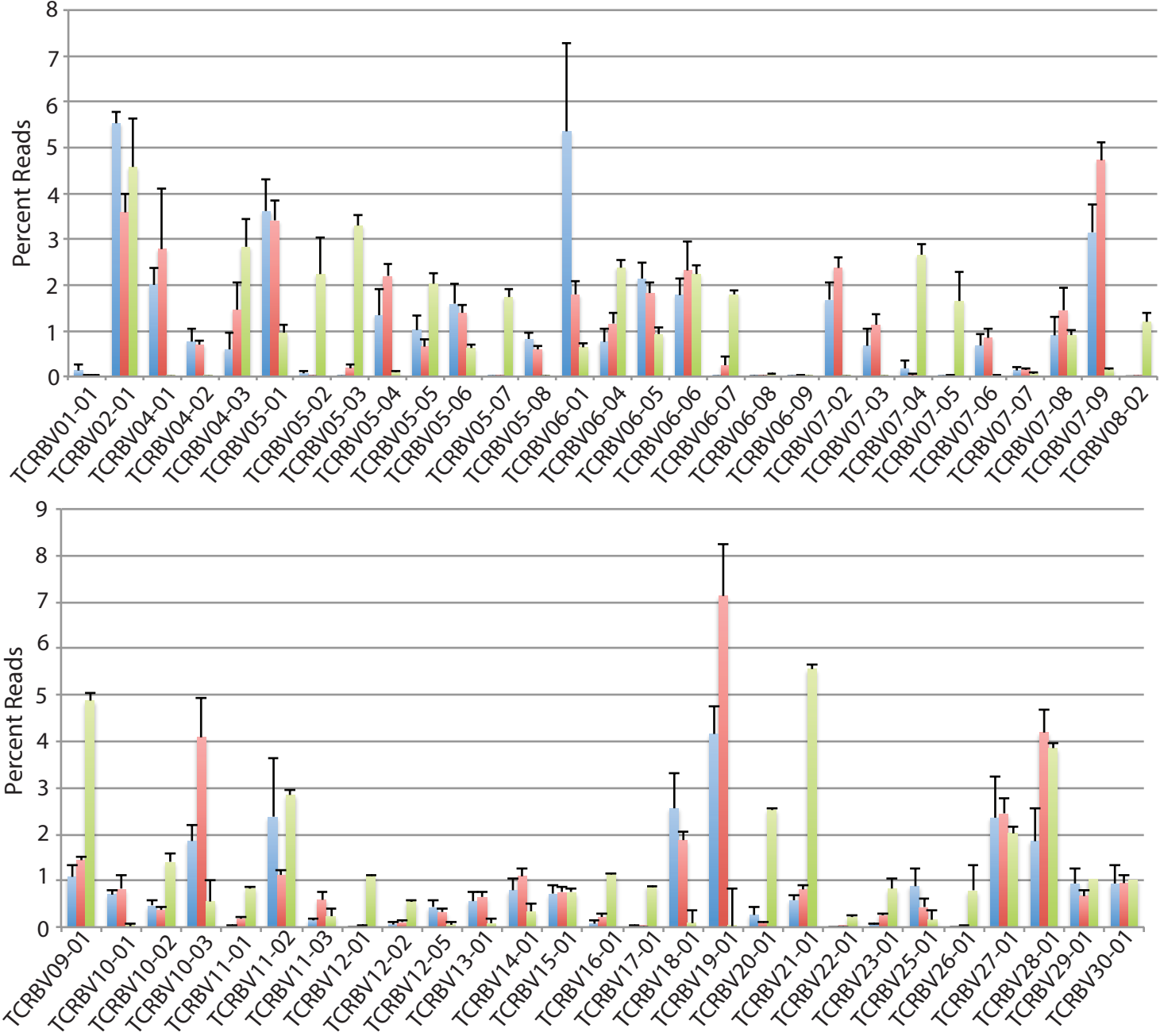


Table S1 – Patient demographics and study information

Sample	Disease Severity (PASI)	Gender	Age (y)	Ethnicity	gDNA (β -chain sequencing)	cDNA (γ -chain sequencing)
Normal 1	n/a	M	41	Black	Y	N
Normal 2	n/a	M	48	Unidentified	Y	N
Normal 3	n/a	M	52	Black	Y	Y
Normal 4	n/a	F	46	Black	Y	Y
Normal 5	n/a	M	55	Black	Y	Y
Normal 6	n/a	M	43	Black	N	Y
Normal 7	n/a	M	40	Black	N	Y
Non-lesional 1	Moderate-severe (17.8)	F	57	Hispanic/Latino	Y	Y
Non-lesional 2	Moderate-severe (26)	M	42	Hispanic/Latino	Y	Y
Non-lesional 3	Moderate-severe (21)	F	62	White	Y	Y
Non-lesional 4	Moderate-severe (32.7)	M	44	Hispanic/Latino	Y	Y
Non-lesional 5	Moderate-severe (12)	M	23	White	Y	Y
Lesional 1	Moderate-severe (17.8)	F	57	Hispanic/Latino	Y	Y
Lesional 2	Moderate-severe (26)	M	42	Hispanic/Latino	Y	Y
Lesional 3	Moderate-severe (21)	F	62	White	Y	Y
Lesional 4	Moderate-severe (32.7)	M	44	Hispanic/Latino	Y	Y
Lesional 5	Moderate-severe (12)	M	23	White	Y	Y
Lesional 6	Moderate-severe (20.5)	M	69	White	Y	N
Lesional 7	Moderate-severe (n/a)	M	63	Asian	Y	N
Lesional 8	Moderate-severe (n/a)	M	25	Black	Y	N

Figure S1

a. TCR β V genes



b. TCR β J genes

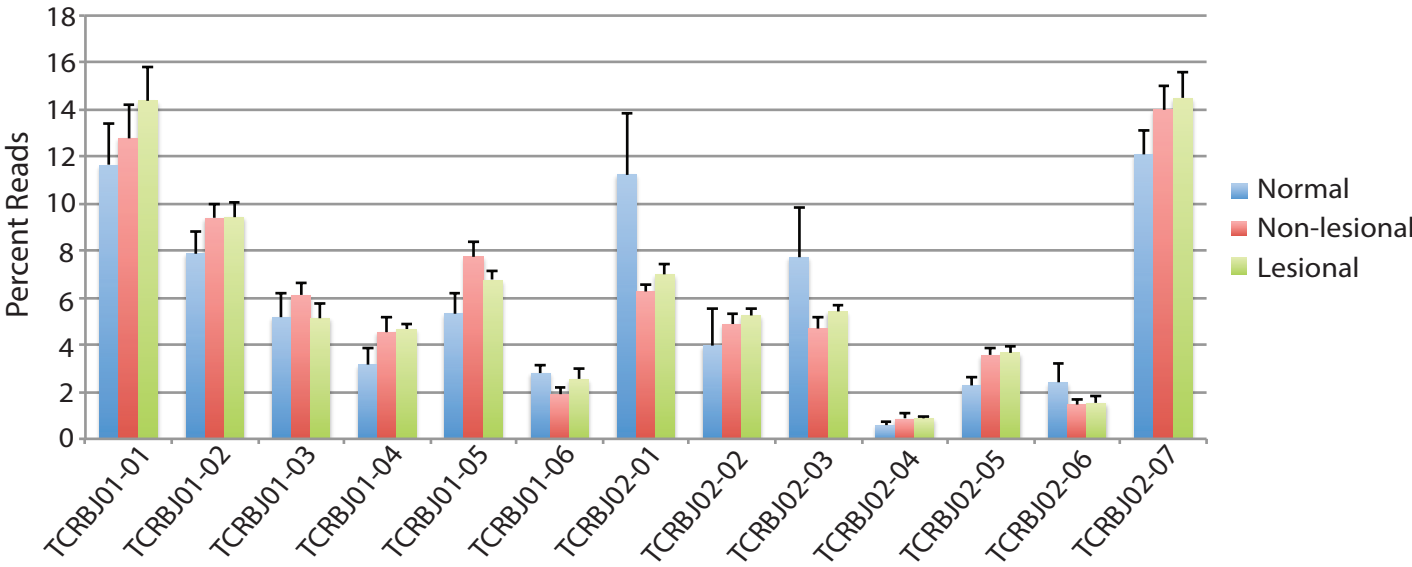


Figure S1 continued

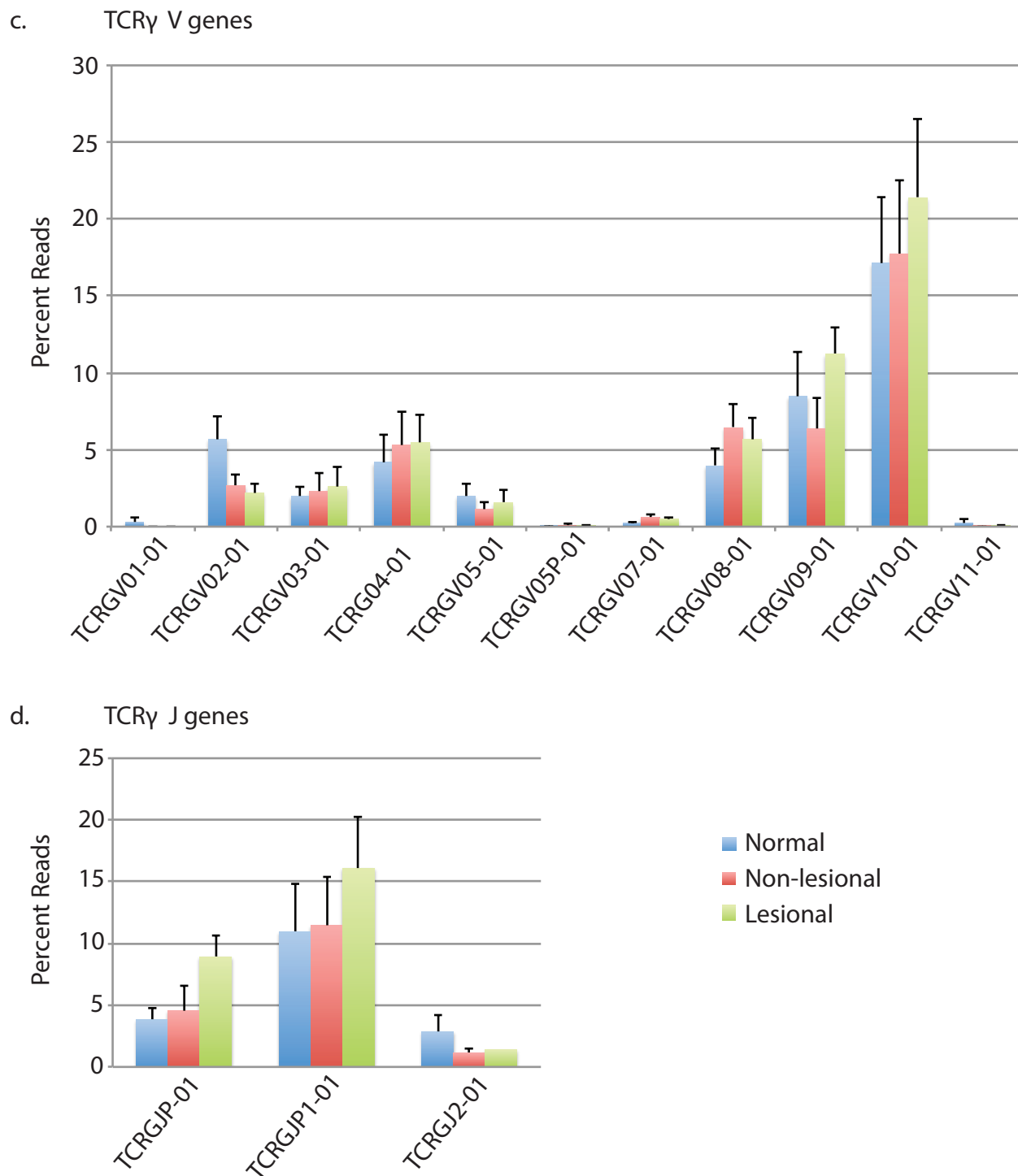


Figure S1: The expression of all TCR γ and TCR β V- and J- genes in normal, non-lesional and lesional skin. The percent of reads of a gene in normal (blue), non-lesional (red), or lesional (green) skin is shown for (a) TCR β -V genes, (b) TCR β -J genes, (c) TCR γ -V genes, and (d) TCR γ -J genes. n = 5 for normal, n = 5 for non-lesional, and n = 8 for lesional. Error bars = S.E.M.