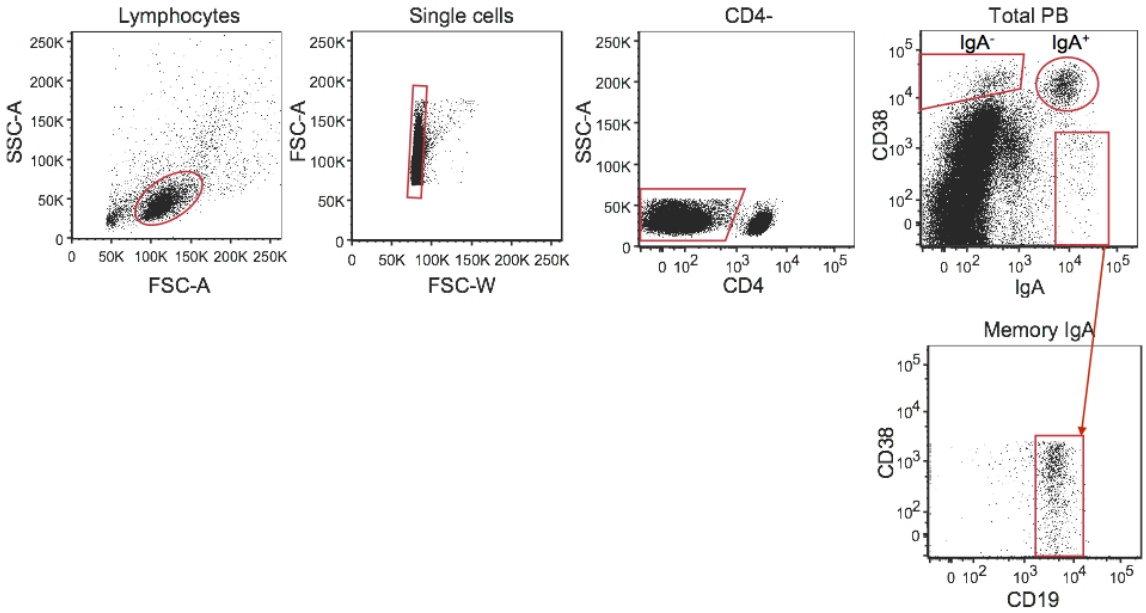
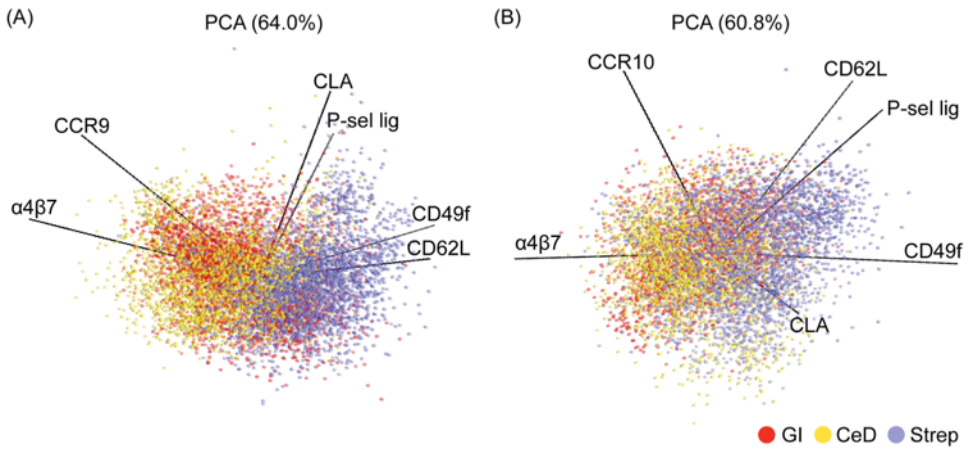
Supplemental data

Trafficking receptor signatures define blood plasmablasts responding to tissue-specific immune challenge

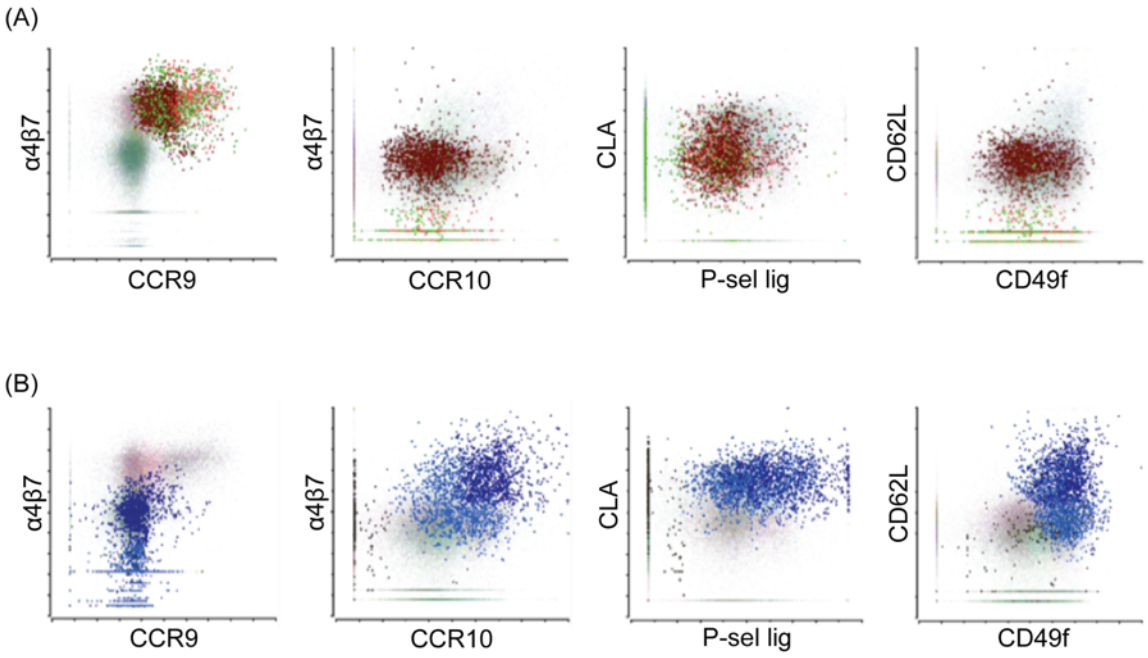
Yekyung Seong[1,2], Nicole H. Lazarus[1,3], Lusijah Sutherland [1,3], Aida Habtezion[4], Tzvia Abramson[5], Xiao-Song He[3,6], Harry B. Greenberg[3,6,7], and Eugene C. Butcher[1,3]



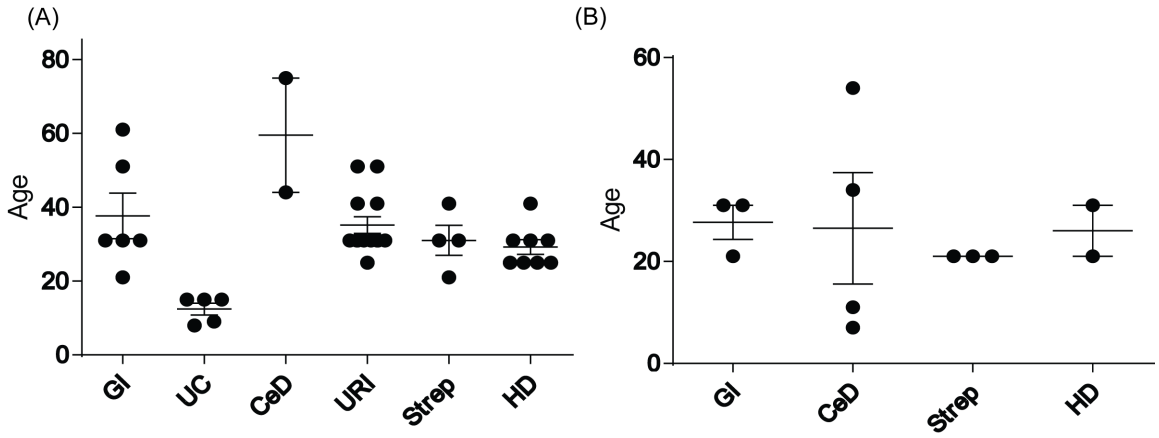
Supplemental Figure 1. IgA^+ and IgA^- plasmablasts (PB) were gated from $CD38^{hi}$ among $CD4^-$ single lymphocytes. Memory IgA^+ cells were gated as $CD19^+$ cells among $CD38^{low}IgA^+$ cells.



Supplemental Figure 2. Principal Component Analysis (PCA) from patient cohort 2 (PC2) supports the PCA result from patient cohort 1. In PC2 (GI=3, CeD=4, Strep=3), for technical reasons blood was stained with panels containing only (A) CCR9 or (B) CCR10, not both.



Supplemental Figure 3. 2x2 flow cytometry plots of plasmablasts (PB) from statistically enriched clusters in samples from patient cohort 2 with celiac disease (CeD) (A) or strep throat (B). As in Figure 4, 1,000 IgA^+ and 1,000 IgA^- cells from each patient were combined and t-SNE was used to define clusters. In addition to the patients included in the analysis in Figure 4, clustering included PB from 3 additional strep throat patients and 4 additional CeD patients whose staining panel lacked either CCR9 or CCR10 (thus either CCR9 or CCR10 was not used for clustering). Enrichment analysis (ANOVA on correspondence tables of PB frequency in clusters for CeD vs. all other samples combined) for (A) included only the CeD patients not included in enrichment analysis for Figure 4. (That is, PB from all patients were used to define the clusters, but for the enrichment analysis the 2 patients with CeD in patient cohort 1 were excluded.) Similarly, enrichment analysis for (B) included only the second cohort of strep throat patients. Comparison in (B) is to all upper respiratory infection patients. PB from the top 4 or 5 most significantly enriched clusters are shown: $P<0.001$.



Supplemental Figure 4. Age distribution of recruited patients within each patient class of (A) patient cohort 1 (same individuals as Figure 1 with ≥ 0.25% plasmablasts) and (B) patient cohort 2 (GI=3, CeD=4, Strep=3, HD=2). Mean ± SEM are shown.

Disease	Site/Etiology	Defining features
Gastrointestinal Infection	Colon and/or small intestine (unknown etiology)	Diarrhea with upper abdominal cramps and/or nausea with or without vomiting
Ulcerative Colitis	Colon	Clinical classification as Active based on PUCAI scoring system (scale 0-100, >10 is active)
Celiac Disease	Small intestine	Clinical classification as Active based on Marsh scoring system (scale 0-4, 2-4 active)
Upper Respiratory Tract Infection	Upper respiratory tract	Cough Nasal discharge ±Sore throat ±Malaise ±Fever
Strep Throat	Throat	Symptoms limited to sore throat and fever. Culture proven streptococcus infection.

Supplemental Table 1. Disease and symptoms defining patient classes. These features were included in the questionnaire provided to the patients.