Table S6. Most frequent TCRβ V-D-J sequence of Vβ22-negative ERBB2IP-mutation-reactive T cells*

TCR Vβ	V-D-J nucleotide sequence (CDR3 highlighted)	V-D-J amino acid sequence (CDR3 highlighted)	Number of TOPO-TA clones with indicated V-D-J
Vβ5.2 (TRBV5-6)	GACGCTGGAGTCACCCAAAGTCCCACACACCTGAT CAAAACGAGAGGACAGCAAGTGACTCTGAGATGC TCTCCTAAGTCTGGGCATGACACTGTGTCCTGGTAC CAACAGGCCCTGGGTCAGGGGCCCCAGTTTATCTT TCAGTATTATGAGGAGGAAGAGAGACAGAGAGGC AACTTCCCTGATCGATTCTCAGGTCACCAGTTCCCT AACTATAGCTCTGAGCTGAATGTGAACGCCTTGTT GCTGGGGGACTCGGCCCTCTATCTCTGT**GCCAGCA** **GCAAAGGCCCGGGAGGCAACTACGAGCAGTAC**TT CGGGCCGGGCACCAGGCTCACGGTCACAG	DAGVTQSPTHLIKTR GQQVTLRCSPKSGHD TVSWYQQALGQGPQ FIFQYYEEEERQRGNF PDRFSGHQFPNYSSE LNVNALLLGDSALYLC **ASSKGPGGNYEQY**F GPGTRLTVT	3/7

* Vβ22-negative cells that upregulated OX40 upon stimulation with mutated ERBB2IP were sorted and expanded. RNA from these cells was then isolated and underwent 5'RACE with TCR-β constant chain primers to identify the expressed TCR-Vβ sequences. TOPO-TA cloning was performed on the PCR products and individual colonies were then sequenced. Flow cytometry demonstrated that 40-50% of these T cells were Vβ5.2 (TRBV5-6). By Sanger sequencing, 3/7 TOPO-TA colonies were Vβ5.2 (TRBV5-6) with the indicated sequence above.