

# Optimization of the HA-1-specific T-cell receptor for gene therapy of hematologic malignancies

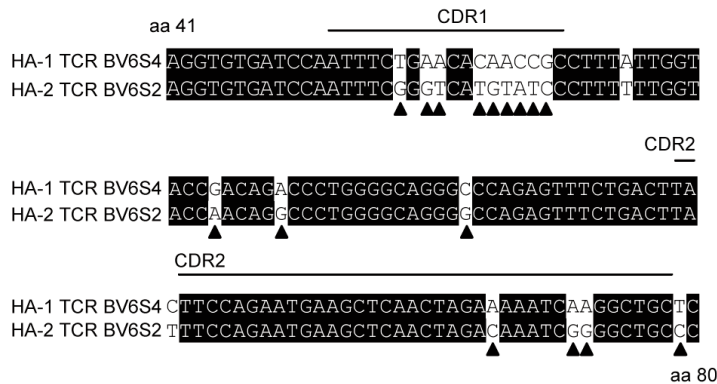
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Online Supplementary Table S1. Primers used for PCR and sequencing.

purpose	name	sequence
HA-1-TCR + HA-2-TCR CDR1	fw HA-1-TCRβ	5' TAGAGAATTCACCATGGGCACCAGCCTCCTC 3'
	rv HA-1-TCRβ	5' TATACCGCTCGAGTCAGAAATCCTTTCTCTTGACC 3'
	fw CDR1 HA-2	5' ATTTCCGGTTCATGTATCCCTTTATTGGTACCGACAGAC 3'
	rv CDR1 HA-2	5' GGATACATGACCCGAAATTGGATCACACCTGAAAGTTAC 3'
Cα	sense	5' CCTGTGATGTCAAGCT GGTCCG 3'
	anti-sense	5' AGCAGATTAACCCGGCCA 3'
	probe	5' TTGAAACAGATACGAACCTAAACTTTCAAACCTGTCA 3'
Cβ	sense	5' AGGATAGGGCCAAACCCGT 3'
	anti-sense	5' AGACAGG ACCCCTTGCTGGT 3'
	probe	5' AGGCCTGGGGTAGAGCAGACTGTG GC 3'
PBGD	sense	5' GGCAATGCGGCTGCAA 3'
	anti-sense	5' GGGTACCCACGCGAATCAC 3'
	probe	5' CTCATCTTTGGGCTGTTT TCTCCGCC 3'



Online Supplementary Figure S1. Sequence alignment of TCRs known to be highly expressed with the HA-1-TCR demonstrate clustered sequence differences in the CDR1-region. Different TCR-BV6 chains that demonstrate high cell surface expression after TCR gene transfer and the HA-1-TCR BV6S4 chains that demonstrate low cell surface expression after TCR gene transfer were aligned and differences in nucleotide sequences were analyzed. Thirty shared nucleotide differences were observed in the 309 aa long variable region between the highly expressed HA-2-TCR BV6S2, the JBBun-TCR BV6S3 and the 10G5-TCR BV6S7 and the marginally expressed HA-1-TCR BV6S4. Sequences shown are from amino acid 41 to 80 of the BV6 chains (total aa 309) containing the CDR1- and CDR2-region of the HA-1-TCRβ and the HA-2-TCRβ chain. The shared differences between all the other BV6 TCR chains and the HA-1-TCRβ chain are indicated with arrows.