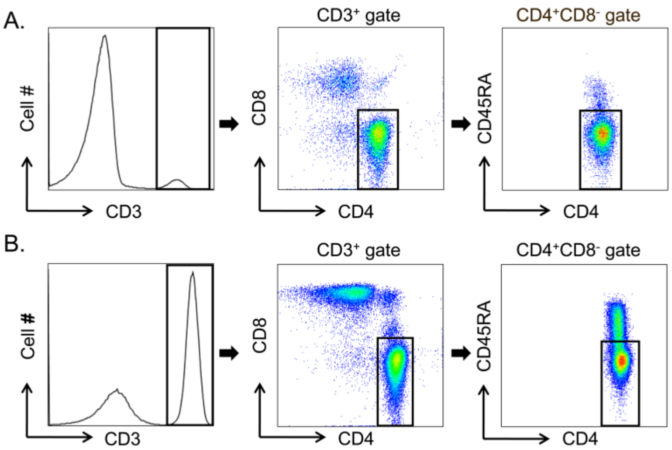
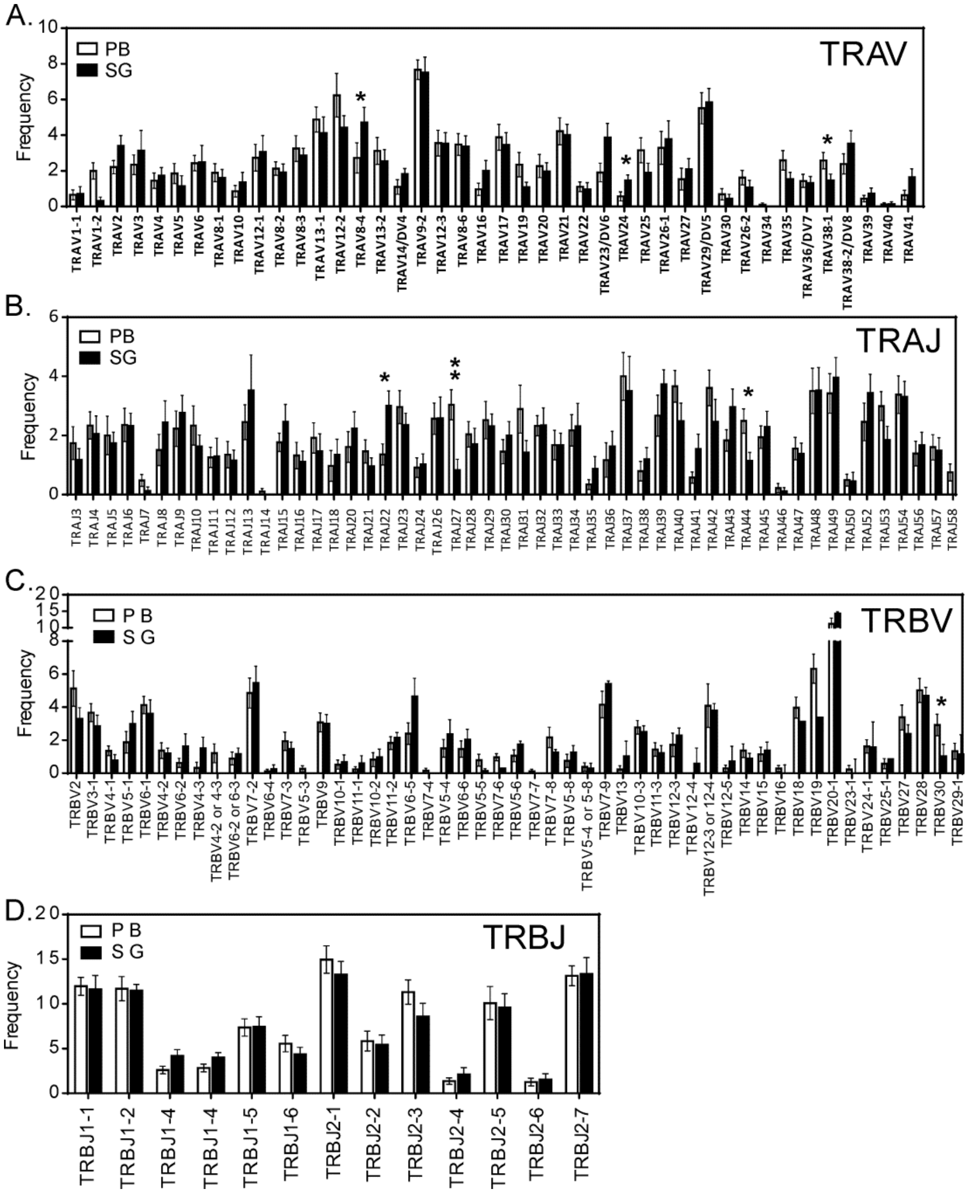
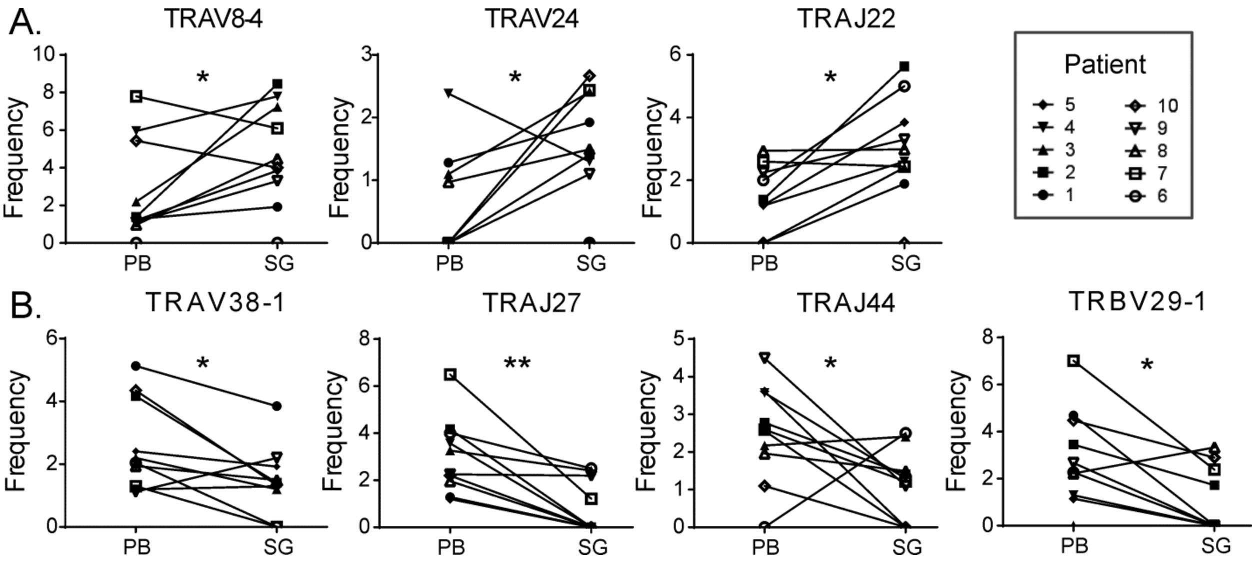


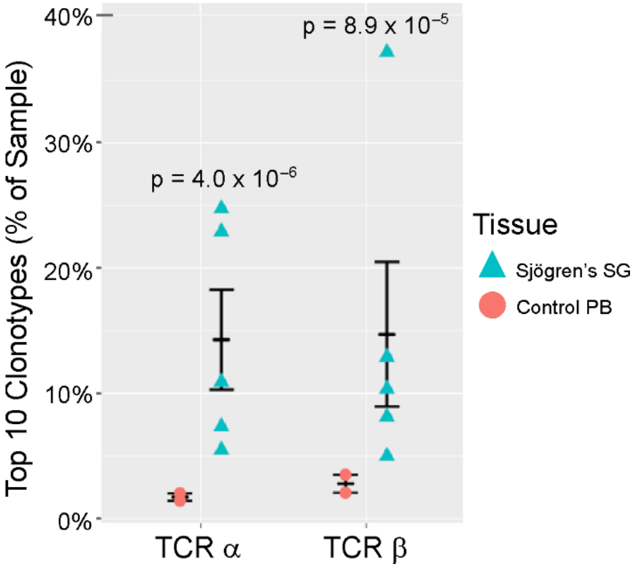
Supplemental Figure 1. Gating scheme for sorting antigen-experienced CD4$^+$ T cells from salivary gland (SG) and peripheral blood (PB). CD3$^+$CD4$^+$CD8$^-$CD45RA$^-$ T cells were bulk sorted from SG (**A**) or PB (**B**) single cell suspensions prior to single cell sorting into 96-well PCR plates. Boxes depict successive gates.



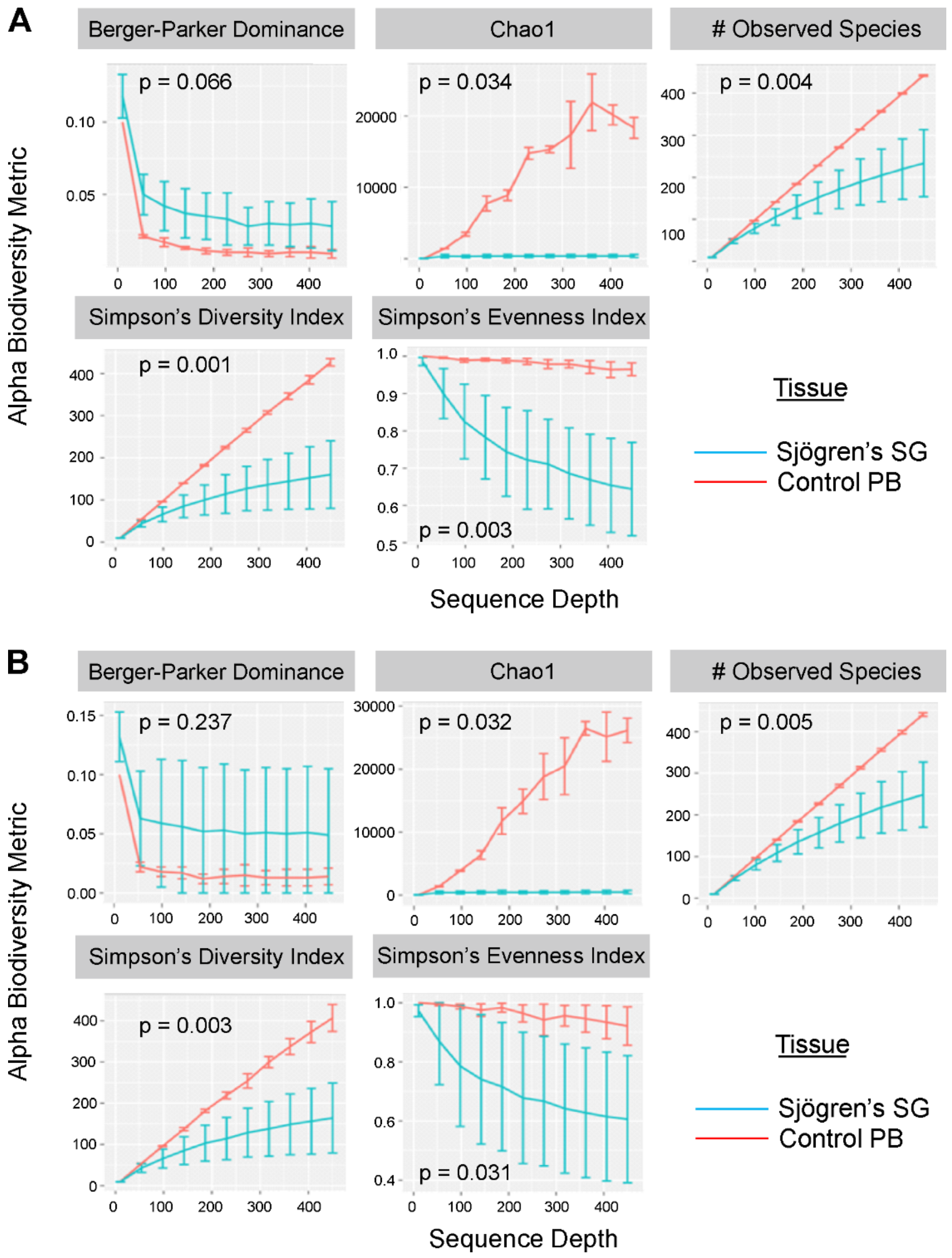
Supplemental Figure 2. Frequencies of T cell receptor (TCR) gene usage in salivary gland (SG) compared to peripheral blood (PB). Mean frequencies of TRAV (A), TRAJ (B), TRBV (C) and TRBJ (D) usage among unique TCR sequences of 10 subjects. Genes are listed in chromosomal order. TRAV7, TRAV8-7, TRAV9-1, TRAV18, TRAJ19, TRAJ25, TRAJ55, TRBV7-1, TRBV6-3, TRBV6-7, TRBV6-8, TRBV5-7, TRBV6-9, and TRBV17, were not detected. Error bars represent SEM. Enrichment in SG or PB was evaluated by matched-pairs Wilcoxon rank sum test with no post-test applied. * $p<0.05$; ** $p<0.01$.



Supplemental Figure 3. Biased TCR gene usage in salivary gland (SG) compared to peripheral blood (PB). A) Frequencies of T cell receptor (TCR) genes that were significantly enriched in SG compared to PB (n=10). **B)** Frequencies of TCR genes that were significantly enriched in PB compared to SG (n=10). Each symbol represents an individual subject (upper right). Only unique TCR sequences were included in the analysis. Enrichment in SG or PB was evaluated by matched-pairs Wilcoxon rank sum test with no post-test applied. * $p<0.05$; ** $p<0.01$.



Supplemental Figure 4. Percentage of TCR repertoire comprised of the 10 most frequently observed clonotypes in the peripheral blood (PB) of two healthy controls (Control PB, red) and the salivary glands (SG) of five subjects with Sjögren's syndrome (Sjögren's SG, blue) as assessed by TCR deep sequencing. P-values are from two-tailed unequal variances t-tests. Horizontal lines indicate mean and SEM.



Supplemental Figure 5. Diversity metrics from T cell receptor (TCR) α (A) and TCR β (B) deep sequencing data as a function of sequence depth. TCR deep sequence data from Sjögren's syndrome salivary gland (Sjögren's SG, blue) were compared to healthy control peripheral blood (Control PB, red). P-values are from non-parametric, two-tailed, two-sample t-tests. Error bars are SD.

Supplemental Table 1: HLA alleles imputed from GWAS data[A]

		DQA1			**DQB1**			**DRB1**		
Subject	**Race**[B]	**All 1**	**All 2**	**Prob**[C]	**All 1**	**All 2**	**Prob**	**All 1**	**All 2**	**Prob**
1	C/NA	05:01	03:01	**0.822**	02:01	03:02	**0.897**	03:01	04:02	0.796
2	C	02:01	02:01	**0.989**	02:02	03:03	**0.965**	07:01	07:01	**0.995**
3	C	05:01	02:01	**0.960**	02:01	02:02	**0.969**	03:01	07:01	**0.997**
4	C	05:01	01:03	0.684	02:01	06:03	0.728	03:01	13:01	0.697
5	C	05:01	01:03	0.671	02:01	06:03	0.664	03:01	13:01	**0.835**
6	C/NA	05:01	03:01	0.738	02:01	03:02	**0.958**	03:01	04:05	0.414
7	C	05:01	02:01	**0.965**	02:01	02:02	**0.971**	03:01	07:01	**0.997**
8	C/NA	05:01	01:03	**0.883**	02:01	06:03	**0.901**	03:01	13:01	**0.973**
9	C	05:01	01:02	**0.959**	02:01	06:02	**0.968**	03:01	15:01	**0.995**
10	C/NA	05:01	03:03	0.532	02:01	03:01	0.655	03:01	04:03	0.345

[A] All=allele; [B] C=self-reported Caucasian race; C/NA=self-reported mixed Caucasian/Native American mixed race; [C] Prob=estimated probability of the maximum likelihood model. Probability values equal to or exceeding 80% are commonly accepted values of certainty for the HLA Imputation using attribute BAGging (HIBAG) method and appear in bold. The predicted haplotypes coincide with those predicted by the PCR screening test in 9 of 10 subjects. GWAS=genome-wide association study.

Supplemental Table 2: SG sample descriptions and sorting recoveries

Subject	Focus Score	No. SG	No. SG $CD4^+$ T cells	No. SG $CD4^+$ T cells sorted into plates
1	1.3	8	1513	378
2	9	5	20900	378
3	4	7	14000	378
4	5.7	4	8307	378
5	12	8	48629	378
6	1.8	3	1013	252
7	2	6	936	252
8	3	NR	408	210
9	4.6	4	809	168
10	4	8	8000	378

NR=not recorded.

Supplemental Table 3: Number of cells evaluated and PCR efficiencies by subject[A]

Subj	SG[B] Total cells	SG[C] Exp cells	SG[D] % Exp cells	SG[E] %Paired cells	SG[F] % α Single	SG[G] % β Single	PB[B] Total cells	PB[C] Exp cells	PB[D] % Exp cells	PB[E] %Paired cells	PB[F] % α Single	SG[G] % β Single
1	62	0	0	48.4	33.9	17.7	92	2	2.2	56.5	14.1	29.3
2	80	2	2.5	62.5	25	12.5	75	0	0	69.3	8	22.7
3	91	4	4.4	63.7	21.9	14.3	120	4	3.3	47.5	21.7	30.8
4	95	6	6.3	61.1	19	20	119	2	1.7	44.5	21.8	33.6
5	91	9	9.9	38.5	23	38.5	111	0	0	55.0	25.2	19.8
6	50	8	16	62.0	26	12	73	0	0	32.9	30.1	37
7	115	19	16.5	55.7	19.1	25.2	96	3	3.1	38.5	20.8	40.6
8	83	15	18	60.2	21.7	18.1	121	0	0	59.5	16.5	24
9	114	22	19.3	62.3	26.3	11.4	105	7	6.7	61.0	12.4	26.7
10	113	32	28.3	68.1	16.8	15	110	0	0	47.3	16.4	36.4
Totals	894	116	Med= 11.95	58.2	23.3	18.5	1022	18	Med= 0.85	51.2	18.7	30

[A] SG=salivary gland, PB=peripheral blood, Subj=Subject; [B] Numbers of cells yielding T cell receptor (TCR) sequences; [C] Numbers of cells that were part of clonal expansions; [D] Percentages of cells that were part of clonal expansions; [E] Percentages of cells that yielded paired TCR α and β sequences; [F] Percentages of cells that yielded only TCR α sequences; [G] Percentages of cells that yielded only TCR β sequences.