Figure S1

Schematic of the in silico TCRminer and MiXCR validation.

1,000 in silico simulated alpha, beta, gamma and delta TCR repertoires were created. Then, 100,000 simulated 80 bp RNA-Seq reads were generated using R package Polyester(50). Number of reads recovered by TCRminer and MiXCR are shown.

Figure S2

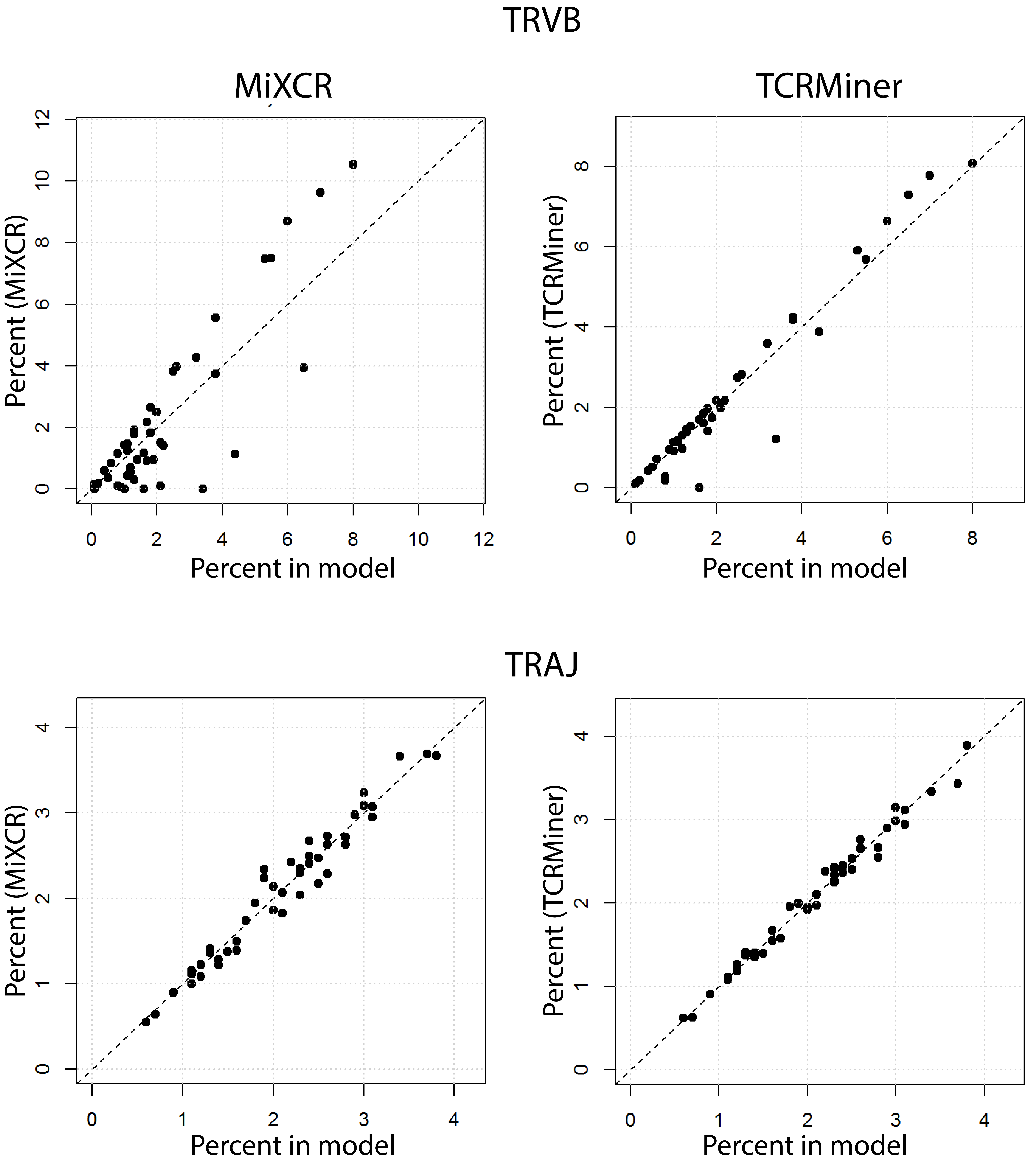
TCR gene segment recovery from in silico-generated simulated NGS TCR reads by TCRminer and MiXCR. V and J sequences were extracted from simulated RNA-Seq datasets using MiXCR or TCRMiner. The abundance of the recovered TCR sequences is plotted along the Y-axis. The abundance of the simulated TCR sequences is plotted on the X-axis.

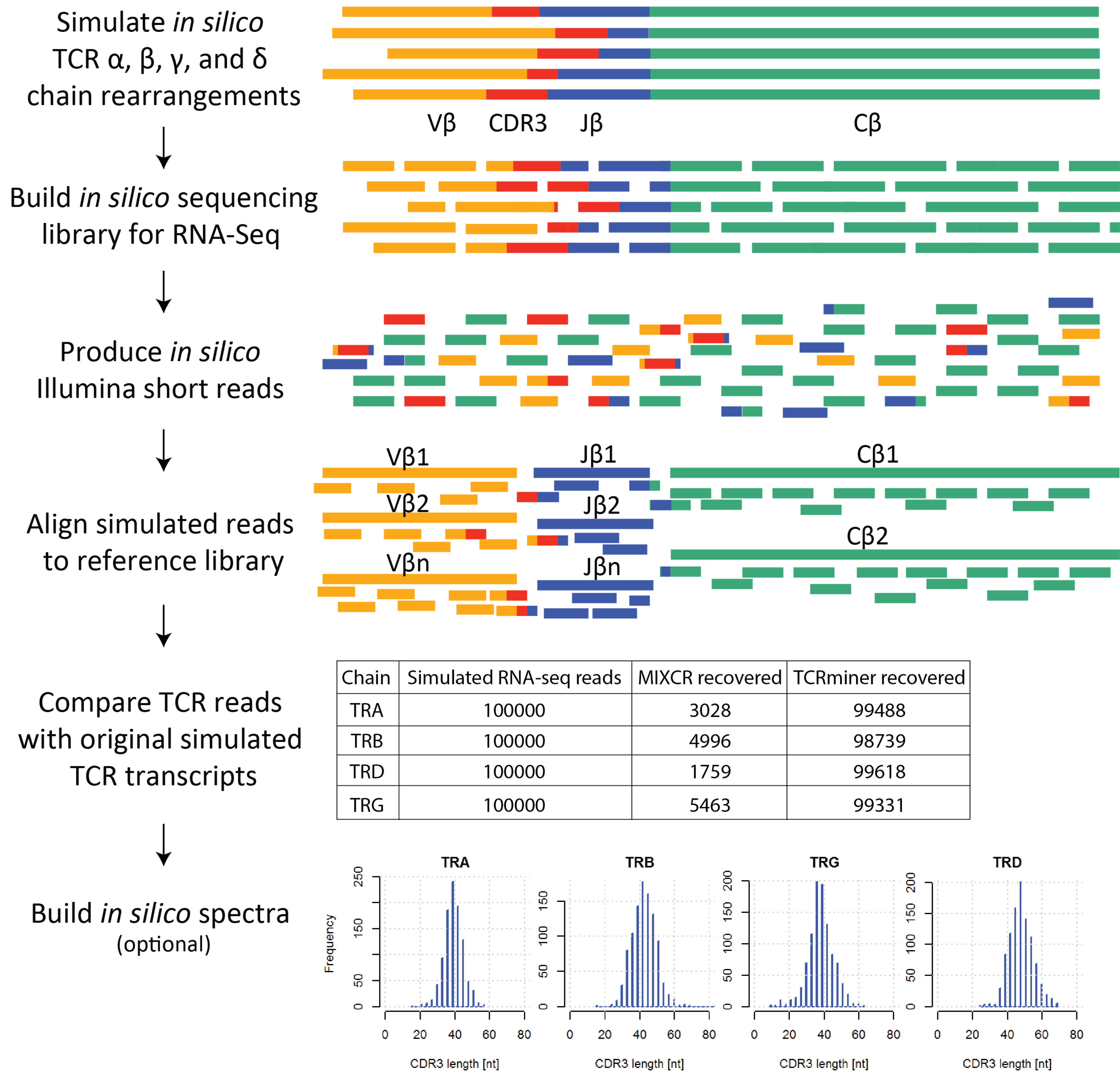
Figure S3

TCR gene correlations with T cell surface markers and transcription factors. For all graphs, discovery RNA-Seq dataset was used and the Spearman correlation coefficients and p-values are displayed on each plot. P-values for Spearman's test were calculated using the asymptotic t approximation. Significant correlations are outlined in blue. Psoriasis RNA-Seq datasets are depicted with red dots and healthy control RNA-Seq datasets are depicted with blue dots. **(A)** Scatter plots of *TRA* versus *TRB* and *TRG* versus *TRD* gene expression correlation levels in psoriatic plaque samples are shown. **(B)** Expression of *CCR6*, a psoriasis-associated T cell marker, correlated with both *TRB* and *TRD.* (**C)** *CD4* and *CD8A* correlations with *TRB* and *TRD* in healthy controls. **(D)** *TRB* and *TRD* correlation with transcription factors in psoriatic plaque samples.**(E)** Correlation of transcription factors with psoriasis-associated cytokines in psoriatic plaque samples.

Figure S4

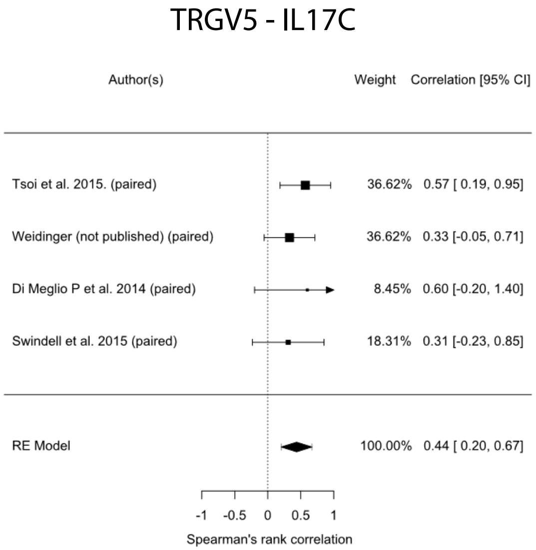
Meta-analysis of *TRGV5, TRAJ39* and *TRBV3-1* correlations with psoriasis-relevant cytokines. Differences in gene expressions were calculated (normalized gene expression of non-lesional samples were subtracted from their corresponding normalized gene expression within the matching lesional sample). Spearman correlation coefficients for differences in gene expressions were then calculated. Forest plots of correlation coefficients are shown. Each black box is representative of the study weight for each data set and horizontal lines are 95% CI. Diamonds represent Standardized Mean Differences for results of all studies combined. Extremes of diamonds give 95% CI.


TRVB
MiXCR
TCRMiner
Percent (MiXCR)
0
2
4
6
8
10
12
Percent in model
0
2
4
6
8
10
12
Percent (TCRMiner)
0
2
4
6
8
Percent in model
0
2
4
6
8
TRAJ
Percent (MiXCR)
0
1
2
3
4
Percent in model
0
1
2
3
4
Percent (TCRMiner)
0
1
2
3
4
Percent in model
0
1
2
3
4

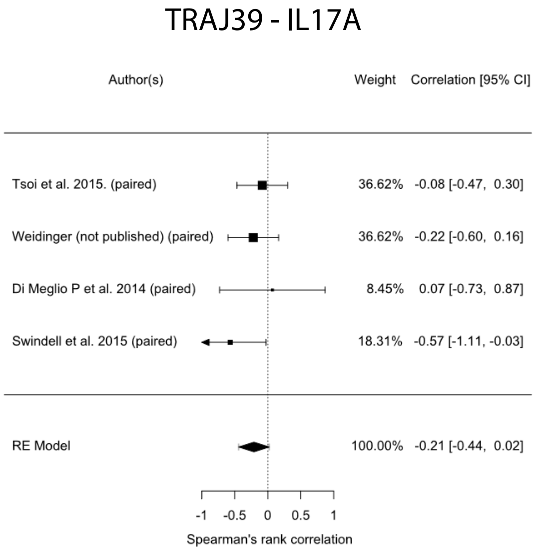


Chain	Simulated RNA-seq reads	MIXCR recovered	TCRminer recovered
TRA	100000	3028	99488
TRB	100000	4996	98739
TRD	100000	1759	99618
TRG	100000	5463	99331

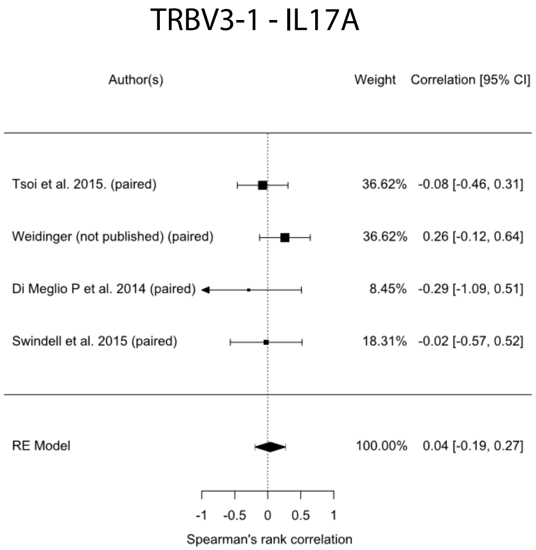

A
Psoriasis
Psoriasis lesion skin
r = 0.91, p.val: <2e-16
TRB
TRA
Psoriasis lesion skin
r = 0.5, p.val: 1.6e-07
TRD
TRG
B
Psoriasis
Psoriasis lesion skin
r = 0.5, p.val: 3.1e-07
CCR6
TRB
Psoriasis lesion skin
r = 0.32, p.val: 0.0015
TRD
C
Healthy Control
Normal skin
r = 0.53, p.val: 1.1e-07
CD4
TRB
Normal skin
r = -0.04, p.val: 0.68
TRD
Normal skin
r = 0.64, p.val: <2e-16
CD8
TRB
Normal skin
r = -0.18, p.val: 0.088
TRD
D
Psoriasis
Psoriasis lesion skin
r = 0.51, p.val: 1.6e-07
TBX21 (T-bet)
TRB
Psoriasis lesion skin
r = 0.28, p.val: 0.0047
TRD
Psoriasis lesion skin
r = 0, p.val: 0.96
GATA3
TRB
Psoriasis lesion skin
r = -0.27, p.val: 0.0068
TRD
Psoriasis lesion skin
r = 0.16, p.val: 0.11
RORC
TRB
Psoriasis lesion skin
r = 0.03, p.val: 0.73
TRD
Psoriasis lesion skin
r = 0.72, p.val: <2e-16
FOXP3
TRB
Psoriasis lesion skin
r = 0.22, p.val: 0.028
TRD
E
Transcription Factor Correlations
Psoriasis lesion skin
r = 0.41, p.val: 3.2e-05
TNF
TBX21
Psoriasis lesion skin
r = 0.55, p.val: 5.4e-09
IL12RB1
TBX21
Psoriasis lesion skin
r = 0.43, p.val: 8.5e-06
CXCL9
TBX21
Psoriasis lesion skin
r = 0.41, p.val: 3.4e-05
CXCL10
TBX21
Psoriasis lesion skin
r = 0.33, p.val: 0.00089
IL17B
RORC
Psoriasis lesion skin
r = -0.12, p.val: 0.24
IL17A
RORC
Psoriasis lesion skin
r = 0.51, p.val: 1.3e-07
CCL27
GATA3
Psoriasis lesion skin
r = 0.37, p.val: 0.00023
IL34
GATA3
Psoriasis lesion skin
r = 0.33, p.val: 0.0011
IL37
GATA3
Psoriasis lesion skin
r = 0.29, p.val: 0.0045
IL18
GATA3
Psoriasis lesion skin
r = -0.14, p.val: 0.16
IL17F
RORC
Psoriasis lesion skin
r = -0.24, p.val: 0.018
IL17C
RORC
Psoriasis lesion skin
r = 0.24, p.val: 0.015
IFNG
STAT1
Psoriasis lesion skin
r = 0.57, p.val: 9.4e-10
IL12RB2
STAT1
Psoriasis lesion skin
r = 0.32, p.val: 0.0013
IL36A
STAT1
Psoriasis lesion skin
r = 0.49, p.val: 5.2e-07
CXCL9
STAT1
Psoriasis lesion skin
r = 0.44, p.val: 7.8e-06
CXCL10
STAT1
Psoriasis lesion skin
r = 0.67, p.val: <2e-16
CCL22
FOXP3
Psoriasis lesion skin
r = 0.59, p.val: <2e-16
CTLA4
FOXP3
Psoriasis lesion skin
r = 0.56, p.val: 4.1e-09
CCL19
FOXP3
Psoriasis lesion skin
r = 0.49, p.val: 5.6e-07
IDO1
FOXP3
Psoriasis lesion skin
r = 0.46, p.val: 3.1e-06
LAG3
FOXP3
0
20
40
60
80
100


TRGV5 - IL17C

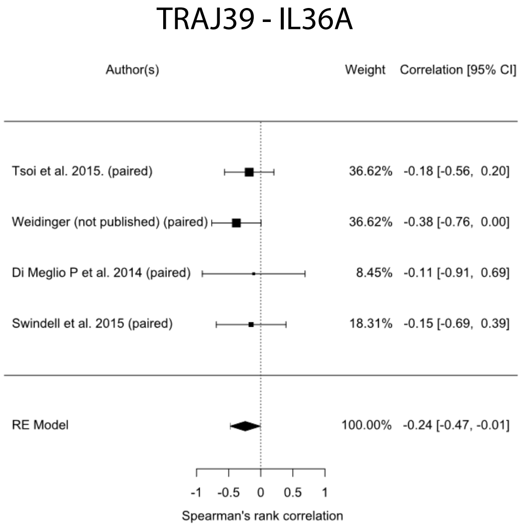
Author(s)	Weight	Correlation [95% CI]
Tsoi et al. 2015. (paired)	36.62%	0.57 [0.19, 0.95]
Weidinger (not published) (paired)	36.62%	0.33 [-0.05, 0.71]
Di Meglio P et al. 2014 (paired)	8.45%	0.60 [-0.20, 1.40]
Swindell et al. 2015 (paired)	18.31%	0.31 [-0.23, 0.85]
RE Model	100.00%	0.44 [0.20, 0.67]


TRAJ39 - IL17A

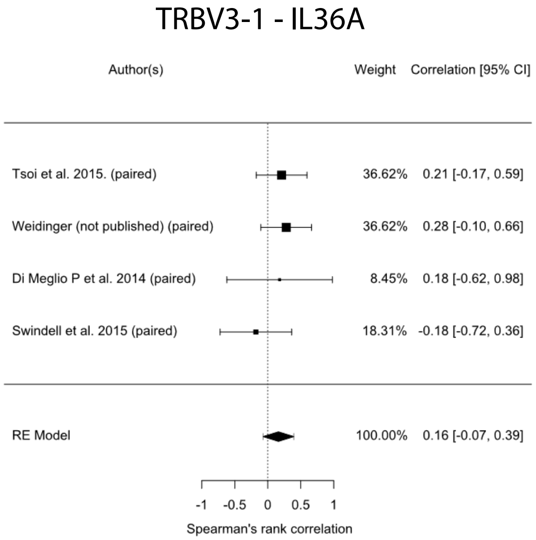
Author(s)	Weight	Correlation [95% CI]
Tsoi et al. 2015. (paired)	36.62%	-0.08 [-0.47, 0.30]
Weidinger (not published) (paired)	36.62%	-0.22 [-0.60, 0.16]
Di Meglio P et al. 2014 (paired)	8.45%	0.07 [-0.73, 0.87]
Swindell et al. 2015 (paired)	18.31%	-0.57 [-1.11, -0.03]
RE Model	100.00%	-0.21 [-0.44, 0.02]


TRBV3-1 - IL17A

Author(s)	Weight	Correlation [95% CI]
Tsoi et al. 2015. (paired)	36.62%	-0.08 [-0.46, 0.31]
Weidinger (not published) (paired)	36.62%	0.26 [-0.12, 0.64]
Di Meglio P et al. 2014 (paired)	8.45%	-0.29 [-1.09, 0.51]
Swindell et al. 2015 (paired)	18.31%	-0.02 [-0.57, 0.52]
RE Model	100.00%	0.04 [-0.19, 0.27]


TRAJ39 - IL36A

Author(s)	Weight	Correlation [95% CI]
Tsoi et al. 2015. (paired)	36.62%	-0.18 [-0.56, 0.20]
Weidinger (not published) (paired)	36.62%	-0.38 [-0.76, 0.00]
Di Meglio P et al. 2014 (paired)	8.45%	-0.11 [-0.91, 0.69]
Swindell et al. 2015 (paired)	18.31%	-0.15 [-0.69, 0.39]
RE Model	100.00%	-0.24 [-0.47, -0.01]


TRBV3-1 - IL36A

Author(s)	Weight	Correlation [95% CI]
Tsoi et al. 2015. (paired)	36.62%	0.21 [-0.17, 0.59]
Weidinger (not published) (paired)	36.62%	0.28 [-0.10, 0.66]
Di Meglio P et al. 2014 (paired)	8.45%	0.18 [-0.62, 0.98]
Swindell et al. 2015 (paired)	18.31%	-0.18 [-0.72, 0.36]
RE Model	100.00%	0.16 [-0.07, 0.39]

Supplementary Tables

Table S1. Benchmarking TCR extraction efficiency by rna-seq of cultured skin cells with no TCR

Extraction TCR rearranged clones with MIXCR - Human

Cell type	Sample	Total reads	TRA	TRB	TRG	TRD
Fibroblast	ENCFF065GSV	43710884	0	0	0	0
Fibroblast	ENCFF509HFH	23119342	0	0	0	0
Fibroblast	ENCFF627NPY	45481510	0	0	0	0
Fibroblast	ENCFF737TKD	22008878	0	0	0	0
Keratinocyte	ENCFF000IDC	98244162	0	0	0	0
Keratinocyte	ENCFF000IDF	108353593	0	0	0	0
Keratinocyte	SRR403879	68505523	0	0	0	0
Keratinocyte	SRR403880	79128508	0	0	0	0
Keratinocyte	SRR403881	79079729	0	0	0	0
Total per millon RNA-Seq reads			<0.001	<0.001	<0.001	<0.001

Extraction TCR reads with TCRminer - Human

Cell type	Sample	Total reads	TRA	TRB	TRG	TRD
Fibroblast	ENCFF065GSV	43710884	7	6	7	0
Fibroblast	ENCFF509HFH	23119342	3	3	1	0
Fibroblast	ENCFF627NPY	45481510	7	5	4	0
Fibroblast	ENCFF737TKD	22008878	2	2	3	0
Keratinocyte	ENCFF000IDC	98244162	35	6	0	0
Keratinocyte	ENCFF000IDF	108353593	69	5	0	0
Keratinocyte	SRR403879	68505523	12	40	0	0
Keratinocyte	SRR403880	79128508	30	9	0	0
Keratinocyte	SRR403881	79079729	5	11	0	0
Total per millon RNA-Seq reads			0.3	0.2	0.03	<0.002

Table S2. Benchmarking TCR extraction efficiency using simulated data

MIXCR test with simulated TCR transcriptome

	TRA	TRB	TRG	TRD
Simulated clones	1000	1000	1000	1000
Found clones	1000	1000	998	1000
Not uniquely or incorrect identified V-regions	0	0	0	0
Not uniquely or incorrect identified J-regions	0	0	450	0
CDR3 errors	0	0	0	0
TCRminer test with simulated TCR transcriptome				
Simulated clones	1000	1000	1000	1000
Found TCR chains	1000	1000	1000	1000
Found V-regions	1000	1000	1000	1000
Found J-regions	992	986	963	988
Not uniquely or incorrect identified V-regions	0	16	0	0
Not uniquely or incorrect identified J-regions	0	0	259	0

Table S3. TCR recovery rate using simulated data

Chain	Simulated RNA-Seq reads	MiXCR recovery rate	TCR miner recovery rate	MiXCR recovery percent	TCR miner recovery percent
TRA	100000	3028	99488	3.03	99.49
TRB	100000	4996	98739	5.00	98.74
TRD	100000	1759	99618	1.76	99.62
TRG	100000	5463	99331	5.46	99.33

Table S4. TCR V/J gene usage in the setting of psoriasis vs healthy controls in Tsoi et al. 2015 dataset.

TCR Segment	Normal	Psoriasis	Segment Type		Fold Change	p-value	FDR	Bonferroni
			Normal	Psoriasis				
TRAJ12	6.92e-03	1.41e-02	26	56	2.04	1.22e-04	1.24e-03	2.48e-02
TRAJ23	2.69e-02	7.01e-02	55	89	2.60	3.03e-29	3.09e-27	6.19e-27
TRAJ39	0.34	9.66e-02	90	88	0.29	7.02e-251	1.43e-248	1.43e-248
TRAJ43	7.5e-03	1.5e-02	28	54	2.00	1.03e-04	1.23e-03	2.10e-02
TRAJ44	9.61e-03	1.99e-02	32	63	2.07	2.61e-06	5.33e-05	5.33e-04
TRB20/OR9-2	1.94e-03	5.45e-04	17	39	0.28	1.21e-04	1.24e-03	2.47e-02
TRBV26/OR9-2	1.1e-02	2.84e-03	56	10	0.26	7.93e-22	5.39e-20	1.62e-19
TRBV3-2	4.47e-03	1.27e-03	36	27	0.28	6.57e-09	1.91e-07	1.34e-06
TRBV5-7	5.06e-04	7.27e-05	5	2	0.14	1.16e-02	4.14e-02	1.00
TRBV5-8	1.18e-03	2.58e-03	13	38	2.19	6.08e-03	2.59e-02	1.00
TRGV5	9.01e-02	0.17	60	77	1.88	2.96e-16	1.51e-13	6.03e-13
TRGVA	1.88e-02	1.88e-03	20	6	0.10	3.12e-10	1.09e-08	6.37e-08

Table S5. Unpaired analysis of TCR V/J gene usage for lesional versus non-lesional samples in Tsoi et al. 2015 dataset.

TCR Segment	Normal	Psoriasis	Segment Type		Sample Number		Fold Change	p-value	FDR	Bonferroni
			Normal	Psoriasis	Normal	Psoriasis				
TRAJ13	20	64	1751	2772	15	23	2.02	4.50e-03	3.12e-02	8.73e-01
TRAJ23	41	198	1751	2772	19	27	3.05	1.81e-13	1.75e-11	3.51e-11
TRAJ32	22	71	1751	2772	14	22	2.04	2.45e-03	1.98e-02	4.75e-01
TRAJ34	15	52	1751	2772	10	20	2.19	5.25e-03	3.51e-02	1.00e+00
TRAJ39	525	260	1751	2772	27	26	0.31	3.23e-69	6.26e-67	6.26e-67
TRAJ42	23	78	1751	2772	14	22	2.14	8.57e-04	1.04e-02	1.66e-01
TRAJ5	23	81	1751	2772	13	26	2.22	3.32e-04	4.30e-03	6.45e-02
TRBV26/OR9-2	52	32	4405	9741	19	14	0.28	7.65e-09	3.71e-07	1.48e-06
TRBV29/OR9-2	54	56	4405	9741	17	21	0.47	1.08e-04	1.49e-03	2.09e-02
TRBV3-1	33	180	4405	9741	16	27	2.47	1.97e-07	7.63e-06	3.82e-05
TRBV3-2	21	10	4405	9741	13	9	0.22	3.91e-05	6.32e-04	7.59e-03
TRBV5-5	48	47	4405	9741	13	16	0.44	8.29e-05	1.24e-04	1.61e-02
TRGV5	53	193	567	1079	20	23	1.91	2.82e-06	5.46e-05	5.46e-04
TRGVA	8	2	567	1079	7	2	0.13	4.20e-03	3.02e-02	8.15e-01

Table S6. TCR V/J gene usage in the setting of psoriasis vs healthy controls in Weidinger dataset

TCR Segment	Normal	Psoriasis	Segment Type		Sample Number		Fold Change	p-value	FDR	Bonferroni
			Normal	Psoriasis	Normal	Psoriasis				
TRAJ22	39	95	2005	2334	18	23	2.09	4.60e-05	1.05e-03	9.47e-03
TRAJ23	57	221	2005	2334	23	23	3.33	5.15e-20	5.30e-18	1.06e-17
TRAJ39	332	75	2005	2334	37	23	0.19	1.92e-53	3.96e-51	3.96e-51
TRAJ9	18	48	2005	2334	12	14	2.29	1.76e-03	2.42e-02	3.63e-01
TRAV12-2	17	143	794	2346	10	23	2.85	3.58e-06	1.23e-04	7.37e-04
TRBV12-4	6	56	1363	3212	6	20	3.96	2.17e-04	3.86e-03	4.47e-02
TRBV20/OR9-2	6	1	1363	3212	5	1	0.07	3.62e-03	4.39e-02	7.46e-01
TRBV26/OR9-2	24	17	1363	3212	12	6	0.30	1.94e-04	3.86e-03	3.99e-02
TRBV3-2	44	19	1363	3212	19	10	0.18	4.67e-11	3.21e-09	9.63e-09
TRBV30	48	39	1363	3212	26	16	0.34	6.85e-07	2.82e-05	1.41e-04
TRBV5-3	5	0	1363	3212	3	0	0.00	2.33e-03	3.01e-02	4.81e-01
TRBV7-9	24	175	1363	3212	14	23	3.09	2.54e-09	1.31e-07	5.23e-07
TRDV3	18	5	74	101	11	5	0.20	2.25e-04	3.86e-03	4.63e-02
TRGV5	14	89	332	709	9	18	2.98	1.10e-05	3.24e-04	2.27e-03
TRGVA	6	7	332	709	5	3	0.55	3.68e-01	7.02e-01	1.00e+00

Table S7. Association between HLA-C*06 and TCR V- J- gene usage in psoriasis in Tsoi et al. 2015 dataset.

TCR Segment	Other HLA	HLA-C06	Sample Number		Fold change	p-value	FDR	Bonferroni
			Other HLA	HLA-C06				
TRAJ40	2.36e-02	8.90e-03	33	24	0.41	4.99e-06	6.62e-04	1.02e-03
TRBV26/ OR9-2	2.07e-03	3.79e-03	14	24	2.10	1.88e-03	3.03e-02	3.83e-01

Table S8. Association between HLA-C*06 and TCR V- J- gene usage in healthy individuals in Tsoi et al. 2015 dataset.

TCR Segment	Other HLA	HLA-C06	Sample Number		Fold change	p-value	FDR	Bonferroni
			Other HLA	HLA-C06				
TRAV38-1	3.33e-02	9.56e-03	37	16	2.04	2.32e-05	1.58e-03	4.74e-03
TRBV15-2	4.53e-02	7.71e-03	50	13	0.44	4.83e-05	1.97e-03	9.85e-03
TRAJ3	5.36e-02	1.59e-03	37	5	0.24	1.04e-04	3.52e-03	2.11e-02
TRAJ33	2.69e-02	8.16e-03	24	9	2.55	1.83e-04	5.05e-03	3.74e-02
TRBV23-1	9.89e-03	3.77e-03	20	5	2.61	1.98e-04	5.05e-03	4.04e-02
TRBV14	3.23e-02	2.14e-03	39	10	0.45	7.64e-04	1.42e-02	1.56e-01
TRBV24	4.33e-02	3.00e-03	39	12	0.48	1.45e-03	2.46e-02	2.95e-01

Table S9. T cell clones that were discovered in multiple psoriatic plaques or control biopsies

Chain	AA. Seq. CDR3	Normal skin samples	Psoriasis lesional skin samples
TRA	CAVNDYKLSF	1	4
TRA	CAVMDSSYKLIF	0	3
TRA	CAAMDSSYKLIF	0	2
TRA	CALDAGNNRKLIW	0	2
TRA	CALDSGGYQKVTF	0	2
TRA	CALNTDKLIF	1	1
TRA	CALYSGGGADGLTF	0	2
TRA	CAVNGNARLMF	0	2
TRA	CAVNRDDKIIF	0	2
TRA	CAVQGSQGNLIF	2	0
TRA	CAVRDGDYKLSF	1	1
TRA	CAVRRMDSSYKLIF	0	2
TRA	CAVSGTGRRALTF	0	2
TRA	CAVSNQAGTALIF	0	2
TRA	CAVYSGAGSYQLTF	0	2
TRA	CLVGYNTDKLIF	1	1
TRB	CASSDSSGSYNEQFF	2	0
TRB	CASSTINSPLHF	1	1
TRB	CATSRDSNTGVGNQPQHF	0	2
TRG	CATWD_DKKLF	1	1

Table S10. The Shannon Diversity Index for healthy and psoriatic CDR3 sequences

Chain	Healthy Control	Psoriasis	p-value
TRA	1.6 +- 0.07	2.1 +- 0.1	1.34e-07
TRB	1.6 +- 0.08	2.2 +- 0.1	3.70e-08

Table S11. The Shannon Diversity Index for healthy and psoriatic V/J sequences

Chain	Healthy Control	Psoriasis	p-value
TRA	3.5 +- 0.04	3.8 +- 0.05	1.14e-14
TRB	3.2 +- 0.03	3.4 +- 0.04	2.57e-08
TRG	1.6 +- 0.04	1.7 +- 0.5	1.31e-01
TRD	0.79+- 0.05	0.91 +- 0.5	9.41e-02

Table S12. TCR gene segments correlation with T cell markers

TCRminer								
Gene	**TRA**	**TRA p-val**	**TRB**	**TRB p-val**	**TRG**	**TRG p-val**	**TRD**	**TRD p-val**
CD4	0.58	3.6e-10	0.61	<2e-16	0.41	2.9e-05	0.47	1.5e-06
CD8A	0.64	<2e-16	0.67	<2e-16	0.5	1.8e-07	0.22	0.027
GATA3	-0.04	0.69	0	0.97	-0.13	0.19	-0.27	0.007
TBX21	0.49	5.5e-07	0.51	1.6e-07	0.42	1.7e-05	0.28	0.0047
RORC	0.04	0.67	0.16	0.11	-0.02	0.86	0.03	0.73

MIXCR								
Gene	**TRA clones**	**TRA clones p-val**	**TRB clones**	**TRB clones p-val**	**TRG clones**	**TRG clones p-val**	**TRD clones**	**TRD clones p-val**
CD4	0.56	2.9e-09	0.53	1.5e-08	0.33	0.00098	NA	NA
CD8A	0.45	2.7e-06	0.26	0.01	0.22	0.035	NA	NA
GATA3	-0.02	0.84	0.11	0.3	0.16	0.11	NA	NA
TBX21	0.44	4.4e-06	0.28	0.0043	0.15	0.15	NA	NA
RORC	0.07	0.48	0.08	0.45	0.11	0.29	NA	NA

Table S13. TCRminer correlation with psoriasis-related genes

Gene	TRA	TRA p-val	TRB	TRB p-val	TRG	TRG p-val	TRD	TRD p-val
IFNG	0.23	0.021	0.19	0.057	0.2	0.05	0.12	0.24
IL1A	-0.09	0.4	-0.11	0.29	0.02	0.86	0.05	0.65
IL1B	0.13	0.22	0.14	.17	0.2	0.044	0.15	0.15
IL6	0.05	0.61	0.03	0.76	0.08	0.46	0.23	0.024
IL6R	0.28	0.0048	0.3	0.0027	0.2	0.051	-0.03	0.74
IL8	-0.08	0.45	-0.03	0.79	0.04	0.68	0.12	0.24
IL12A	0.17	0.1	0.11	0.28	-0.07	0.47	-0.06	0.55
IL12B	0.11	0.28	0.05	0.62	0.17	0.1	0.2	0.044
IL17A	0.13	0.22	0.06	0.54	0.03	0.75	-0.08	0.44
IL17B	0.13	0.19	0.11	0.26	0.1	0.32	0.31	0.002
IL17C	0.15	0.15	0.19	0.057	0.03	0.76	-0.02	0.83
IL17D	0.18	0.075	0.15	0.15	-0.03	0.76	0.01	0.96
IL17F	0.1	0.31	0.11	0.3	0.06	0.58	0	0.97
IL17RA	0.3	0.0032	0.39	8.3e-05	0.28	0.0057	0.1	0.32
IL17RC	0.13	0.21	0.28	0.0051	-0.15	0.14	-0.15	0.14
IL18	-0.2	0.051	-0.24	0.019	-0.18	0.087	-0.13	0.21
IL22	0.01	0.92	0.03	0.8	0.14	0.17	0.04	0.72
IL22RA1	-0.05	0.63	0.09	0.38	-0.03	0.77	-0.29	0.0035
IL22RA2	0.14	0.17	0.03	0.75	0.15	0.14	0.13	0.2
IL23A	0.07	0.47	0.16	0.13	0.18	0.076	-0.07	0.51
IL23R	0.2	0.045	0.12	0.23	0.1	0.34	0.22	0.034
CXCL3	0.2	0.046	0.23	0.024	0.24	0.019	0.21	0.037
CXCL5	0.01	0.96	-0.02	0.85	0.21	0.034	0.22	0.031
CCR6	0.57	1.6e-09	0.5	3.1e-07	0.49	2.7e-07	0.32	0.0015
CCL20	-0.17	0.1	-0.26	0.009	-0.06	0.56	0.03	0.75
TNF	0.63	<2e-16	0.6	<2e-16	0.45	3.5e-06	0.25	0.015
TNFSF11	0.38	9.9e-05	0.41	3.3e-05	0.37	0.00016	0.25	0.014
TGFB1	0.47	1.7e-06	0.6	<2e-16	0.2	0.043	0.17	0.088
TGFB2	-0.23	0.023	-0.34	0.00056	-0.01	0.94	0.26	0.0097
TGFB3	0.22	0.031	0.23	0.024	0.24	0.017	0.5	2.6e-07
RORgammaT	-0.02	0.84	0.06	0.53	0.07	0.52	0.08	0.45

Table S14. TCR gene segments correlation with IL-17

TRGV

Gene	**IL17A**	**P-val**
TRGV1	0.03	0.76
TRGV10	0.01	0.94
TRGV2	-0.05	0.64
TRGV3	0.02	0.83
TRGV4	-0.01	0.9
TRGV5	-0.01	0.9
TRGV5P	0.04	0.7
TRGV8	0.1	0.35
TRGV9	0.13	0.21

TRDV

Gene	**IL17A**	**P-val**
TRDV1	-0.01	0.94
TRDV2	-0.09	0.36
TRDV3	-0.09	0.39

TRBV

Gene	**IL17A**	**P-val**
TRBV10-1	0.02	0.87
TRBV10-2	0.11	0.28
TRBV10-3	0.04	0.68
TRBV11-1	-0.02	0.86
TRBV11-2	-0.05	0.61
TRBV11-3	0.12	0.26
TRBV12-3	-0.04	0.67
TRBV12-4	-0.08	0.44
TRBV12-5	-0.04	0.68
TRBV13	-0.11	0.29
TRBV14	0.11	0.29
TRBV15	0.01	0.95
TRBV18	0.16	0.11
TRBV19	-0.01	0.94
TRBV2	0.07	0.52
TRBV20-1	0.08	0.42
TRBV21-1	-0.14	0.18
TRBV23-1	-0.04	0.72
TRBV24-1	0.14	0.19
TRBV25-1	0.21	0.037
TRBV26/OR9-2	0.01	0.89
TRBV27	0	0.99
TRBV28	0.01	0.92
TRBV29-1	-0.01	0.89
TRBV29/OR9-2	0.07	0.52
TRBV3-1	-0.01	0.94
TRBV3-2	-0.04	0.69
TRBV30	-0.01	0.91

TRBV4-1	0.05	0.64
TRBV4-2	0.07	0.52
TRBV4-3	0.01	0.95
TRBV5-1	0.14	0.18
TRBV5-4	0.12	0.25
TRBV5-5	-0.05	0.62
TRBV5-6	0.08	0.45
TRBV5-8	0.12	0.23
TRBV6-1	0.04	0.67
TRBV6-4	0.15	0.15
TRBV6-5	-0.1	0.34
TRBV6-6	-0.1	0.33
TRBV7-2	-0.15	0.15
TRBV7-3	-0.13	0.21
TRBV7-6	-0.04	0.72
TRBV7-7	0.19	0.068
TRBV7-8	0	1
TRBV7-9	0.08	0.43
TRBV9	0.13	0.21

TRAV

Gene	IL17A	P-val
TRAV1-1	0.12	0.22
TRAV1-2	0.13	0.22
TRAV10	-0.07	0.52
TRAV12-1	0.06	0.55
TRAV12-2	0.04	0.68
TRAV12-3	0.07	0.49
TRAV13-1	0.06	0.56
TRAV13-2	0.12	0.23
TRAV14/DV4	0.03	0.74
TRAV16	0.08	0.42
TRAV17	0.05	0.6
TRAV18	0.19	0.067
TRAV19	0.07	0.52
TRAV2	-0.03	0.81
TRAV20	-0.02	0.87
TRAV21	0.04	0.69
TRAV22	-0.07	0.48
TRAV23/DV6	-0.04	0.69
TRAV24	0	0.99
TRAV25	0.09	0.4
TRAV26-1	0.21	0.039
TRAV26-2	-0.04	0.67
TRAV27	0.07	0.48
TRAV29/DV5	0.22	0.029
TRAV3	0.12	0.23
TRAV30	0.1	0.31
TRAV34	0.11	0.3
TRAV35	0.06	0.53

TRAV36/DV7	0.08	0.46
TRAV38-1	0.02	0.85
TRAV38-2/DV8	-0.13	0.2
TRAV39	0	0.98
TRAV4	0.18	0.075
TRAV41	0	0.99
TRAV5	-0.07	0.5
TRAV6	0.18	0.082
TRAV8-1	0.07	0.52
TRAV8-2	0	0.98
TRAV8-3	-0.03	0.75
TRAV8-4	0.13	0.19
TRAV8-6	0	0.99
TRAV9-2	0.14	0.19

Table S15. TRGV5 correlation with IL-36 genes

Gene	Correlation	p-val	FDR
IL36A	0.43	9.9e-06	4e-05
IL36B	0.36	0.00041	0.00082
IL36RN	0.32	0.00154	0.00205
IL36G	0.29	0.00407	0.00407