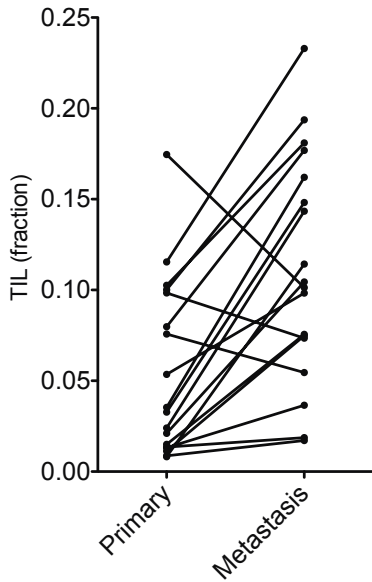
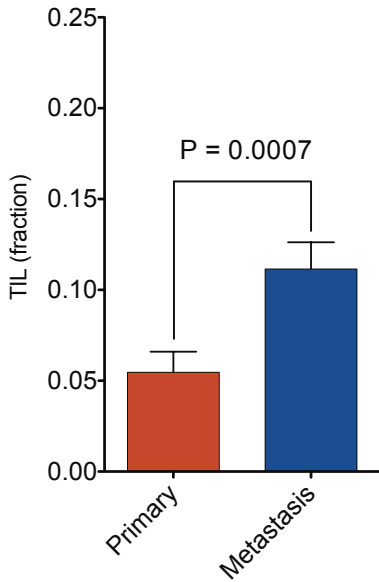


**A****B**

**Supplemental Figure 1.** TIL fraction in patient-matched primary tumor and metastasis.

QuanTILfy was performed on 17 pairs of primary ovarian carcinoma and patient-matched metastatic omentum. When compared pairwise (**a**), in all but 3 cases, metastases displayed higher TIL percentages than their matched primary tumors. On average (**b**), omentum metastases had a more than 2-fold higher TIL fraction than their paired primary tumors (n= 18, two-tailed paired t test,  $p = 0.0007$ ).

**Table S1. Variable gene forward primers**

#	Specificity	Sequence (5' to 3')
1	V02	TTC GAT GAT CAA TTC TCA GTT GAA AGG CC
2	V03-1	CCT AAA TCT CCA GAC AAA GCT CAC TTA AA
3	V04-1	CTG AAT GCC CCA ACA GCT CTC TCT TAA AC
4	V04-2/3	CTG AAT GCC CCA ACA GCT CTC ACT TAT TC
5	V05-1	TGG TCG ATT CTC AGG GCG CCA GTT CTC TA
6	V05-3	TAA TCG ATT CTC AGG GCG CCA GTT CCA TG
7	V05-4	TCC TAG ATT CTC AGG TCT CCA GTT CCC TA
8	V05-5	AAG AGG AAA CTT CCC TGA TCG ATT CTC AGC
9	V05-6	GGC AAC TTC CCT GAT CGA TTC TCA GGT CA
10	V05-8	GGA AAC TTC CCT CCT AGA TTT TCA GGT CG
11	V06-1	GTC CCC AAT GGC TAC AAT GTC TCC AGA TT
12	V06-2/3	GCC AAA GGA GAG GTC CCT GAT GGC TAC AA
13	V06-4	GTC CCT GAT GGT TAT AGT GTC TCC AGA GC
14	V06-5	AAG GAG AAG TCC CCA ATG GCT ACA ATG TC
15	V06-6	GAC AAA GGA GAA GTC CCG AAT GGC TAC AAC
16	V06-7	GTT CCC AAT GGC TAC AAT GTC TCC AGA TC
17	V06-8	CTC TAG ATT AAA CAC AGA GGA TTT CCC AC
18	V06-9	AAG GAG AAG TCC CCG ATG GCT ACA ATG TA
19	V07-1	TCC CCG TGA TCG GTT CTC TGC ACA GAG GT
20	V07-2	AGT GAT CGC TTC TCT GCA GAG AGG ACT GG
21	V07-3	GGC TGC CCA ACG ATC GGT TCT TTG CAG T
22	V07-4	GGC GGC CCA GTG GTC GGT TCT CTG CAG AG
23	V07-6/7	ATG ATC GGT TCT CTG CAG AGA GGC CTG AGG
24	V07-8	GCT GCC CAG TGA TCG CTT CTT TGC AGA AA
25	V07-9	GGT TCT CTG CAG AGA GGC CTA AGG GAT CT
26	V09	GTT CCC TGA CTT GCA CTC TGA ACT AAA C
27	V10-1	AAC AAA GGA GAA GTC TCA GAT GGC TAC AG
28	V10-2	GAT AAA GGA GAA GTC CCC GAT GGC TAT GT
29	V10-3	GAC AAA GGA GAA GTC TCA GAT GGC TAT AG
30	V11-1/2/3	CTA AGG ATC GAT TTT CTG CAG AGA GGC TC
31	V12-3/4	TCG ATT CTC AGC TAA GAT GCC TAA TGC
32	V12-5	TTC TCA GCA GAG ATG CCT GAT GCA ACT TTA
33	V13	CTG ATC GAT TCT CAG CTC AAC AGT TCA GT
34	V14	TCT TAG CTG AAA GGA CTG GAG GGA CGT AT
35	V15	GCC GAA CAC TTC TTT CTG CTT TCT TGA C
36	V16	TTC AGC TAA GTG CCT CCC AAA TTC ACC CT
37	V18	ATT TTC TGC TGA ATT TCC CAA AGA GGG CC

38	V19	TAT AGC TGA AGG GTA CAG CGT CTC TCG GG
39	V20-1	ATG CAA GCC TGA CCT TGT CCA CTC TGA CA
40	V24-1	ATC TCT GAT GGA TAC AGT GTC TCT CGA CA
41	V25-1	TTT CCT CTG AGT CAA CAG TCT CCA GAA TA
42	V27	TCC TGA AGG GTA CAA AGT CTC TCG AAA AG
43	V28	TCC TGA GGG GTA CAG TGT CTC TAG AGA GA
44	V29-1	CAT CAG CCG CCC AAA CCT AAC ATT CTC AA
45	V30	GAC CCC AGG ACC GGC AGT TCA TCC TGA GT

**Table S2. Joining gene reverse primers**

#	Specificity	Sequence (5' to 3')
1	J1-1	TTACCTACAACCTGTGAGTCTGGTGCCTTGTCCAAA
2	J1-2	ACCTACAACGGTTAACCTGGTCCCCGAACCGAA
3	J1-3	ACCTACAACAGTGAGCCAACCTTCCCTCTCCAAA
4	J1-4	CCAAGACAGAGAGCTGGGTTCCACTGCCAAA
5	J1-5	ACCTAGGATGGAGAGTCGAGTCCCATCACAAA
6	J1-6	CCATACCTGTCACAGTGAGCCTGGTCCCGTT
7	J2-1	CGGTGAGCCGTGTCCCTGGCCCGAA
8	J2-2	CCAGTACGGTCAGCCTAGAGCCTTCTCCAAA
9	J2-3	ACTGTCAGCCGGGTGCCTGGGCCAAA
10	J2-4	AGAGCCGGTCCC GGCGCCGAA
11	J2-5	GGAGCCGCGTGCCTGGCCCGAA
12	J2-6	CCAGCACGGTCAGCCTGCTGCCG
13	J2-7	GTGAGCCTGGTGCCCGGCCCGAA

**Table S3. Variable gene TaqMan probes (each with FAM fluorophore)**

#	Name	Specific to	Sequence (5' to 3')
1	V02	V02	TCCGGTCCACAAAGCTGGAG
2	V03	V03-1, V03-2p	CTGGAGCTTGGTGA CTCTGC
3	V04a	V04-1	TCACCTACACGCCCTGC
4	V04b	V04-2, V04-3	ACACACCCTGCAGCCAG
5	V05a1	V05-1	AGCACCTTGGAGCTGGG
6	V05a2	V05-3	TGAGTGCCTTGGAGCTGG
7	V05b	V05-4, V05-5, V05-6, V05-7, V05-8	TGAGCTGAATGTGAACGCCTT
8	V06a	V06-1, V06-2, V06-3	TGGAGTCGGCTGCTCC
9	V06b	V06-7, V06-9	CTGGAGTCAGCTGCTCCC
10	V06c	V06-4	CACAGATGATTTCCCCTC
11	V06d	V06-1, V06-5, V06-6, V06-8, V06-9	TGCTCCCTCCCAGACATC
12	V07a1	V07-1	CTGAAGTTCCAGCGCACA
13	V07a2	V07-2	TCCGTCTCCACTCTGACGA
14	V07b	V07-3, V07-4, V07-8	ACTCTGAAGATCCAGCGCA
15	V07c	V07-4, V07-6, V07-9	TCCAGCGCACAGAGCA
16	V07d	V07-7	CAGCGGGACTCAGCCA
17	V09	V09	TGAGCTCTCTGGAGCTGG
18	V10a1	V10-1	TCAAACACAGAGGACCTCCC
19	V10a2	V10-2	CACTCTGGAGTCAGCTACCC
20	V10b	V10-3	TCACTCTGGAGTCCGCTACC
21	V11	V11-1, V11-2, V11-3	AGTAGACTCCACTCTCAAGATCCA
22	V12c	V12-3, V12-4, V12-5	ATCCAGCCCTCAGAACCCAG
23	V13	V13	ACATGAGCTCCTTGGAGCTG
24	V14	V14	TGCAGAACTGGAGGATTCTGG
25	V15	V15	TGTACCTGTGTGCCACCAGC
26	V16	V16	CCTTGAGATCCAGGCTACG
27	V18	V18	ATCCAGCAGGTAGTGCGAGG
28	V19	V19	CACTGTGACATCGGCCCAA
29	V20	V20-1	CAGTGCCCATCCTGAAGACA
30	V24	V24-1	TGTCCCTAGAGTCTGCCATCC
31	V25	V25-1	CAGGCCCTCACATACCTCTC
32	V27	V27-1	TGGAGTCGCCAGCC
33	V28	V28	AGGAGCGCTTCTCCCTG
34	V29	V29-1	TGTGAGCAACATGAGCCCTG
35	V30	V30	TCCTTCTCAGTGA CTCTGGC

**Table S4. Reference assay oligo sequences**

#	Name	Sequence (5' to 3')
1	RPP30 FOR	AGATTTGGACCTGCGAGC
2	RPP30 REV	GAGCGGCTGTCTCCACAAGT
3	RPP30-VIC probe	CCGCGCAGAGCCTTC

**Table S5. Assay subgroup assignments**

<b>Subgroup</b>	<b>Probes</b>	<b>Specificity</b>	<b>Well</b>
A	V02	V02	B04
	V04a	V04-1	C05
	V14	V14	A10
	V15	V15	A11
	V29	V29-1	B12
B	V04b	V04-2	C06 (C06)
		V04-3	
	V05a1	V05-1	C07
	V06a	V06-1	D01
		V06-2	D02
V06-3		(D02)	
V13	V13	A09	
V28	V28	B11	
C	V05b	V05-4	C09
		V05-5	C10
		V05-6	C11
		V05-8	C12
	V06c	V06-4	D03
	V09	V09	E04
	V25	V25-1	B08
V27	V27-1	B10	
D	V06b	V06-7	D06
		V06-9	D08
	V06d	V06-1	D01
		V06-5	D04
		V06-6	D05
V06-8		D07	
V06-9	(D08)		
V18	V18	B02	
V20	V20-1	B05	
E	V05a2	V05-3	C08
	V12c	V12-3	A07
		V12-4	(A07)
		V12-5	A08
V24	V24-1	B07	
V30	V30	C04	
F	V07c	V07-4	D12
		V07-6	E01
		V07-9	E03
	V07d	V07-7	(E01)
	V10a1	V10-1	A01
V10a2	V10-2	A02	
G	V07a1	V07-1	D09
	V11	V11-1	A04
		V11-2	(A04)
		V11-3	(A04)
	V16	V16	A12
V19	V19	B03	
H	V03	V03-1	C02



V07a2	V07-2	D10
V07b	V07-3	D11
	V07-4	D12
	V07-8	E02
V10b	V10-3	A03

Table S6. TCR $\beta$  clone identified by sequencing.

ID	quanTILfy Subgroup of Clone	Clone %	TCRB CDR3 Sequence	Vgene/family	J gene
PT.1	A	90.2	TGTGCCAGCATTATTTTAGGGTACCCTAACTATGGCTA	TRBV2	TRBJ1-2
PT.2	B	99.8	TGTGCCAGCAGTTTATTAGGAGAGGAGACCCA	TRBV28	TRBJ2-5
PT.3	G	91.9	TGTGCCAGTAGTCACCCTCACACAGATACGCA	TRBV19	TRBJ2-3
PT.4	A	97.7	TGCGCCAGCAGCCAAGATAGAGAGCGGGAGGATCGCACAGATACGCA	TRBV4-1	TRBJ2-3
PT.5	C	93.4	TGTGCCAGCAGTTTGAAACACAAACCGGCAGTGGCGCGAGCTAACTATGGCTA	5	TRBJ1-2