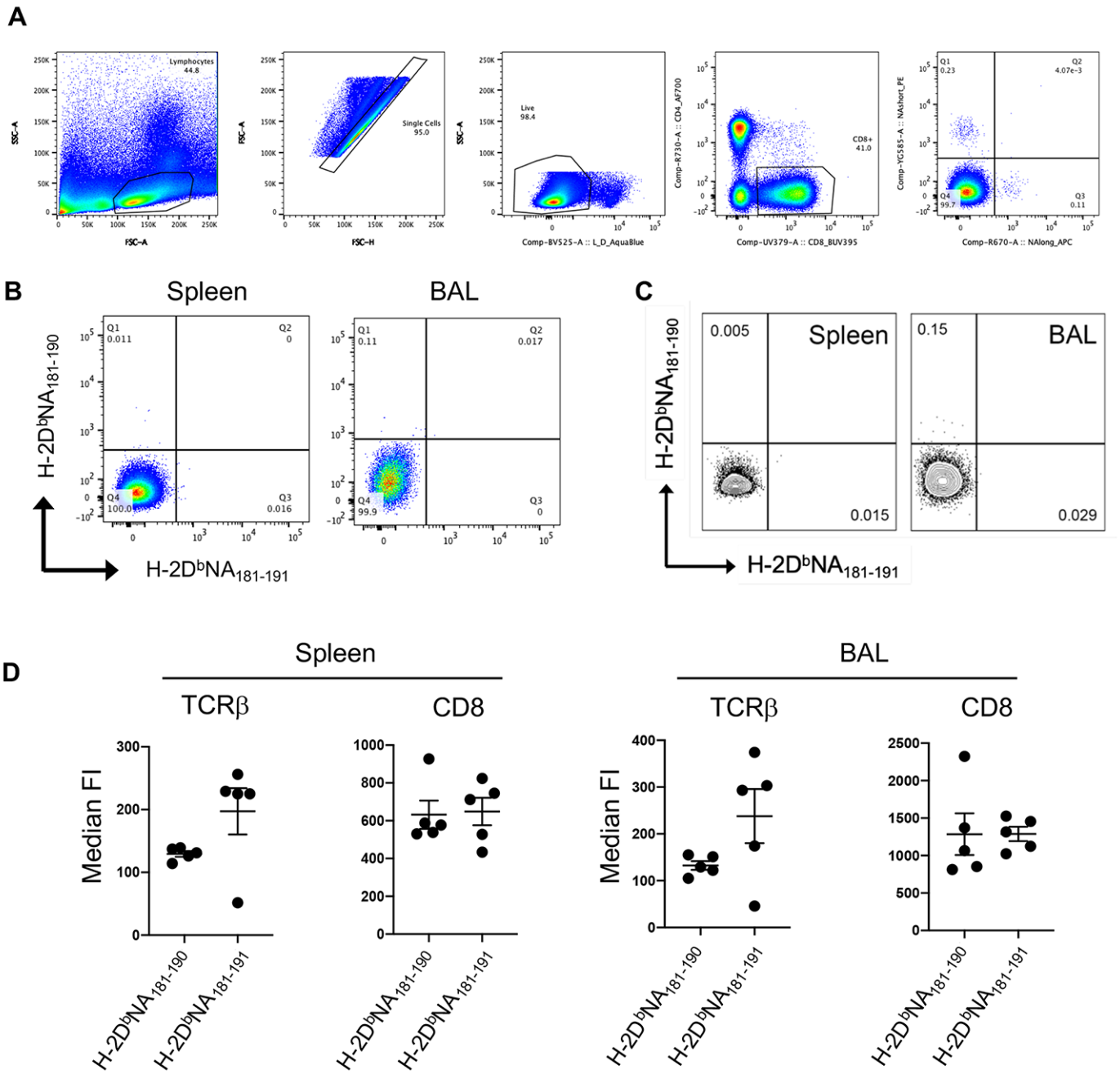
Supplementary Table 1. Data Collection and Refinement Statistics

Data Collection Statistics	**H-2Db-NA(10)**	**H-2Db-NA(11)**
Temperature	100K	100K
Space group	$P2_1$	$P2_1$
Cell Dimensions (a,b,c)(Å)	68.72, 44.96, 71.77 $\beta = 98.23°$	69.01, 44.75, 71.66 $\beta = 98.45°$
Resolution (Å)	45.95 – 1.50 (1.53 – 1.50)	45.91 – 1.55 (1.58 – 1.55)
Total number of observations	247455 (12308)	228178 (11040)
Number of unique observations	69128 (3413)	62822 (3067)
Multiplicity	3.6 (3.6)	3.6 (3.6)
Data completeness (%)	99.1 (99.4)	99.5 (99.6)
I/σ_I	17.6 (2.0)	12.7 (2.0)
R_{pim}[a] (%)	2.8 (39.0)	5.6 (43.9)
Refinement Statistics		
Non-hydrogen atoms	3774	3769
Protein	3202	3175
Water	572	594
R_{factor}[b] (%)	17.81 (26.52)	18.30 (28.80)
R_{free}[b] (%)	20.88 (30.02)	21.25 (31.93)
Rms deviations from ideality		
Bond lengths (Å)	0.013	0.013
Bond angles (°)	1.57	1.58
Ramachandran plot (%)		
Favored	99	99
Allowed	0.79	1.3
Outliers	0	0

[a] $R_{p.i.m} = \Sigma_{hkl} [1/(N-1)]^{1/2} \Sigma_i | I_{hkl,\,i} - \langle I_{hkl} \rangle | / \Sigma_{hkl} \langle I_{hkl} \rangle$

[b] $R_{factor} = \Sigma_{hkl} \; | \, | F_o | - | F_c | \, | / \Sigma_{hkl} | F_o |$ for all data except ≈ 5% which were used for R_{free} calculation

Supplemental Fig. 1



Supplemental Fig. 1. (**A**) Dot plots showing consecutive gating strategy for analysis of tetramer staining on splenic CD8+ T cells. (**B**) Dot plots showing detection of tetramer staining in spleen and BAL samples stained with all antibodies but no tetramers (FMO control). (**C**) Tetramer staining on CD4+ T cells from samples shown in Figure 1A. (**D**) Median fluorescence intensity of TCRβ and CD8 staining on spleen and BAL samples from tetramer dissociation experiment shown in Figure 2E.