

Supplementary Table 2. Quality control of RNA used for sequencing of TRB via Illumina MiSeq and number of TRB sequences (total and distinct) for each sample.

Sample	# cells culture seeded with	# cells RNA purified from ^a	A260/A280 ^b	RIN ^b	# Total Sequences	# Distinct Sequences
Tumor T-T0	n/a	4.4 x 10 ⁶	1.66	7.2	51,713	1,854
Baseline T0	n/a	5 x 10 ⁶	1.78	9.2	56,748	9,664
Baseline WT	0.1 x 10 ⁶	5.5 x 10 ⁶	2.01	8.8	58,896	2,840
Baseline MT	10.5 x 10 ⁶	5.5 x 10 ⁶	1.76	9.6	49,826	158
Post-IT-AG T0	n/a	6 x 10 ⁶	1.67	8.9	47,602	5,162
Post-IT-AG WT	0.1 x 10 ⁶	2 x 10 ⁶	1.66	9.1	53,435	4,585
Post-IT-AG MT	5 x 10 ⁶	2 x 10 ⁶	1.78	9.1	58,217	182
Post-Ipi (1 mo.) T0	n/a	7.8 x 10 ⁶	1.76	9.1	51,983	7,528
Post-Ipi (1 mo.) WT	0.1 x 10 ⁶	5 x 10 ⁶	1.73	9.1	49,799	2,709
Post-Ipi (1 mo.) MT	10 x 10 ⁶	5 x 10 ⁶	1.80	8.4	49,035	156
Post-Ipi (4 mo.) T0	n/a	13.8 x 10 ⁶	1.77	9.3	58,588	6,006
Post-Ipi (4 mo.) WT	0.1 x 10 ⁶	5 x 10 ⁶	1.75	9.0	52,277	2,091
Post-Ipi (4 mo.) MT	20 x 10 ⁶	5 x 10 ⁶	1.86	9.0	35,527	84
Post-Ipi (13 mo.) T0	n/a	2 x 10 ⁶	1.83	7.8	54,284	4,693
Post-Ipi (13 mo.) WT	0.1 x 10 ⁶	5 x 10 ⁶	1.83	9.8	51,711	2,209
Post-Ipi (13 mo.) MT	18 x 10 ⁶	5 x 10 ⁶	1.76	9.8	46,575	133

^a RNA was purified with Qiagen RNeasy Mini kits.

^b Quantity and quality assessed via QUBIT fluorometer and Agilent RNA Pico Chip on a 2100 BioAnalyzer, respectively.

TRB cDNA libraries prepared from 500 ng RNA, using Clontech SMARTer RACE 5'/3' Kit with a human TRBC gene specific primer. Following library preparation via Illumina TruSeq workflow, samples were sequenced using the Illumina MiSeq platform.

TRB, T cell receptor beta; RIN, RNA Integrity Number; T-T0, Tumor, freshly cryopreserved; T0, time zero; WT, wild-type; MT, mutant; IT-AG, intratumoral α -gal glycolipids; Ipi, Ipilimumab; mo., months.