**Supplemental Material and Methods**

***In vitro* transcription (IVT) of RNAs**

The OVA plasmid used for this study was previously described (17).The coding region for human dopachrome tautomerase (TRP2) was amplified by polymerase chain reaction (PCR) using oligo(dT)-primed cDNA from human melanoma cell line, 624 MEL cell (kindly provided by Dr. S.A. Rosenberg (NIH, Bethesda, MD) RNA as template and primers as follows: 5’-ATAGGGAGACAAGCTTCCACCATGAGCCCCCTTTGGTG-3’ (forward) and 5’-TATAGAATACGAATTCTAGGCTTCTTCTGTGTATCTCTT-3’ (reverse), in which the start and stop codons are underlined. The resulting 1.6-kb DNA fragments were purified by gel extraction and cloned into the *Hin*dIII and *Eco*RI sites of pGEM-4Z vector (Promega) by In-Fusion HD Cloning Kit (Clontech). By sequence analysis, we confirmed that the cloned sequence coded for TRP2 isoform 1. Before IVT, the TRP2 plasmid was linearized with *Eco*RI and purified by QIAquick PCR Purification Kit (Qiagen). The cDNA for the longest isoform (isoform D) of human Wilms tumor 1 (WT1) was purchased from OriGene Technologies, Inc. and was used as template to amplify the coding region by PCR. The primers used were as follows: 5’-CCAAGCTTCCACC**ATG**CAGGACCCGGCTTCCACG-3’ (forward) and 5’-CGGAATTCTCAAAGCGCCAGCTGGAGTTTGG-3’ (reverse), in which *Hin*dIII and *Eco*RI sites are underlined and the CTG-to-ATG substitution is shown in bold. The resulting 1.6-kb DNA fragments were purified by gel extraction and subcloned using Zero Blunt TOPO PCR Cloning Kit (Invitrogen). After sequence analysis, the cloned sequence was excised with *Hin*dIII and *Eco*RI and inserted into the pGEM-4Z vector with Ligation high Ver.2 (Toyobo). Before IVT, the WT1 plasmid was linearized and purified as above. IVT was carried out using mMessage mMachine T7 Ultra Kit (Ambion) according to manufacturer’s instructions. RNA was purified by RNeasy Mini/Midi Kit (Qiagen) and the integrity was verified by denaturing agarose gel electrophoresis.

**T cell receptor Vβ repertoire assay**

For the evaluation of TCR Vβ Repertoire, total RNA was extracted from highly sorted OVA-tetramer+CD8+ T cells and reverse transcribed for synthesis of first-strand cDNA using a SMARTer RACE cDNA amplification kit (Clontech). Both universal mix primer and primers specific for the T cell receptor β (TCRβ) constant region sequence were used for second-strand amplifications, resulting in TCRβ PCR products of high purity which were then submitted for high-throughput DNA sequencing using an Illumina Miseq sequencing system. All reads of the TCRα and the TCRβ repertoire sequence were analyzed using Python and Perl scripts based on the USEARCH algorithm (<http://drive5.com/>usearch/). V-region consensus sequences in each cluster were searched on the ImMunoGeneTics (IMGT) sites (www.imgt.org/IMGT\_vquest/share/textes/).