*Bold* denotes Vβ population that was also dominant in the infusion product

**Supplementary Table 1.** Dominant TCR Vβ populations in the CD8+ compartment

The TCR Vβ repertoire of the CD8+ compartment of TIL infusion products, and peripheral blood at 1 and 4 weeks post-infusion were analyzed using the IOTest Beta Mark Kit (Beckman-Coulter). Shown are the dominant TCR Vβ populations, as defined by any Vβ chain whose frequency was considered to be a statistical outlier in the repertoire of the 24 Vβ chains that were analyzed. An outlier test was used to define a Vβ as dominant if its frequency was at least three interquartile distances away from the third quartile of all the Vβ chains analyzed.
| Patient | Infusion Product | Week 1 post-infusion | Week 4 post-infusion |
|---------|------------------|----------------------|----------------------|
| 1       |                  | Vβ5.1 (10%)          | Vβ2 (12%)            |
| 2       |                  |                      | Vβ2 (17%)            |
| 3       |                  |                      |                      |
| 4       |                  | Vβ2 (16%)            |                      |
| 5       |                  | Vβ2 (18%)            | Vβ17 (30%)           |
|         |                  |                      | Vβ2 (16%)*           |
| 6       |                  | Vβ17 (8.3%)          | Vβ2 (11%)            |
| 7       |                  |                      |                      |
| 8       |                  | Vβ4 (23%)            | Vβ4 (55%)            |
| 9       |                  | Vβ23 (12%)           | Vβ8 (12%)            |
| 10      |                  |                      |                      |
| 11      |                  |                      | Vβ2 (11%)            |
| 12      |                  | Vβ2 (11%)            | Vβ17 (8.9%)          |

Vβ, T cell receptor beta chain

*Bold denotes Vβ population that was also dominant in the infusion product

**Supplementary Table 2.** Dominant TCR Vβ populations in the CD4+ compartment

The TCR Vβ repertoire of the CD4+ compartment of TIL infusion products, and peripheral blood at 1 and 4 weeks post-infusion were analyzed using the IOTest Beta Mark Kit (Beckman-Coulter). Shown are the dominant TCR Vβ populations, as defined by any Vβ chain whose frequency was considered to be a statistical outlier in the repertoire of the 24 Vβ chains that were analyzed. An outlier test was used to define a Vβ as dominant if its frequency was at least three interquartile distances away from the third quartile of all the Vβ chains analyzed.
Supplementary Figure 1. Survival curves

a. Progression-free survival. Twelve patients were included in the analysis and eight events (both RECIST and irRC PD or death) were observed. The estimated median PFS time was 5.1 months (95% CI: 1.2 – 6.4 months).

b. Overall survival. Twelve patients were included in the analysis and five events (death) were observed. Median OS was estimated to be 6.2 months (95% CI: 1.5 to not reached).
Peripheral blood mononuclear cells taken before TIL therapy (Baseline) and after TIL infusion (WK1 – WK140) were analyzed by flow cytometry for the proportion of various TCR Vβ chains present in the CD8+ T cell compartment. This analysis was also performed on a sample of the TIL infusion product. The legend describes the color coding for three TCR Vβ populations of interest that are exploded from the pie charts: Vβ13.1, which was dominant in the infusion product and at many time points post-infusion; Vβ16, which was not dominant in the infusion product but expanded in peripheral blood post-infusion; and Vβ8, which was dominant in the infusion product and then declined post-infusion. The legend also indicates the population of T cells expressing TCR Vβ chains that were not interrogated by the Vβ antibody panel used (unknown Vβ chains).
Supplementary Figure 3. Flow cytometric analysis of post-treatment biopsy (Patient 7).

A subcutaneous lesion was surgically removed from Patient 7 at 17 weeks following TIL infusion. After enzymatic dissociation of the tissue, the above gating strategy was applied to identify CD3+ lymphocytes for analysis of CD8 and PD-1 expression by flow cytometry.