Table S1: Summary of the number of reads and sequences that were used to analyze the TRB repertoire in naïve CD8$^+$ T cells and influenza specific CTLs

Sample Code	Sample Description	No. of total sequences	No. of unique sequences	No. of productive sequences	No. of unique productive sequences	Gene Rearrangements	Clonality: Pielou's evenness
3_day_Neo 1	Naïve, CD8$^+$CD44$^-$	636	57	363	23	66	0.07
3_day_Neo 2	Naïve, CD8$^+$CD44$^-$	1650	179	1018	104	202	0.08
3_day_Neo 3	Naïve, CD8$^+$CD44$^-$	3721	283	2336	177	309	0.07
3_day_Neo 4	Naïve, CD8$^+$CD44$^-$	285	31	180	22	35	0.14
7_day_Neo 1	Naïve, CD8$^+$CD44$^-$	68,489	6150	50,152	4387	6981	0.04
7_day_Neo 2	Naïve, CD8$^+$CD44$^-$	19,548	1709	14,374	1242	1819	0.04
7_day_Neo 3	Naïve, CD8$^+$CD44$^-$	44,538	2043	32,764	1473	2182	0.03
7_day_Neo 4	Naïve, CD8$^+$CD44$^-$	83,158	2686	60,074	1890	2851	0.03
7_day_Neo 5	Naïve, CD8$^+$CD44$^-$	6150	411	4439	295	425	0.04
Adult 1	Naïve, CD8$^+$CD44$^-$	482,749	53,414	358,073	38,991	56,978	0.02
Adult 2	Naïve, CD8$^+$CD44$^-$	197,827	21,069	144,729	15,049	21,608	0.02
Adult 3	Naïve, CD8$^+$CD44$^-$	148,382	17,076	108,254	12,284	17,902	0.04
Adult 4	Naïve, CD8$^+$CD44$^-$	1,079,304	82,662	789,667	59,232	88,520	0.03
Adult 5	Naïve, CD8$^+$CD44$^-$	742,911	54,504	538,712	38,756	57,665	0.03
3_day Neo 1 Flu	10 DPI, CD8+ NP$_{(366–374)}^+$	148,975	1649	80,028	1164	6611	0.46
3_day Neo 2 Flu	10 DPI, CD8+ NP$_{(366–374)}^+$	156,588	939	107,832	648	3590	0.44
3_day Neo 3 Flu	10 DPI, CD8+ NP$_{(366–374)}^+$	37,202	723	29,149	519	2358	0.34
Adult 1 Flu	10 DPI, CD8+ NP$_{(366–374)}^+$	1,211,772	2795	878,101	1895	50112	0.55
Adult 2 Flu	10 DPI, CD8+ NP$_{(366–374)}^+$	680,199	966	440,679	637	49080	0.49
Adult 3 Flu	10 DPI, CD8+ NP$_{(366–374)}^+$	948,075	1805	842,455	1245	30967	0.62

Table S2: Shared amino acid sequences for the adult and 3-day neonatal samples infected with influenza.

Number of reads within the sample (percentage of total productive sequences)

Adult Shared Sequences	**Adult 1 Flu**	**Adult 2 Flu**	**Adult 3 Flu**	**3_day Neo 1 Flu**	**3_day Neo 2 Flu**	**3_day Neo 3 Flu**
CASSGGSNTGQLYF	235741 (26.9)	27265 (6.2)	229052 (27.2)	0	0	0
CASSGGANTGQLYF	158643 (18.1)	55902 (12.7)	32410 (3.9)	0	0	1237 (4.2)
CASRGGANTGQLYF	41949 (4.8)	56457 (12.8)	15650 (1.9)	0	0	0
CASSGGGNTGQLYF	69866 (8.0)	35049 (8.0)	567 (0.1)	0	0	0
CASSQDRRNSYNSPLYF	2739 (0.3)	9285 (2.1)	8275 (1.0)	0	0	0
CASSLARDEQYF	3342 (0.4)	5150 (1.2)	5134 (0.6)	0	0	0
CASSGDSAETLYF	4562 (0.5)	23 (0.01)	1006 (0.1)	0	0	0
CASSQDSAETLYF	1021 (0.1)	224 (0.1)	919 (0.1)	0	123 (0.1)	2 (0.001)
CASRDSANTEVFF	284 (0.03)	4 (0.001)	1482 (0.2)	0	0	0
CASSPDSAETLYF	122 (0.01)	46 (0.01)	1422 (0.2)	23 (0.03)	0	0
Neonatal Shared Sequences						
CASSLGGEQYF	104 (0.01)	0	0	4547 (5.7)	367 (0.3)	61 (0.2)
CASSLGAEQFF	35 (0.004)	0	0	32 (0.04)	4481 (4.2)	2 (0.01)
CASSMGAEVFF	204 (0.02)	0	0	807 (1.0)	275 (0.3)	112 (0.4)
CASSMGGQNTLYF	0	0	0	36 (0.04)	7 (0.01)	676 (2.3)
CASSLGQGGNTLYF	14 (0.002)	9 (0.002)	0	17 (0.02)	47 (0.04)	389 (1.3)
CASSRDWGGTGQLYF	0	0	0	5 (0.006)	28 (0.03)	297 (1.0)
CASSLGSGNTLYF	0	0	0	58 (0.07)	75 (0.1)	98 (0.3)
CASSDWGQNTLYF	0	0	0	17 (0.02)	186 (0.2)	7 (0.02)
CASSWGGYAEQFF	0	0	0	2 (0.003)	71 (0.1)	64 (0.2)
CASSLDWGGYEQYF	15 (0.002)	0	17 (0.002)	81 (0.1)	37 (0.03)	3 (0.01)