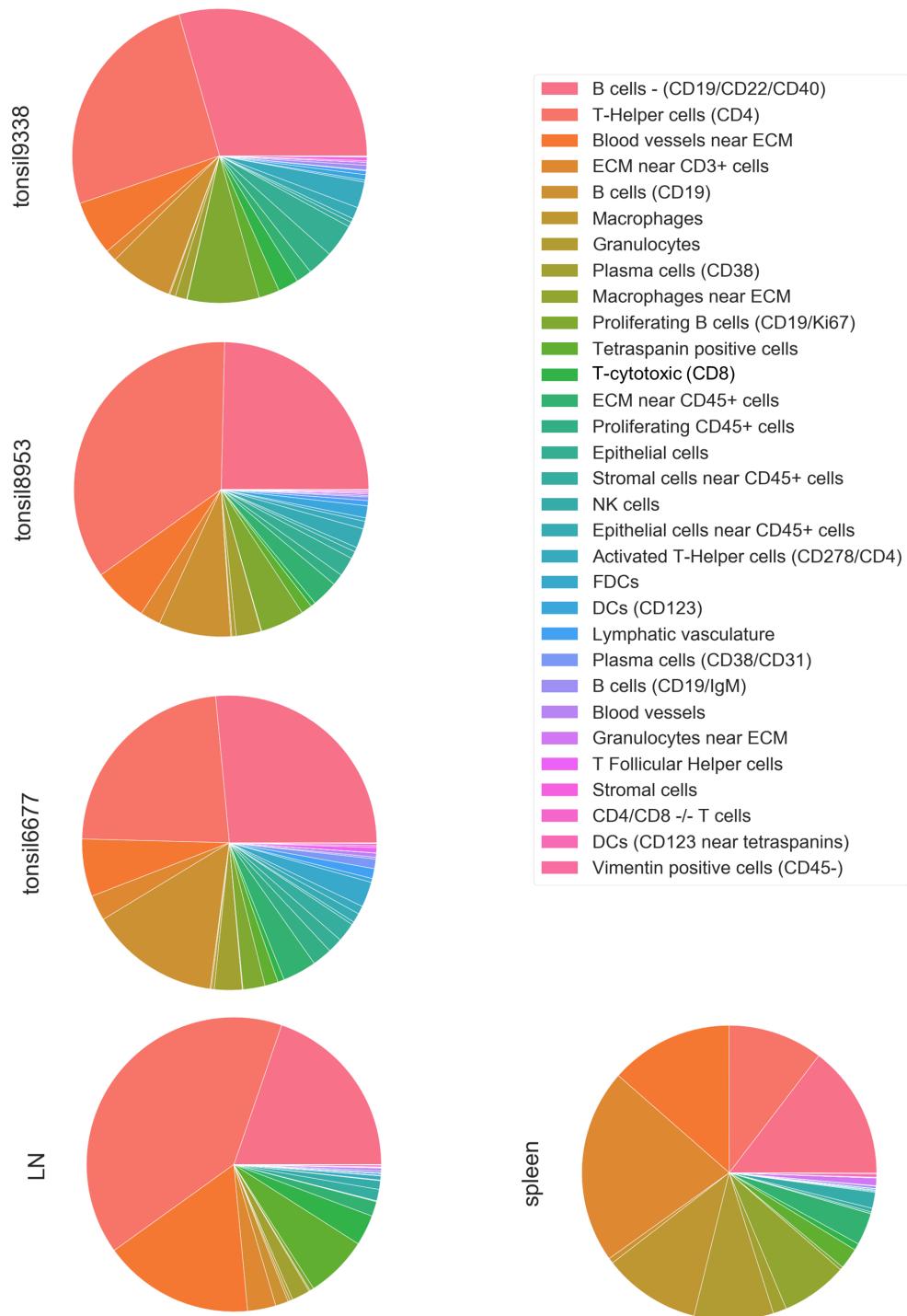
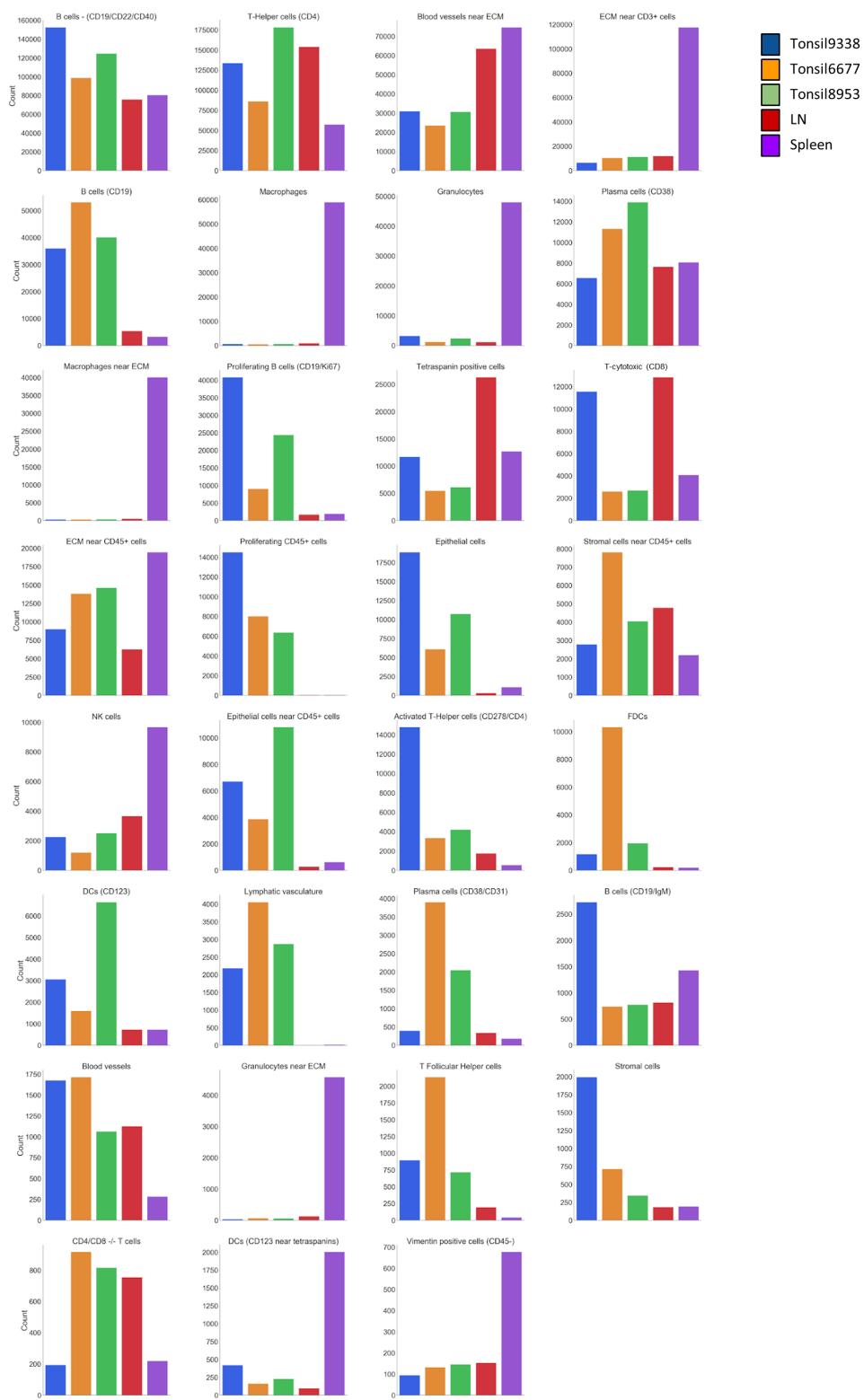


Supporting Information

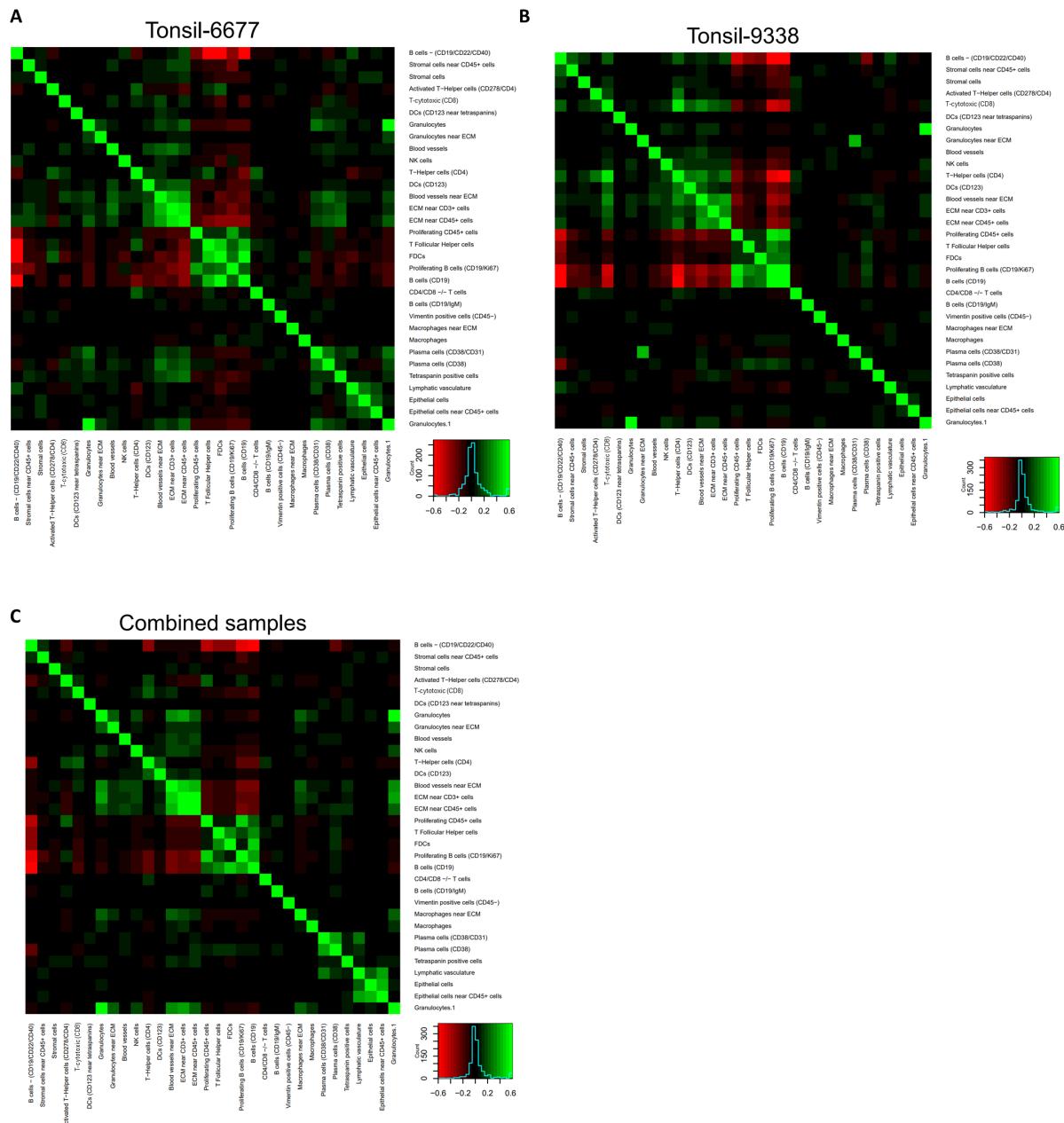
Herein contains Supporting Information Figures 1-3 and Supporting Tables 1-2:



Supporting Information Figure 1: Pie charts of cell-type compositions for all tissues imaged.



Supporting Information Figure 2: Bar graphs of the numbers of each cell type in all tissues imaged.



Supporting Information Figure 3: Cell-cell density correlation analysis across lymphoid tissues determined by evaluating 100 x 100 pixel squares for (A) tonsil 6677, (B) tonsil 9338, and (C) all samples combined.

Supporting Table 1: CODEX multicycle panel, order, oligo number, and antibody clones

	CH1	A488			Cy3			Cy5		
Cycle		antibody	oligo	clone	antibody	oligo	clone	antibody	oligo	clone
1	Hoechst	CD38	A2	HIB7	CD19	A0	HIB19	CD31	A1	WM59
2	Hoechst	Vimentin	A4	RV202	CD22	A6	HIB22	Ki67	A3	B56
3	Hoechst	CD8	A5	SK1	CD90	A7	5E10.00E+10	CD123	A9	7G3
4	Hoechst	CD15	A8	HI98	CD3	B0	UCHT1	CD152	B2	BN13
5	Hoechst	CD21	B1	Bu32	cytokeratin	B3	AE1/AE3	CD2	B4	RPA-2.10
6	Hoechst	CD66	C4	B1.1/CD66	collagen IV	B6	poly	CD81	B5	5A6
7	Hoechst	HLA-DR	C7	L243	CD57	B9	HCD57	CD4	B7	A161A1
8	Hoechst	CD7	D8	CD7-6B7	CD278	C2	C398.4A	podoplanin	C0	NC-08
9	Hoechst	CD45RA	E2	HI100	CD34	C3	561	CD54	C1	HA58
10	Hoechst	CD9	E4	HI9a	IGM	D0	MHM-88	CD117	C5	YB5.B6
11	Hoechst				CD56	D1	HCD56	CD279	C8	EH12.2H7
12	Hoechst				CD45	D6	HI30	CD49f	D2	GoH3
13	Hoechst				CD5	D7	UCHT2	CD16	D3	3G8
14	Hoechst				Ecadherin	E6	2.40E+11	FAPalpha	D4	BMS168
15	Hoechst				CD63	E7	H5C6	CD11b	D9	ICRF44
16	Hoechst				CD1c	F2	L161	CD40	E0	HB14
17	Hoechst				CD274	F3	29E.2A3	CD27	E1	M-T271
18	Hoechst							CD104	F5	450-9D
19	Hoechst							CD273	F6	24F.10C12

Supporting Table 2: CODEX Oligonucleotide sequences

Name	Top oligo sequence (5'-3')	dye sequence	Dye	# in cross-validation
A0	ATAGCAGTCCAGTTGCTGATGGTTAGGACTACGG	GTAGTCCTAAACCAT	Cy3	2
A1	ATAGCAGTCCAGGATAATAGTACTCCTCGCCGCAA	CGGCGAGGAGTA	A488	3
A2	ATAGCAGTCCAGGCCACTCTCCCATTAGTCGGAA	CCGACTAATGGGAGA	A488	1
A3	ATAGCAGTCCAGCACAGGTGGATGTGTTACGATGG	ATCGTAACACATCCA	Cy5	6
A4	ATAGCAGTCCAGAGCCGCTAACGATATTCTAAGTT	CTTAGAATATCTAGCG	A488	4
A5	ATAGCAGTCCAGGCCTAACGCAGATGAATATTCAA	GAATATTCATCTGCG	A488	7
A6	ATAGCAGTCCAGATCGAAGGGTTATACACTCGTGG	ACGAGTGTATAACCC	Cy3	5
A7	ATAGCAGTCCAGCGATGGAGATTCACTCTCGGG	CGAGAGACTGAATCT	Cy3	8
A8	ATAGCAGTCCAGCGAGCACTGTAATAGGCACTATT	TAGTGCCTATTACAG	A488	10
A9	ATAGCAGTCCAGGGAACAAAGCGGTCTACGGTT	ACCGTAAGACCGCTT	Cy5	9
B0	ATAGCAGTCCAGAACGATGGATGTAGGATGGCTCGG	GAGACCATCCTACAT	Cy3	11
B1	ATAGCAGTCCAGGTACCGGACGTGCCGTTCACTT	GTGAAACGGCACG	A488	13
B2	ATAGCAGTCCAGCTCGCGGTTCTCAGACACGG	GTGTCTGAGGAAACC	Cy5	12
B3	ATAGCAGTCCAGTTAAGAATAAGGGCTATTGTTT	ACAATGAGCCTTAT	Cy3	14
B4	ATAGCAGTCCAGAGGCAGAGGCACGCCCTTAA	TAAAAGGGCGTGC	Cy5	15
B5	ATAGCAGTCCAGCGGATCCACTTGTCTAACCAATT	TTGGTTAGACAAGTG	Cy5	18
B7	ATAGCAGTCCAGTATGATTGGTCCACTAACGTAGG	TACGTTAGTGGACCA	A488	24
B8	ATAGCAGTCCAGCGCGTGTAGGGCATTGAAGGG	CTTCAAATGCCCTAT	Cy5	21
B9	ATAGCAGTCCAGCCCCTACACATGAGCGAACGAGG	TGATTGCTCATGTG	Cy3	20
C0	ATAGCAGTCCAGAACGACTACCAAATCCTGATG	CATCAGGATTGGTA	Cy5	27
C1	ATAGCAGTCCAGCTATTATCATGAGGAGCGCG	CGCTCCTCATGATAA	Cy5	30
C2	ATAGCAGTCCAGGTGTCCACCTACACAATGCTA	TAGCATTGTGTAGGT	Cy3	23
C3	ATAGCAGTCCAGCGCATTGCGTCACTTATAAG	CTTATAAGTAGACGC	Cy3	26
C4	ATAGCAGTCCAGTTACTGTATGAGTAGTAATCT	AGATTACTACTCATACA	A488	16

C5	ATAGCAGTCCAGGGCTACCTCTAAGTCAGAGAGC	GCTCTCTGACTTAGA	Cy5	33
C6	ATAGCAGTCCAGGGCTCGTACATTATCCGTGAT	ATCACGGATAATGTC	A488	19
C7	ATAGCAGTCCAGTTCTCACTACTATTAGTACT	AGTACTAATAGTAGTGA	A488	22
C8	ATAGCAGTCCAGCCTGTTGCCAGAACATGCCA	TGGCATTCTGGC	Cy5	36
C9	ATAGCAGTCCAGCTTCCGACTCGAACCTGAG	CTCAGGTTGAGTC	A488	25
D0	ATAGCAGTCCAGCATGGCCTGCACGGCAAAGTG	CACTTGCCTGTC	Cy3	29
D1	ATAGCAGTCCAGATGGCAATAACGCCCGTATC	GATACGAGGCCTTAT	Cy3	32
D2	ATAGCAGTCCAGTCCGTCTCCGTGCGGGAAAAT	ATTTTCCCGCACG	Cy5	39
D3	ATAGCAGTCCAGATACTAACCAAGGTGATTGCAT	ATGCAATCACCTGGT	Cy5	42
D4	ATAGCAGTCCAGGGCGCACTATCCCCTAAACTTC	GAAGTTTACGGGATA	Cy5	45
D5	ATAGCAGTCCAGTCAAGGCAGGTCAACTCGCAC	GTGCGAGTTGACCT	Cy3	35
D6	ATAGCAGTCCAGAGTGAGGGTCACATGGTCGTT	AACGACCATGTGACC	Cy3	38
D7	ATAGCAGTCCAGAGAAGTGCCTGGATTCTGTATT	AAATACGAAATCCGC	Cy3	41
D8	ATAGCAGTCCAGGGCAGCTCGTCAGTACTTCAG	CTGAAAGTACTGACG	A488	28
D9	ATAGCAGTCCAGGTGACGCTTATTATGGACTTC	GAAGTCCATAATAAGC	Cy5	48
E0	ATAGCAGTCCAGGTGTAACACAAACTGCTGTCG	CGACAGCAGTTTTGT	Cy5	51
E1	ATAGCAGTCCAGGTGAATTCTTATTCCGAATA	TATTGGGAATAAGA	Cy5	53
E2	ATAGCAGTCCAGGAAGCCTAGGGGACAGGTTG	CAACCTGTTCCCTA	A488	31
E3	ATAGCAGTCCAGGTTAATTAGCTTAAGAGAGT	ACTCTCTTAAGCTAATT	A488	34
E4	ATAGCAGTCCAGACGTTGATAAAATTTTACAGAGT	ACTCTGAAATATTATC	A488	37
E5	ATAGCAGTCCAGACTCGCGATGTACGTGCTTGGTT	AACCAAAGCACGTA	A488	40
E6	ATAGCAGTCCAGAGCGGGAGTTGCCGACGACGAAGGC	GCCTTCGTCGTC	Cy3	44
E7	ATAGCAGTCCAGCAAGGAGATGCTTCTGTGGAACC	GGTTCACAAGAAG	Cy3	47
E8	ATAGCAGTCCAGCAATACATACGTGGCCCCGGCAGTT	AACTGCCGGG	A488	43
E9	ATAGCAGTCCAGCCCCCTGTCCAACCAAACGTGACCG	CGGTCAAGTTGGTT	A488	46
F0	ATAGCAGTCCAGCGGGTTGAGCGTGTACCCCCCAGC	GCTGGGGGTGA	Cy3	50
F1	ATAGCAGTCCAGCGACGGCGCGACAACGCGACGGAT	ATCCGTCGCGTT	A488	49
F2	ATAGCAGTCCAGCTTATCACATTGCTTCGACGA	TCGTCGAAGCAAAT	Cy3	52
F3	ATAGCAGTCCAGCTGCGGGGCGCTTGGGTGTTA	TAAACACCCAAGCG	Cy3	54

F4	ATAGCAGTCCAGGACGCTGGGATCTGTCGGTCGTCA	TGACGACCGACAG	Cy5	55
F5	ATAGCAGTCCAGGAGGTCAATTCAACAAATATTGTT	AACAATATTGTTGAAAT	Cy5	56
F6	ATAGCAGTCCAGTCTTAATGAATGGCCGGAAGTGGT	ACCACTTCCGGC	Cy5	57
F7	ATAGCAGTCCAGTGGTCCCCAGACGCCGGGCACCA	TGGTGCCCCG	Cy5	58
F8	ATAGCAGTCCAGTTTCTATCGCAAGGAACTACCGA	TCGGTAGTTCTTG	Cy5	59