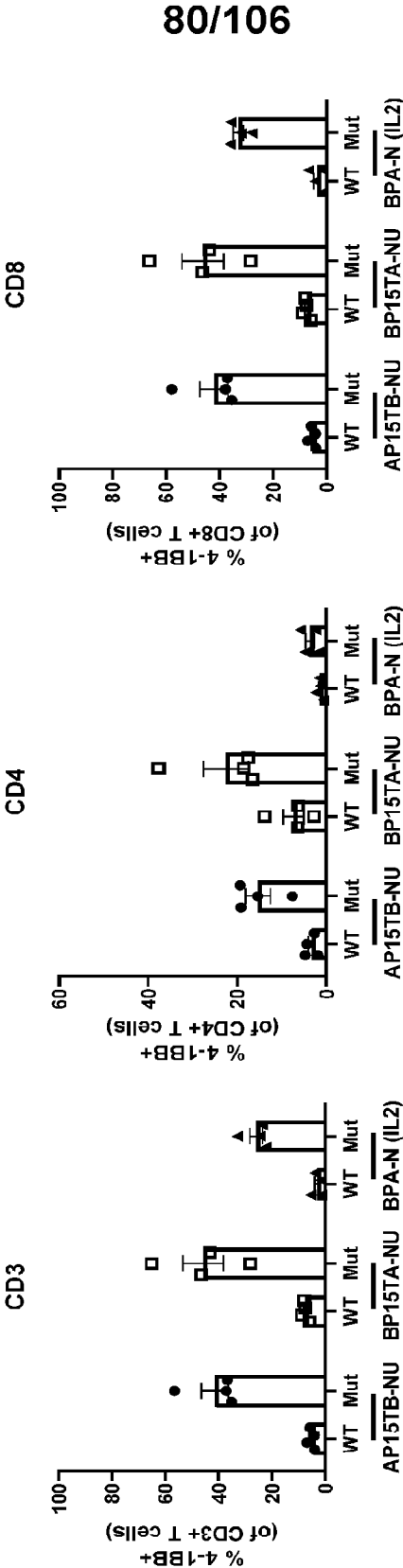


FIG. 35B

4-1BB Induction after LTWD culture

TCR009

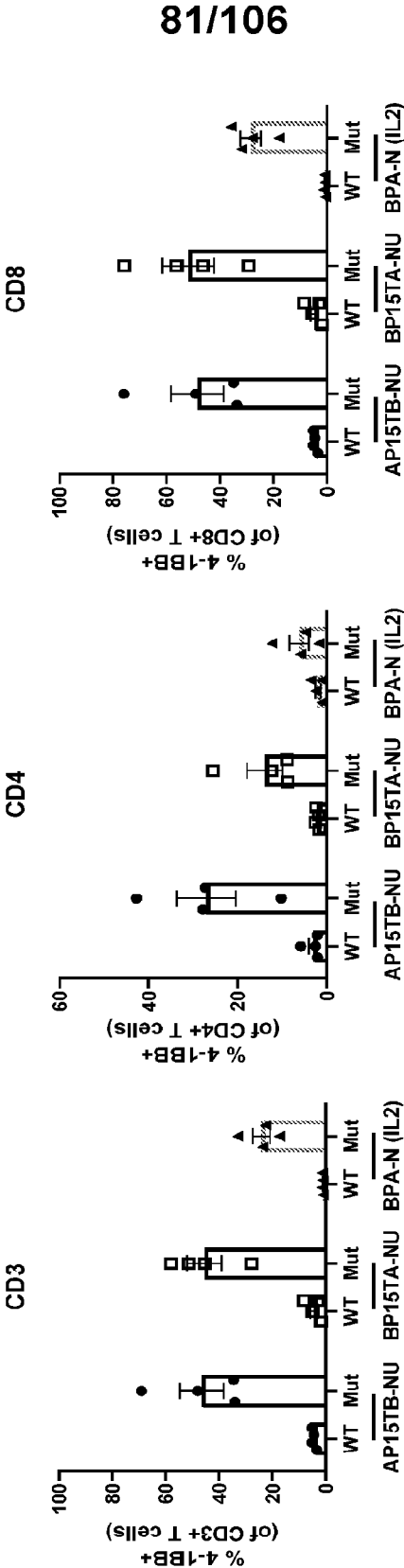


FIG. 35C

4-1BB Induction after LTWD culture

TCR016

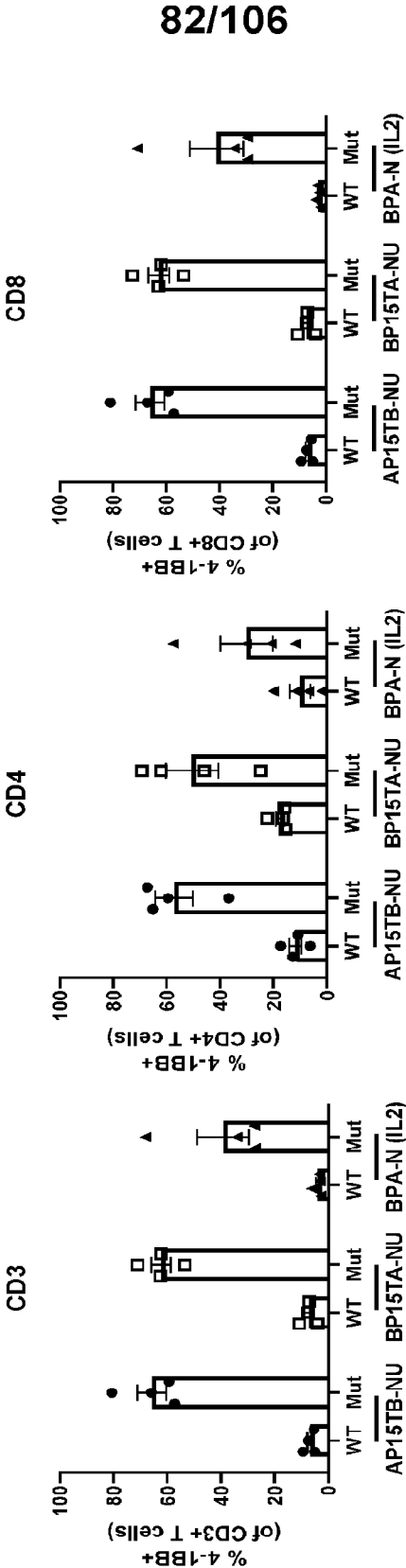


FIG. 35D

4-1BB Induction after LTWD culture

TCR022

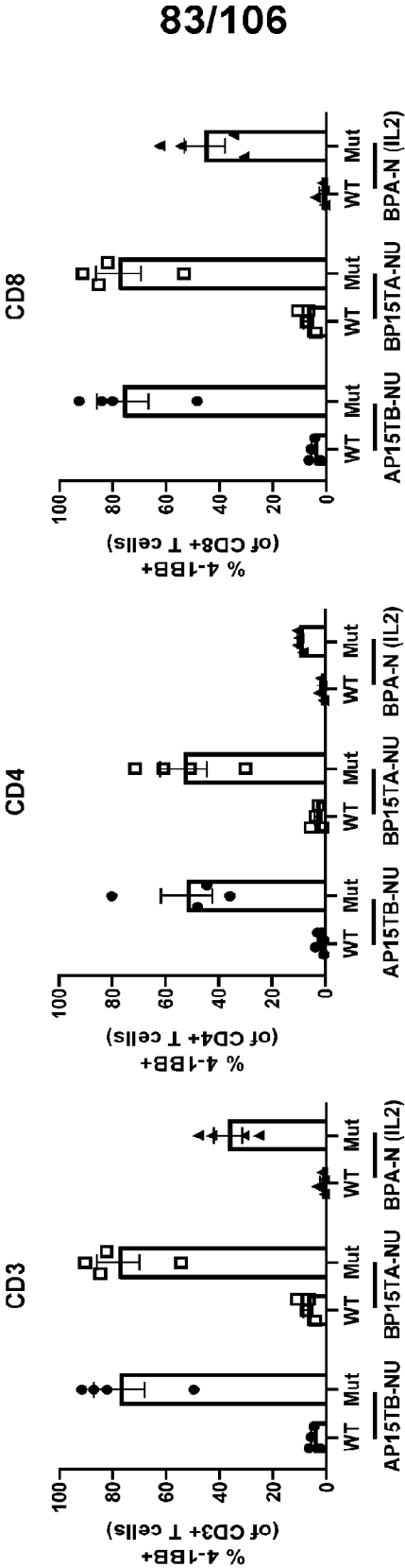


FIG. 35E

4-1BB Induction after LTWD culture

TCR075

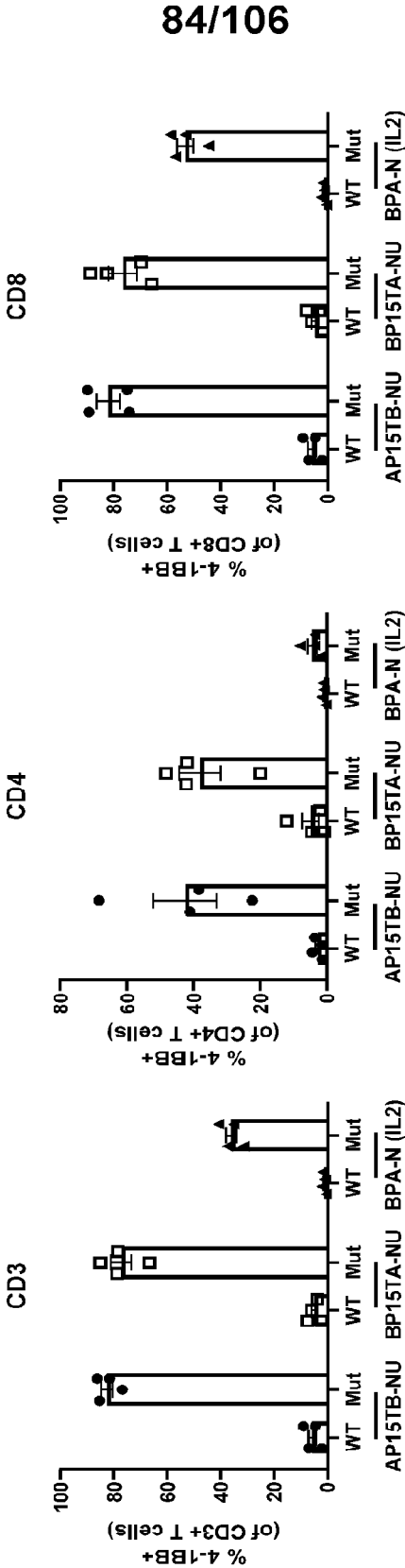


FIG. 35F

4-1BB Induction after LTWD culture

TCR055

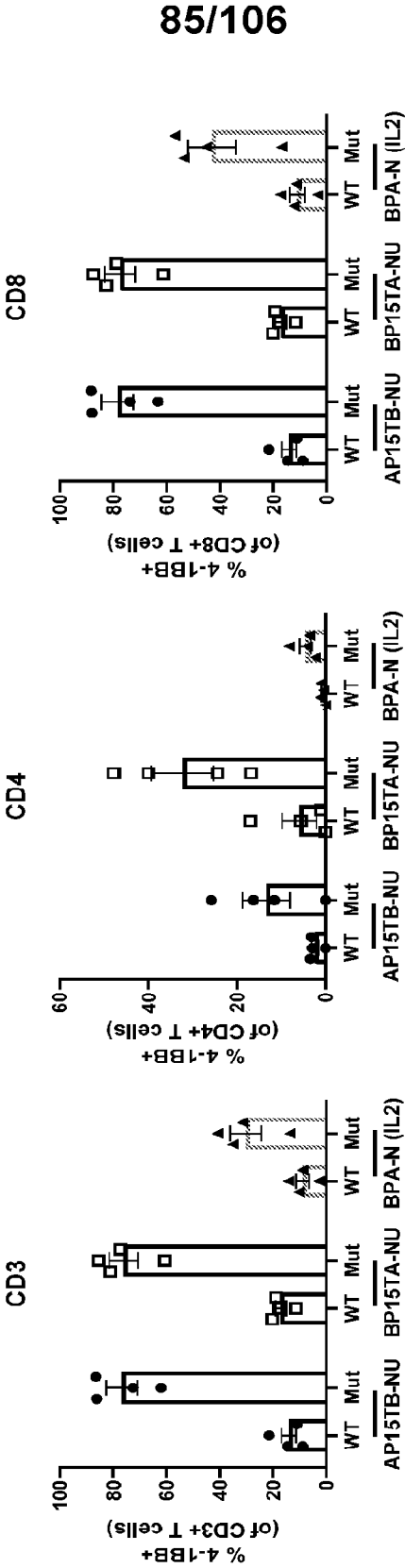


FIG. 35G

4-1BB Induction after LTWD culture

TCR064

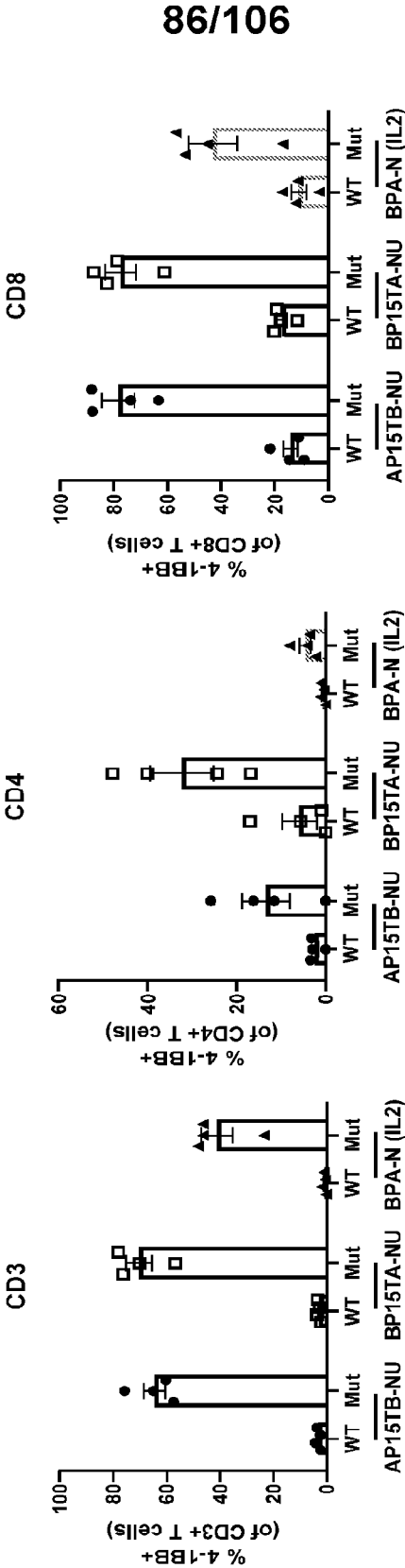


FIG. 35H

4-1BB Induction after LTWD culture

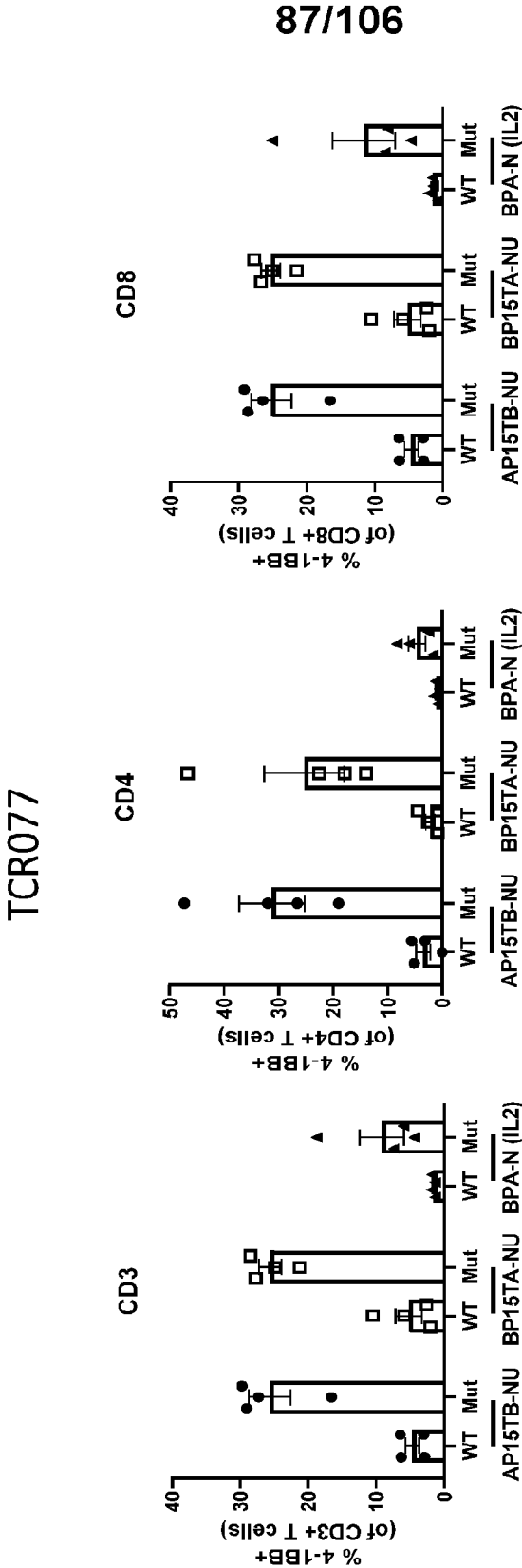


FIG. 35I

IFN- γ after LTWD culture

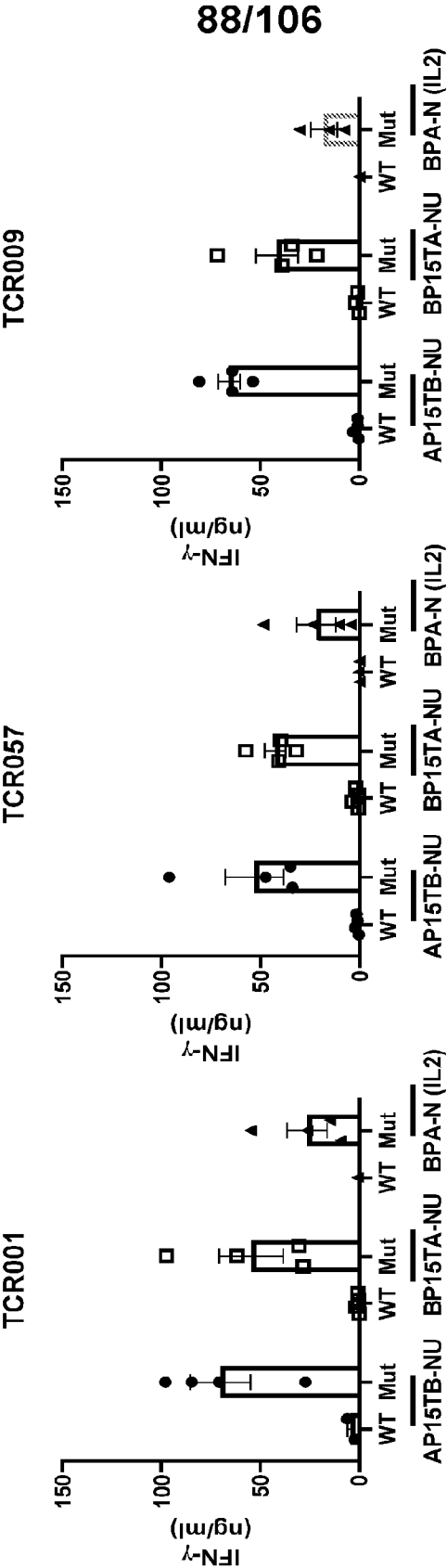


FIG. 36A

IFN- γ after LTWD culture

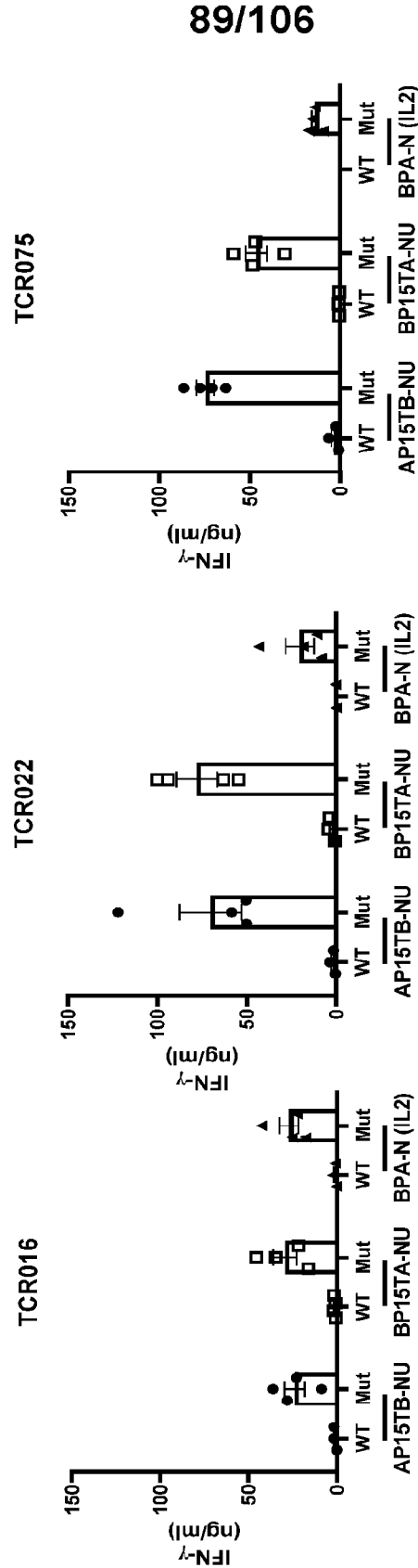


FIG. 36B

IFN- γ after LTWD culture

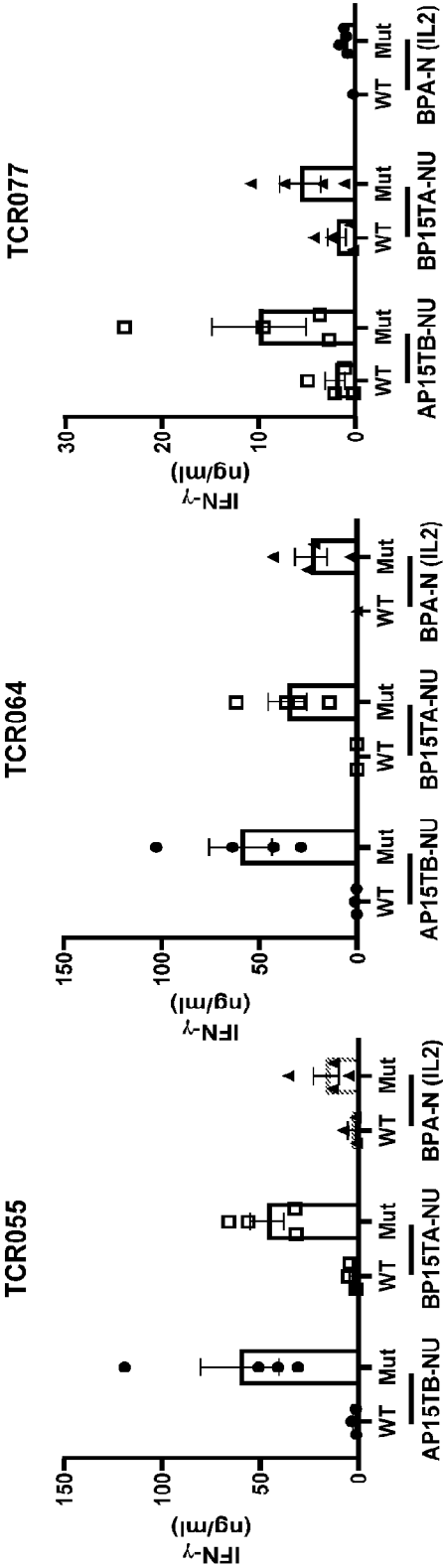


FIG. 36C

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR0001

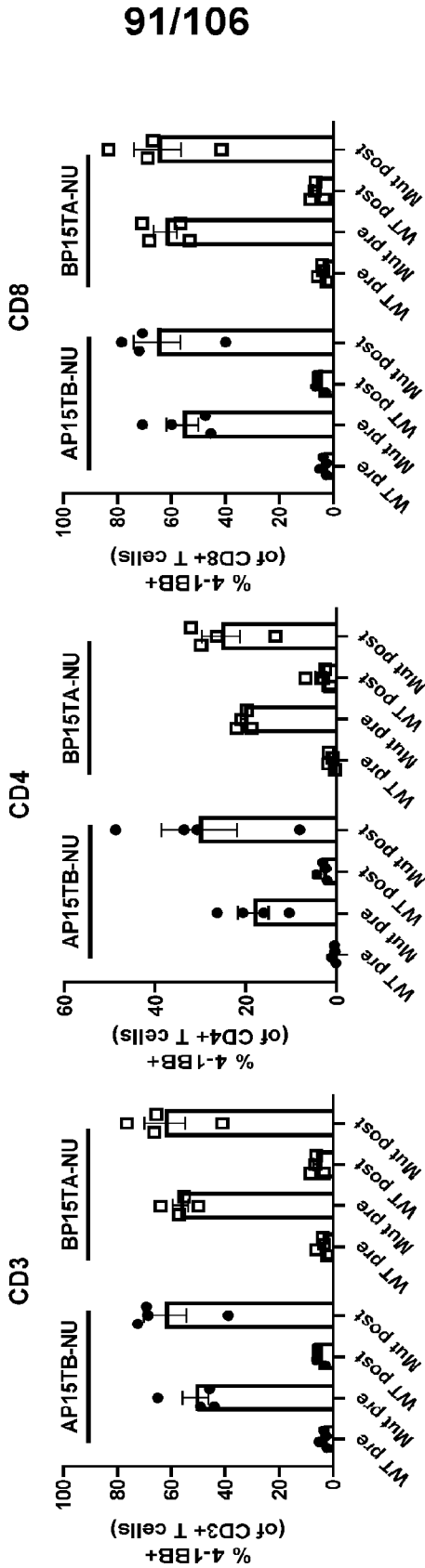


FIG. 37A

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR057

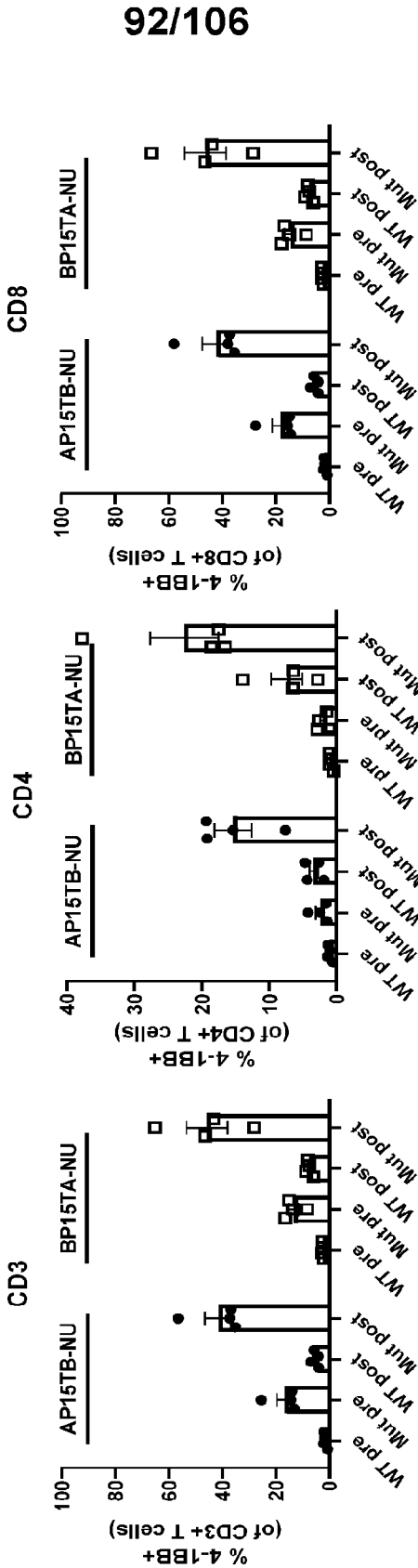


FIG. 37B

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR009

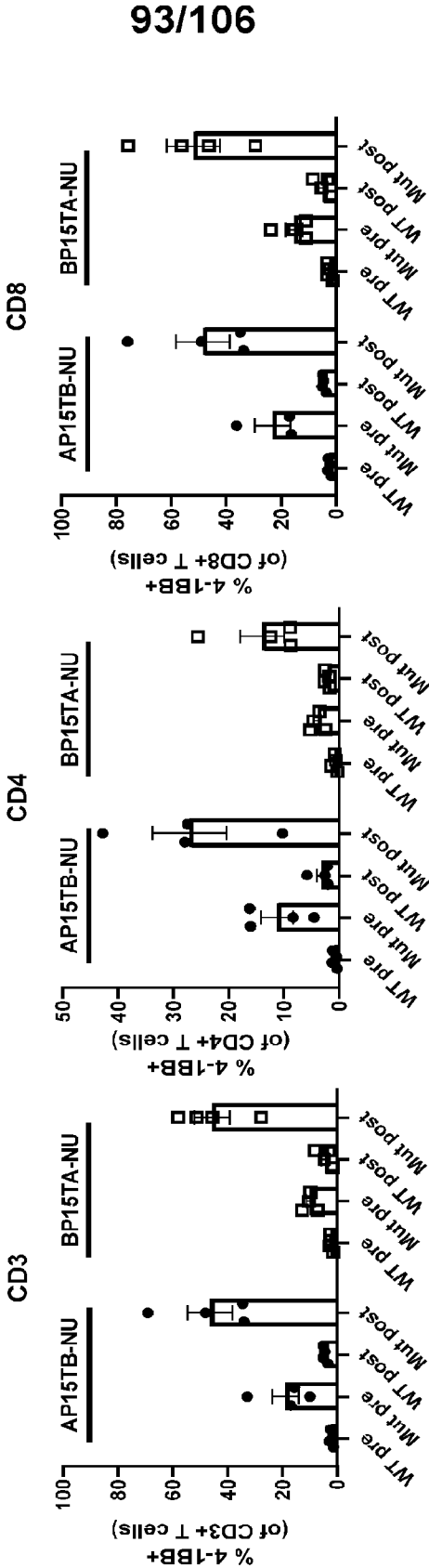


FIG. 37C

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR016

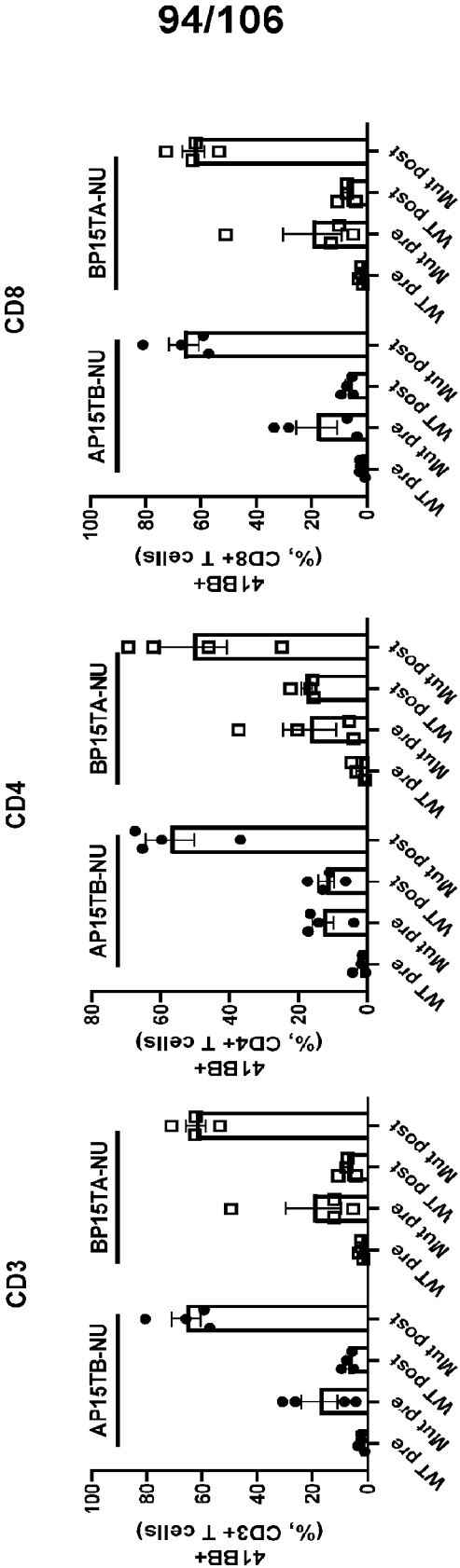


FIG. 37D

Comparison of 4-1BB Induction pre- and post- LTWD culture

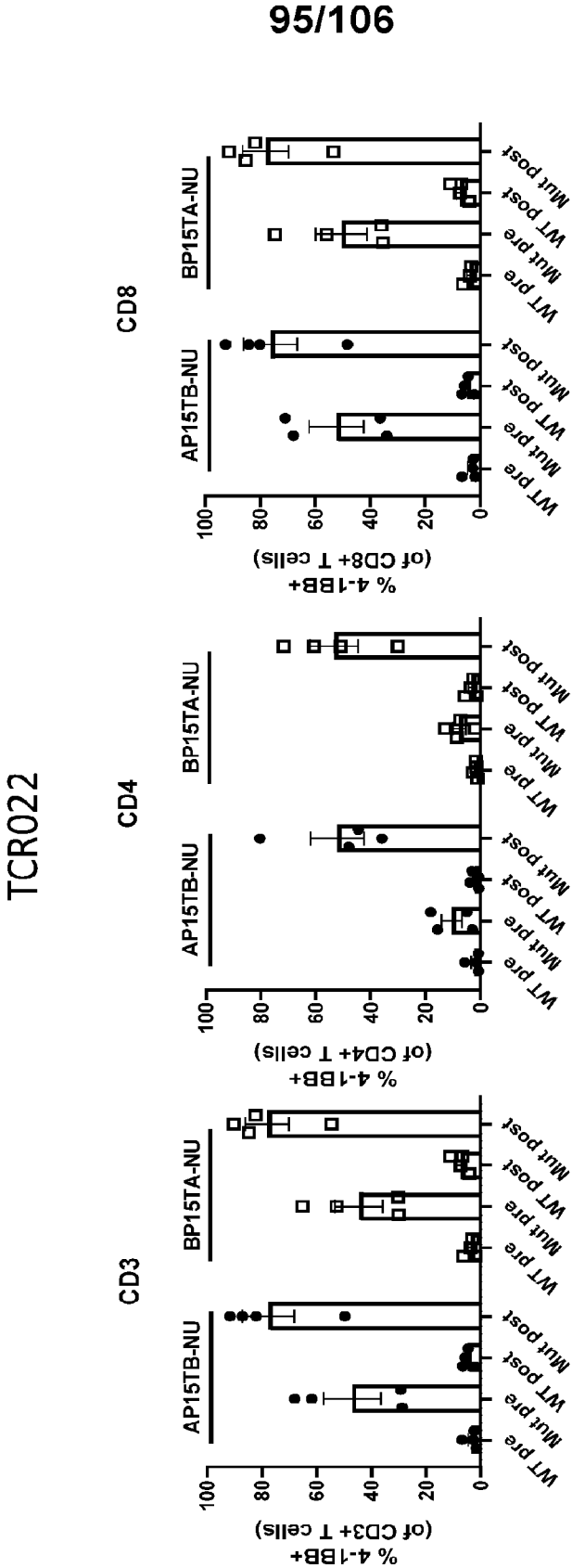


FIG. 37E

Comparison of 4-1BB Induction pre- and post- LTWD culture

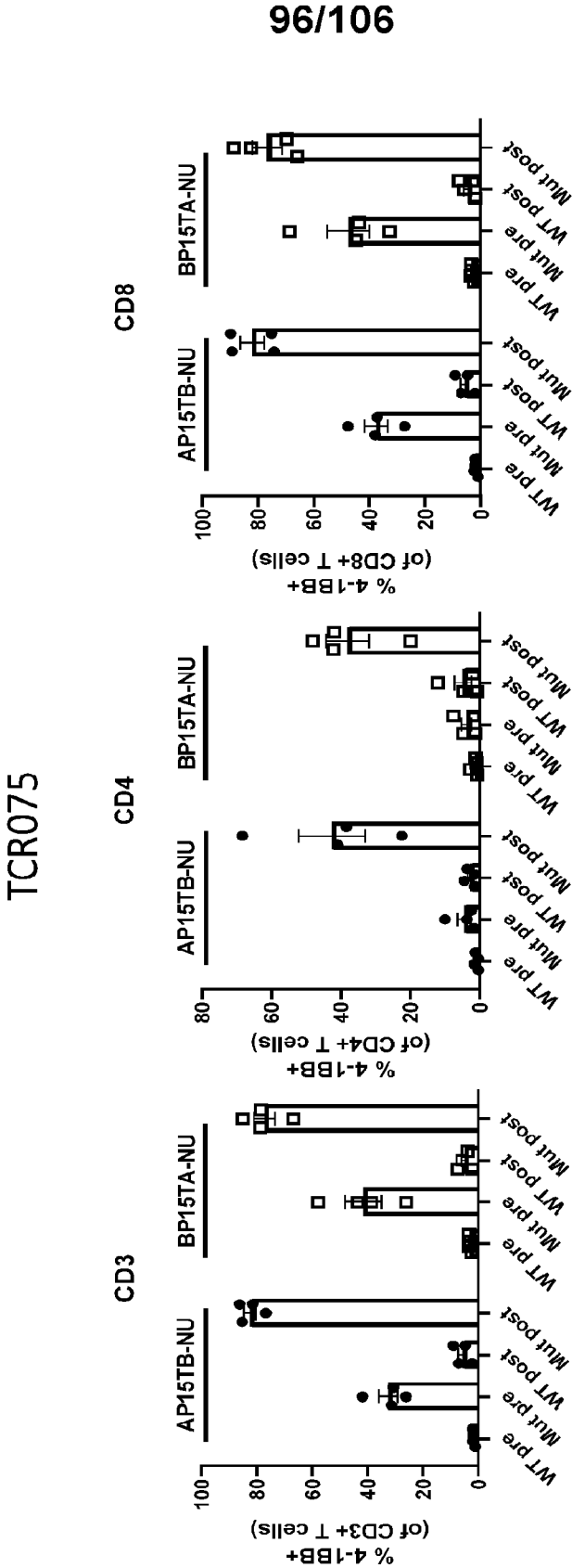


FIG. 37F

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR055

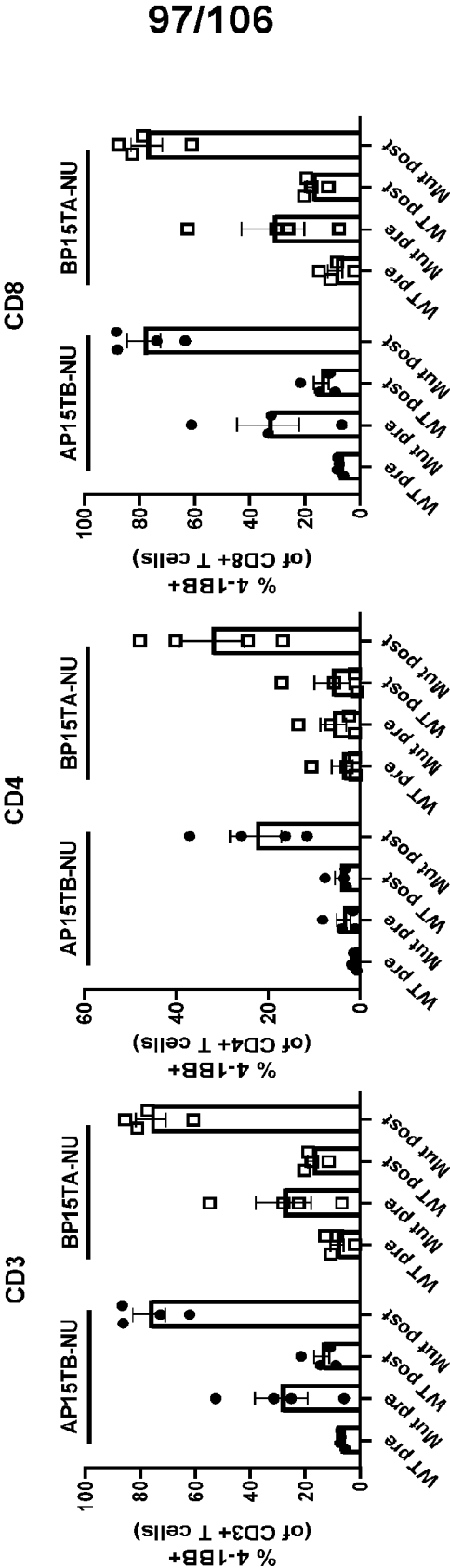


FIG. 37G

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR064

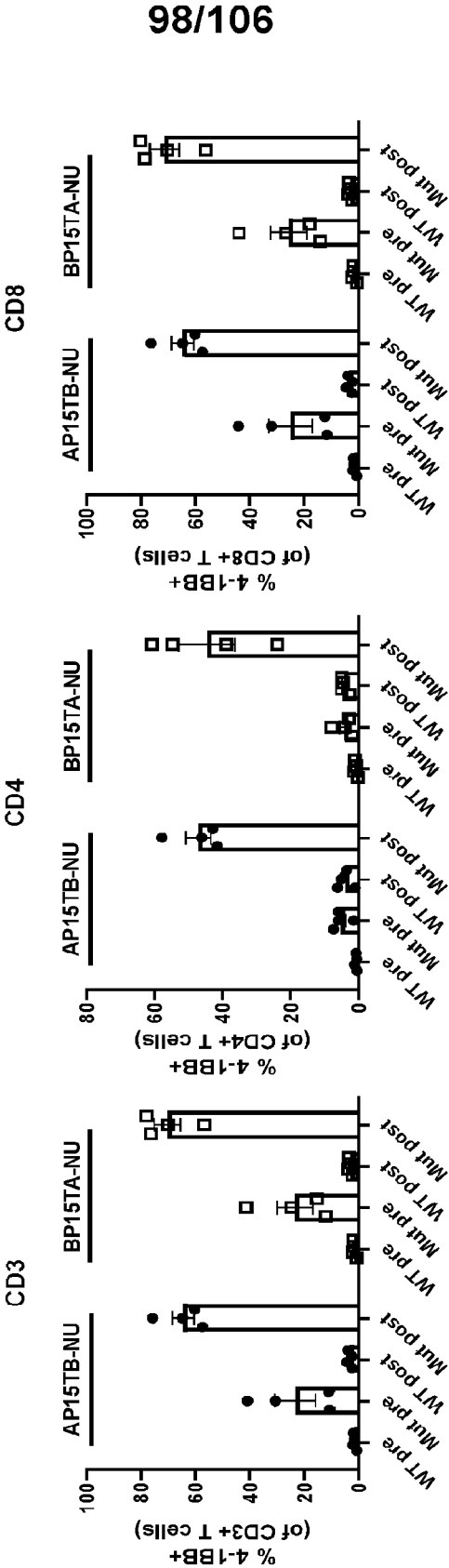


FIG. 37H

Comparison of 4-1BB Induction pre- and post- LTWD culture

TCR077

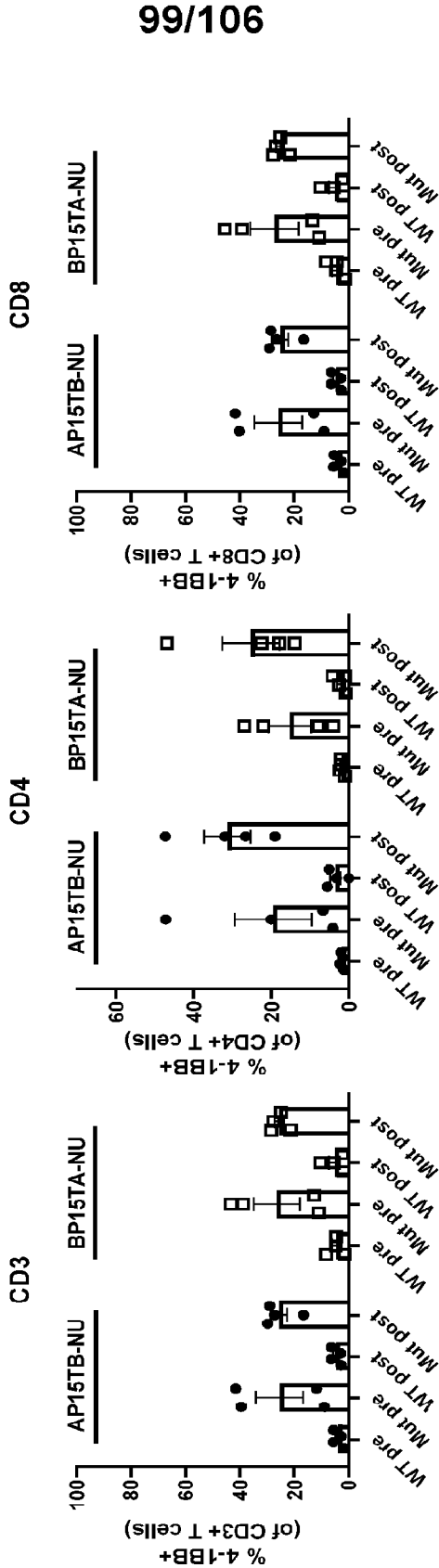


FIG. 37I

Memory Phenotype of Engineered T cells at D11

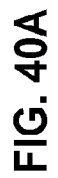


FIG. 38

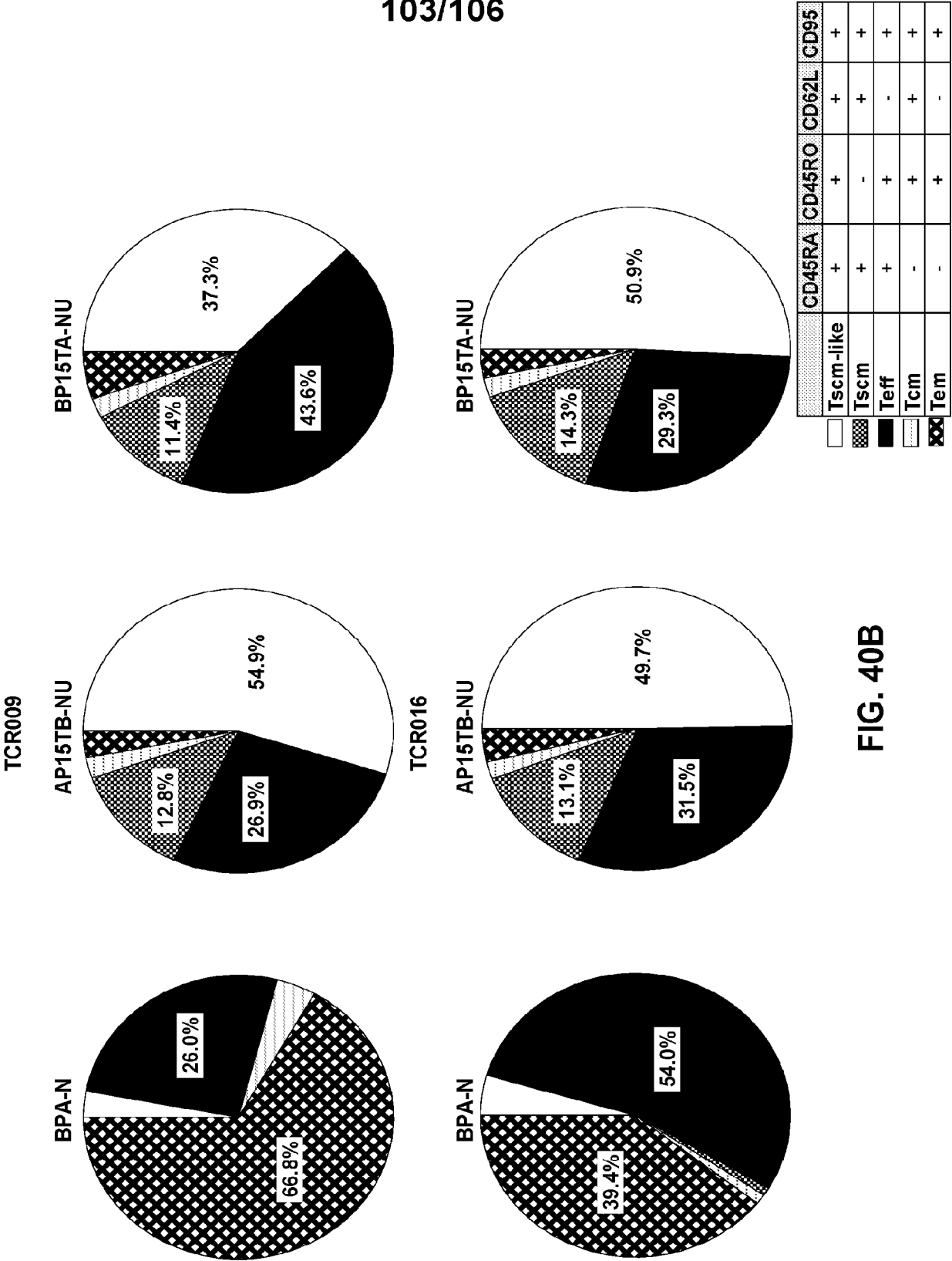
Memory Phenotype of Engineered T cells at D22



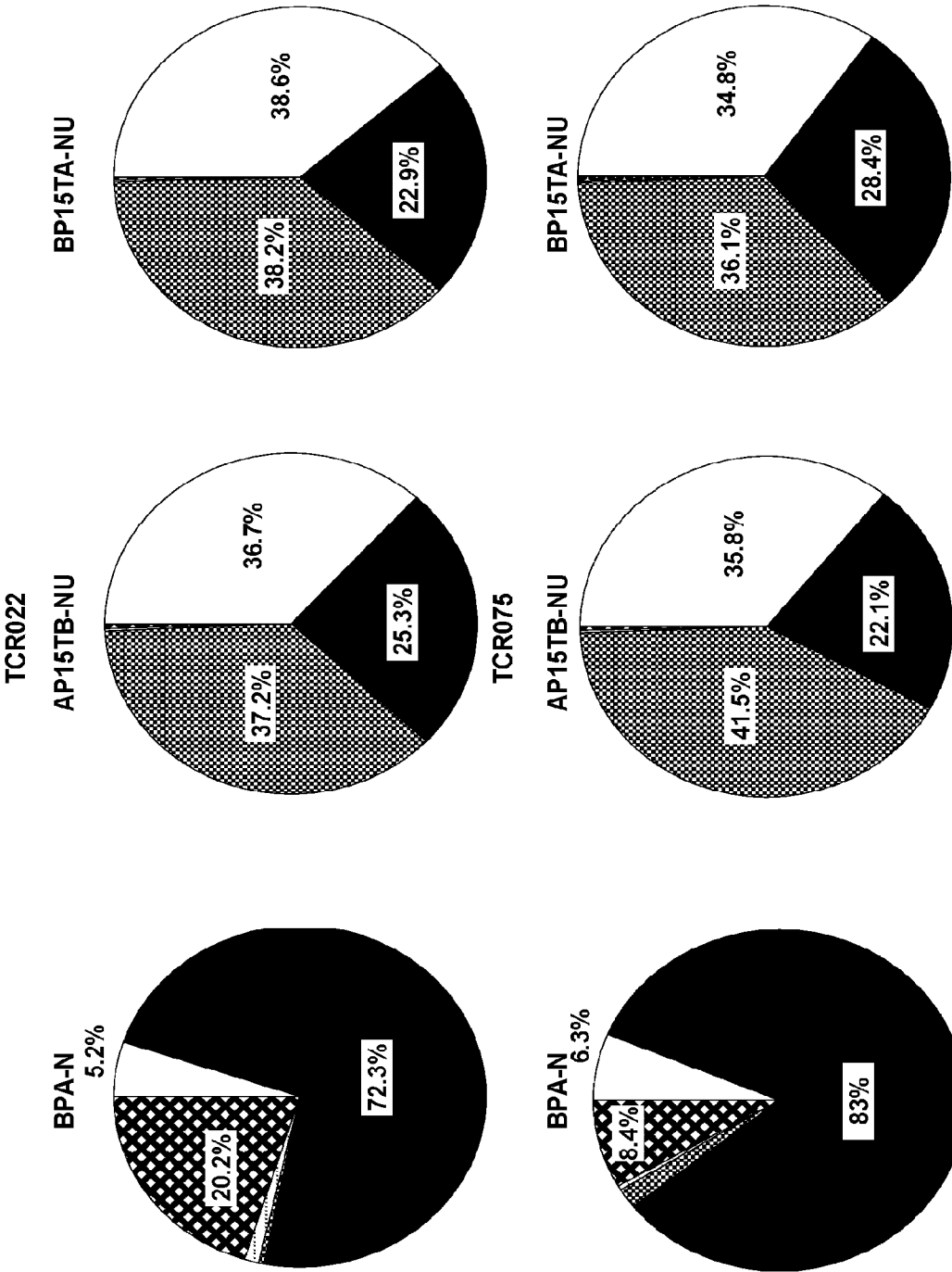
FIG. 39



Memory Phenotype of Engineered T cells after LTWD



Memory Phenotype of Engineered T cells after LTWD



	CD45RA	CD45RO	CD62L	CD95
Tscm-like	+	+	+	+
Tscm	+	-	+	+
Teff	+	+	-	+
Tcm	-	+	+	+
Tem	-	+	-	+

FIG. 40C

Memory Phenotype of Engineered T cells after LTWD

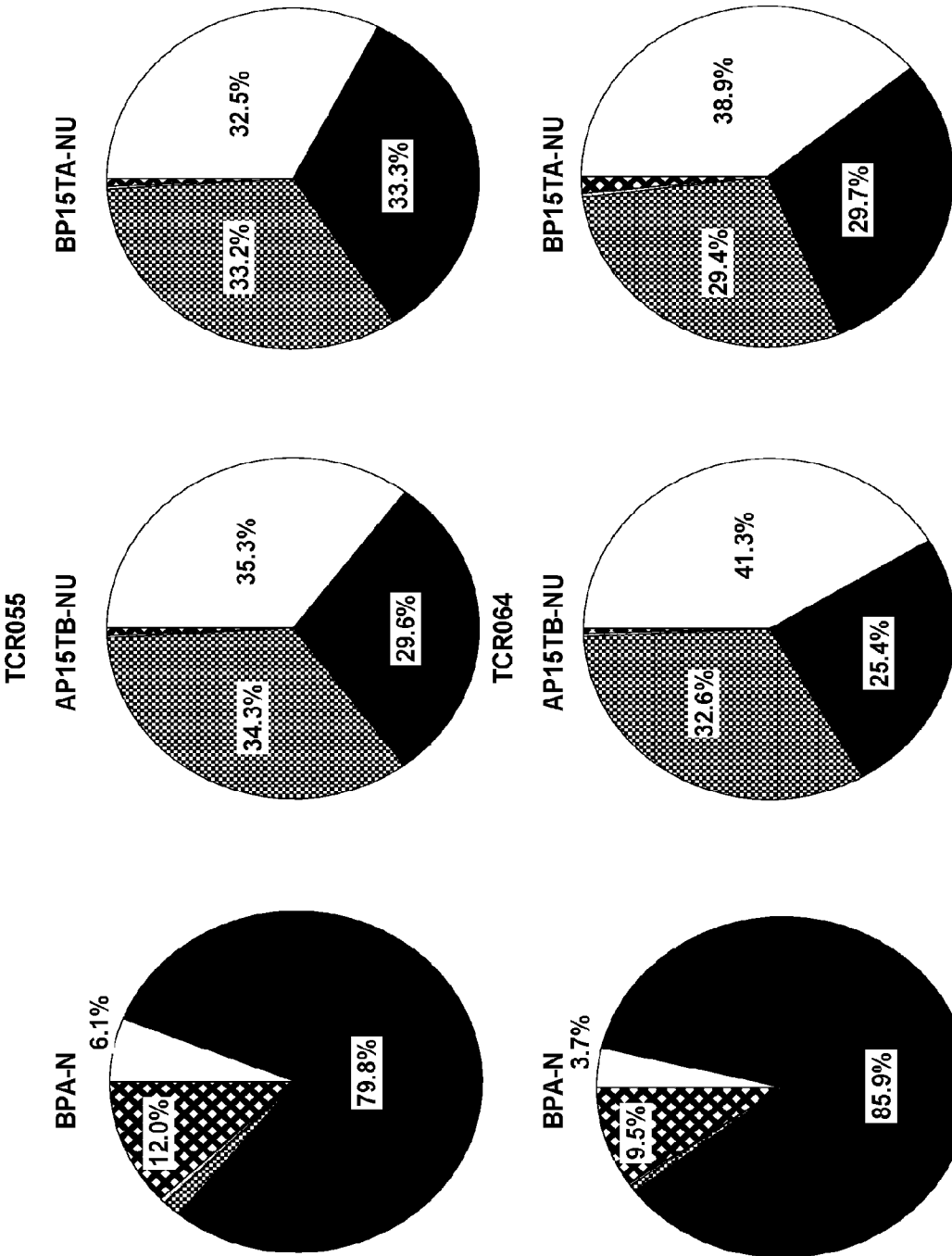


FIG. 40D

Memory Phenotype of Engineered T cells after LTWD

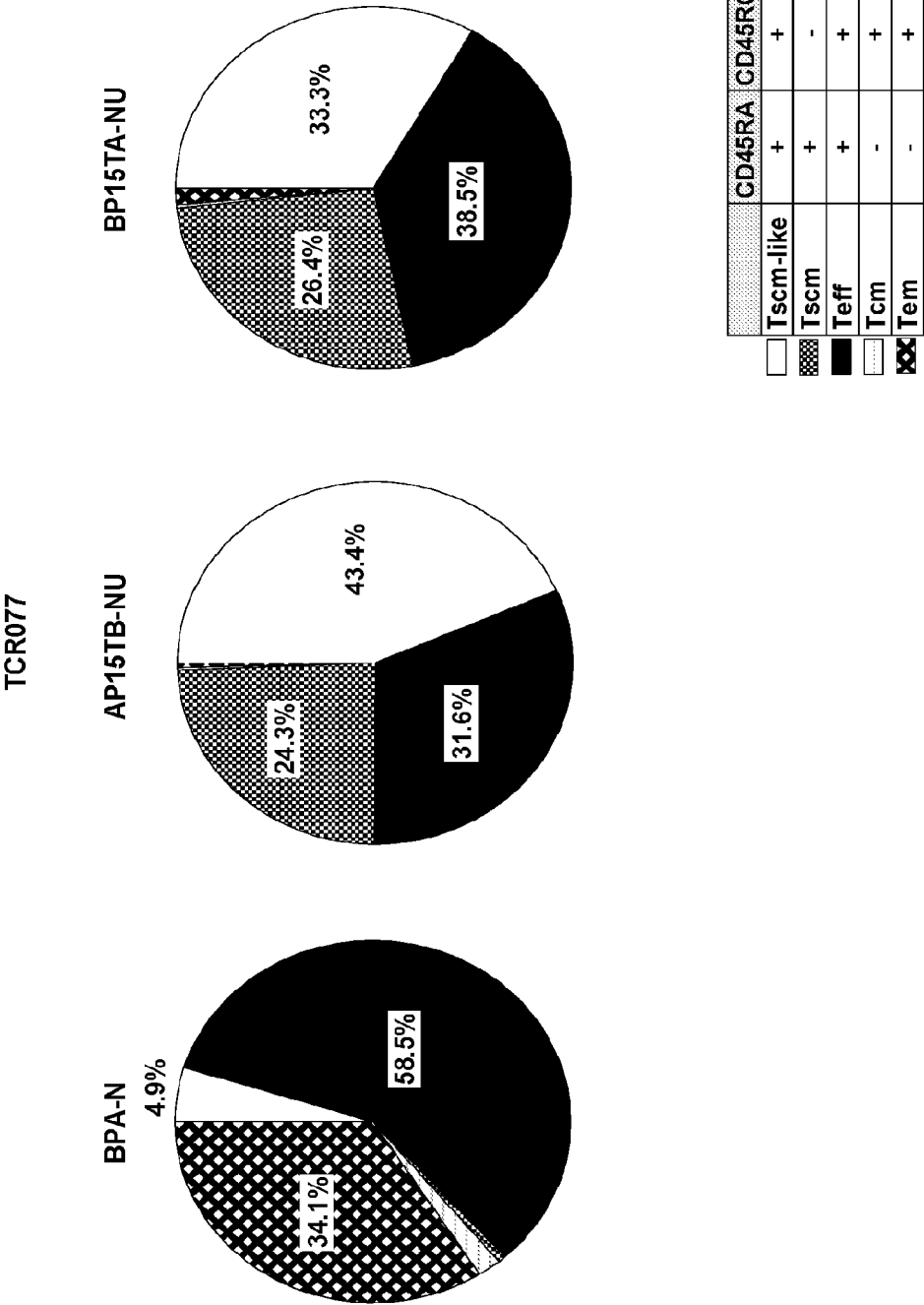


FIG. 40E