

Antibody Repertoire Profiling Using Bacterial Display Identifies Reactivity Signatures of Celiac Disease

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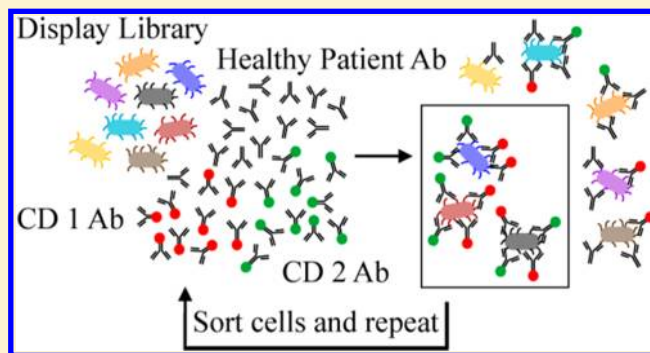
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S Supporting Information

ABSTRACT: A general strategy to identify serum antibody specificities associated with a given disease state and peptide reagents for their detection was developed using bacterial display peptide libraries and multiparameter flow cytometry (MPFC). Using sera from patients with celiac disease (CD) ($n = 45$) or healthy subjects ($n = 40$), bacterial display libraries were screened for peptides that react specifically with antibodies from CD patients and not with those from healthy patients. The libraries were screened for peptides that simultaneously cross-react with CD patient antibodies present in two separate patient groups labeled with spectrally distinct fluorophores but do not react with unlabeled non-CD antibodies, thus affording a quantitative separation. A panel of six unique peptide sequences yielded 85% sensitivity and 91% specificity (AUC = 0.91) on a set of 60 samples not used for discovery, using leave-one-out cross-validation. Individual peptides were dissimilar with known CD-specific antigens tissue transglutaminase (tTG) and deamidated gliadin, and the classifier accuracy was independent of anti-tTG antibody titer. These results demonstrate that bacterial display/MPFC provides a highly effective tool for the unbiased discovery of disease-associated antibody specificities and peptide reagents for their detection that may have broad utility for diagnostic development.



The circulating antibody repertoire provides a rich source of potential diagnostic information. Serum antibodies serve as one of the largest classes of clinical disease biomarkers,^{1–3} owing to their intrinsic affinity and specificity, analytical stability, and amplification by the immune system. Thus, antibody detection assays can enable rapid and accurate diagnosis of diseases with high sensitivity and specificity and are amenable to point-of-care diagnostic applications. Unique antibody reactivity patterns or signatures, generated by multiple distinct antibody specificities, have been observed in many diseases including cancer,⁴ autoimmune,⁵ neurodegenerative,⁶ and infectious diseases.⁷ Additionally, since some disease-associated antibodies play a role in pathology,⁸ monitoring their concentration in blood can provide valuable information to guide therapy.^{9,10} Despite their established utility, the identification of serum antibody specificities that indicate disease and reagents for their detection has proven remarkably challenging. Consequently, there remains a need for robust and

unbiased serum antibody specificity profiling technologies to identify signatures of disease for known and unknown etiology.

Several distinct methodologies have been developed to identify serum antibody specificities associated with disease. Protein arrays have been used to identify antibody specificities associated with breast¹¹ and colorectal cancer,¹² Alzheimer's disease,^{6,13} and rheumatoid arthritis.¹⁴ However, antigen arrays do not enable a complete search of the human proteome and are biased toward a limited subset of human antigens comprising the array.¹⁵ For example, short peptides and membrane proteins are not represented by current array platforms. An alternative approach to access a larger number of candidate antigens uses random peptide, cDNA, or genomic libraries displayed on the surface of M13 or T7 bacteriophage. The panning of phage display cDNA libraries constructed from

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prostate and colon cancer tissue^{4,16} and an ovarian cancer cell line¹⁷ has enabled identification of peptide sequences with potential diagnostic utility. Even so, phage cDNA libraries are biased toward soluble proteins that are expressed efficiently in *Escherichia coli*, and their effective use generally requires knowledge of which tissues are most relevant to the pathology. In an effort to overcome these problems, phage display peptide libraries have been constructed using overlapping 36-mer linear fragments, spanning the human proteome.¹⁸ Nevertheless, since a majority of antibody specificities are likely directed toward structural rather than linear epitopes,¹⁹ small libraries of linear peptides do not generally yield mimotopes with sufficient affinity and specificity to mimic structural epitopes. Both cDNA- and proteome-derived peptide libraries are less useful when nonhuman antigens are involved in disease.^{20–22} Furthermore, when compared to random peptide libraries, the use of protein antigen arrays and cDNA libraries may not provide adequate diversity to effectively mimic post-translationally modified peptides.

To address these limitations and enable identification of antibody biomarkers or signatures for arbitrary pathological processes, we sought to develop a robust and quantitative screening method using unbiased bacterial display peptide libraries in conjunction with quantitative library screening using fluorescence-activated cell sorting (FACS). We demonstrated previously that very large random peptide libraries displayed on *E. coli*^{23,24} can be screened quantitatively based on both affinity and specificity, enabling identification of those mimotopes exhibiting the highest specificity for a mock disease sample.²⁵ Here, we investigated the utility of specificity-based screening of bacterial display libraries for the identification of disease-specific antibody signatures and peptide reagents for their detection. Our results demonstrate that bacterial display coupled with FACS provides a highly effective route to identify diagnostically useful antibody signatures of disease and may enable development of effective and versatile diagnostic tests for a broad range of unmet medical needs.

EXPERIMENTAL SECTION

Reagents and Strains. All experiments were performed with the *E. coli* strain MC1061.²⁶ A pool of three bacterial display libraries with the format X₁₅, X₁₂CX₃, or X₄CX₂CX₄ displayed at the N-terminus of the enhanced circularly permuted OmpX (eCPX) display scaffold²⁷ were used for peptide discovery. Bacterial cultures were grown at 37 °C with vigorous shaking in Luria-Bertani (LB) media supplemented with chloramphenicol (CM) (34 µg/mL) for expansion. The medium was supplemented with arabinose (final concentration of 0.02–0.04% w/v) to induce the peptide display. Reagents were supplied as follows: streptavidin-R-phycoerythrin (SA-PE) (Invitrogen), EZ-Link NHS-PEG₄-biotin (Thermo Scientific), Alexa Fluor 488 reactive dye (Invitrogen), Dynabeads MyOne streptavidin C1 1 µm magnetic beads (Invitrogen).

Study Subjects and Samples. Sera used in this study were provided by the University of Tampere (Finland) and the Mayo Clinic (Rochester, MN) (Table 1). The discovery phase patient cohort contained 25 celiac disease (CD) and 20 healthy patient samples from the University of Tampere and 20 CD and 20 healthy samples from the Mayo Clinic. The entire 88 patient training and cross-validation cohort was provided by the University of Tampere. Each sample was from a distinct individual, and the discovery phase cohorts were independent of the training and cross-validation cohort. Samples were

Table 1. Clinical Information About the Patient Samples Used in the Study^a

variable	discovery	training & validation
summary		
no. of patients	85	88
age (yr)	44.6 ± 10.2	45.9 ± 16.2
male	26	29
female	59	59
celiac disease patients		
no. of patients	45	26
age (yr)	45.6 ± 11.0	45.4 ± 16.9
male	14	6
female	31	20
biopsy results available	25	26
Marsh 3a	0	2
Marsh 3b	14	15
Marsh 3c	11	9
double seropositive (tTG & EMA)	45	23
tTG titer		
mean (units/mL)	44.4 ± 38.0	51.1 ± 38.6
<10 units/mL	11	5
10–50 units/mL	15	8
50–80 units/mL	8	5
> 80 U/mL	11	8
healthy controls		
no. of patients	40	34
age (yr)	43.5 ± 9.2	50.5 ± 15.9
male	12	14
female	28	20
tTG serology available	40	34
tTG positive	0	0

^aPlus-minus values are means ± SD.

shipped frozen at –20 °C and 50 µL aliquots were made upon initial thawing. All CD sera were collected at initial diagnosis while patients were still on a gluten-containing diet. Celiac patients from Finland underwent a complete small intestine mucosal biopsy, and their Marsh classification was reported. Patients from the Mayo clinic cohort did not undergo biopsies but tested positive for both antiendomysial antibodies (anti-EMA) and antitissue transglutaminase (anti-tTG) antibodies, which gives a high positive predictive value (~99%) for CD. Healthy controls tested negative for anti-tTG antibodies (and anti-EMA in borderline cases) and were asymptomatic. Disease control samples from the University of Tampere were tTG negative and underwent a biopsy to rule out CD.

Antibody Fractionation and Depletion. Antibody purification was carried out using the Thiophilic Adsorbent kit (Thermo Scientific). Pooled serum purification was performed after pooling 50 µL of serum from each patient. Serum samples (University of Tampere) were divided into pools of 12 and 13 CD patients and 20 healthy patients. Serum samples (Mayo Clinic) were divided into two pools of 10 tTG and EMA double-positive patients and a pool of 20 tTG-negative samples. Individual patient antibody purifications were performed with 50 µL of serum per patient. Eluted antibody fractions were concentrated using 100 kDa molecular weight cutoff filters (Millipore). To deplete antibody fractions of *E. coli* binding antibodies, overnight cultures of cells overexpressing the library scaffold eCPX without a displayed peptide were diluted (1:50) in fresh LB/CM media and grown until the optical density at 600 nm (OD₆₀₀) was between 0.45 and 0.65

(~2 h). Cells were induced with arabinose for 1 h at 37 °C. Cells were centrifuged at 3000 rcf for 5 min. The supernatant was removed, and the cell pellet was resuspended with antibody solution ($>2 \times 10^9$ cells per 1 mg of antibody). Samples were incubated at room temperature on a rotary shaker for 2 h and centrifuged as above, and the supernatant was recovered.²⁵

Library Screening. To reduce the library size to one allowing fluorescence-activated cell sorting (FACS), a pre-enrichment was performed by magnetic-activated cell sorting (MACS)²⁸ with the following change to the protocol to minimize healthy patient antibody binding: unlabeled pooled healthy patient antibodies (50 μ M) were preincubated with the library for 30 min prior to the addition of biotinylated CD antibodies (5 μ M). The overnight culture (post-MACS) was subcultured and induced as above. A volume representing a 10-fold oversampling of the number of cells retained after magnetic separation was centrifuged and resuspended in pooled healthy patient immunoglobulin (Ig). Following 30 min incubation at 4 °C, disease Ig was added to the cell and Ig suspension. One pool of the CD Ig was biotin-labeled and the other pool was labeled with Alexa Fluor 488 dye. Total Ig ratio was 5:1 healthy:CD for the first round of FACS and 10:1 for subsequent rounds. Samples were incubated 45 min at 4 °C, washed, and labeled with 10 nM SA-PE. Cells were washed by centrifugation at 4 °C, resuspended in ice-cold PBS, and sorted or analyzed on a FACSria cell sorter (Becton Dickinson). Sorted cells were grown overnight, and the procedure was repeated for enrichment.²⁸ Three rounds of sorting against the first cohort of samples were performed, followed by a single round of enrichment against a new cohort of samples. Similarly, for single clonal analysis by flow cytometry, biotinylated Ig (200 nM) was used.

Statistical Analysis and Classification Algorithm.

Statistical analysis and optimization of the classification algorithm were performed using R environment version 2.14.2.²⁹ The e1071,³⁰ pROC,³¹ and ROCR³² packages were used to train a support vector machine classification algorithm, calculate the area under the curve (AUC) and 95% confidence intervals, and obtain receiver operating characteristic (ROC) curves, respectively. The raw fluorescent signals from single patient flow cytometry assays were normalized to a “Z score”.^{4,33} The fluorescence signal of each sample’s antibodies binding to *E. coli* that do not display peptides was subtracted from the raw fluorescence signal and then a Z-transformation was applied so that each clone had a mean reactivity of zero and standard deviation of 1.0 across all 60 samples used for training and cross-validation. To determine statistical significance between CD patient antibody and healthy sample antibody reactivity, the Wilcoxon rank-sum test was performed. Support vector machines (SVMs) were used for peptide mimotope classification training.^{34,35} Between 27 and 33 support vectors, depending on the random seed, were required for the highest classifier accuracy using a sigmoid kernel function. The algorithm was optimized by using the tune.svm algorithm in R to select the cost, gamma, and coef0 parameters.³⁰ The classification accuracy was determined by leave-one-out cross-validation (LOOCV) within the training set of samples from 60 CD and healthy patients. The final reported classifier accuracy, area under the curve (AUC), sensitivity and specificity are averages from four trials of LOOCV, each trial having a different random seed. Sensitivity was calculated by dividing the true positives by the sum of the true positives and false negatives. Specificity was calculated by dividing the true

negatives by the sum of the true negatives and false positives. The peptide classifier was further validated using an independent test set of 28 disease control patient sera. Heatmap representations were created using a heatmap builder program.³⁶

RESULTS AND DISCUSSION

Discovery of Celiac Disease Specific Antibody Signatures Using Bacterial Display. To enable the identification of antibody signatures of disease with diagnostic utility, we developed a quantitative, specificity-based screening method to identify peptide mimotopes from random peptide libraries that capture disease-specific serum antibodies (Figure 1). Celiac disease was selected to demonstrate the utility of this

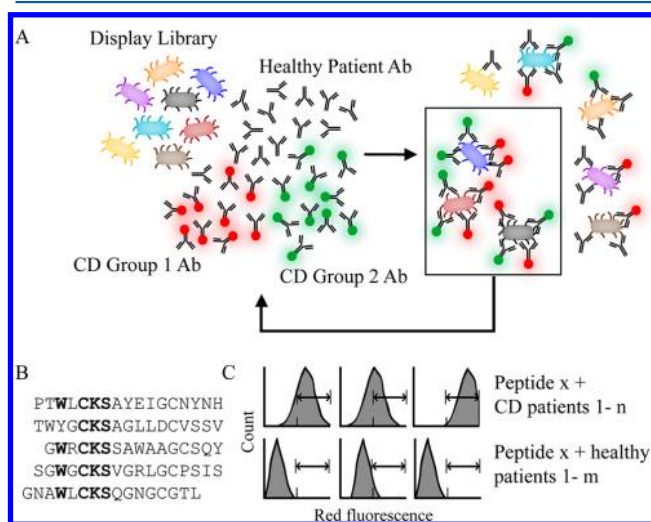


Figure 1. Antibody repertoire profiling methodology using bacterial display and multiparameter flow cytometry (MPFC). (A) Pools of CD patient antibodies are labeled with spectrally distinct fluorophores and incubated with the peptide display library, simultaneously. Pooled unlabeled healthy patient antibodies in excess are used as competition for peptide binding sites. Cells exhibiting both high red and high green fluorescence were collected using FACS. (B) Peptides sequences are identified by DNA sequencing from colonies and grouped into consensus families. Five of the 44 unique peptide sequences isolated from the library screening possessed a WXCKS motif. (C) Unique bacterial clones are assayed with individual patient’s serum antibodies by flow cytometry to assess each peptide’s diagnostic sensitivity and specificity.

approach since it involves a relatively well-understood pathology³⁷ and is known to involve disease-specific serum antibodies against tissue transglutaminase (tTG)³ and deamidated gliadin peptides (dGP).²⁰ The recent identification of tTG and dGP as CD-specific antigens with diagnostic utility required roughly 40 years of basic research. Celiac disease is a complex systemic disease propagated by an abnormal immune response to peptides in dietary wheat gluten and similar prolamins in barley and rye. Diagnosis of CD is facilitated by serological testing for tTG and/or dGP antibodies and confirmed by histological examination of a biopsy of the small intestine. Prompt diagnosis is important to prevent substantial morbidity and possible mortality associated with untreated CD.^{37,38} Yet, definitive diagnosis has been estimated to require 11 years on average from the first presentation,³⁹ and many individuals remain undiagnosed.⁹ Antibody specificities other than those against tTG and dGP have been reported to

be present in patients with CD,⁴⁰ but their diagnostic utility has not been systematically examined. A previous attempt to profile CD patient antibodies using a small peptide display library and a nonquantitative panning method did not identify diagnostically useful mimotopes.⁴¹ Given this, we sought to determine whether the coupling of quantitative specificity-based screening via FACS with high quality bacterial display peptide libraries could provide an effective route to identify antibody signatures of CD.

To increase the probability that the peptides recovered would be both disease specific and cross-reactive with multiple patients' Ig, four pools of CD patient sera from two geographically distinct cohorts, exhibiting diverse severity as assessed by Marsh staging and tTG titers (Table 1), were used for library screening. In order to minimize the nonspecific binding of antibodies present in the non-CD population to peptide binding sites, pools of unlabeled healthy patient sera were used as competition during screening (Figure 1A). Healthy controls were those without symptoms and with negative tTG serology. A bacterial display peptide library comprised of three distinct pooled libraries of the form X_{15} , $X_{12}CX_3$, and $X_4CX_7CX_4$ with 1.2×10^{10} members used for mimotope discovery.²⁷ To facilitate quantitative specificity-based screening via FACS (Figure 2), in an Ig isotype

react with Ig present in two distinct CD patient pools [clones with high red and high green fluorescence (Figure 2)] and that are not blocked by unlabeled Ig from healthy patient pools. The specificity of the enriched library pools for CD patient Ig over healthy patient Ig was explicitly quantified during each cycle of screening (Figure S1 of the Supporting Information). Thus, unlike reported phage-based profiling methods that involve sequential panning with one or two separate disease samples,^{7,42} our method recovered only clones that bind simultaneously to Ig from two distinct CD patient groups.

Reported antibody profiling strategies typically rely upon the use of defined protein arrays^{11,12} that provide fractional coverage of the human proteome or use cDNA libraries derived from specific organs or tissues in conjunction with phage display.^{4,16,17} In contrast, the present approach using a diverse random peptide library coupled with a quantitative library screening requires no prior knowledge about the disease of interest or tissue origin of the antibody biomarkers. Furthermore, this random peptide library approach is not limited to autoantigen discovery since antigens derived from pathogens and allergens can be effectively mimicked. Although not a prerequisite for diagnostic development, the use of a high quality random peptide library can enable direct antigen identification,^{43,44} without bias toward human open reading frames. Here, both linear and disulfide-constrained peptide libraries were pooled to provide a broad range of potential structures for antigen epitope mimicry. Such libraries would be expected to yield mimotopes of both structural and linear epitopes but, aside from amidation and deamidation, would not capture certain post-translational modifications including glycosylation, hydroxylation, and phosphorylation.

The capability to quantify mimotope specificity during MPFC screening offers important advantages over panning of phage libraries. In the latter approach, each round of positive selection is based primarily on affinity between ligand and antibody, and specificity is not explicitly accounted for, despite its obvious importance. Consequently, peptides identified using panning may not possess sufficient disease Ig specificity or desired cross-reactivity to improve diagnostic sensitivity. Both affinity and specificity were favored during MPFC screening because disease and control patient antibodies were incubated simultaneously with the peptide library. With the use of MPFC, the stringency of each round of screening can be adjusted quantitatively in response to a quantitative measurement of cross-reactivity (green and red fluorescence) and disease specificity (signal intensity) (Figure 2).

Down-Selection of Library Isolated Peptides. The final enriched library population was plated, and peptide sequences from individual colonies were determined (Figure 1B). Roughly 200 peptide sequences were obtained from the sorted library population, yielding 44 unique peptide sequences. To identify clones exhibiting maximal cross-reactivity and specificity for CD Ig, the unique clones were first assayed for binding to Ig from at least four disease patients from the discovery phase using flow cytometry (Figure 1C). The assay described here can be performed using very small patient samples, including finger prick volumes as low as 2 μ L per patient, although typical Ig purifications were performed with 50 μ L of serum to ensure a single purification produced enough antibodies for assays with all 44 unique peptides. A total of 22 clones with mean fluorescence intensities greater than 2-fold above the background (i.e., *E. coli* that do not display peptides) were retained for training. In addition, five of the best performing clones were

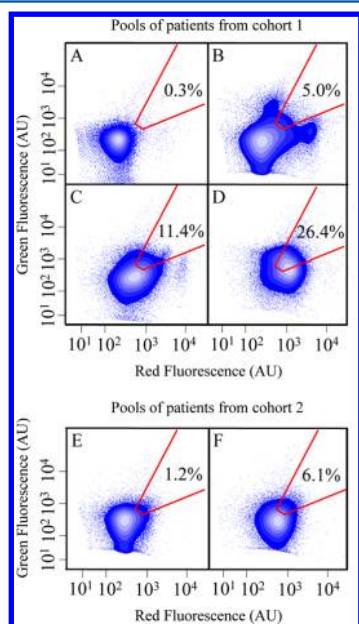


Figure 2. Multicolor FACS enables direct screening for library clones binding to multiple CD patients' antibody fractions. Representative sorting gates are indicated by the red lines. Contour plots of the library population after (A) MACS, (B) one, (C) two, and (D) three cycles of FACS with patient cohort 1 from the University of Tampere. (E) The library population obtained from D, after incubation with the second cohort of CD and healthy patients from the Mayo Clinic. (F) The final enriched library population after one cycle of FACS with the second patient cohort. Each panel is labeled with the percentage of cells from the library that lie within the sorting gate.

independent manner, antibody fractions were conjugated with spectrally distinct fluorophores. Antibodies that recognize native antigens on *E. coli* were depleted from the pool by incubation with *E. coli* cells prior to antibody labeling with biotin or Alexa488 dye.²⁵ Use of two-color screening enabled direct enrichment of clones that display peptides that cross-

further assayed with Ig fractions from 14 CD patients and 22 healthy controls from the discovery cohorts to assess whether the peptides could cross-react with Ig from CD patients and not bind appreciably to healthy patient Ig (Figure S2 of the Supporting Information). Antibody reactivity with these clones was significantly higher for CD patients than for healthy patients (Wilcoxon rank-sum test p value < 0.001), as measured by flow cytometry.

To identify individual peptides from the set of 22 with the highest utility for CD patient diagnosis, clones were assayed for binding to new patient samples that were not used for discovery (Figure 3). First, each clone was assayed for binding to ten

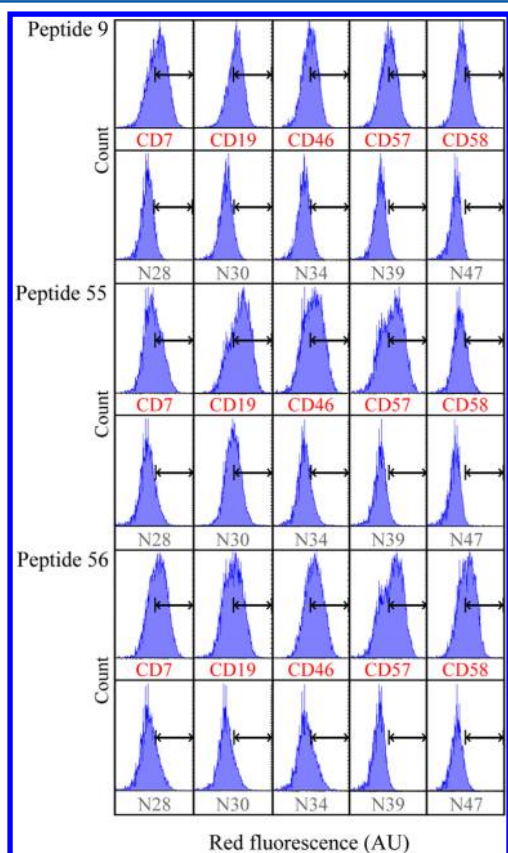


Figure 3. Library-isolated peptides were down-selected and characterized by assaying individual patient's serum antibodies by flow cytometry. Representative histograms of three peptides assayed for binding with five CD patient antibodies and five non-CD healthy controls (N) not used in the discovery phase. The data shown here was typical of the peptide performance seen throughout individual patient analysis during the training and cross-validation phases of the study. Arrows represent red fluorescence from 300 AU to 10000 AU. Red fluorescence is shown on the logarithmic scale.

healthy patient samples, and clones exhibiting fluorescence signals less than 3-fold above background were retained. Ten clones that met this condition were further assayed with 10 CD samples. Six peptides yielded significant ($p < 0.05$) differences in reactivity between CD and healthy patient Ig and were retained for combined array training and cross-validation phases. The remaining peptides (Figure 4) were dissimilar with the primary amino acid sequence of tTG and deamidated gliadin. Four of the remaining peptides (9, 10, 55, 56) possessed a Cys-Lys consensus motif with a preference for an aromatic residue (W/Y) N-terminal to cysteine. However,

these sequences did not enable unambiguous candidate antigen identification using protein database search algorithms. Further epitope elucidation may be possible through directed evolution.²⁵ Three clones (9, 55, 56) originated from the X₁₂CX₃ library, two clones (10, 168) originated from the X₄CX₇CX₄ library, and one (7) was derived from the X₁₅ library. Assaying these six clones with 16 additional CD patients and 24 additional healthy patient antibody fractions revealed that these peptides maintained desired CD patient Ig cross-reactivity and specificity for CD over healthy patients in the training set (Figure 4A). These peptides, with the exception of peptide 7, retained statistically significant reactivity differences between CD and healthy patients with the inclusion of more patient samples (Figure 4C).

Classification model Development and Cross-Validation of the Peptide Panel. Because no single peptide identified provided high specificity alone and because each peptide's reactivity pattern with the 60 new samples was unique, the peptides were used in combination to improve classification accuracy. A support vector machine (SVM) algorithm was applied to classify patients as either CD or non-CD.^{30,33,34} A sigmoid kernel function was used to project the data to higher dimensions and allow for separation between classes, and model parameters were tuned to optimize classification. To measure the performance of the algorithm, future sample prediction accuracy was estimated using LOOCV in quadruplicate using random sampling (Table S1 of the Supporting Information). Thus, the model was trained using 59 of the 60 samples and used to predict the class of the remaining sample. This process was repeated 60 times for each of the four random samplings so that each sample was used as the validation sample exactly once per sampling. The predictions for each sample were averaged over the four trials and prediction error was calculated (Table S1 of the Supporting Information).

The true positive rate (sensitivity) was plotted against the false positive rate (1-specificity) in a receiver operating characteristic (ROC) curve as a function of varying thresholds of class prediction probabilities (Figure 5). Use of a six peptide panel enabled discrimination of CD patients from healthy controls with an area under the curve (AUC) of 0.91 (95% confidence interval range, 0.88 to 0.95). Using a predicted class probability threshold of 0.45, sixty patients were classified with 88% overall classifier accuracy, with 85% sensitivity and 91% specificity. A cutoff of 0.5 similarly classifies patients with 87% accuracy but a higher specificity of 94% and a lower sensitivity of 77%. Since the prevalence of CD is approximately 1 in 100 Caucasians on the population level but may be as high as 1 in 10 in first degree relatives,^{45–47} multiple prediction probability thresholds may be useful, depending on the type of screening being performed. Thus, using a relatively small panel of nonoptimized peptide reagents, we were able to obtain sensitivity and specificity values that approach those of current serological tests. The accuracy of anti-tTG IgA ELISA tests has demonstrated variable diagnostic sensitivity (85–98%) and specificity (95–98%) in several different studies^{48–50} but may be lower in routine clinical use.⁵¹ Similarly, tests for the presence of IgA antibodies against deamidated gliadin have been reported to yield average sensitivities of 88% and specificities of 95%.⁵⁰

Classifier accuracy was independent of tTG titer, suggesting the peptides were not mimotopes of tTG (Figure S3 of the Supporting Information). Interestingly, each of three CD

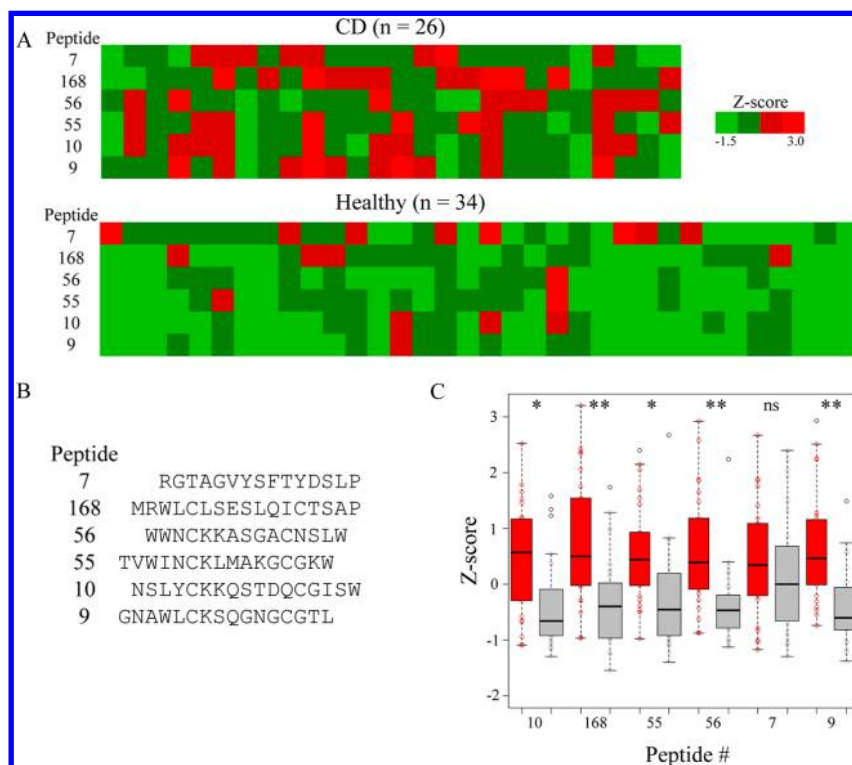


Figure 4. Reactivity of the peptides with 60 training phase samples. (A) Heatmap representation of 6 peptides assayed for binding with 26 CD patient antibodies and 34 healthy controls not used in the discovery phase by flow cytometry. Individual peptides are represented in rows and patients' antibodies are represented in columns. Red indicates high reactivity, dark green indicates signal above background, and light green indicates nonreactivity. (B) Amino acid sequences of the six peptides. (C) Box plot representation of the training phase sample response to the six peptides. Red boxes represent the CD samples and gray boxes represent the healthy controls: *, $P < 0.005$; **, $P < 0.0001$; ns, not significant. P values were calculated from the Wilcoxon-rank-sum test with $P < 0.05$ considered statistically significant.

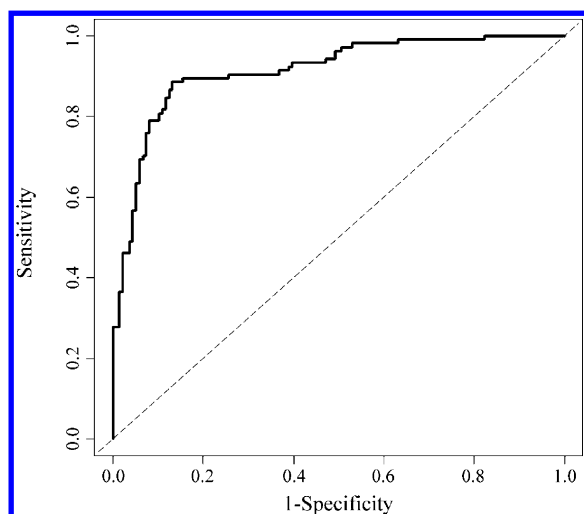


Figure 5. Receiver-operating characteristic (ROC) curve for the six peptide CD classifier with 60 patients not used in reagent discovery. The ROC curve is calculated using the true positive rate and false positive rate from the average class probabilities from four trials of LOOCV predicted by the support vector machine (SVM) algorithm. The area under the curve (AUC) for the peptide classifier is 0.91 (95% confidence interval, 0.88 to 0.95). A classification probability threshold of 0.45 yields a sensitivity of 85% and a specificity of 91%.

patients in the test set that were negative for either EMA or tTG antibodies when both tests were performed were classified correctly using the peptide panel. It is possible that additional tTG/dGP negative but biopsy positive CD patients could be

correctly classified using the peptide panel; however, the scarcity of such samples makes evaluation problematic for this application. Diagnostic sensitivity obtained with the panel was apparently independent of the severity of villous atrophy since there was no trend between the Marsh stage of the 26 untreated CD patients and the peptide classifier predictions (Figure S4 of the Supporting Information).

Independent Validation Set of Disease Control Patients. To investigate whether the peptide classifier was specific to CD and not related conditions, 28 disease control patients were classified using the peptide panel. This group included 13 patients that possessed the necessary CD genotype (HLA-DQ2 or -DQ8) but were confirmed by biopsy not to have the characteristic histology required for CD diagnosis. To rigorously test our peptide panel against patients that suffer from symptoms that overlap with those occurring in CD, patients with irritable bowel syndrome (IBS, $n = 10$), dyspepsia ($n = 10$), lactose intolerance ($n = 3$), collagenous colitis ($n = 1$), colitis ulcerosa ($n = 1$), and nonspecific discomfort ($n = 3$) were classified as CD or non-CD using our SVM model. With a probability threshold of 0.5, 22/28 patients (79%) were correctly classified as not having CD (Figure S5 of the Supporting Information). The six misclassifications were from four dyspepsia patients (two with HLA-DQ2), one patient with IBS, and one collagenous colitis patient, although no disease showed a statistically significant difference of reactivity in comparison to the other groups. Additionally, we cannot definitively rule out the possibility that biopsy results were falsely negative.⁵² Interestingly, patients with dyspepsia and IBS

have been reported to exhibit positive tTG serology more frequently than the general population.⁵³

CONCLUSIONS

In summary, our results demonstrate that cell display technology provides a remarkably effective route to identify diagnostically useful serum antibody signatures of disease and peptide-capture reagents for their detection. The coupling of multicolor screening with bacterial display peptide libraries provides an alternative to phage cDNA and peptidome libraries, enabling an unbiased search of peptide sequence space. Consequently, the present approach may allow the identification of both self- and nonself antigens from heterologous organisms without prior knowledge of the autoantigens' tissue expression patterns or organisms involved in disease onset or progression. For these reasons, specificity-based screening of bacterial display libraries may be generally useful to identify novel antibody biomarkers and reagents for diagnostic assay development.

ASSOCIATED CONTENT

Supporting Information

Quantitative fluorescence histograms of pooled antibody reactivity during library sorting, heatmap of discovery phase patient reactivity with five peptides, cross-validation predictions using the SVM model, relationships between serology and histology with CD prediction probabilities, and CD classification with 28 disease control patients. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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Notes

The authors declare no competing financial interest.

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Antibody repertoire profiling using bacterial display identifies reactivity signatures of celiac disease

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The supporting information contains: quantitative fluorescence histograms of pooled antibody reactivity during library sorting, heatmap of discovery phase patient reactivity with five peptides, cross-validation predictions using the SVM model, relationships between serology and histology with CD prediction probabilities, and CD classification with 28 disease control patients.

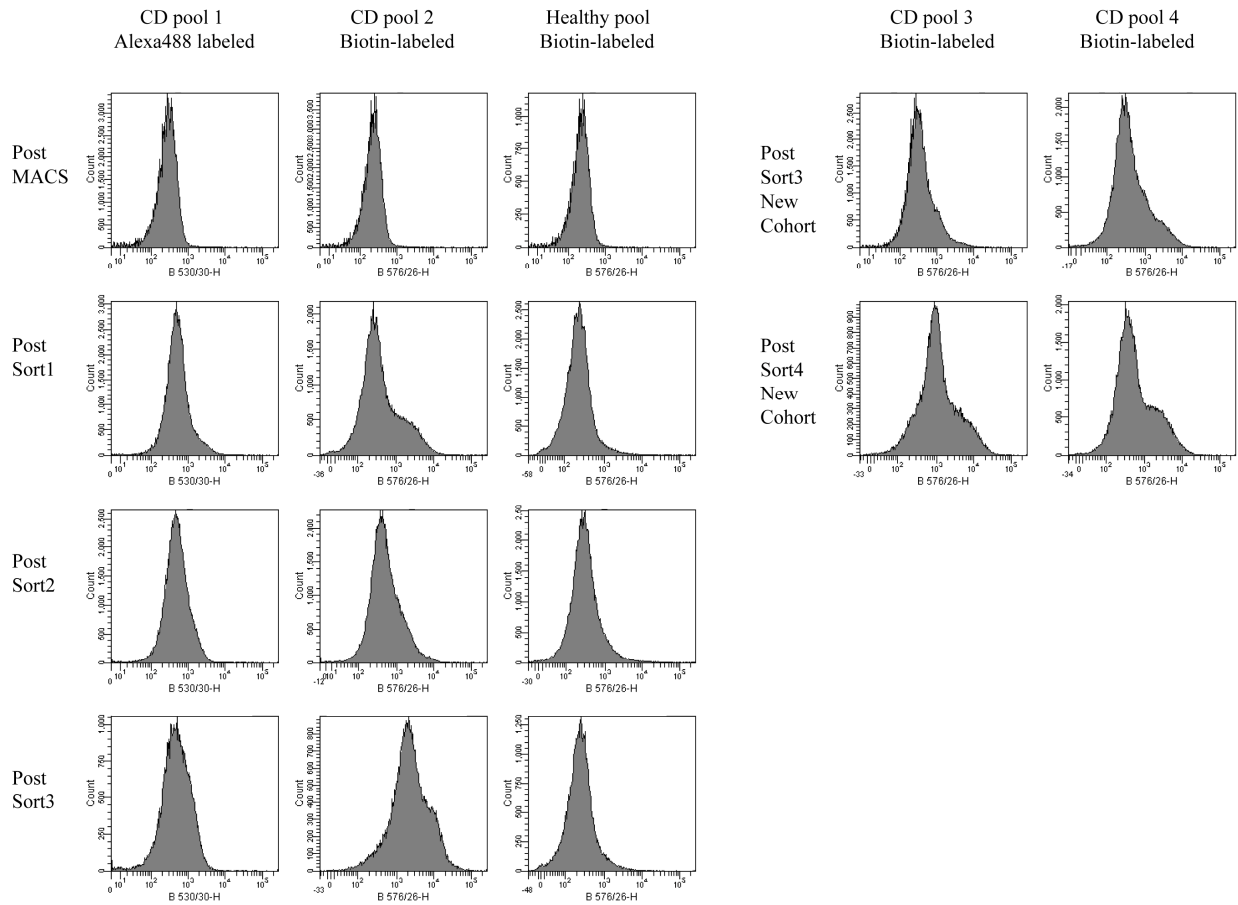


Figure S1. Quantification of bacterial display peptide library enrichment for specific binding to CD patient Ig but not healthy patient Ig. Fluorescence histograms obtained by flow cytometry for antibody pools incubated separately with the enriched library population after each round of sorting. To monitor the relative specificity of the enriched library, the mean fluorescence of the library assayed with CD patients' antibodies was compared to the mean fluorescence of the library assayed with healthy patient pools. CD pools 1 and 2 were provided by the University of Tampere, and CD pools 3 and 4 were provided by the Mayo Clinic.

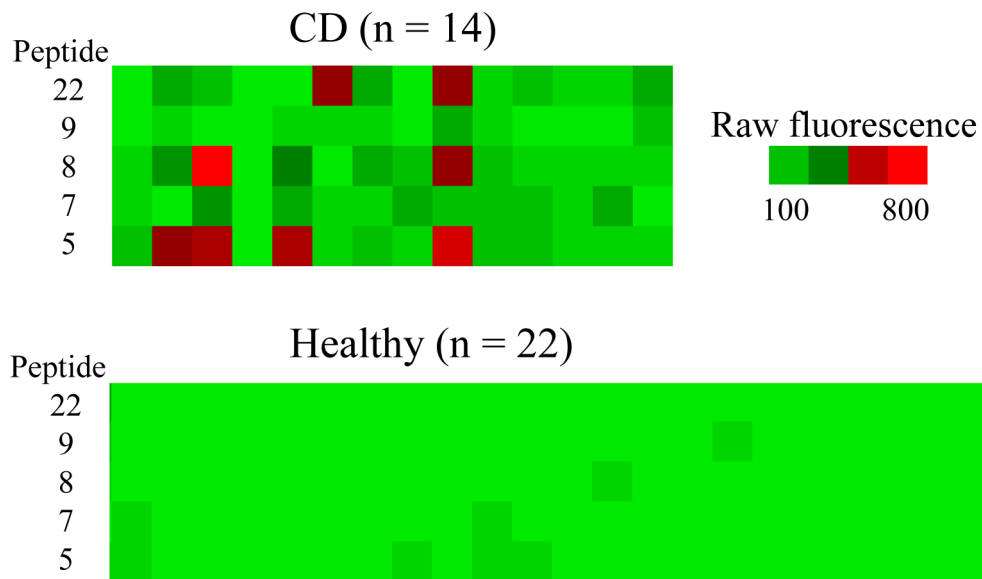


Figure S2. Heatmap representation of five distinct peptide-displaying bacteria assayed for binding to 36 discovery phase Ig samples. Individual peptide clones are represented in rows and patients' antibodies are represented in columns. Fourteen CD patients and 14 healthy patients were provided by the Mayo Clinic, and the remaining eight healthy patients shown here were provided by the University of Tampere. All patients shown here were used in the peptide screening phases. Peptides 5, 8, and 22 were not retained in the final six peptide panel used for disease prediction because of poor specificity with healthy controls not used in screening (data not shown).

Table S1. LOOCV predictions using SVM model with 60 patients from the University of Tampere. A class prediction probability of greater than 0.5 is considered to be CD. A class prediction probability of less than 0.5 is considered to be normal (N).

Sample ID	Prediction	Probability	Error	Class	Misclassification
1	N	0.045	0.018	N	
2	N	0.271	0.053	CD	*
3	N	0.037	0.018	N	
4	CD	0.651	0.036	CD	
5	CD	0.531	0.052	CD	
6	N	0.102	0.033	N	
7	CD	0.902	0.033	CD	
8	CD	0.544	0.054	CD	
9	CD	0.684	0.032	CD	
10	N	0.471	0.034	N	
11	N	0.334	0.069	CD	*
12	N	0.188	0.067	N	
13	CD	0.607	0.028	CD	
14	N	0.338	0.038	N	
15	N	0.081	0.018	N	
16	N	0.220	0.013	N	
17	N	0.366	0.042	CD	*
18	N	0.326	0.011	N	
19	CD	0.906	0.036	CD	
20	N	0.324	0.029	N	
21	CD	0.852	0.019	CD	
22	CD	0.617	0.031	N	*
23	N	0.281	0.041	N	
24	CD	0.637	0.044	CD	
25	CD	0.932	0.034	CD	
26	N	0.052	0.014	N	
27	N	0.294	0.035	N	
28	N	0.239	0.014	N	
29	N	0.273	0.036	N	
30	N	0.102	0.035	N	
31	CD	0.916	0.050	CD	
32	N	0.153	0.055	N	
33	N	0.165	0.073	N	

34	N	0.183	0.031	N	
35	N	0.468	0.094	CD	*
36	CD	0.775	0.036	N	*
37	CD	0.614	0.121	CD	
38	N	0.264	0.024	N	
39	N	0.077	0.031	N	
40	N	0.056	0.018	N	
41	N	0.343	0.060	N	
42	N	0.114	0.027	N	
43	CD	0.701	0.055	CD	
44	N	0.087	0.020	N	
45	N	0.128	0.031	N	
46	CD	0.945	0.020	CD	
47	N	0.049	0.006	N	
48	CD	0.912	0.020	CD	
49	N	0.185	0.028	N	
50	N	0.378	0.051	N	
51	CD	0.738	0.063	CD	
52	N	0.057	0.028	N	
53	N	0.152	0.040	N	
54	N	0.116	0.028	N	
55	CD	0.553	0.044	CD	
56	N	0.140	0.041	CD	*
57	CD	0.790	0.090	CD	
58	CD	0.614	0.055	CD	
59	CD	0.678	0.085	CD	
60	N	0.457	0.054	CD	*

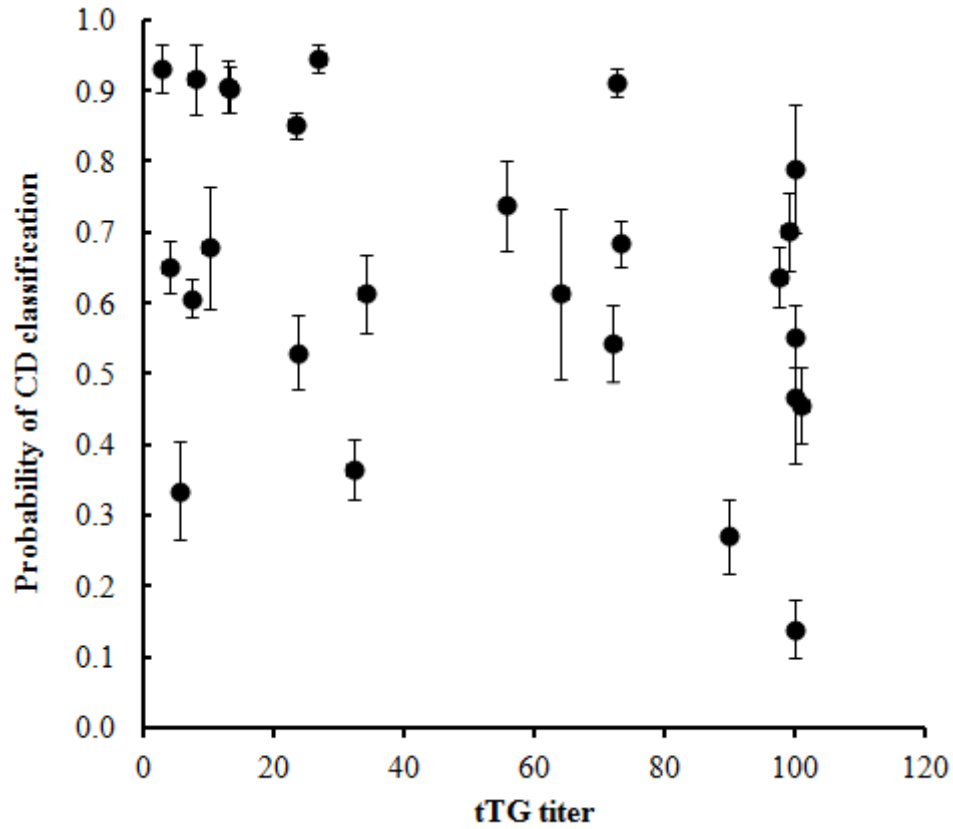


Figure S3. The probability of CD classification as a function of tTG titer for the 26 training phase CD antibody samples. Each circle signifies a distinct patient. Error bars represent the standard error of the mean for four trials of the classification algorithm, each with a unique random seed. The two samples with the lowest tTG titers were considered to be negative for the tTG ELISA blood test.

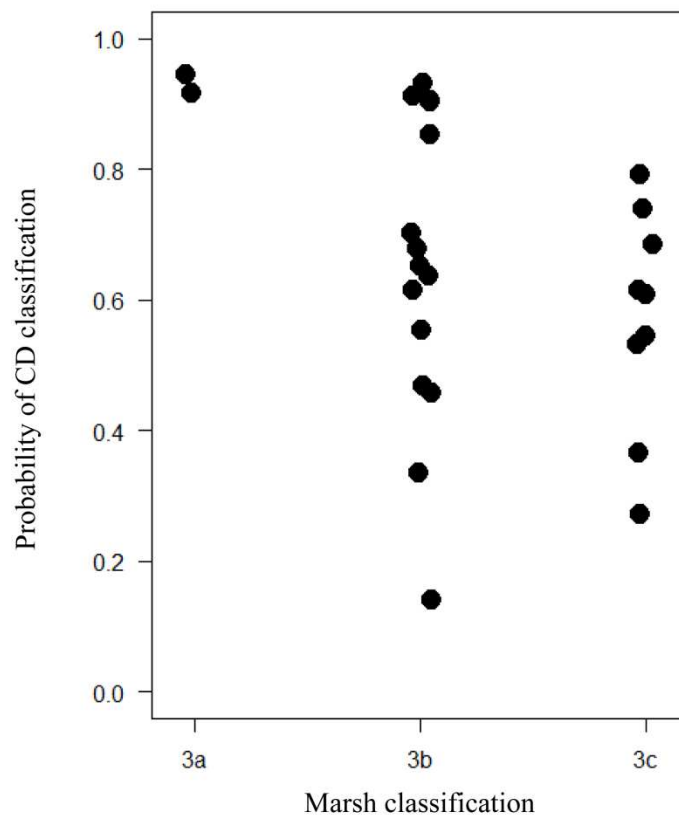


Figure S4. The probability of CD classification as a function of intestinal mucosal histology for the 26 training phase CD samples. Each circle represents an distinct individual patient from the University of Tampere.

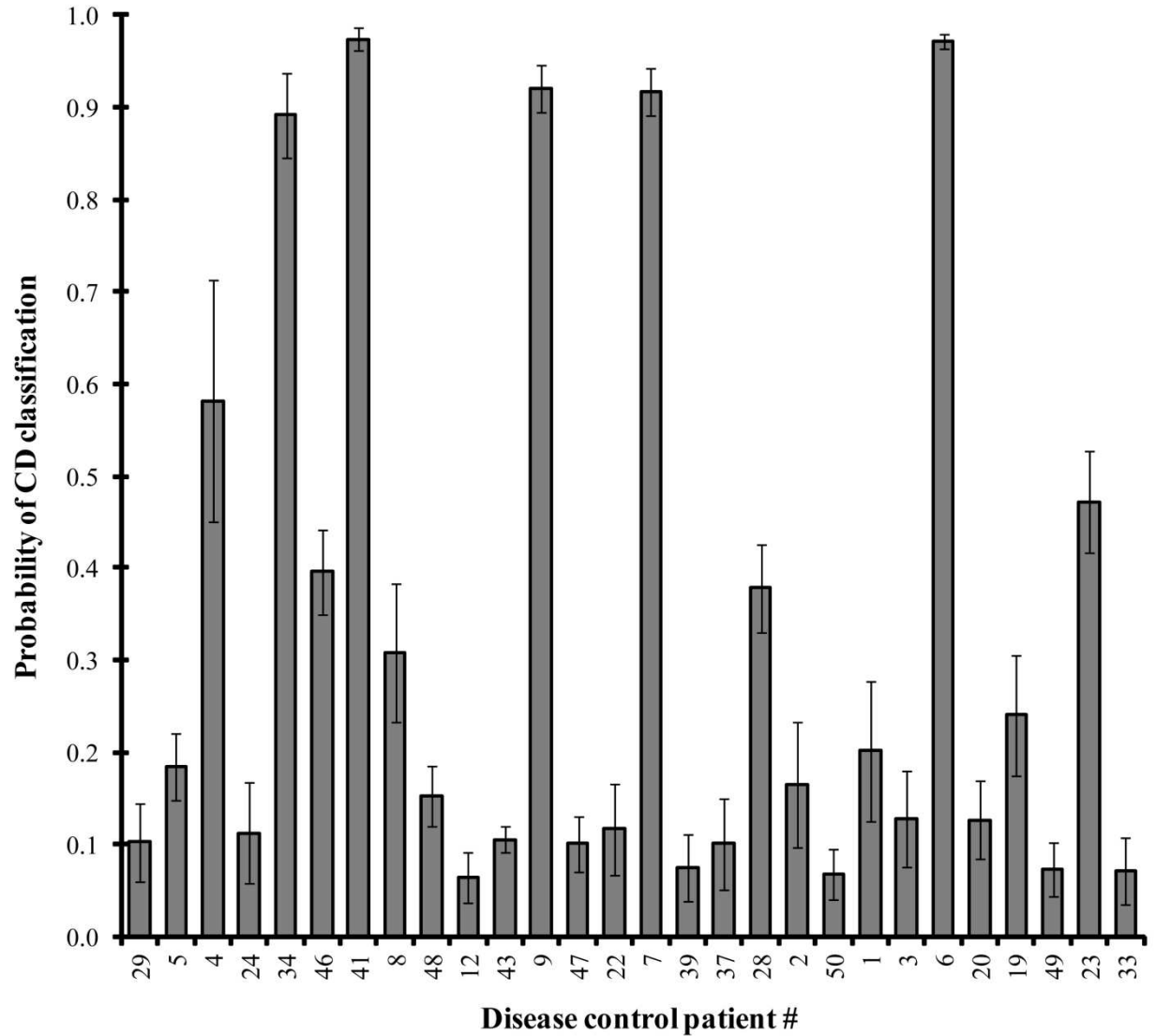


Figure S5. Classification probabilities for the validation cohort of 28 disease control patients from the University of Tampere. With a class prediction probability threshold of 0.5, 79% of disease control patients are correctly classified as non-Celiac. When the threshold is decreased to 0.45, the classifier accuracy drops to 75%. Error bars represent the standard error of the mean for four trials of the classification model, each with a unique random seed.