Award Number: W81XWH-12-1-0388

TITLE: Subgrouping Chronic Fatigue Syndrome Patients by Genetic and Immune Profiling

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REPORT DATE: December 2015

TYPE OF REPORT: Final

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for Public Release;
Distribution Unlimited

REPORT DOCUMENTATION PAGE		*Form Approved* *OMB No. 0704-0188*

1. REPORT DATE December 2015	**2. REPORT TYPE** Final	**3. DATES COVERED** 08 Sep 2012 - 7Sep2015
4. TITLE AND SUBTITLE Subgrouping Chronic Fatigue Syndrome Patients By Genetic And Immune Profiling		**5a. CONTRACT NUMBER** W81XWH-12-1-0388
		5b. GRANT NUMBER
		5c. PROGRAM ELEMENT NUMBER
6. AUTHOR(S) Dr. Jose Montoya, Tyson Holmes, Donn Gavert, Holden Maecker, Michael Mindrinos, Rosemary Fernandez, Luciana Mendiola E-Mail: lucianam@stanford.edu		**5d. PROJECT NUMBER**
		5e. TASK NUMBER
		5f. WORK UNIT NUMBER
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) THE LELAND STANFORD JUNIOR UNIVERSITY 450 SERRA MALL STANFORD CA 94305-2004		**8. PERFORMING ORGANIZATION REPORT NUMBER**
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012		**10. SPONSOR/MONITOR'S ACRONYM(S)**
		11. SPONSOR/MONITOR'S REPORT NUMBER(S)
12. DISTRIBUTION / AVAILABILITY STATEMENT Approved for Public Release; Distribution Unlimited		
13. SUPPLEMENTARY NOTES		

14. ABSTRACT

We have successfully performed all testing of the approximately 600 samples (200 CFS/ME patients vs 397 healthy controls) we set up to do under this grant at the Stanford Human Immune Monitoring Center (HIMC) and the Stanford HLA Mindrinos lab. These samples were tested by two novel methods (CyTOF-phosphoflow and HLA Typing, respectively) to help us better understand the roles of immune responses and genetics in the pathogenesis of chronic fatigue syndrome (CFS)/myalgic encephalomyelitis (ME). It is likely that these findings will also result in an improved understanding of the pathogenesis of Gulf War Illness (GWI). For both methods, CyTOF-phosphoflow and HLA Typing, we have reviewed in excruciating detail all the potential sources of technical error in both methods, systematically cleaned all confounders and plate effects, and have set up a statistical plan.

Our statistical team worked closely with the lab that generated the phospho-CyTOF assay results (The HIMC) to ensure that the phospho-CyTOF database for this analysis was complete. Our statistical team was also able to work in close collaboration with Dr. Fernandez-Vina, Professor (a world authority in HLA genetics and close collaborator of Dr. Mindrinos), Department of Pathology, Stanford University School of Medicine regarding HLA type coding. Below please find initial results on basic and descriptive statistics of the results from both methods.

ABSTRACT(CONTINUED)

A more complex statistical analysis is underway; please see below details of the major statistical analysis that is being currently performed. Utilizing funds from a major Stanford donor we have been able to hire a full time and high-level statistician and programmer (Donn Gavert) who will work 100% with our team and under the direction of Dr. Tyson Holmes (a Stanford authority in the analysis of complex and big data). Our primary goal is to unveil the pathogenesis of ME/CFS and subsequently of GWI. It appears that we will gain a significant understanding of the immune responses and genetics of these illnesses with the analysis of the results in CyTOF-phosphoflow and HLA Typing that it is underway. We aim at submitting an amendment to this report with the final analysis, biological/clinical meaning of our results and publications in major journals we hope to achieve.

15. SUBJECT TERMS

CyTOF, human leukocyte antigens (HLA) types, Chronic Fatigue Syndrome(CFS), novel testing, autoimmune disease, dynamic range, analytes, phospho-flow, flow cytometry, pico-green, quality control, Chronic Fatigue Immune Dysfunction, genetic, immune, infectious disease

16. SECURITY CLASSIFICATION OF:			**17. LIMITATION OF ABSTRACT**	**18. NUMBER OF PAGES**	**19a. NAME OF RESPONSIBLE PERSON** USAMRMC
a. REPORT U	**b. ABSTRACT** U	**c. THIS PAGE** U	UU	185	**19b. TELEPHONE NUMBER** *(include area code)*

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INTRODUCTION:

We are excited to report that we have completed the CyTOF and HLA before September 8 2015 testing as scheduled and reported in our previous report. We hope to be able to further elucidate the roles that the immune system and genetics play in the pathogenesis of CFS/ME by comparing cases vs. healthy controls. We believe that we will also gain significant insights by analyzing these data by severity of ME/CFS. Below please see the demographics and main ME/CFS symptoms in the participants by cases vs healthy controls.

Characteristics	*Untreated Cases*		*Healthy Controls*	
	n	*(%)*	*n*	*(%)*
Total N	200	(100.0)	397	(100.0)
Age, Mean ± SD	50.0 ± 12.5		50.1 ± 12.5	
Gender, N (%)				
Female	154	(77.0)	305	(76.8)
Male	46	(23.0)	92	(23.2)
Race, N (%)				
Asian	5	(2.5)	40	(10.1)
Hispanic	3	(1.5)	21	(5.3)
Black	1	(0.5)	32	(8.1)
White	183	(91.5)	281	(70.8)
All other	1	(0.5)	19	(4.8)
No data	7	(3.5)	4	(1.0)
Family History of CFS, N (%)				
Yes	26	(13.0)	6	(1.5)
No	167	(83.5)	389	(98.0)
No data	7	(3.5)	2	(0.5)
Fukuda Criteria				
Impaired memory	192	(96.0)	4	(1.0)
Sore throat	124	(62.0)	1	(0.3)
Tender cervical or lymph nodes	124	(62.0)	2	(0.5)
Muscle pain	182	(91.0)	10	(2.5)
Multi-joint pain	139	(69.5)	22	(5.5)
New headaches	144	(72.0)	30	(7.6)
Unrefreshing sleep	193	(96.5)	8	(2.0)
Post-exertional malaise	193	(96.5)	3	(0.8)

All team members are aware of the goals for this DOD Grant and we look forward to completing all the tasks as needed in order to complete the project together. We will be analyzing the CyTOF-phosphoflow and HLA Typing by case/control status, severity, age, gender, race and some of the Fukuda criteria.

BODY (CyTOF):

Analyses to date:

Data Preparation

Upon receipt, data were thoroughly reviewed by our statistical team to check for accuracy and completeness. Our statistical team worked closely with the lab that generated the phospho-CyTOF assay results (The Human Immune Monitoring Center, Stanford University) to ensure that the phospho-CyTOF database for this analysis was complete. Completeness of participant inclusion was also verified against our master demographic file. This process revealed that only a small percentage of participants ($n = 36$, 6.03%) did not provide sufficient sample to provide readings on all 39 cell subsets percentages plus $31 \times 8 = 248$ intensities or $f = 248$ features in total. Initial drafts of data summaries were reviewed by Dr. Holden Maecker, Director, The Human Immune Monitoring Center, Stanford University.

Initial Detailed Descriptive Summaries

1) Separately for cases and controls, for each stimulation condition, we calculated the sample means for each cell subset expressed as a percentage of intact cells.
2) Separately for cases and controls, for each stimulation condition, we calculated the sample mean *median intensity* of each of the eight intracellular-staining phospho-epitopes within each of the 31 cell subsets. Minimum possible median intensity is 1.

Proposed analyses:

Analysis by Feature

This analysis is designed to conduct formal hypothesis testing for purposes of identifying those phospho-CyTOF features that distinguish cases and controls. Regression modeling will account for the possibility that differences between case and control responses may differ among the different stimulation conditions examined. Covariates will be included for age and gender, those two factors that were used to match cases and controls in the original sampling design, plus an additional covariate for race. Finally, because participants' samples were assayed in a sequence of multiple batches, we will employ two means of correcting for any batch effects that may be present.

1) By design, a sample from a standard control was to be included within each batch. As such, we will include this control reading as a covariate in the regression model.
2) Because batch effects may exhibit *carryover* from one batch to the next over the sequence of batches (e.g., due to drift in instrumentation, materials, or assay operation), we will employ the mean response from the prior batch as a covariate and also account for the fact that the strength of this carryover effect may vary depending upon the amount of time elapsed between consecutive batches.

The regression model specification for each of outcome will be as follows.

$$\begin{aligned} g(Y) = \beta_0 + \beta_1 c + \sum_{i=1}^{7} \beta_{i+1} s_i + \sum_{j=1}^{7} \beta_{j+8} s_j\, c + \beta_{16} m_{t-1} \\ + \sum_{k=1}^{7} \beta_{k+16} m_{t-1} b_k[d_t - d_{t-1}] + \beta_{24} u_t + \beta_{25} a + \beta_{26} g + \beta_{27} w + E, \end{aligned} \quad \text{[E1]}$$

where Y is outcome, $g(\cdot)$ is an appropriate link function, $c = 1$ for case and $c = 0$ for control, s_i is an indicator variable for i^{th} stimulated condition, a is age of the participant, g is an indicator variable for gender of the participant, w is an indicator variable for white race, m_{t-1} is batch mean of outcome for previous batch ($m_{t-1} = 0$ for first batch), d is days elapsed from first batch, the $b_k[d_t - d_{t-1}]$, $k \in \{\mathbb{Z}^+ | k \leq 7\}$, is a cubic b-spline basis on three knots, u_t is value of outcome for batch control, and E is residual error, as appropriate. Regression model E1 will be fit separately to each the $f = 248$ features as the outcome. Attained significance levels (p-values) for the case vs. control effect will be adjusted to account for accumulation of Type I error (false positive error) across multiple hypothesis tests. Specifically, p-value adjustments will employ an adaptive two-stage linear step-up procedure to control the FDR at 5% (Benjamani et al. 2006, Kim and van de Weil 2008) across the $f = 248$ features. Unadjusted (raw) p-values will provided as well for those whose interest is limited a priori to a specific feature.

Multivariate Immunophenotype Discovery

This analysis is designed to 1) identify those multivariate feature constellations that represent distinct immunophenotypes and 2) compare prevalences of cases and controls between these immunophenotypes. We will test for differences in multivariate feature structure between cases and controls, employing the full set of $f = 248$ features. Analysis will begin by identifying *phenotypes* (clusters). Cluster analysis will be performed on a data matrix that consists of eight rows per person, one row per person per stimulation condition, and one column for each feature ($f = 248$). This matrix will be denoised (Peterson and Ford 2013, Chi and Lange 2014) prior to clustering to ensure that clustering is on structure (signal) rather than noise. A combination of ragged pruning of the hierarchical clustering via a minimum cluster size criterion (Bruggner et al. 2014) and equal weighting per cluster of the cluster quality criterion will permit identification of phenotypes *whether common or rare*. We will test for association between each phenotype and case status (by stimulation condition) by employing presence/absence of each derived phenotype as a binary outcome variable in a logistic regression structured per model E1.

BODY (HLA Typing):

Analyses to date:

Data Preparation

Upon receipt, data were thoroughly reviewed by our statistical team to check for accuracy and completeness of the data. Completeness of participant inclusion was also verified against our master demographic file. The statistical team was able to resolve those few questions that arose during this quality-control process, namely regarding HLA type coding, in consultation with Dr. Fernandez-Vina, Professor, Department of Pathology, Stanford University School of Medicine, and co-Director of the Histocompatibility, Immunogenetics and Disease Profiling Laboratory. Dr. Fernandez-Vina also inspected initial summaries of the data. Missing data for an entire gene was assumed to be due to poor quality sequencing reads. The number of observed misreads varied by gene loci: HLA-A = 4 (0.67%), HLA-B = 19 (3.22%), HLA-C = 5 (0.85%), HLA-DPA1 = 4 (0.67%), HLA-DPB1 = 4 (0.67%), HLA-DQA1 = 5 (0.85%), HLA-DQB1 = 33 (5.59%), HLA-DRB1 = 10 (1.69%), and HLA-DRBo = 74 (12.54%).

After completion of these quality-control procedures, initial estimation summaries were prepared of allele prevalences.

Allele Prevalence per Copy: Prevalence Characterization

The primary objective of this analysis was to provide individual allele prevalence estimates. Per traditional reporting practices (e.g., Smith et al. 2005), prevalences here are *per copy*. In other words, in a sample of n participants, prevalence was calculated with a denominator of $2n$ (hereafter, "$2n$-allele prevalence"). Separately for each allele, Bayesian point estimates (posterior means) of $2n$-allele prevalences were calculated for cases and, separately, for controls as well as for the difference in prevalences between cases and controls. Along with each point estimate, a Bayesian 95% credible interval (highest density) was calculated, which encompasses *the 95% most plausible values of the parameter*. Alleles were classified as common or rare for purposes of statistical modeling. For common alleles, a logistic regression model was fit for beta-binomial outcome y, $y \in \{0, 1, 2\}$, $m = 2$ via Bayesian estimation. A beta-binomial model was employed because alleles are sampled in pairs (Guedj et al. 2006), a fact that is often overlooked in analyses of prevalence per copy (e.g., Smith et al. 2005). Conjugation of a binomial distribution with a beta distribution allows for the possibility of *overdispersion*—that is, variation in $2n$-allele prevalence p among individuals and/or among subpopulations *within* the case population and/or *within* the control population. Alleles were classified as rare where average sample $2n$-allele prevalence across cases and controls, combined, was 5% or less (Raychaudhuri 2011), a threshold that was confirmed by Dr. Fernandez-Vina. Given that a rare allele, by definition, was absent from nearly all participants, estimation of overdispersion was not possible. As such, for rare alleles, a logistic regression model was fit for binomial outcome $y \sim \text{Bin}(m, p)$, $y \in \{0, 1, 2\}$, $m = 2$, via Bayesian estimation, where the necessary simplifying assumption was made that $2n$-allele prevalence p was identical across all individuals within each population (case or control). Also, in common alleles, where we found that the beta binomial model fit the observed data poorly, estimation employed this simpler binomial model. Bayesian estimation was employed for its ability to account for sampling of pairs and for any complex variation due to subpopulation structure, which is anticipated for the HLA region. Bayesian estimation was also employed for its capacity to rigorously and explicitly account for uncertainty in parameter estimation (Holmes and Lewis 2014). To illustrate this latter point, Bayesian estimation admits the possibility that an allele of observed frequency of zero does not necessarily indicate that allele is truly absent from the population but merely very rare (e.g., estimated prevalence of 0.0083% for A69 in cases). Results are reported separately for 2-digit alleles (e.g., A01) and 4-digit alleles (e.g., A0101). In addition to tables of results, we prepared caterpillar plots of the Bayesian 95% credible intervals for differences in 2n-allele prevalences for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

Allele Prevalence per Person: Case v. Control Prevalence Comparisons

The primary objective of this analysis was to compare individual allele prevalences between case and controls. Here, prevalence was defined by presence/absence of one or more copies of a specific allele *per person* (i.e., with a denominator of *n* sample participants). This allele prevalence was compared between cases and controls. Expected prevalence may be close to zero or zero for many of the alleles. Exact testing is useful in this circumstance. Boschloo's (1970) exact *unconditional* test was employed as Mehrotra et al. (2003) has shown that this procedure is uniformly more powerful than the Fischer's exact test. A relative risk point estimate was calculated for each allele comparing cases to controls. Attained significance levels (p-values) were adjusted to account for accumulation of Type I error (false positive error) across multiple hypothesis tests. Specifically, p-value adjustments employed an adaptive two-stage linear step-up procedure to control the false discovery rate (FDR) at 5% (Benjamani et al. 2006), here across all alleles within each gene,—a procedure that has been shown to have good error-control properties for possibly dependent hypothesis tests (Kim and van de Weil 2008). Separate FDR control by gene allows for possibility that % true nulls varies among genes. 95% exact unconditional confidence intervals were calculated for the relative risk (Chan and Zang, 1999). Results are reported separately for 2-digit alleles and 4-digit alleles.

Proposed analyses:

Accounting for Disease Severity

After this final report, we will begin by preparing an additional set of tables that provide Bayesian estimates of $2n$-allele prevalences for controls *compared to each disease severity category (mild, moderate and severe) for cases*. Results will be reported separately for 2-digit alleles and 4-digit alleles. Comparisons of per-person allele prevalences between controls and each disease severity category will also be performed.

Expansive Hypothesis Testing

We will also commence additional work on formal hypothesis testing to examine associations between case status (case vs. control) and 1) each individual allele and 2) potentially interacting alleles (Cordell 2009).

1) Testing for Association between Case Status and Copy Number: The first set of analyses will examine the association of individual alleles with case status. Separately for each allele, a binary variable for case status (0 = control, 1 = case) will be regressed on the main effect of that allele, with the value of each allele coded by copy number (0, 1, 2). Three additional adjustment covariates will be included for age, gender, and race. This will permit estimation of *the (covariate-adjusted) increase in the probability (and odds) of being a case per each additional copy of that allele*. Attained significance levels (p-values) will be adjusted to account for accumulation of Type I error (false positive error) across multiple hypothesis tests. Specifically, p-value adjustments will employ an adaptive two-stage linear step-up procedure to control the FDR at 5% (Benjamani et al. 2006; Kim and van de Weil 2008), here across all alleles within each gene. Separate FDR control by gene

allows for possibility that % true nulls varies among genes. Unadjusted (raw) p-values will be provided as well for those whose interest is limited a priori to a specific allele. Results will be reported separately for 2-digit alleles and 4-digit alleles.

2) Testing Genetic Interactions and Case Status: We will perform additional exploratory analyses to test for *the presence of epistasis, wherein the impact of an allele depends upon the presence of another allele* (i.e., two-way interactions between alleles), at the level of 2-digit alleles. Separately for each allele, a binary variable for case status (0 = control, 1 = case) will be regressed on the main effect of that allele as well as the two-way interaction between that allele and each of the remaining 134 alleles, with the value of each allele coded by copy number (0, 1, 2). Three additional adjustment covariates will be included for age, gender and race. Model will be fit using sparse partial least squares discriminant analysis (Perez-Enciso and Tenenhaus 2003). An approximate t-statistic will be computed for each of the 135 allele regression coefficients within each allele's logistic regression model. Estimates of coefficients' standard errors will be obtained via the bootstrap; and approximate degrees of freedom will be determined per Krämer and Sugiyama (2011). These 135 logistic regression analyses will generate a total of $135^2 = 18{,}225$ t-statistics; and discovery of significant main effects and interactions will be based on correlation-adjusted t-scores per methods detailed in Zuber and Strimmer (2009).

KEY RESEARCH ACCOMPLISHMENTS:

- Year 3 allowed us to finish testing of all 597 subjects (200 CFS/ME patients and 597 healthy controls) by CyTOF-phosphoflow and HLA Typing.
- Set up the world-class statistical team for data completion and accuracy so that a major statistical analysis for complex and big data can begin.
- Provide initial report on the statistical analysis that is underway.

For CyTOF, all samples were tested.

- Preliminary analysis of completed and clean data has been provided and major statistical analysis is underway.
- Multiple meetings with Statisticians and Scientists to visualize the data and understand the processes to handle the complexity of the data
- Batch-to-batch variability has been corrected.
- Have a statistical plan in place

For HLA Typing, all samples were tested.

- Preliminary analysis of completed and clean data has been provided and major statistical analysis is underway.
- Multiple meetings with Statisticians and Scientists to visualize the data and understand the processes to handle the complexity of the data
- Batch-to-batch variability has been corrected.
- Have a statistical plan in place

REPORTABLE OUTCOMES:

Major results from statistical analysis are underway.

CONCLUSIONS:

The results of this study will provide additional basis to the biological nature of ME/CFS and enhance the understanding of its pathogenesis.

For the CyTOF testing and HLA test results, a well thought out and comprehensive statistical plan has been created and it is underway. We continue to have meetings to move the statistical analysis forward and hope to submit an amendment to this report with final results and their clinical/biological meaning.

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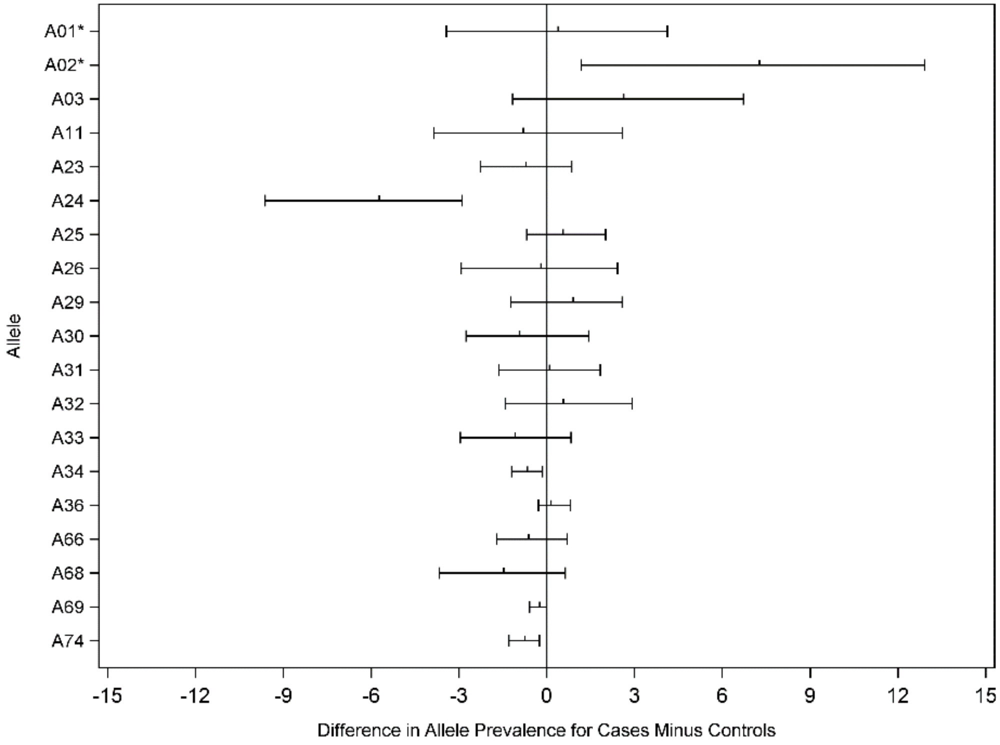
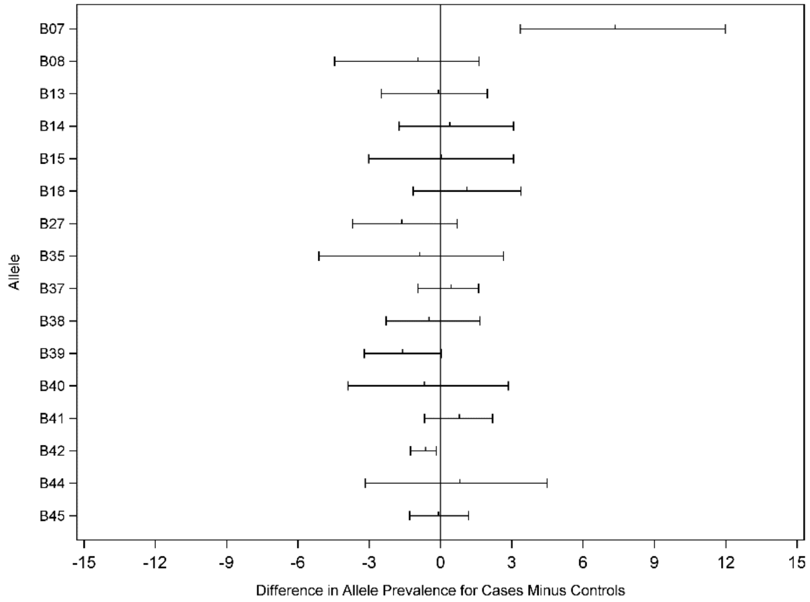
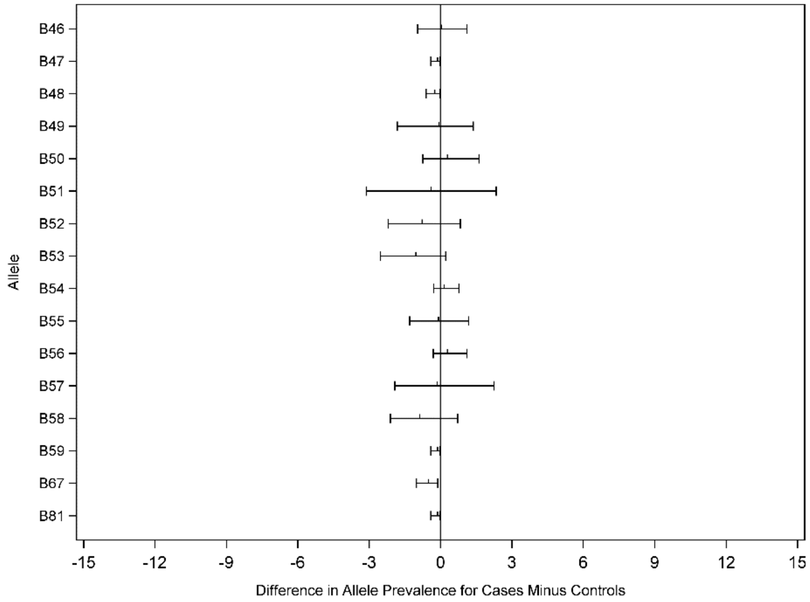
Appendix A

HLA-A



HLA-B

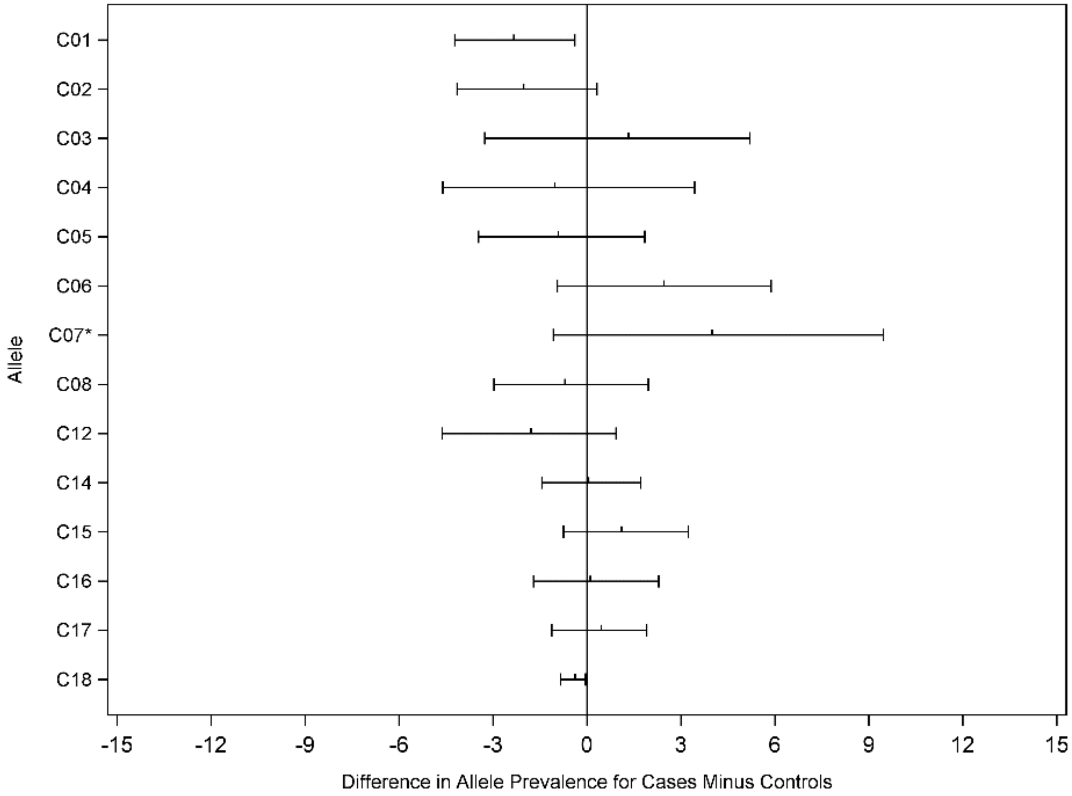




* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

HLA-C



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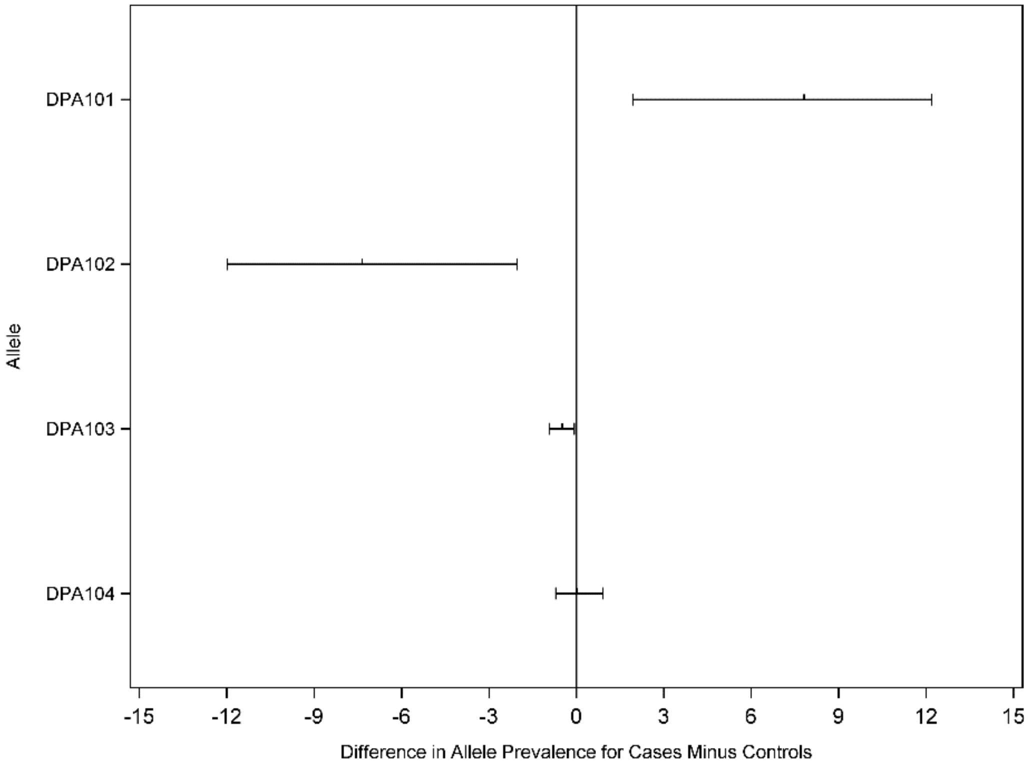
HLA-DPA1



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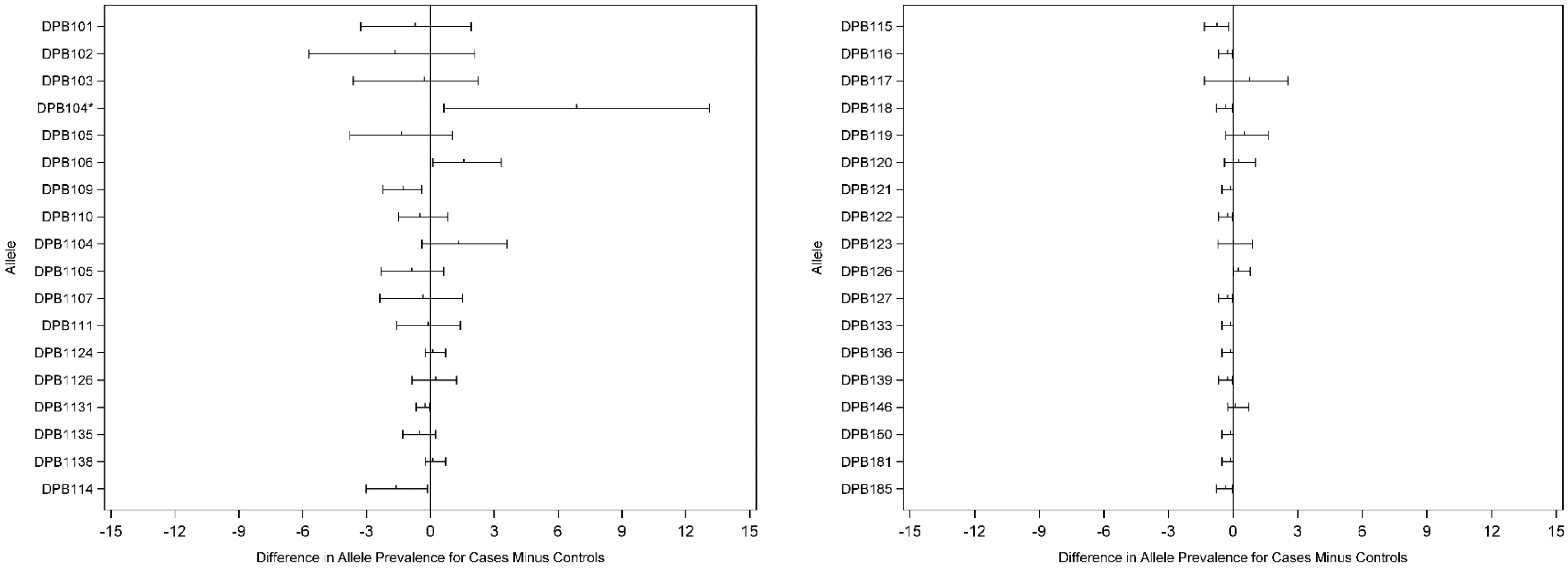
HLA-DPB1



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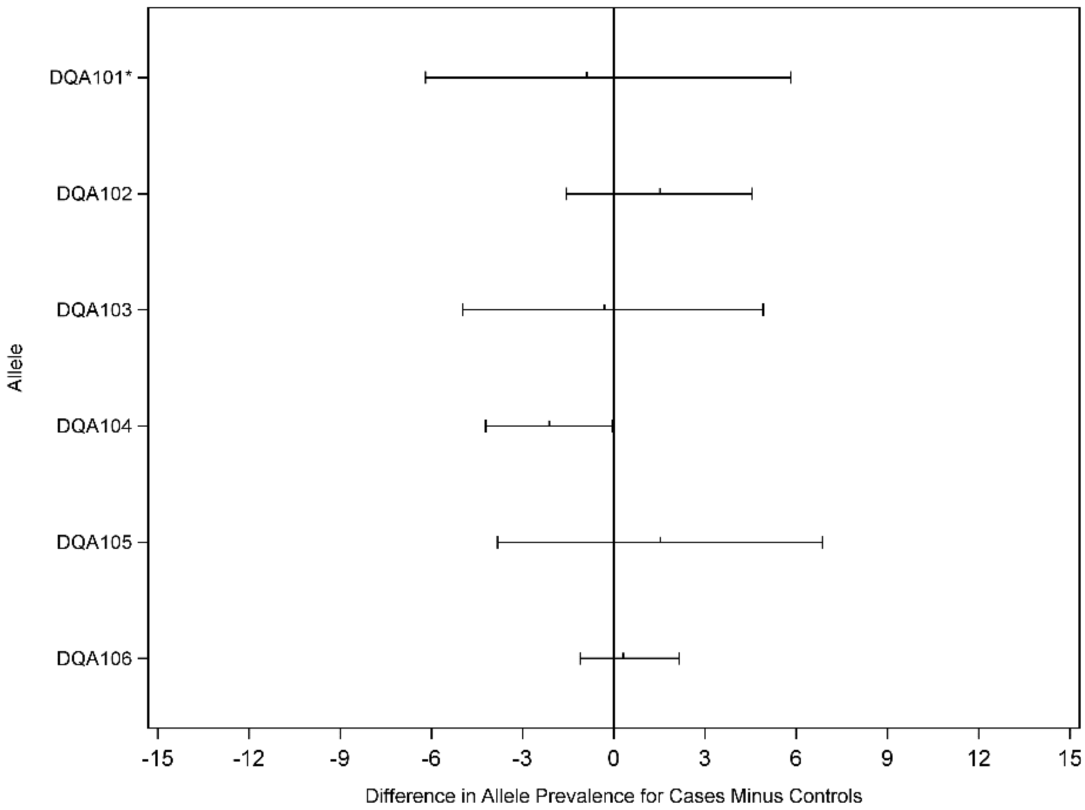
HLA-DQA1



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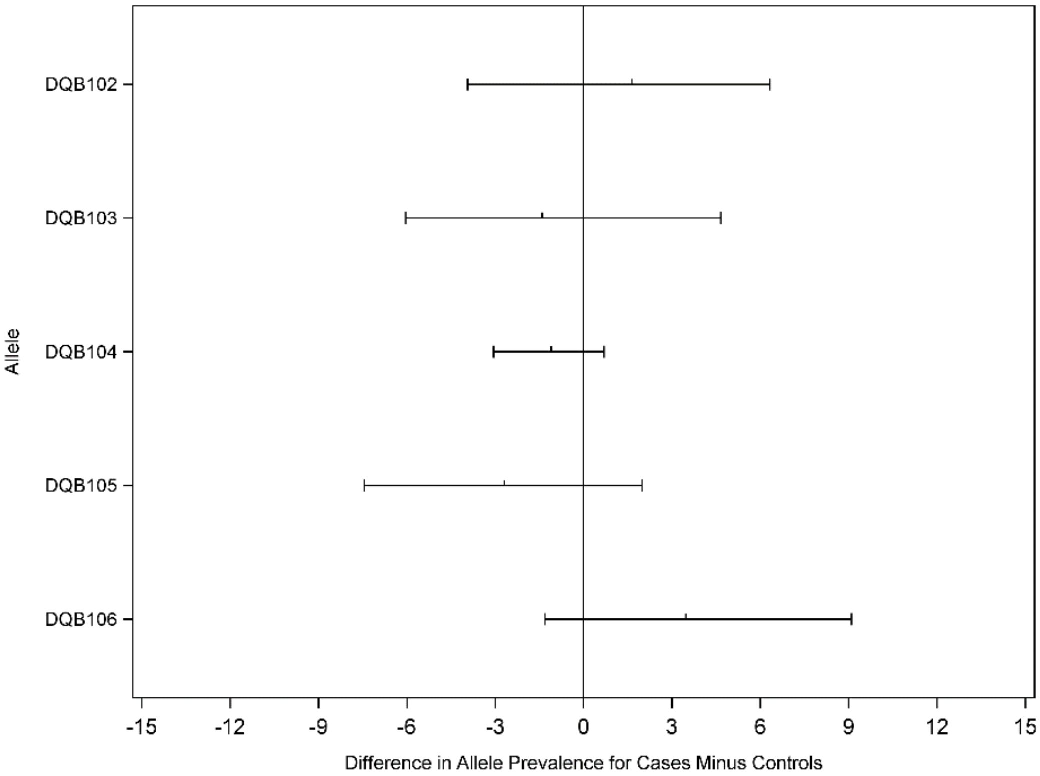
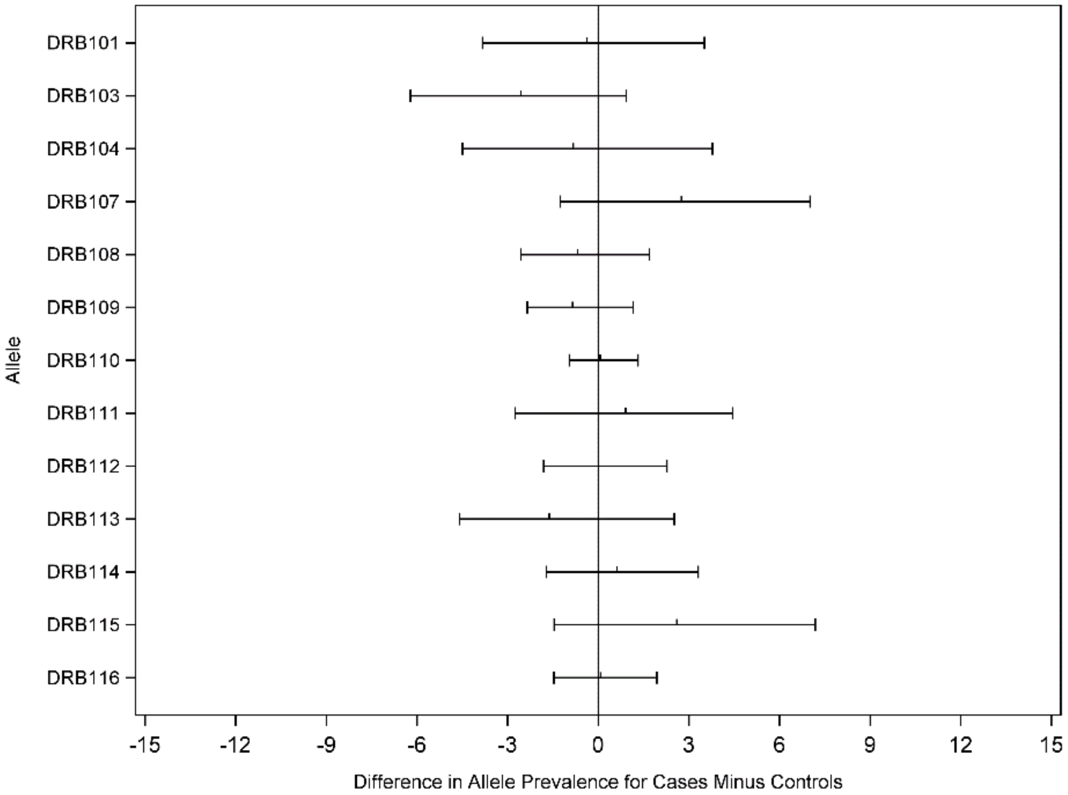
HLA-DQB1



* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

HLA-DRB1



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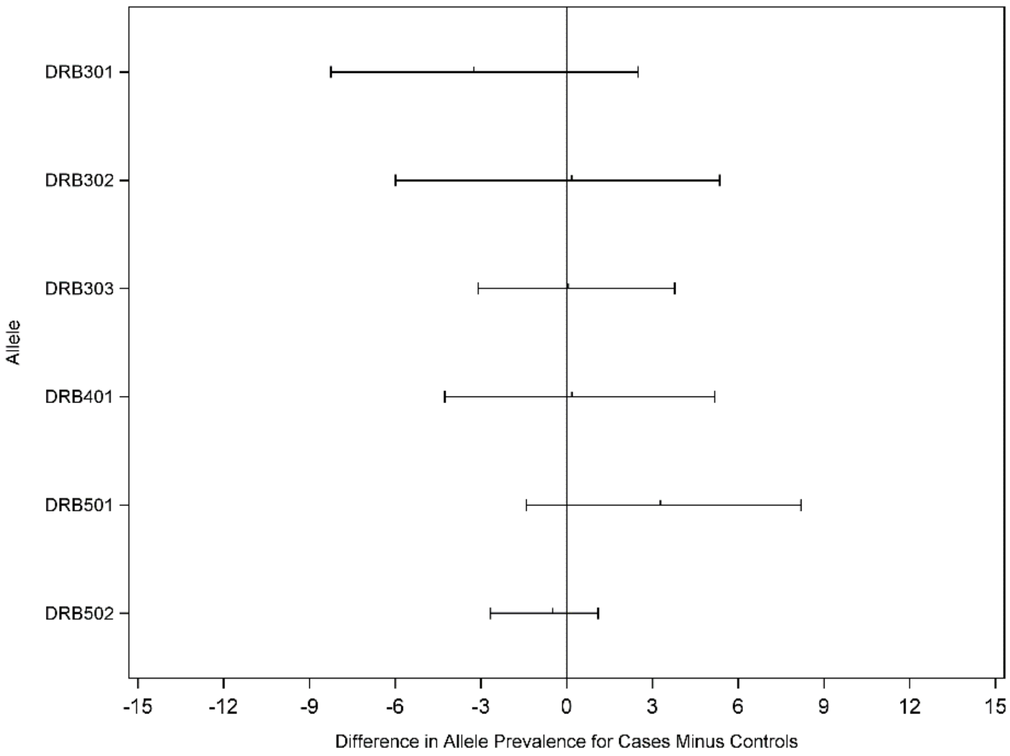
HLA-DRBo



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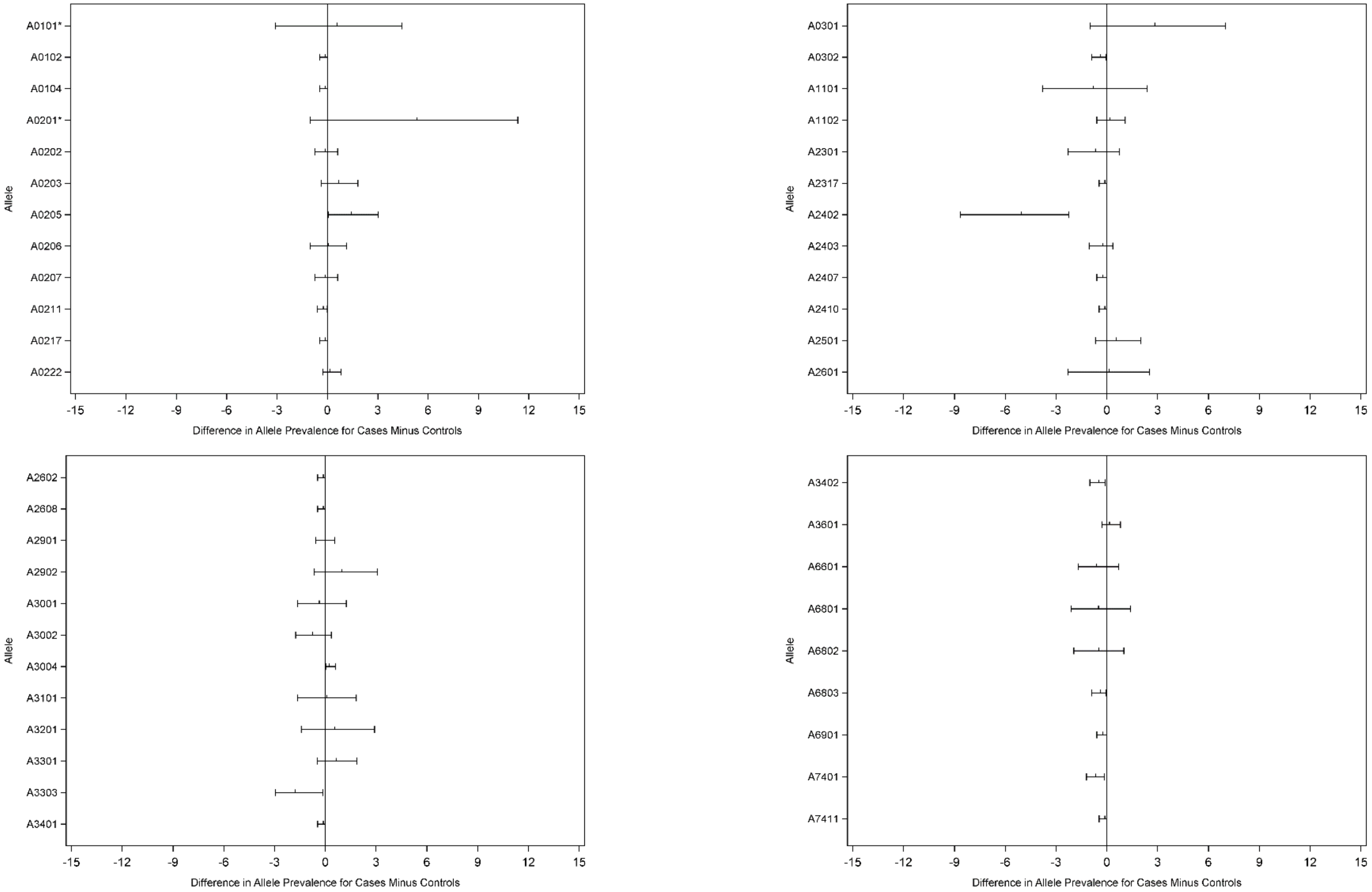
Appendix B

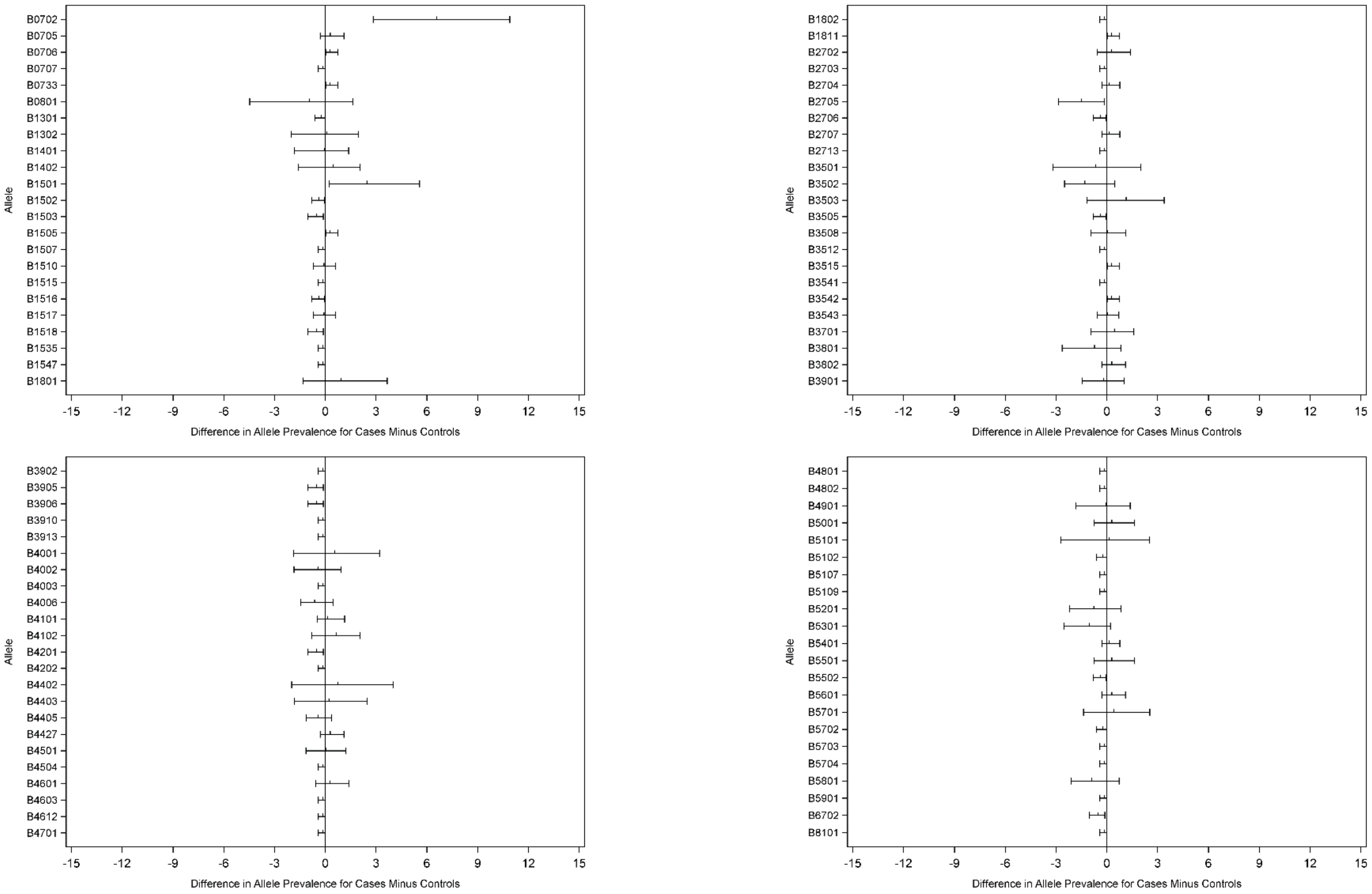
HLA-A



* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

HLA-B



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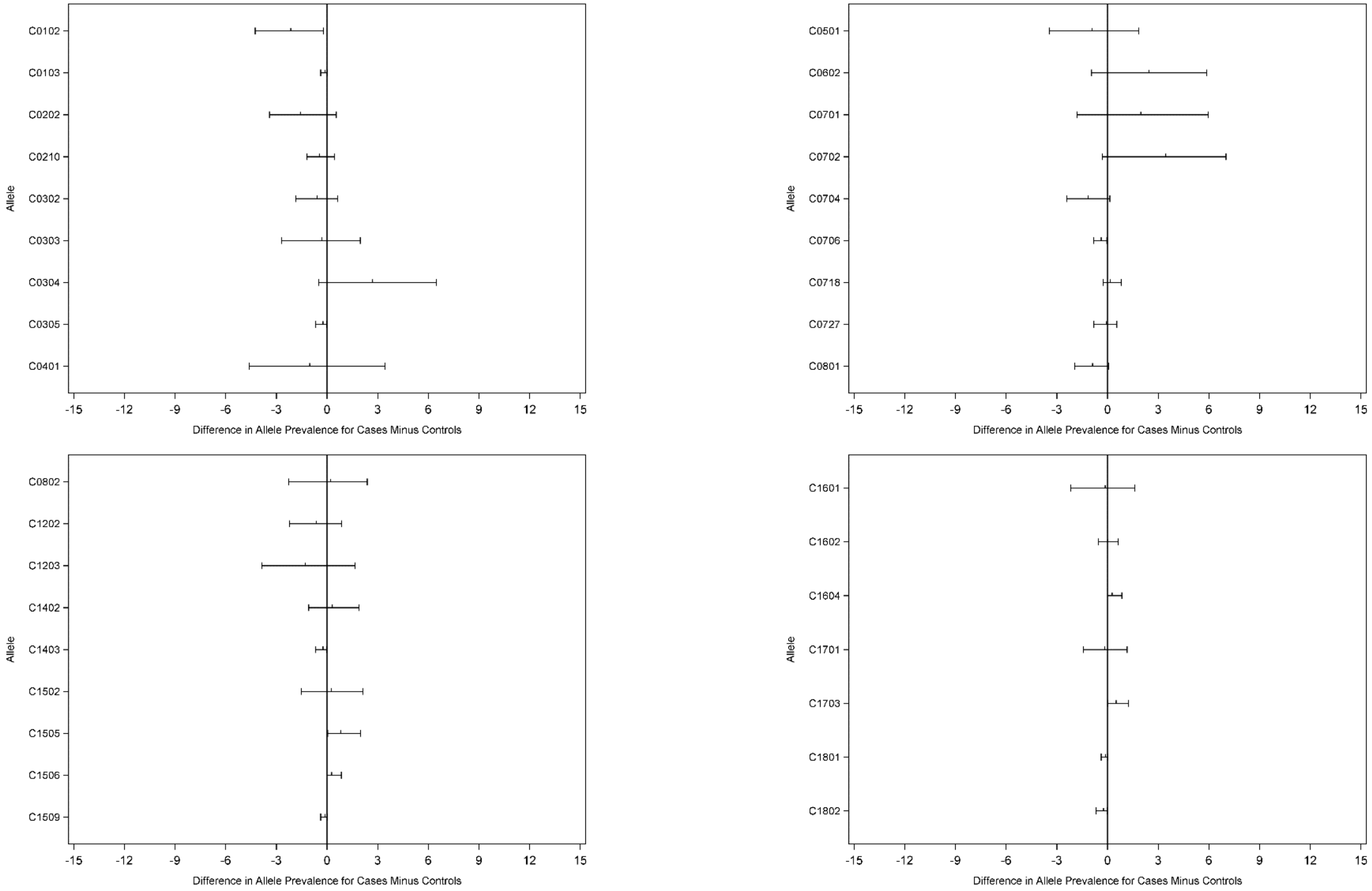
Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

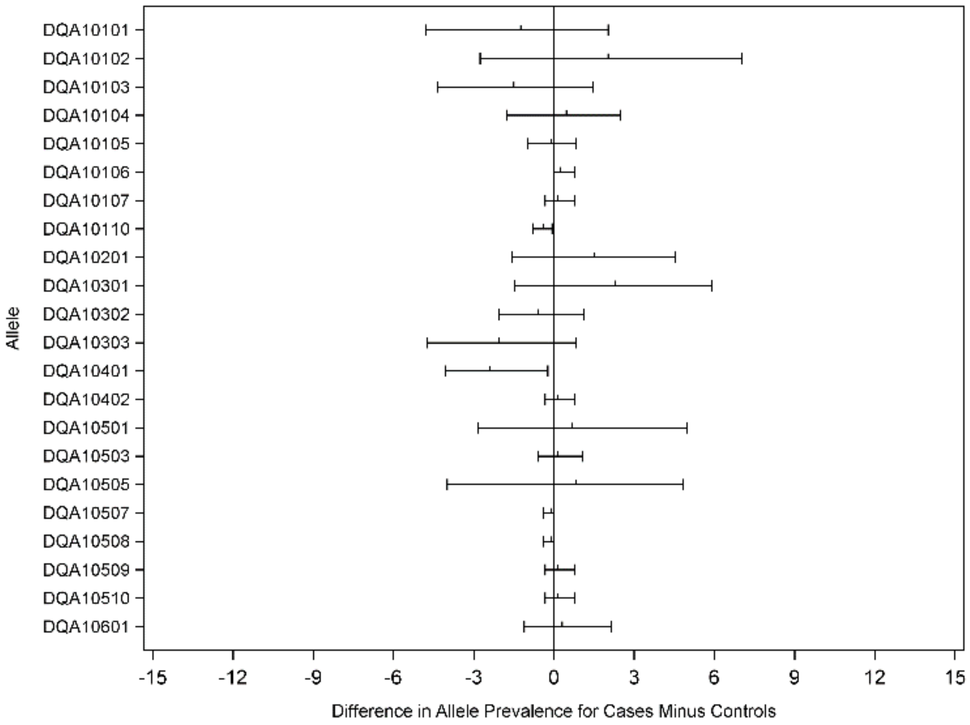
HLA-C



* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

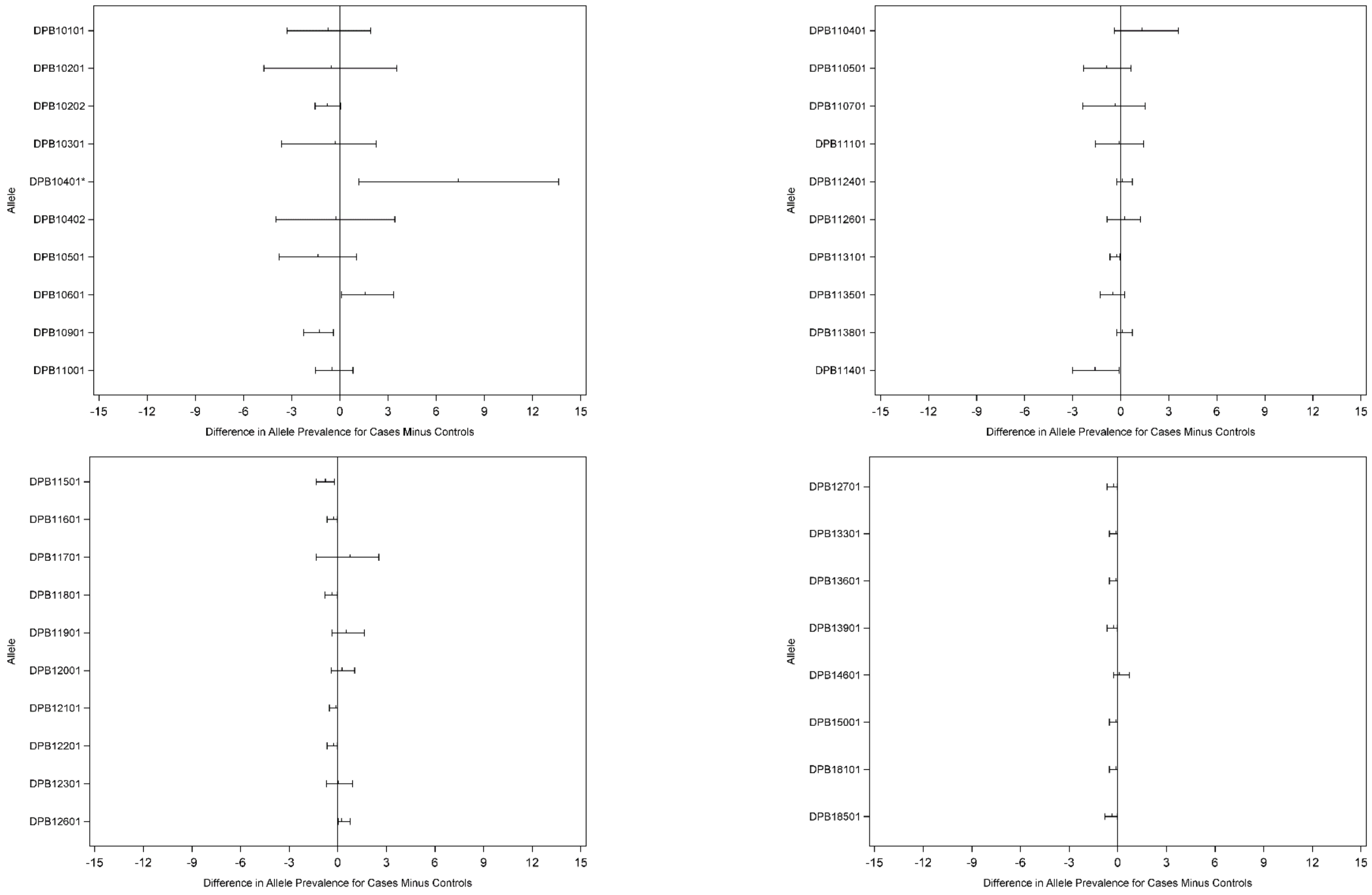
HLA-DPA1



* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

HLA-DPB1



* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

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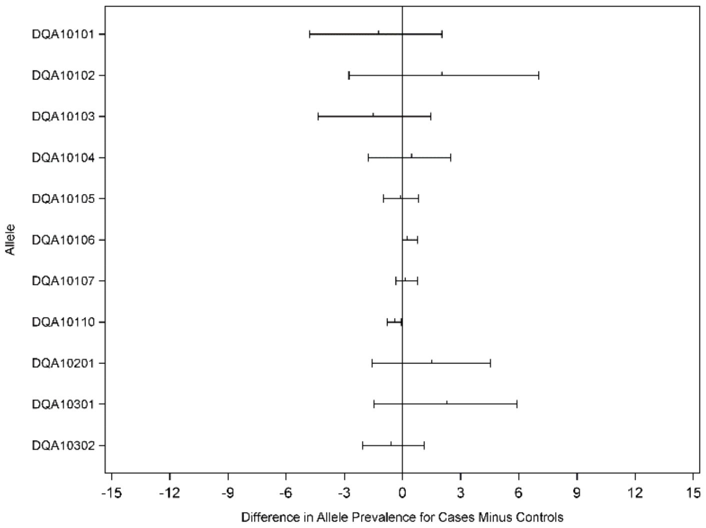
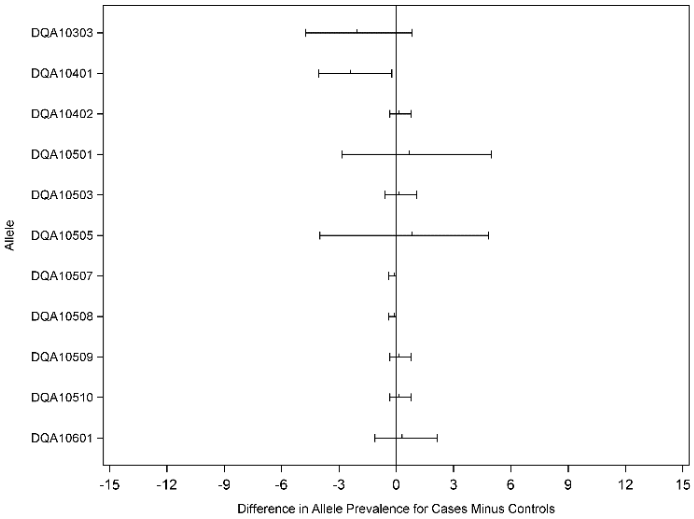
HLA-DQA1

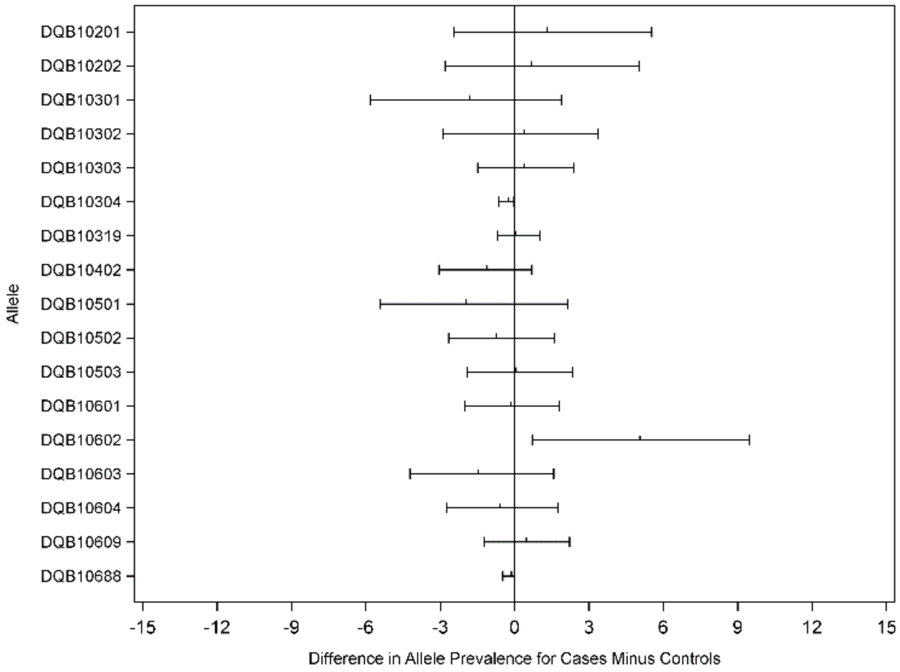




* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

HLA-DQB1



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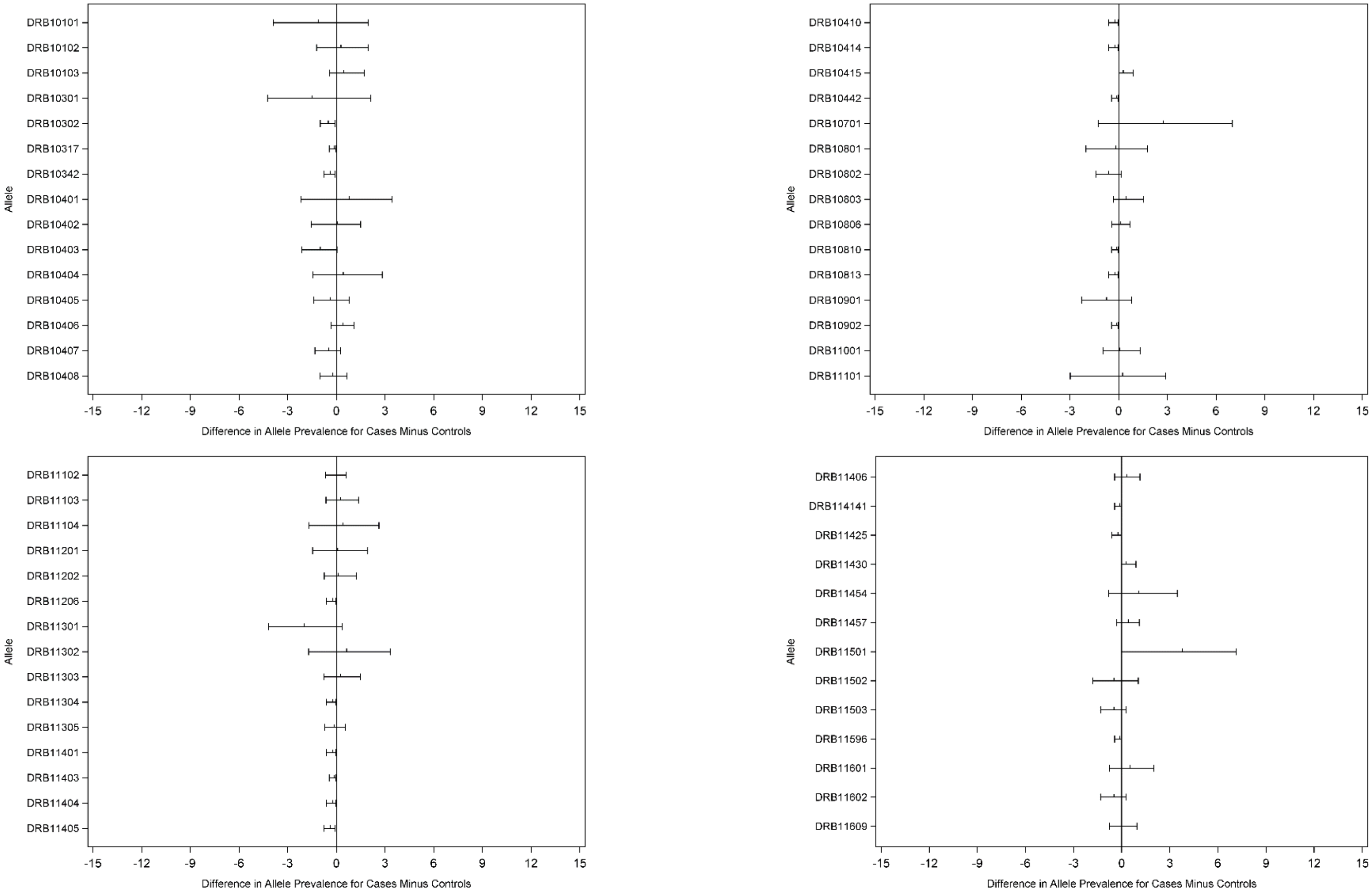
Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

HLA-DRB1



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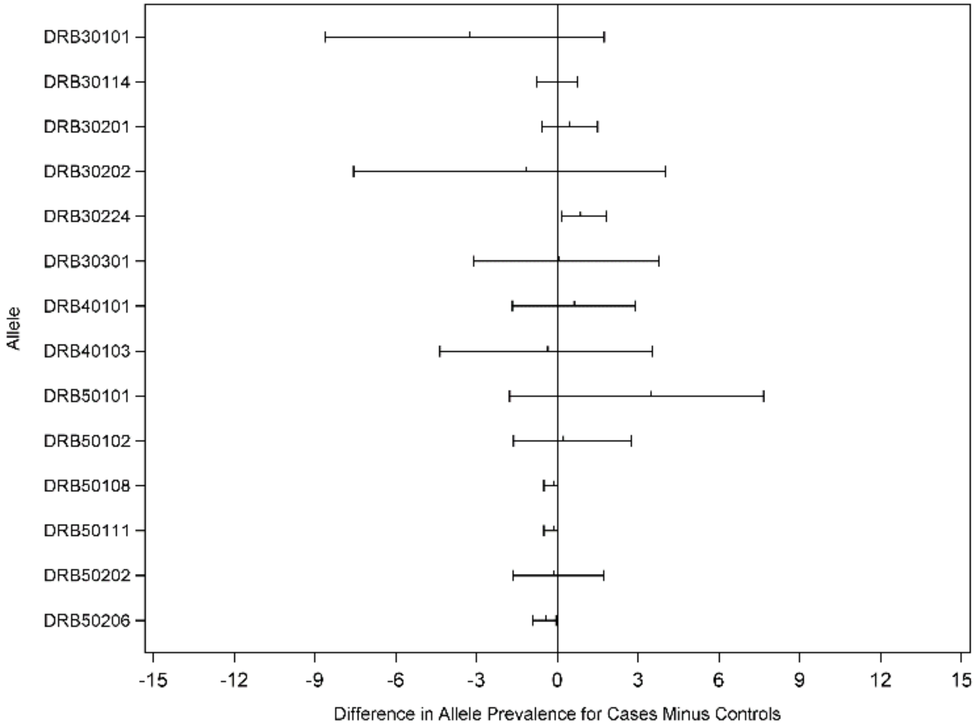
HLA-DRBo



* Bayesian estimates of allele prevalence made using the beta-binomial distribution.

Shown are Bayesian 95% credible intervals for differences in 2n-allele prevalence for cases minus controls. Each credible interval extends from its lower bound on left to its upper bound on right. Center tick marks estimate of difference in 2n-allele prevalence for cases minus controls. An interval that does not include zero (center vertical line) indicates that a difference between cases and controls is highly plausible.

GENE=A

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
A01	50	26.04	94	23.86	0.5967	0.7380	1.09	0.76	1.46
A02	102	53.13	168	42.64	0.0167	0.1586	1.25	1.02	1.48
A03	47	24.48	77	19.54	0.1840	0.6991	1.25	0.88	1.72
A11	29	15.10	67	17.01	0.6214	0.7380	0.89	0.57	1.32
A23	6	3.13	18	4.57	0.4864	0.7282	0.68	0.18	1.66
A24	25	13.02	90	22.84	0.0057	0.1086	0.57	0.34	0.86
A25	7	3.65	10	2.54	0.4184	0.7282	1.44	0.50	3.79
A26	17	8.85	35	8.88	1.0000	1.0000	1.00	0.55	1.73
A29	12	6.25	17	4.31	0.2957	0.7282	1.45	0.62	3.08
A30	9	4.69	25	6.35	0.4450	0.7282	0.74	0.27	1.53
A31	8	4.17	15	3.81	0.8134	0.9091	1.09	0.42	2.52
A32	17	8.85	28	7.11	0.4927	0.7282	1.25	0.62	2.23
A33	8	4.17	23	5.84	0.4252	0.7282	0.71	0.22	1.54
A34	0	0.00	5	1.27	0.1646	0.6991	0.00	0.00	1.58
A36	1	0.52	1	0.25	0.5211	0.7282	2.05	0.10	68.65
A66	3	1.56	11	2.79	0.5365	0.7282	0.56	0.09	1.86
A68	12	6.25	32	8.12	0.4873	0.7282	0.77	0.35	1.44
A69	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.57
A74	0	0.00	6	1.52	0.1290	0.6991	0.00	0.00	1.32

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=B

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
B07	52	27.96	61	15.84	0.0019	0.0609	1.76	1.24	2.45
B08	28	15.05	62	16.10	0.7990	1.0000	0.93	0.59	1.40
B13	10	5.38	22	5.71	1.0000	1.0000	0.94	0.39	1.94
B14	17	9.14	32	8.31	0.7408	1.0000	1.10	0.59	1.92
B15	24	12.90	52	13.51	0.8915	1.0000	0.96	0.58	1.49
B18	15	8.06	26	6.75	0.5912	1.0000	1.19	0.61	2.20
B27	8	4.30	31	8.05	0.1006	1.0000	0.53	0.17	1.12
B35	39	20.97	84	21.82	0.9098	1.0000	0.96	0.63	1.34
B37	5	2.69	6	1.56	0.3195	1.0000	1.72	0.50	6.54
B38	10	5.38	22	5.71	1.0000	1.0000	0.94	0.39	1.94
B39	4	2.15	21	5.45	0.0710	1.0000	0.39	0.09	1.09
B40	27	14.52	59	15.32	0.8961	1.0000	0.95	0.59	1.44
B41	7	3.76	8	2.08	0.2497	1.0000	1.81	0.63	5.57
B42	0	0.00	5	1.30	0.1648	1.0000	0.00	0.00	1.60
B44	41	22.04	81	21.04	0.8205	1.0000	1.05	0.71	1.46
B45	4	2.15	9	2.34	1.0000	1.0000	0.92	0.17	2.93
B46	3	1.61	6	1.56	1.0000	1.0000	1.03	0.17	4.33
B47	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B48	0	0.00	2	0.52	1.0000	1.0000	0.00	0.00	5.61
B49	5	2.69	13	3.38	0.7883	1.0000	0.80	0.18	2.14
B50	4	2.15	6	1.56	0.7133	1.0000	1.38	0.29	5.28
B51	17	9.14	35	9.09	1.0000	1.0000	1.01	0.55	1.74
B52	5	2.69	16	4.16	0.4569	1.0000	0.65	0.17	1.68
B53	2	1.08	13	3.38	0.1357	1.0000	0.32	0.03	1.25
B54	1	0.54	1	0.26	0.5190	1.0000	2.07	0.10	69.30
B55	4	2.15	9	2.34	1.0000	1.0000	0.92	0.17	2.93
B56	2	1.08	2	0.52	0.5809	1.0000	2.07	0.17	30.95
B57	11	5.91	26	6.75	0.8484	1.0000	0.88	0.38	1.71
B58	5	2.69	15	3.90	0.6071	1.0000	0.69	0.17	1.80

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=B

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
B59	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B67	0	0.00	4	1.04	0.2971	1.0000	0.00	0.00	2.05
B81	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

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Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=C

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL***[3]	***Upper CL***[3]
C01	9	4.69	37	9.41	0.0445	0.4068	0.50	0.17	1.01
C02	11	5.73	41	10.43	0.0581	0.4068	0.55	0.20	1.04
C03	52	27.08	98	24.94	0.6025	0.8435	1.09	0.77	1.44
C04	49	25.52	106	26.97	0.7561	0.8875	0.95	0.66	1.26
C05	20	10.42	49	12.47	0.4846	0.8435	0.84	0.47	1.35
C06	35	18.23	56	14.25	0.2122	0.5940	1.28	0.82	1.88
C07	97	50.52	170	43.26	0.1074	0.5013	1.17	0.96	1.40
C08	18	9.38	41	10.43	0.7607	0.8875	0.90	0.49	1.51
C12	24	12.50	65	16.54	0.2084	0.5940	0.76	0.46	1.16
C14	8	4.17	16	4.07	1.0000	1.0000	1.02	0.37	2.32
C15	13	6.77	18	4.58	0.3047	0.6490	1.48	0.65	3.07
C16	12	6.25	24	6.11	1.0000	1.0000	1.02	0.48	2.00
C17	7	3.65	11	2.80	0.5995	0.8435	1.30	0.46	3.36
C18	0	0.00	3	0.76	0.3245	0.6490	0.00	0.00	3.07

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

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Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DPA1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DPA101	185	95.85	351	89.31	0.0073	0.0218	1.07	1.02	1.12
DPA102	67	34.72	169	43.00	0.0570	0.0855	0.81	0.62	1.01
DPA103	0	0.00	3	0.76	0.3155	0.3155	0.00	0.00	3.05
DPA104	2	1.04	4	1.02	1.0000	1.0000	1.02	0.14	5.70

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DPB1

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DPB101	21	10.88	44	11.20	1.0000	1.0000	0.97	0.56	1.58
DPB102	45	23.32	95	24.17	0.8313	1.0000	0.96	0.66	1.31
DPB103	24	12.44	48	12.21	1.0000	1.0000	1.02	0.61	1.60
DPB104	145	75.13	276	70.23	0.2284	1.0000	1.07	0.95	1.18
DPB105	13	6.74	37	9.41	0.3263	1.0000	0.72	0.34	1.30
DPB106	10	5.18	8	2.04	0.0402	0.6325	2.55	0.97	6.75
DPB109	1	0.52	12	3.05	0.0527	0.6325	0.17	0.01	1.03
DPB110	3	1.55	10	2.54	0.5327	1.0000	0.61	0.13	2.07
DPB1104	12	6.22	13	3.31	0.1166	0.9694	1.88	0.79	4.26
DPB1105	5	2.59	17	4.33	0.3391	1.0000	0.60	0.16	1.55
DPB1107	10	5.18	23	5.85	0.8419	1.0000	0.89	0.37	1.81
DPB111	6	3.11	13	3.31	1.0000	1.0000	0.94	0.26	2.40
DPB1124	1	0.52	1	0.25	0.5231	1.0000	2.04	0.10	68.10
DPB1126	4	2.07	6	1.53	0.7303	1.0000	1.36	0.29	5.20
DPB1131	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB1135	1	0.52	6	1.53	0.3931	1.0000	0.34	0.01	2.26
DPB1138	1	0.52	1	0.25	0.5231	1.0000	2.04	0.10	68.10
DPB114	3	1.55	19	4.83	0.0519	0.6325	0.32	0.05	1.02
DPB115	0	0.00	6	1.53	0.1346	0.9694	0.00	0.00	1.31
DPB116	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB117	10	5.18	14	3.56	0.3607	1.0000	1.45	0.62	3.26
DPB118	0	0.00	3	0.76	0.3155	1.0000	0.00	0.00	3.05
DPB119	4	2.07	4	1.02	0.3960	1.0000	2.04	0.46	9.05
DPB120	2	1.04	2	0.51	0.5819	1.0000	2.04	0.17	30.42
DPB121	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB122	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB123	2	1.04	4	1.02	1.0000	1.0000	1.02	0.14	5.70
DPB126	1	0.52	0	0.00	0.2856	1.0000	.	.	.
DPB127	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

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[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DPB1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DPB133	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB136	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB139	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB146	1	0.52	1	0.25	0.5231	1.0000	2.04	0.10	68.10
DPB150	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB181	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB185	0	0.00	3	0.76	0.3155	1.0000	0.00	0.00	3.05

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DQA1

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DQA101	122	63.87	259	65.74	0.7012	1.0000	0.97	0.83	1.10
DQA102	25	13.09	44	11.17	0.4814	1.0000	1.17	0.68	1.85
DQA103	62	32.46	129	32.74	1.0000	1.0000	0.99	0.74	1.27
DQA104	8	4.19	32	8.12	0.0750	0.4502	0.52	0.17	1.08
DQA105	83	43.46	171	43.40	1.0000	1.0000	1.00	0.79	1.22
DQA106	7	3.66	12	3.05	0.7906	1.0000	1.20	0.44	3.09

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DQB1

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DQB102	67	36.41	141	37.80	0.7725	0.8437	0.96	0.74	1.21
DQB103	62	33.70	130	34.85	0.8437	0.8437	0.97	0.72	1.23
DQB104	6	3.26	19	5.09	0.3675	0.8014	0.64	0.16	1.53
DQB105	53	28.80	119	31.90	0.4808	0.8014	0.90	0.64	1.18
DQB106	85	46.20	158	42.36	0.4003	0.8014	1.09	0.87	1.32

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DRB1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DRB101	35	18.32	71	18.25	1.0000	1.0000	1.00	0.64	1.44
DRB103	33	17.28	79	20.31	0.4179	1.0000	0.85	0.56	1.22
DRB104	48	25.13	101	25.96	0.9162	1.0000	0.97	0.68	1.30
DRB107	55	28.80	97	24.94	0.3508	1.0000	1.15	0.84	1.53
DRB108	14	7.33	31	7.97	0.8634	1.0000	0.92	0.46	1.68
DRB109	6	3.14	18	4.63	0.4859	1.0000	0.68	0.18	1.64
DRB110	3	1.57	6	1.54	1.0000	1.0000	1.02	0.17	4.26
DRB111	39	20.42	72	18.51	0.5638	1.0000	1.10	0.74	1.56
DRB112	12	6.28	24	6.17	1.0000	1.0000	1.02	0.48	1.98
DRB113	35	18.32	80	20.57	0.5664	1.0000	0.89	0.59	1.27
DRB114	19	9.95	32	8.23	0.5192	1.0000	1.21	0.62	2.07
DRB115	52	27.23	87	22.37	0.2028	1.0000	1.22	0.87	1.63
DRB116	7	3.66	17	4.37	0.8158	1.0000	0.84	0.26	1.95

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DRBo

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DRB301	49	27.84	109	32.06	0.3504	0.7772	0.87	0.61	1.15
DRB302	69	39.20	143	42.06	0.5584	0.7772	0.93	0.71	1.16
DRB303	23	13.07	44	12.94	1.0000	1.0000	1.01	0.59	1.61
DRB401	43	24.43	76	22.35	0.6477	0.7772	1.09	0.74	1.51
DRB501	54	30.68	97	28.53	0.5994	0.7772	1.08	0.78	1.42
DRB502	5	2.84	13	3.82	0.6138	0.7772	0.74	0.17	2.00

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

gene=A

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
A01*	192	50	12.8999	9.8522	16.3168	394	99	12.5146	10.3678	14.7482	0.3853	-3.4547	4.1409
A02*	192	125	32.5167	27.5820	36.9663	394	199	25.2486	21.7074	28.1134	7.2682	1.1555	12.9429
A03	192	50	13.0586	10.0560	15.9755	394	82	10.4284	8.3603	12.7883	2.6301	-1.1915	6.7410
A11	192	31	7.9874	5.5957	10.6545	394	69	8.7836	6.9235	10.6478	-0.7963	-3.8783	2.6052
A23	192	6	1.5524	0.5424	2.8098	394	18	2.2689	1.3486	3.3944	-0.7165	-2.2850	0.8691
A24	192	28	7.2130	4.5360	9.5654	394	102	12.9392	10.7650	15.0888	-5.7261	-9.6479	-2.8755
A25	192	7	1.8024	0.8564	3.1445	394	10	1.2441	0.4823	2.0145	0.5583	-0.7011	2.0338
A26	192	17	4.4150	2.3931	6.4543	394	36	4.6178	3.2828	6.0462	-0.2028	-2.9403	2.4446
A29	192	12	3.0732	1.5658	4.7188	394	17	2.1670	1.3214	3.2232	0.9062	-1.2519	2.6013
A30	192	9	2.2744	0.9312	3.8991	394	25	3.1946	2.1136	4.4919	-0.9202	-2.7759	1.4474
A31	192	8	2.1002	0.7623	3.5776	394	16	2.0097	1.2063	3.1023	0.0905	-1.6469	1.8561
A32	192	17	4.3572	2.4670	6.1438	394	30	3.7910	2.5579	5.1210	0.5662	-1.4420	2.9366
A33	192	8	2.0655	0.8354	3.5567	394	25	3.1433	1.9823	4.4066	-1.0778	-2.9745	0.8503
A34	192	0	0.0072	0.0000	0.0316	394	5	0.6674	0.1265	1.2238	-0.6602	-1.2238	-0.1266
A36	192	1	0.2725	0.0005	0.7774	394	1	0.1212	0.0005	0.3384	0.1513	-0.2996	0.8306
A66	192	3	0.7600	0.1022	1.5349	394	11	1.3796	0.6424	2.2479	-0.6196	-1.7222	0.7195
A68	192	12	3.0385	1.6500	4.9345	394	35	4.5139	3.1284	6.0748	-1.4755	-3.6878	0.6567
A69	192	0	0.0083	0.0000	0.0471	394	2	0.2528	0.0143	0.6057	-0.2445	-0.6130	0.0064
A74	192	0	0.0105	0.0000	0.0626	394	6	0.7541	0.2784	1.3357	-0.7435	-1.3107	-0.2279

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=B

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
B07	186	58	15.6990	12.1425	19.5164	385	64	8.3570	6.5800	10.1332	7.3420	3.3353	12.0053
B08	186	29	7.9800	5.3561	10.6792	385	69	8.9381	6.9359	10.9937	-0.9581	-4.4863	1.6472
B13	186	10	2.7630	1.1553	4.7036	385	22	2.8475	1.7138	3.9794	-0.0846	-2.5138	1.9852
B14	186	17	4.6798	2.7241	6.9286	385	33	4.2886	2.7899	5.5918	0.3912	-1.7707	3.0923
B15	186	26	6.9634	4.5118	9.1112	385	53	6.9236	5.2697	9.0069	0.0397	-3.0438	3.0931
B18	186	17	4.6009	2.7993	6.6055	385	27	3.4941	2.2978	4.8872	1.1069	-1.1690	3.4036
B27	186	9	2.4307	1.1521	4.0035	385	31	4.0622	2.6464	5.4190	-1.6315	-3.7210	0.7146
B35	186	43	11.4902	8.6134	14.7824	385	95	12.3672	10.1586	14.7642	-0.8770	-5.1367	2.6677
B37	186	5	1.3532	0.3497	2.4999	385	7	0.9046	0.3274	1.5262	0.4486	-0.9733	1.6227
B38	186	10	2.6385	1.2436	4.3269	385	24	3.1245	2.0089	4.3430	-0.4860	-2.3126	1.6737
B39	186	4	1.0813	0.2505	2.0906	385	21	2.6818	1.6662	3.9326	-1.6005	-3.2302	0.0588
B40	186	27	7.1840	4.7374	9.9147	385	61	7.8643	5.8606	9.7302	-0.6803	-3.9184	2.8731
B41	186	7	1.8272	0.4750	3.0678	385	8	1.0416	0.4150	1.8417	0.7857	-0.6926	2.2088
B42	186	0	0.0046	0.0000	0.0099	385	5	0.6404	0.1801	1.2900	-0.6358	-1.2900	-0.1568
B44	186	44	11.7162	9.2056	15.2656	385	84	10.9106	8.9063	13.2143	0.8056	-3.1849	4.5006
B45	186	4	1.0661	0.2004	2.0449	385	9	1.1571	0.5533	1.9495	-0.0910	-1.3200	1.1944
B46	186	3	0.8129	0.0671	1.6681	385	6	0.7901	0.2314	1.4123	0.0229	-0.9811	1.1227
B47	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B48	186	0	0.0047	0.0000	0.0218	385	2	0.2534	0.0051	0.6200	-0.2487	-0.6261	0.0070
B49	186	6	1.6090	0.4409	2.8422	385	13	1.6721	0.8573	2.5486	-0.0631	-1.8377	1.3904
B50	186	4	1.0600	0.0777	2.0524	385	6	0.7705	0.2404	1.4294	0.2894	-0.7681	1.6375
B51	186	17	4.5043	2.2852	6.4936	385	38	4.9055	3.3786	6.6210	-0.4012	-3.1441	2.3510
B52	186	5	1.3492	0.4312	2.5979	385	16	2.1250	1.1115	3.0753	-0.7758	-2.2246	0.8558
B53	186	3	0.8119	0.1347	1.7210	385	14	1.8536	0.9608	2.8877	-1.0416	-2.5483	0.2336
B54	186	1	0.2687	0.0029	0.7895	385	1	0.1192	0.0001	0.3512	0.1496	-0.3027	0.7893
B55	186	4	1.0661	0.2004	2.0449	385	9	1.1571	0.5533	1.9495	-0.0910	-1.3200	1.1944
B56	186	2	0.5316	0.0468	1.2531	385	2	0.2426	0.0273	0.5923	0.2890	-0.3262	1.1175
B57	186	12	3.2087	1.6751	5.1709	385	26	3.3506	2.0439	4.5098	-0.1420	-1.9446	2.2683

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=B

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
B58	186	5	1.2997	0.3081	2.3721	385	17	2.1760	1.1830	3.1597	-0.8763	-2.1363	0.7379
B59	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B67	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B81	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=C

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
C01	192	9	2.3265	1.0281	3.7450	393	37	4.6650	3.2114	6.0220	-2.3385	-4.2470	-0.3629
C02	192	12	3.1627	1.6042	4.9045	393	41	5.1857	3.8421	7.0649	-2.0230	-4.1691	0.3388
C03	192	57	14.6613	11.1773	18.2746	393	105	13.3330	10.6934	15.5200	1.3283	-3.2830	5.2229
C04	192	51	13.1884	9.9467	16.0922	393	112	14.2186	11.5084	16.4236	-1.0302	-4.6274	3.4533
C05	192	20	5.2650	3.1408	7.3894	393	49	6.1823	4.6730	7.8511	-0.9173	-3.4834	1.8665
C06	192	38	9.9043	7.0111	12.9400	393	59	7.4525	5.7937	9.2166	2.4518	-0.9652	5.9008
C07*	192	114	29.7173	25.3847	34.1643	393	203	25.7197	22.8254	28.8790	3.9976	-1.0970	9.4784
C08	192	18	4.6627	2.5306	6.6991	393	42	5.3657	3.9563	7.0867	-0.7030	-2.9902	1.9771
C12	192	25	6.5625	4.3663	9.0296	393	66	8.3510	6.5264	10.2976	-1.7885	-4.6494	0.9458
C14	192	8	2.0506	0.8388	3.6855	393	16	1.9938	0.9837	2.9032	0.0568	-1.4654	1.7359
C15	192	13	3.3636	1.6066	4.9722	393	18	2.2535	1.3489	3.2422	1.1102	-0.7643	3.2575
C16	192	12	3.1384	1.5673	5.1637	393	24	3.0337	1.8958	4.2148	0.1047	-1.7249	2.3072
C17	192	7	1.8448	0.6101	3.1769	393	11	1.3910	0.6451	2.2399	0.4538	-1.1484	1.9316
C18	192	0	0.0073	0.0000	0.0211	393	3	0.3815	0.0567	0.8594	-0.3742	-0.8616	-0.0311

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DPA1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
DPA101	193	311	80.5046	76.2134	84.1138	393	571	72.6945	69.4045	76.0062	7.8101	1.9167	12.2191
DPA102	193	73	18.9186	14.9534	22.5088	393	207	26.2781	23.6105	29.8709	-7.3595	-11.997	-2.0115
DPA103	193	0	0.0068	0.0000	0.0166	393	4	0.4906	0.0890	0.9454	-0.4838	-0.9454	-0.0581
DPA104	193	2	0.5328	0.0197	1.2292	393	4	0.5119	0.0974	0.9513	0.0209	-0.7309	0.9300

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DPB1

	Bayesian Credible Interval [1] Cases n=195					**Bayesian Credible Interval [1] Controls n=395**					**Bayesian Credible Interval [1] Comparing Cases & Controls**		
Allele	**n^2**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**n^2**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DPB101	193	21	5.4801	3.4599	7.7373	393	49	6.2030	4.5896	7.6093	-0.7229	-3.2992	1.9399
DPB102	193	47	11.9837	8.8238	14.8277	393	107	13.6360	11.1412	15.7130	-1.6523	-5.7323	2.1027
DPB103	193	24	6.1606	4.1198	8.3967	393	51	6.4385	4.8337	8.1330	-0.2779	-3.6479	2.2733
DPB104*	193	203	52.4998	47.3925	57.1524	393	358	45.6179	41.9615	49.0673	6.8819	0.6223	13.1444
DPB105	193	14	3.6281	1.9109	5.3197	393	39	4.9760	3.5374	6.3386	-1.3479	-3.8070	1.0626
DPB106	193	10	2.5581	1.0078	3.9379	393	8	0.9891	0.3604	1.6990	1.5690	0.0881	3.3607
DPB109	193	1	0.2790	0.0001	0.7621	393	12	1.5515	0.7536	2.4501	-1.2725	-2.2697	-0.3885
DPB110	193	3	0.8071	0.1631	1.7939	393	10	1.2930	0.6660	2.1617	-0.4859	-1.5374	0.8323
DPB1104	193	12	3.0299	1.3123	4.8176	393	13	1.7083	0.8132	2.6191	1.3217	-0.4265	3.6134
DPB1105	193	5	1.3003	0.3253	2.3414	393	17	2.1721	1.3374	3.2957	-0.8719	-2.3421	0.6594
DPB1107	193	10	2.5881	1.2065	4.2974	393	23	2.9447	1.8727	4.0941	-0.3566	-2.4039	1.5377
DPB111	193	6	1.5657	0.4570	2.8767	393	13	1.6632	0.8685	2.5085	-0.0976	-1.6135	1.4376
DPB1124	193	1	0.2305	0.0001	0.6802	393	1	0.1346	0.0007	0.3983	0.0959	-0.2613	0.7394
DPB1126	193	4	1.0180	0.1683	1.9304	393	6	0.7636	0.2076	1.3549	0.2544	-0.8842	1.2541
DPB1131	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB1135	193	1	0.2563	0.0008	0.7548	393	6	0.7596	0.2233	1.3680	-0.5033	-1.3088	0.2679
DPB1138	193	1	0.2305	0.0001	0.6802	393	1	0.1346	0.0007	0.3983	0.0959	-0.2613	0.7394
DPB114	193	3	0.7864	0.1216	1.6218	393	19	2.3956	1.3984	3.5052	-1.6092	-3.0531	-0.0989
DPB115	193	0	0.0094	0.0000	0.0365	393	6	0.7733	0.3199	1.4592	-0.7639	-1.3612	-0.1855
DPB116	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB117	193	10	2.6579	1.1538	4.3470	393	15	1.9077	0.8795	2.7937	0.7502	-1.3615	2.5628
DPB118	193	0	0.0053	0.0000	0.0172	393	3	0.3520	0.0201	0.7924	-0.3467	-0.7997	-0.0111
DPB119	193	4	1.0440	0.2480	1.9346	393	4	0.5172	0.0955	0.9945	0.5268	-0.3686	1.6532
DPB120	193	2	0.5154	0.0101	1.1153	393	2	0.2571	0.0105	0.6396	0.2583	-0.4347	1.0540
DPB121	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB122	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB123	193	2	0.5328	0.0197	1.2292	393	4	0.5119	0.0974	0.9513	0.0209	-0.7309	0.9300
DPB126	193	1	0.2466	0.0003	0.7634	393	0	0.0030	0.0000	0.0071	0.2436	0.0003	0.8055

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DPB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DPB127	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB133	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB136	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB139	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB146	193	1	0.2305	0.0001	0.6802	393	1	0.1346	0.0007	0.3983	0.0959	-0.2613	0.7394
DPB150	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB181	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB185	193	0	0.0053	0.0000	0.0172	393	3	0.3520	0.0201	0.7924	-0.3467	-0.7997	-0.0111

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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gene=DQA1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
DQA101*	191	160	41.6495	36.9950	46.4729	394	336	42.5360	39.1323	46.1568	-0.8865	-6.2229	5.8455
DQA102	191	29	7.4621	4.8900	9.9741	394	47	5.9398	4.4818	7.7739	1.5222	-1.5790	4.5768
DQA103	191	74	19.4702	15.3903	23.2800	394	156	19.7795	17.2498	22.4817	-0.3093	-4.9860	4.9344
DQA104	191	9	2.4412	1.0032	3.8128	394	36	4.5591	3.1987	6.0136	-2.1178	-4.2375	-0.0225
DQA105	191	103	27.0829	22.2904	30.9695	394	201	25.5496	22.4285	28.6742	1.5333	-3.8475	6.8753
DQA106	191	7	1.8426	0.6008	3.2192	394	12	1.5326	0.7713	2.3091	0.3101	-1.1326	2.1673

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DQB1

	Bayesian Credible Interval [1] Cases n=195					**Bayesian Credible Interval [1] Controls n=395**					**Bayesian Credible Interval [1] Comparing Cases & Controls**		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DQB102	184	92	24.8043	20.3041	28.6893	373	173	23.1689	20.2551	25.8378	1.6354	-3.9633	6.3502
DQB103	184	79	21.4066	17.4850	25.8154	373	170	22.8182	20.0796	25.6360	-1.4116	-6.0628	4.6812
DQB104	184	6	1.6389	0.4596	2.8294	373	20	2.7450	1.6151	4.0844	-1.1061	-3.0754	0.7154
DQB105	184	67	18.2113	14.3756	22.3810	373	157	20.9101	18.6300	23.7615	-2.6988	-7.4639	2.0085
DQB106	184	124	33.6676	28.8895	37.8874	373	226	30.1939	27.0773	33.2116	3.4737	-1.3373	9.1193

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DRB1

	Bayesian Credible Interval [1] Cases n=195					**Bayesian Credible Interval [1] Controls n=395**					**Bayesian Credible Interval [1] Comparing Cases & Controls**		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DRB101	191	37	9.6161	7.0436	12.5708	389	78	9.9823	8.0771	11.9685	-0.3662	-3.8529	3.5387
DRB103	191	35	9.2052	6.8885	12.3690	389	91	11.7676	9.5043	13.9692	-2.5625	-6.2417	0.9524
DRB104	191	52	13.7271	10.2588	17.0068	389	113	14.5492	12.1992	16.9571	-0.8220	-4.5186	3.7989
DRB107	191	60	15.5201	11.9373	19.2470	389	99	12.7621	10.7466	15.3479	2.7580	-1.2819	7.0287
DRB108	191	14	3.6438	2.2493	5.5286	389	34	4.3237	2.9395	5.6044	-0.6798	-2.5756	1.7083
DRB109	191	6	1.5749	0.5640	2.9272	389	19	2.4266	1.5026	3.4761	-0.8516	-2.3736	1.1717
DRB110	191	3	0.8230	0.0878	1.7030	389	6	0.7617	0.2330	1.4629	0.0614	-0.9750	1.3354
DRB111	191	40	10.5560	7.2729	13.2287	389	75	9.6484	7.3715	11.5217	0.9076	-2.7722	4.4708
DRB112	191	12	3.2138	1.6791	5.0572	389	25	3.2061	1.9992	4.3216	0.0077	-1.8297	2.3024
DRB113	191	37	9.7271	7.0299	12.7775	389	88	11.3493	9.3268	13.6570	-1.6222	-4.6180	2.5376
DRB114	191	20	5.1858	3.1753	7.2853	389	36	4.5597	3.1339	5.7789	0.6261	-1.7440	3.3310
DRB115	191	57	14.9822	11.2565	18.4985	389	96	12.3773	10.0617	14.7072	2.6050	-1.4824	7.2101
DRB116	191	9	2.3825	1.2346	4.0926	389	18	2.3069	1.3801	3.4414	0.0757	-1.4923	1.9558

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DRBo

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DRB301	176	69	19.5783	15.2723	23.2526	340	156	22.8248	19.7975	25.8146	-3.2465	-8.2727	2.5130
DRB302	176	111	31.6018	26.6240	36.0107	340	214	31.4259	27.8840	34.6548	0.1759	-6.0027	5.3787
DRB303	176	31	8.7600	6.1137	11.3086	340	59	8.7101	6.6775	10.8847	0.0499	-3.1202	3.8028
DRB401	176	55	15.5475	11.6123	19.1912	340	104	15.3604	12.5082	18.1805	0.1871	-4.2931	5.2037
DRB501	176	79	22.4283	18.8354	26.6715	340	130	19.1515	16.2884	22.3661	3.2767	-1.4408	8.2189
DRB502	176	7	1.9973	0.5205	3.2892	340	17	2.4815	1.3522	3.6182	-0.4842	-2.6865	1.1237

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* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=A

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
A0101*	192	50	12.9425	9.6918	15.8977	394	97	12.3623	10.0772	14.4801	0.5802	-3.1360	4.4453
A0102	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A0104	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A0201*	192	107	27.3748	22.3800	32.2764	394	175	22.0416	19.0803	24.9407	5.3332	-1.0481	11.3561
A0202	192	1	0.2594	0.0004	0.8121	394	3	0.3888	0.0502	0.8259	-0.1294	-0.7494	0.6273
A0203	192	4	1.0288	0.2403	2.0460	394	3	0.3701	0.0443	0.8226	0.6587	-0.3961	1.8371
A0205	192	8	2.0675	0.8910	3.6833	394	5	0.6324	0.1247	1.1536	1.4351	0.0469	3.0421
A0206	192	3	0.7925	0.0593	1.6831	394	6	0.7475	0.2174	1.3434	0.0450	-1.0358	1.1531
A0207	192	1	0.2594	0.0004	0.8121	394	3	0.3888	0.0502	0.8259	-0.1294	-0.7494	0.6273
A0211	192	0	0.0083	0.0000	0.0471	394	2	0.2528	0.0143	0.6057	-0.2445	-0.6130	0.0064
A0217	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A0222	192	1	0.2725	0.0005	0.7774	394	1	0.1212	0.0005	0.3384	0.1513	-0.2996	0.8306
A0301	192	50	12.9438	9.8476	16.3519	394	79	10.1192	8.0597	12.0484	2.8246	-1.0072	7.0270
A0302	192	0	0.0068	0.0000	0.0326	394	3	0.3864	0.0619	0.9124	-0.3796	-0.9048	-0.0358
A1101	192	29	7.5841	5.0958	10.3743	394	66	8.4018	6.6535	10.3405	-0.8177	-3.8251	2.3997
A1102	192	2	0.5513	0.0138	1.3660	394	3	0.3869	0.0496	0.8095	0.1644	-0.6187	1.1058
A2301	192	6	1.5186	0.4976	2.7168	394	17	2.1981	0.9472	3.2097	-0.6796	-2.3061	0.7774
A2317	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A2402	192	27	7.0566	4.4505	9.3753	394	95	12.1210	9.8917	14.1986	-5.0644	-8.6728	-2.2275
A2403	192	1	0.2667	0.0016	0.7934	394	4	0.5190	0.0874	1.0419	-0.2523	-1.0724	0.3714
A2407	192	0	0.0083	0.0000	0.0471	394	2	0.2528	0.0143	0.6057	-0.2445	-0.6130	0.0064
A2410	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A2501	192	7	1.8024	0.8564	3.1445	394	10	1.2441	0.4823	2.0145	0.5583	-0.7011	2.0338
A2601	192	17	4.3987	2.0776	6.3867	394	34	4.2598	2.9570	5.5734	0.1389	-2.3167	2.5270
A2602	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A2608	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A2901	192	1	0.2472	0.0003	0.7552	394	2	0.2503	0.0123	0.5692	-0.0031	-0.6061	0.5609
A2902	192	11	2.8712	1.4871	4.7361	394	15	1.9019	1.0127	2.8084	0.9693	-0.6642	3.1004

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=A

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
A3001	192	6	1.5632	0.4265	2.7992	394	15	1.9248	0.8525	2.7575	-0.3616	-1.6705	1.2518
A3002	192	2	0.5289	0.0230	1.3046	394	10	1.2723	0.5595	2.0616	-0.7434	-1.7751	0.3725
A3004	192	1	0.2329	0.0013	0.6343	394	0	0.0015	0.0000	0.0042	0.2314	0.0003	0.6343
A3101	192	8	2.1002	0.7623	3.5776	394	16	2.0097	1.2063	3.1023	0.0905	-1.6469	1.8561
A3201	192	17	4.3572	2.4670	6.1438	394	30	3.7910	2.5579	5.1210	0.5662	-1.4420	2.9366
A3301	192	5	1.2972	0.3312	2.4114	394	5	0.6532	0.1216	1.1808	0.6440	-0.4887	1.8905
A3303	192	3	0.7813	0.1005	1.5541	394	20	2.5572	1.5314	3.5700	-1.7759	-2.9633	-0.1064
A3401	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216
A3402	192	0	0.0093	0.0000	0.0436	394	4	0.4970	0.0747	0.9584	-0.4877	-1.0263	-0.0744
A3601	192	1	0.2725	0.0005	0.7774	394	1	0.1212	0.0005	0.3384	0.1513	-0.2996	0.8306
A6601	192	3	0.7600	0.1022	1.5349	394	11	1.3796	0.6424	2.2479	-0.6196	-1.7222	0.7195
A6801	192	7	1.8273	0.5654	3.3087	394	18	2.3273	1.3393	3.2915	-0.5000	-2.1240	1.4006
A6802	192	5	1.3199	0.3954	2.4249	394	14	1.7828	0.8818	2.8780	-0.4629	-1.9714	1.0197
A6803	192	0	0.0068	0.0000	0.0326	394	3	0.3864	0.0619	0.9124	-0.3796	-0.9048	-0.0358
A6901	192	0	0.0083	0.0000	0.0471	394	2	0.2528	0.0143	0.6057	-0.2445	-0.6130	0.0064
A7401	192	0	0.0072	0.0000	0.0316	394	5	0.6674	0.1265	1.2238	-0.6602	-1.2238	-0.1266
A7411	192	0	0.0079	0.0000	0.0257	394	1	0.1333	0.0009	0.3856	-0.1254	-0.4779	0.0216

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=B

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
B0702	186	54	14.4660	11.1642	17.6558	385	61	7.8875	6.2147	9.7788	6.5785	2.8087	10.9255
B0705	186	2	0.5316	0.0468	1.2531	385	2	0.2426	0.0273	0.5923	0.2890	-0.3262	1.1175
B0706	186	1	0.2630	0.0003	0.7421	385	0	0.0040	0.0000	0.0219	0.2591	-0.0044	0.7536
B0707	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B0733	186	1	0.2630	0.0003	0.7421	385	0	0.0040	0.0000	0.0219	0.2591	-0.0044	0.7536
B0801	186	29	7.9800	5.3561	10.6792	385	69	8.9381	6.9359	10.9937	-0.9581	-4.4863	1.6472
B1301	186	0	0.0047	0.0000	0.0218	385	2	0.2534	0.0051	0.6200	-0.2487	-0.6261	0.0070
B1302	186	10	2.6592	1.0610	4.1438	385	20	2.5626	1.5154	3.7287	0.0965	-2.0277	1.9688
B1401	186	6	1.6090	0.4409	2.8422	385	13	1.6721	0.8573	2.5486	-0.0631	-1.8377	1.3904
B1402	186	11	2.9894	1.6047	4.5515	385	20	2.5100	1.6505	3.6326	0.4794	-1.6159	2.0703
B1501	186	23	6.2571	4.0569	8.8553	385	29	3.8016	2.6455	5.1424	2.4555	0.1988	5.5924
B1502	186	0	0.0081	0.0000	0.0412	385	3	0.3822	0.0393	0.8175	-0.3740	-0.8124	-0.0191
B1503	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B1505	186	1	0.2630	0.0003	0.7421	385	0	0.0040	0.0000	0.0219	0.2591	-0.0044	0.7536
B1507	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B1510	186	1	0.3009	0.0029	0.9156	385	3	0.3819	0.0480	0.7729	-0.0810	-0.7356	0.6229
B1515	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B1516	186	0	0.0081	0.0000	0.0412	385	3	0.3822	0.0393	0.8175	-0.3740	-0.8124	-0.0191
B1517	186	1	0.3009	0.0029	0.9156	385	3	0.3819	0.0480	0.7729	-0.0810	-0.7356	0.6229
B1518	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B1535	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B1547	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B1801	186	16	4.2519	2.3754	6.3982	385	26	3.3419	2.2127	4.6854	0.9100	-1.3247	3.6775
B1802	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B1811	186	1	0.2630	0.0003	0.7421	385	0	0.0040	0.0000	0.0219	0.2591	-0.0044	0.7536
B2702	186	3	0.7808	0.0813	1.6926	385	4	0.5093	0.1022	1.0872	0.2715	-0.5861	1.4260
B2703	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B2704	186	1	0.2687	0.0029	0.7895	385	1	0.1192	0.0001	0.3512	0.1496	-0.3027	0.7893

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=B

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
B2705	186	4	1.0816	0.2391	2.0271	385	20	2.5745	1.5307	3.6511	-1.4929	-2.8812	-0.1372
B2706	186	0	0.0081	0.0000	0.0412	385	3	0.3822	0.0393	0.8175	-0.3740	-0.8124	-0.0191
B2707	186	1	0.2687	0.0029	0.7895	385	1	0.1192	0.0001	0.3512	0.1496	-0.3027	0.7893
B2713	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B3501	186	17	4.5610	2.5560	6.4149	385	40	5.2193	3.8161	6.9974	-0.6583	-3.2057	2.0164
B3502	186	4	1.0696	0.1395	2.1678	385	18	2.3649	1.3139	3.3454	-1.2953	-2.5218	0.4943
B3503	186	16	4.2792	2.0592	6.1607	385	24	3.1435	1.9667	4.4110	1.1357	-1.2035	3.4019
B3505	186	0	0.0081	0.0000	0.0412	385	3	0.3822	0.0393	0.8175	-0.3740	-0.8124	-0.0191
B3508	186	3	0.8129	0.0671	1.6681	385	6	0.7901	0.2314	1.4123	0.0229	-0.9811	1.1227
B3512	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B3515	186	1	0.2630	0.0003	0.7421	385	0	0.0040	0.0000	0.0219	0.2591	-0.0044	0.7536
B3541	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B3542	186	1	0.2630	0.0003	0.7421	385	0	0.0040	0.0000	0.0219	0.2591	-0.0044	0.7536
B3543	186	1	0.2933	0.0001	0.9331	385	2	0.2444	0.0118	0.5701	0.0489	-0.5867	0.7344
B3701	186	5	1.3532	0.3497	2.4999	385	7	0.9046	0.3274	1.5262	0.4486	-0.9733	1.6227
B3801	186	8	2.1503	0.9661	3.7105	385	22	2.8799	1.7846	4.0020	-0.7296	-2.6630	0.8372
B3802	186	2	0.5316	0.0468	1.2531	385	2	0.2426	0.0273	0.5923	0.2890	-0.3262	1.1175
B3901	186	4	1.1056	0.2126	2.2179	385	10	1.2901	0.5625	2.1403	-0.1845	-1.4913	1.0365
B3902	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B3905	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B3906	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B3910	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B3913	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4001	186	21	5.6609	3.5333	7.9476	385	39	5.1107	3.7168	6.6421	0.5502	-1.9002	3.2152
B4002	186	5	1.3658	0.4782	2.5093	385	14	1.8069	0.9340	2.6970	-0.4411	-1.8788	0.9525
B4003	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4006	186	1	0.2828	0.0002	0.7939	385	7	0.9197	0.3191	1.6136	-0.6369	-1.4874	0.4730
B4101	186	2	0.5327	0.0221	1.2829	385	3	0.3845	0.0468	0.7930	0.1482	-0.5109	1.1599

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=B

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	*n*[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
B4102	186	5	1.3312	0.3095	2.5359	385	5	0.6809	0.2010	1.2656	0.6503	-0.8388	2.0698
B4201	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B4202	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4402	186	25	6.7027	4.3803	9.0448	385	46	5.9542	4.5377	7.6120	0.7485	-2.0117	4.0396
B4403	186	16	4.2914	2.4717	6.2943	385	31	4.0833	2.7501	5.5439	0.2080	-1.8375	2.4821
B4405	186	1	0.2638	0.0008	0.7387	385	5	0.6841	0.1860	1.2754	-0.4204	-1.1588	0.3801
B4427	186	2	0.5316	0.0468	1.2531	385	2	0.2426	0.0273	0.5923	0.2890	-0.3262	1.1175
B4501	186	4	1.0539	0.3131	2.0829	385	8	1.0333	0.4119	1.7122	0.0205	-1.1742	1.2456
B4504	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4601	186	3	0.7808	0.0813	1.6926	385	4	0.5093	0.1022	1.0872	0.2715	-0.5861	1.4260
B4603	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4612	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4701	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4801	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4802	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B4901	186	6	1.6090	0.4409	2.8422	385	13	1.6721	0.8573	2.5486	-0.0631	-1.8377	1.3904
B5001	186	4	1.0600	0.0777	2.0524	385	6	0.7705	0.2404	1.4294	0.2894	-0.7681	1.6375
B5101	186	17	4.5738	2.6701	6.9124	385	34	4.4326	3.0770	5.9771	0.1412	-2.7473	2.5337
B5102	186	0	0.0047	0.0000	0.0218	385	2	0.2534	0.0051	0.6200	-0.2487	-0.6261	0.0070
B5107	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B5109	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B5201	186	5	1.3492	0.4312	2.5979	385	16	2.1250	1.1115	3.0753	-0.7758	-2.2246	0.8558
B5301	186	3	0.8119	0.1347	1.7210	385	14	1.8536	0.9608	2.8877	-1.0416	-2.5483	0.2336
B5401	186	1	0.2687	0.0029	0.7895	385	1	0.1192	0.0001	0.3512	0.1496	-0.3027	0.7893
B5501	186	4	1.0600	0.0777	2.0524	385	6	0.7705	0.2404	1.4294	0.2894	-0.7681	1.6375
B5502	186	0	0.0081	0.0000	0.0412	385	3	0.3822	0.0393	0.8175	-0.3740	-0.8124	-0.0191
B5601	186	2	0.5316	0.0468	1.2531	385	2	0.2426	0.0273	0.5923	0.2890	-0.3262	1.1175
B5701	186	12	3.2581	1.6101	4.9616	385	22	2.8432	1.8658	3.9349	0.4149	-1.4001	2.5602

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=B

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	n^2	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	n^2	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
B5702	186	0	0.0047	0.0000	0.0218	385	2	0.2534	0.0051	0.6200	-0.2487	-0.6261	0.0070
B5703	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B5704	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B5801	186	5	1.2997	0.3081	2.3721	385	17	2.1760	1.1830	3.1597	-0.8763	-2.1363	0.7379
B5901	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082
B6702	186	0	0.0094	0.0000	0.0325	385	4	0.5214	0.0998	1.0226	-0.5120	-1.0374	-0.0998
B8101	186	0	0.0054	0.0000	0.0137	385	1	0.1332	0.0002	0.4055	-0.1277	-0.4351	0.0082

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=C

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	**n^2**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**n^2**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
C0102	192	9	2.3930	1.1047	3.8062	393	36	4.5432	3.1783	5.9285	-2.1502	-4.2796	-0.1973
C0103	192	0	0.0062	0.0000	0.0233	393	1	0.1305	0.0002	0.3962	-0.1243	-0.4043	0.0336
C0202	192	11	2.8550	1.3334	4.4927	393	35	4.4383	3.0553	5.8618	-1.5833	-3.4332	0.5700
C0210	192	1	0.2902	0.0048	0.8862	393	6	0.7501	0.2331	1.3219	-0.4599	-1.2049	0.4686
C0302	192	4	1.0489	0.2608	2.1152	393	13	1.6310	0.8568	2.5488	-0.5821	-1.8646	0.6442
C0303	192	15	3.9102	2.1182	6.1799	393	33	4.2190	2.8933	5.4627	-0.3089	-2.7173	1.9891
C0304	192	38	9.8996	7.0985	12.9961	393	57	7.1971	5.6830	8.9264	2.7024	-0.5188	6.4869
C0305	192	0	0.0081	0.0000	0.0185	393	2	0.2494	0.0141	0.6576	-0.2413	-0.6893	-0.0039
C0401	192	51	13.1884	9.9467	16.0922	393	112	14.2186	11.5084	16.4236	-1.0302	-4.6274	3.4533
C0501	192	20	5.2650	3.1408	7.3894	393	49	6.1823	4.6730	7.8511	-0.9173	-3.4834	1.8665
C0602	192	38	9.9043	7.0111	12.9400	393	59	7.4525	5.7937	9.2166	2.4518	-0.9652	5.9008
C0701	192	54	14.0916	11.1723	17.6452	393	95	12.1257	9.7156	14.4875	1.9659	-1.8300	5.9919
C0702	192	55	14.3253	11.2505	17.4750	393	86	10.8734	8.7990	12.7947	3.4520	-0.3373	7.0345
C0704	192	3	0.7592	0.0765	1.5456	393	15	1.8951	0.9862	2.7955	-1.1359	-2.4484	0.1542
C0706	192	0	0.0073	0.0000	0.0211	393	3	0.3815	0.0567	0.8594	-0.3742	-0.8616	-0.0311
C0718	192	1	0.2785	0.0003	0.7397	393	1	0.1154	0.0001	0.3481	0.1631	-0.2971	0.8137
C0727	192	1	0.2821	0.0005	0.8421	393	3	0.3774	0.0645	0.7663	-0.0953	-0.8269	0.5752
C0801	192	2	0.5172	0.0190	1.2351	393	11	1.4146	0.7116	2.2132	-0.8974	-1.9692	0.0906
C0802	192	16	4.1638	2.4465	5.9786	393	31	3.9421	2.7012	5.3356	0.2217	-2.2790	2.4013
C1202	192	6	1.5603	0.4188	2.7605	393	17	2.2002	1.2465	3.4563	-0.6399	-2.2402	0.8803
C1203	192	19	4.9991	3.1080	7.4283	393	49	6.3005	4.6473	8.0738	-1.3014	-3.8943	1.6696
C1402	192	8	2.0746	0.8576	3.4447	393	14	1.7558	0.8426	2.4842	0.3188	-1.1092	1.9216
C1403	192	0	0.0081	0.0000	0.0185	393	2	0.2494	0.0141	0.6576	-0.2413	-0.6893	-0.0039
C1502	192	8	2.1274	0.6425	3.5298	393	15	1.8896	0.9801	2.9109	0.2378	-1.5566	2.1350
C1505	192	4	1.0481	0.2433	2.1508	393	2	0.2471	0.0197	0.5931	0.8011	0.0203	2.0038
C1506	192	1	0.2755	0.0012	0.8505	393	0	0.0030	0.0000	0.0148	0.2725	-0.0256	0.8579
C1509	192	0	0.0062	0.0000	0.0233	393	1	0.1305	0.0002	0.3962	-0.1243	-0.4043	0.0336
C1601	192	10	2.6669	1.2157	4.1380	393	22	2.8088	1.6804	3.8745	-0.1419	-2.2006	1.6295

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=C

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
C1602	192	1	0.2654	0.0009	0.8179	393	2	0.2460	0.0164	0.6295	0.0194	-0.5540	0.6363
C1604	192	1	0.2755	0.0012	0.8505	393	0	0.0030	0.0000	0.0148	0.2725	-0.0256	0.8579
C1701	192	5	1.2835	0.2972	2.3441	393	11	1.4472	0.6498	2.1884	-0.1637	-1.4577	1.1822
C1703	192	2	0.5098	0.0491	1.2606	393	0	0.0041	0.0000	0.0255	0.5057	0.0111	1.2606
C1801	192	0	0.0062	0.0000	0.0233	393	1	0.1305	0.0002	0.3962	-0.1243	-0.4043	0.0336
C1802	192	0	0.0081	0.0000	0.0185	393	2	0.2494	0.0141	0.6576	-0.2413	-0.6893	-0.0039

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DPA1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DPA10103*	193	308	79.9145	75.9758	84.1108	393	564	71.7409	68.2376	74.6732	8.1735	3.1423	13.1201
DPA10104	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPA10105	193	2	0.5154	0.0101	1.1153	393	2	0.2571	0.0105	0.6396	0.2583	-0.4347	1.0540
DPA10109	193	1	0.2466	0.0003	0.7634	393	0	0.0030	0.0000	0.0071	0.2436	0.0003	0.8055
DPA10111	193	0	0.0053	0.0000	0.0172	393	3	0.3520	0.0201	0.7924	-0.3467	-0.7997	-0.0111
DPA10201	193	54	14.0474	10.5270	17.3569	393	145	18.4412	15.9914	21.5220	-4.3937	-8.5863	-0.1558
DPA10202	193	19	4.9636	3.0155	6.9639	393	62	7.8953	5.9335	9.7043	-2.9317	-5.8357	-0.3603
DPA10301	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPA10302	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPA10303	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPA10401	193	2	0.5328	0.0197	1.2292	393	4	0.5119	0.0974	0.9513	0.0209	-0.7309	0.9300

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DPB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DPB10101	193	21	5.4801	3.4599	7.7373	393	49	6.2030	4.5896	7.6093	-0.7229	-3.2992	1.9399
DPB10201	193	46	11.9776	8.8218	15.5549	393	99	12.5000	10.4837	14.6348	-0.5224	-4.7560	3.5577
DPB10202	193	1	0.2352	0.0007	0.7158	393	8	1.0220	0.3535	1.7030	-0.7868	-1.5667	0.0790
DPB10301	193	24	6.1606	4.1198	8.3967	393	51	6.4385	4.8337	8.1330	-0.2779	-3.6479	2.2733
DPB10401*	193	163	42.3313	36.7113	47.3778	393	275	34.9633	31.0687	38.0398	7.3680	1.1605	13.6480
DPB10402	193	40	10.3986	7.4813	13.7016	393	83	10.6350	8.6584	12.6438	-0.2363	-4.0124	3.4478
DPB10501	193	14	3.6281	1.9109	5.3197	393	39	4.9760	3.5374	6.3386	-1.3479	-3.8070	1.0626
DPB10601	193	10	2.5581	1.0078	3.9379	393	8	0.9891	0.3604	1.6990	1.5690	0.0881	3.3607
DPB10901	193	1	0.2790	0.0001	0.7621	393	12	1.5515	0.7536	2.4501	-1.2725	-2.2697	-0.3885
DPB11001	193	3	0.8071	0.1631	1.7939	393	10	1.2930	0.6660	2.1617	-0.4859	-1.5374	0.8323
DPB110401	193	12	3.0299	1.3123	4.8176	393	13	1.7083	0.8132	2.6191	1.3217	-0.4265	3.6134
DPB110501	193	5	1.3003	0.3253	2.3414	393	17	2.1721	1.3374	3.2957	-0.8719	-2.3421	0.6594
DPB110701	193	10	2.5881	1.2065	4.2974	393	23	2.9447	1.8727	4.0941	-0.3566	-2.4039	1.5377
DPB11101	193	6	1.5657	0.4570	2.8767	393	13	1.6632	0.8685	2.5085	-0.0976	-1.6135	1.4376
DPB112401	193	1	0.2305	0.0001	0.6802	393	1	0.1346	0.0007	0.3983	0.0959	-0.2613	0.7394
DPB112601	193	4	1.0180	0.1683	1.9304	393	6	0.7636	0.2076	1.3549	0.2544	-0.8842	1.2541
DPB113101	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB113501	193	1	0.2563	0.0008	0.7548	393	6	0.7596	0.2233	1.3680	-0.5033	-1.3088	0.2679
DPB113801	193	1	0.2305	0.0001	0.6802	393	1	0.1346	0.0007	0.3983	0.0959	-0.2613	0.7394
DPB11401	193	3	0.7864	0.1216	1.6218	393	19	2.3956	1.3984	3.5052	-1.6092	-3.0531	-0.0989
DPB11501	193	0	0.0094	0.0000	0.0365	393	6	0.7733	0.3199	1.4592	-0.7639	-1.3612	-0.1855
DPB11601	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB11701	193	10	2.6579	1.1538	4.3470	393	15	1.9077	0.8795	2.7937	0.7502	-1.3615	2.5628
DPB11801	193	0	0.0053	0.0000	0.0172	393	3	0.3520	0.0201	0.7924	-0.3467	-0.7997	-0.0111
DPB11901	193	4	1.0440	0.2480	1.9346	393	4	0.5172	0.0955	0.9945	0.5268	-0.3686	1.6532
DPB12001	193	2	0.5154	0.0101	1.1153	393	2	0.2571	0.0105	0.6396	0.2583	-0.4347	1.0540
DPB12101	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB12201	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DPB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DPB12301	193	2	0.5328	0.0197	1.2292	393	4	0.5119	0.0974	0.9513	0.0209	-0.7309	0.9300
DPB12601	193	1	0.2466	0.0003	0.7634	393	0	0.0030	0.0000	0.0071	0.2436	0.0003	0.8055
DPB12701	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB13301	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB13601	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB13901	193	0	0.0069	0.0000	0.0201	393	2	0.2553	0.0122	0.6495	-0.2484	-0.6946	-0.0122
DPB14601	193	1	0.2305	0.0001	0.6802	393	1	0.1346	0.0007	0.3983	0.0959	-0.2613	0.7394
DPB15001	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB18101	193	0	0.0104	0.0000	0.0375	393	1	0.1368	0.0007	0.4260	-0.1263	-0.5479	0.0152
DPB18501	193	0	0.0053	0.0000	0.0172	393	3	0.3520	0.0201	0.7924	-0.3467	-0.7997	-0.0111

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DQA1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DQA10101	191	36	9.4154	6.8367	12.4550	394	84	10.6612	8.7634	12.7202	-1.2457	-4.8144	2.0545
DQA10102	191	85	22.5556	17.7621	26.5105	394	162	20.5308	17.6288	23.3394	2.0248	-2.7818	7.0371
DQA10103	191	22	5.8211	3.6839	8.1765	394	58	7.3164	5.6397	9.2904	-1.4953	-4.3589	1.4967
DQA10104	191	13	3.3921	1.7243	5.0312	394	23	2.9241	1.8115	3.9644	0.4680	-1.7743	2.5037
DQA10105	191	2	0.5352	0.0236	1.3066	394	5	0.6411	0.1302	1.1873	-0.1059	-1.0033	0.8395
DQA10106	191	1	0.2570	0.0000	0.7906	394	0	0.0045	0.0000	0.0308	0.2525	-0.0115	0.8041
DQA10107	191	1	0.2680	0.0003	0.8239	394	1	0.1393	0.0001	0.3780	0.1287	-0.3495	0.7869
DQA10110	191	0	0.0081	0.0000	0.0413	394	3	0.3900	0.0648	0.8070	-0.3820	-0.8128	-0.0467
DQA10201	191	29	7.4621	4.8900	9.9741	394	47	5.9398	4.4818	7.7739	1.5222	-1.5790	4.5768
DQA10301	191	49	12.9227	9.5833	16.0186	394	84	10.6333	8.5692	12.5721	2.2894	-1.4994	5.9335
DQA10302	191	6	1.5618	0.2963	2.7201	394	17	2.1500	1.2919	3.2222	-0.5881	-2.0765	1.1587
DQA10303	191	19	4.9711	2.8325	7.1205	394	55	7.0290	5.4401	8.9103	-2.0579	-4.7722	0.8496
DQA10401	191	8	2.0719	0.7352	3.3821	394	35	4.4587	2.8864	5.7883	-2.3868	-4.0864	-0.2059
DQA10402	191	1	0.2680	0.0003	0.8239	394	1	0.1393	0.0001	0.3780	0.1287	-0.3495	0.7869
DQA10501	191	43	11.3692	8.3581	14.9206	394	84	10.6862	8.6484	13.1269	0.6831	-2.8586	5.0007
DQA10503	191	2	0.5051	0.0125	1.1670	394	3	0.3800	0.0387	0.8180	0.1251	-0.6169	1.0880
DQA10505	191	56	14.7415	11.4362	18.2016	394	110	13.9089	11.5410	16.3150	0.8327	-4.0176	4.8542
DQA10507	191	0	0.0098	0.0000	0.0323	394	1	0.1252	0.0004	0.3748	-0.1154	-0.4160	0.0181
DQA10508	191	0	0.0098	0.0000	0.0323	394	1	0.1252	0.0004	0.3748	-0.1154	-0.4160	0.0181
DQA10509	191	1	0.2680	0.0003	0.8239	394	1	0.1393	0.0001	0.3780	0.1287	-0.3495	0.7869
DQA10510	191	1	0.2680	0.0003	0.8239	394	1	0.1393	0.0001	0.3780	0.1287	-0.3495	0.7869
DQA10601	191	7	1.8426	0.6008	3.2192	394	12	1.5326	0.7713	2.3091	0.3101	-1.1326	2.1673

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

[1] Kruschke, J.K., 2011. Doing Bayesian Data Analysis. Academic Press, Burlington.

[2] Sample sizes reported are the result of available data for the specific gene. Not all genes have complete data due to possibly poor quality sequencing reads.

[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DQB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	**n[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**n[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference [3]**	**Lower CB[3]**	**Upper CB[3]**
DQB10201	184	47	12.7985	9.3257	15.9587	373	87	11.4728	8.9166	13.5893	1.3257	-2.4594	5.5503
DQB10202	184	45	12.2883	8.9536	15.7777	373	86	11.6118	9.2199	13.5575	0.6765	-2.8291	5.0530
DQB10301	184	41	11.0661	8.2391	14.2802	373	96	12.8738	10.3653	15.4468	-1.8078	-5.8510	1.9050
DQB10302	184	25	6.8242	4.0474	9.0064	373	49	6.4364	4.5766	8.1625	0.3878	-2.9166	3.3815
DQB10303	184	11	2.9407	1.4313	4.5685	373	19	2.5527	1.5275	3.8530	0.3880	-1.5081	2.3961
DQB10304	184	0	0.0062	0.0000	0.0219	373	2	0.2719	0.0016	0.6381	-0.2657	-0.6615	-0.0016
DQB10319	184	2	0.5587	0.0180	1.3237	373	4	0.5170	0.1326	0.9735	0.0417	-0.7088	1.0468
DQB10402	184	6	1.6389	0.4596	2.8294	373	20	2.7450	1.6151	4.0844	-1.1061	-3.0754	0.7154
DQB10501	184	45	12.3458	9.6264	15.4935	373	107	14.3117	11.7635	16.6994	-1.9659	-5.4357	2.1459
DQB10502	184	10	2.7126	1.2495	4.3685	373	26	3.4681	2.2675	4.6878	-0.7555	-2.6796	1.6090
DQB10503	184	12	3.3169	1.8066	5.3331	373	24	3.2560	2.0886	4.4058	0.0609	-1.9453	2.3721
DQB10601	184	10	2.7038	1.1988	4.4576	373	21	2.8485	1.6493	3.9188	-0.1447	-2.0239	1.8350
DQB10602	184	73	19.7269	15.9243	23.2575	373	110	14.6723	12.2698	17.1857	5.0546	0.6823	9.5097
DQB10603	184	20	5.4218	3.1530	7.4196	373	51	6.8888	5.1808	8.7946	-1.4671	-4.2518	1.6056
DQB10604	184	12	3.1936	1.4059	4.9699	373	28	3.7842	2.3496	5.0787	-0.5906	-2.7487	1.7640
DQB10609	184	9	2.4346	1.1264	3.9818	373	15	1.9741	1.1615	2.9909	0.4605	-1.2539	2.2387
DQB10688	184	0	0.0060	0.0000	0.0244	373	1	0.1355	0.0002	0.4197	-0.1295	-0.4924	0.0281

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DRB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	n[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	n[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
DRB10101	191	25	6.5204	4.2153	9.0771	389	59	7.6217	5.9366	9.4864	-1.1013	-3.9171	1.9818
DRB10102	191	8	2.0829	0.7061	3.4469	389	14	1.8039	0.9212	2.7686	0.2791	-1.2483	1.9817
DRB10103	191	4	1.0588	0.1660	2.0302	389	5	0.6194	0.1633	1.2122	0.4394	-0.4597	1.7446
DRB10301	191	35	9.1802	6.6632	11.7604	389	83	10.6958	8.8808	13.0785	-1.5155	-4.2718	2.1338
DRB10302	191	0	0.0132	0.0000	0.0781	389	4	0.5110	0.1167	0.9989	-0.4978	-1.0134	-0.0798
DRB10317	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031
DRB10342	191	0	0.0045	0.0000	0.0234	389	3	0.3758	0.0348	0.7594	-0.3713	-0.8022	-0.0697
DRB10401	191	22	5.8253	4.0191	8.4021	389	39	5.0336	3.3536	6.4825	0.7916	-2.2186	3.4526
DRB10402	191	7	1.8482	0.7402	3.2794	389	14	1.7891	0.9254	2.6126	0.0591	-1.5638	1.5206
DRB10403	191	2	0.5408	0.0454	1.3097	389	12	1.5288	0.7366	2.4192	-0.9880	-2.1564	0.0520
DRB10404	191	12	3.1363	1.4424	4.9105	389	21	2.7070	1.5558	3.9228	0.4293	-1.4557	2.8404
DRB10405	191	3	0.7812	0.1218	1.6990	389	9	1.1555	0.4663	1.9039	-0.3742	-1.4366	0.8080
DRB10406	191	2	0.5339	0.0319	1.2115	389	1	0.1368	0.0003	0.4347	0.3972	-0.3395	1.1178
DRB10407	191	1	0.2743	0.0003	0.7551	389	6	0.7611	0.2517	1.3590	-0.4868	-1.3447	0.2844
DRB10408	191	2	0.5300	0.0270	1.2629	389	6	0.7517	0.2925	1.3883	-0.2217	-1.0453	0.6625
DRB10410	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB10414	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB10415	191	1	0.2851	0.0006	0.8635	389	0	0.0035	0.0000	0.0133	0.2815	-0.0232	0.9090
DRB10442	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031
DRB10701	191	60	15.5201	11.9373	19.2470	389	99	12.7621	10.7466	15.3479	2.7580	-1.2819	7.0287
DRB10801	191	9	2.3974	0.8965	3.9483	389	20	2.5611	1.5540	3.6072	-0.1637	-2.0454	1.7991
DRB10802	191	1	0.2648	0.0001	0.8109	389	7	0.9001	0.2735	1.5698	-0.6353	-1.4325	0.1765
DRB10803	191	3	0.7994	0.1008	1.6387	389	3	0.3661	0.0445	0.7552	0.4333	-0.3706	1.5458
DRB10806	191	1	0.2614	0.0016	0.7644	389	1	0.1389	0.0000	0.3899	0.1225	-0.4450	0.7023
DRB10810	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031
DRB10813	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB10901	191	6	1.5744	0.4940	2.7048	389	18	2.3263	1.3488	3.4509	-0.7519	-2.3138	0.8290
DRB10902	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: "Prevalence Difference" is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DRB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	n[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	n[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
DRB11001	191	3	0.8230	0.0878	1.7030	389	6	0.7617	0.2330	1.4629	0.0614	-0.9750	1.3354
DRB11101	191	22	5.7913	3.3321	8.1172	389	43	5.5508	4.1434	7.0468	0.2404	-3.0138	2.9133
DRB11102	191	1	0.2699	0.0003	0.8037	389	2	0.2700	0.0071	0.6608	-0.0001	-0.6775	0.6285
DRB11103	191	3	0.7958	0.1189	1.7651	389	4	0.5227	0.0671	1.0104	0.2730	-0.6723	1.3800
DRB11104	191	14	3.7111	1.8649	5.4766	389	26	3.3175	2.1787	4.5737	0.3936	-1.7114	2.6487
DRB11201	191	9	2.3825	1.2346	4.0926	389	18	2.3069	1.3801	3.4414	0.0757	-1.4923	1.9558
DRB11202	191	3	0.7897	0.0846	1.6677	389	5	0.6614	0.1581	1.2239	0.1283	-0.7701	1.2562
DRB11206	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB11301	191	12	3.2122	1.4889	4.9161	389	41	5.1840	3.8188	7.2485	-1.9718	-4.1975	0.3675
DRB11302	191	20	5.1858	3.1753	7.2853	389	36	4.5597	3.1339	5.7789	0.6261	-1.7440	3.3310
DRB11303	191	4	1.0348	0.2302	2.0449	389	6	0.7680	0.3267	1.4469	0.2668	-0.7869	1.4901
DRB11304	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB11305	191	1	0.2550	0.0001	0.7741	389	3	0.3882	0.0535	0.8198	-0.1332	-0.7379	0.5788
DRB11401	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB11403	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031
DRB11404	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB11405	191	0	0.0045	0.0000	0.0234	389	3	0.3758	0.0348	0.7594	-0.3713	-0.8022	-0.0697
DRB11406	191	2	0.5575	0.0045	1.2705	389	2	0.2331	0.0106	0.6255	0.3244	-0.4658	1.1552
DRB114141	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031
DRB11425	191	0	0.0073	0.0000	0.0357	389	2	0.2547	0.0135	0.6178	-0.2474	-0.6344	-0.0071
DRB11430	191	1	0.2851	0.0006	0.8635	389	0	0.0035	0.0000	0.0133	0.2815	-0.0232	0.9090
DRB11454	191	15	3.9411	2.2148	6.1137	389	22	2.8870	1.8310	4.1441	1.0541	-0.8554	3.4858
DRB11457	191	2	0.5339	0.0319	1.2115	389	1	0.1368	0.0003	0.4347	0.3972	-0.3395	1.1178
DRB11501	191	51	13.3834	10.4194	16.3457	389	75	9.6152	7.4673	11.5094	3.7682	-0.0619	7.1530
DRB11502	191	5	1.3072	0.2531	2.3908	389	14	1.8014	0.9875	2.7106	-0.4942	-1.8181	1.0577
DRB11503	191	1	0.2743	0.0003	0.7551	389	6	0.7611	0.2517	1.3590	-0.4868	-1.3447	0.2844
DRB11596	191	0	0.0062	0.0000	0.0337	389	1	0.1275	0.0003	0.4076	-0.1213	-0.4627	0.0031
DRB11601	191	6	1.5636	0.5707	2.7539	389	8	1.0535	0.3688	1.8320	0.5101	-0.7973	2.0235

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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gene=DRB1

	Bayesian Credible Interval [1] Cases n=195					Bayesian Credible Interval [1] Controls n=395					Bayesian Credible Interval [1] Comparing Cases & Controls		
Allele	n[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	n[2]	Observed Allele Frequency	Estimated Allele Prevalence	Lower CB	Upper CB	Prevalence Difference [3]	Lower CB[3]	Upper CB[3]
DRB11602	191	1	0.2743	0.0003	0.7551	389	6	0.7611	0.2517	1.3590	-0.4868	-1.3447	0.2844
DRB11609	191	2	0.5126	0.0200	1.1845	389	4	0.5122	0.1255	1.0253	0.0004	-0.7890	0.9668

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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[3] An interval that does not include zero indicates that a difference between cases and controls is highly plausible.

gene=DRBo

	Bayesian Credible Interval[1] Cases n=195					Bayesian Credible Interval[1] Controls n=395					Bayesian Credible Interval[1] Comparing Cases & Controls		
Allele	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	***n*[2]**	**Observed Allele Frequency**	**Estimated Allele Prevalence**	**Lower CB**	**Upper CB**	**Prevalence Difference[3]**	**Lower CB[3]**	**Upper CB[3]**
DRB30101	176	68	19.3383	15.3650	23.2661	340	154	22.6055	19.8622	25.6435	-3.2672	-8.6451	1.7619
DRB30114	176	1	0.3117	0.0004	1.0105	340	2	0.3160	0.0191	0.7665	-0.0043	-0.8018	0.7825
DRB30201	176	3	0.8803	0.1241	1.8900	340	3	0.4362	0.0673	0.9478	0.4441	-0.5857	1.5214
DRB30202	176	105	29.8578	25.6326	34.4636	340	211	31.0247	27.5207	34.3494	-1.1669	-7.5904	4.0418
DRB30224	176	3	0.8669	0.1426	1.8440	340	0	0.0051	0.0000	0.0242	0.8618	0.1429	1.8440
DRB30301	176	31	8.7600	6.1137	11.3086	340	59	8.7101	6.6775	10.8847	0.0499	-3.1202	3.8028
DRB40101	176	13	3.7186	1.9688	5.9832	340	21	3.0913	2.0437	4.4953	0.6273	-1.6906	2.9131
DRB40103	176	42	11.8845	8.8812	15.2472	340	83	12.2405	9.8643	14.6096	-0.3561	-4.3830	3.5403
DRB50101	176	69	19.7672	15.4932	23.5610	340	110	16.2926	13.5892	18.9245	3.4746	-1.7910	7.6760
DRB50102	176	10	2.8676	1.1440	4.5302	340	18	2.6410	1.6216	3.8764	0.2266	-1.6518	2.7761
DRB50108	176	0	0.0120	0.0000	0.0410	340	1	0.1486	0.0003	0.4798	-0.1366	-0.5286	0.0323
DRB50111	176	0	0.0120	0.0000	0.0410	340	1	0.1486	0.0003	0.4798	-0.1366	-0.5286	0.0323
DRB50202	176	7	1.9361	0.8678	3.4859	340	14	2.0803	1.1063	3.0908	-0.1442	-1.6743	1.7242
DRB50206	176	0	0.0087	0.0000	0.0454	340	3	0.4426	0.0452	0.9452	-0.4339	-0.9452	-0.0344

* Bayesian estimates of allele prevalence made using the beta-binomial distribution.
Note: CB = credible bound.
Note: A Bayesian 95% highest density credible interval encompasses the 95% most plausible values of the parameter.
Note: “Prevalence Difference” is the estimate of the allele prevalence of cases minus the allele prevalence of controls.
Note: Allele prevalences are calculated based on the available 2*n sample sizes for cases and controls, respectively. Allele prevalence estimates are per copy.

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GENE=A

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
A0101	50	26.04	92	23.35	0.4601	1.0000	1.12	0.78	1.50
A0102	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A0104	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A0201	89	46.35	149	37.82	0.0469	0.5860	1.23	0.98	1.49
A0202	1	0.52	3	0.76	1.0000	1.0000	0.68	0.03	6.75
A0203	3	1.56	3	0.76	0.3620	1.0000	2.05	0.34	12.35
A0205	8	4.17	5	1.27	0.0271	0.5860	3.28	1.05	12.18
A0206	3	1.56	6	1.52	1.0000	1.0000	1.03	0.17	4.30
A0207	1	0.52	3	0.76	1.0000	1.0000	0.68	0.03	6.75
A0211	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.57
A0217	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A0222	1	0.52	1	0.25	0.5211	1.0000	2.05	0.10	68.65
A0301	47	24.48	74	18.78	0.1185	1.0000	1.30	0.92	1.80
A0302	0	0.00	3	0.76	0.3340	1.0000	0.00	0.00	3.08
A1101	27	14.06	64	16.24	0.5302	1.0000	0.87	0.55	1.31
A1102	2	1.04	3	0.76	0.6540	1.0000	1.37	0.16	8.50
A2301	6	3.13	17	4.31	0.6324	1.0000	0.72	0.18	1.76
A2317	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A2402	24	12.50	85	21.57	0.0089	0.4002	0.58	0.34	0.89
A2403	1	0.52	4	1.02	1.0000	1.0000	0.51	0.02	3.79
A2407	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.57
A2410	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A2501	7	3.65	10	2.54	0.4184	1.0000	1.44	0.50	3.79
A2601	17	8.85	34	8.63	1.0000	1.0000	1.03	0.55	1.78
A2602	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A2608	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A2901	1	0.52	2	0.51	1.0000	1.0000	1.03	0.05	11.43
A2902	11	5.73	15	3.81	0.2718	1.0000	1.50	0.62	3.28
A3001	6	3.13	15	3.81	0.8039	1.0000	0.82	0.20	2.04

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=A

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
A3002	2	1.04	10	2.54	0.3173	1.0000	0.41	0.05	1.66
A3004	1	0.52	0	0.00	0.2840	1.0000	.	.	.
A3101	8	4.17	15	3.81	0.8134	1.0000	1.09	0.42	2.52
A3201	17	8.85	28	7.11	0.4927	1.0000	1.25	0.62	2.23
A3301	5	2.60	5	1.27	0.2958	1.0000	2.05	0.56	7.45
A3303	3	1.56	19	4.82	0.0521	0.5860	0.32	0.05	1.03
A3401	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06
A3402	0	0.00	4	1.02	0.2958	1.0000	0.00	0.00	2.04
A3601	1	0.52	1	0.25	0.5211	1.0000	2.05	0.10	68.65
A6601	3	1.56	11	2.79	0.5365	1.0000	0.56	0.09	1.86
A6801	7	3.65	17	4.31	0.8161	1.0000	0.84	0.26	1.97
A6802	5	2.60	13	3.30	0.7886	1.0000	0.79	0.18	2.12
A6803	0	0.00	3	0.76	0.3340	1.0000	0.00	0.00	3.08
A6901	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.57
A7401	0	0.00	5	1.27	0.1646	1.0000	0.00	0.00	1.58
A7411	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	30.06

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=B

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
B0702	49	26.34	58	15.06	0.0026	0.2371	1.75	1.22	2.46
B0705	2	1.08	2	0.52	0.5809	1.0000	2.07	0.17	30.95
B0706	1	0.54	0	0.00	0.2818	1.0000	.	.	.
B0707	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B0733	1	0.54	0	0.00	0.2818	1.0000	.	.	.
B0801	28	15.05	62	16.10	0.7990	1.0000	0.93	0.59	1.40
B1301	0	0.00	2	0.52	1.0000	1.0000	0.00	0.00	5.61
B1302	10	5.38	20	5.19	1.0000	1.0000	1.03	0.46	2.16
B1401	6	3.23	12	3.12	1.0000	1.0000	1.03	0.31	2.71
B1402	11	5.91	20	5.19	0.6853	1.0000	1.14	0.50	2.31
B1501	21	11.29	29	7.53	0.1436	1.0000	1.50	0.81	2.57
B1502	0	0.00	3	0.78	0.3538	1.0000	0.00	0.00	3.10
B1503	0	0.00	4	1.04	0.2971	1.0000	0.00	0.00	2.05
B1505	1	0.54	0	0.00	0.2818	1.0000	.	.	.
B1507	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B1510	1	0.54	3	0.78	1.0000	1.0000	0.69	0.03	6.81
B1515	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B1516	0	0.00	3	0.78	0.3538	1.0000	0.00	0.00	3.10
B1517	1	0.54	3	0.78	1.0000	1.0000	0.69	0.03	6.81
B1518	0	0.00	3	0.78	0.3538	1.0000	0.00	0.00	3.10
B1535	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B1547	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B1801	15	8.06	25	6.49	0.4697	1.0000	1.24	0.63	2.30
B1802	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B1811	1	0.54	0	0.00	0.2818	1.0000	.	.	.
B2702	2	1.08	4	1.04	1.0000	1.0000	1.03	0.14	5.80
B2703	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B2704	1	0.54	1	0.26	0.5190	1.0000	2.07	0.10	69.30
B2705	4	2.15	20	5.19	0.1026	1.0000	0.41	0.09	1.14

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=B

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value[1]***	***FDR Adjusted p-value[2]***	***Relative Risk***	***Lower CL[3]***	***Upper CL[3]***
B2706	0	0.00	3	0.78	0.3538	1.0000	0.00	0.00	3.10
B2707	1	0.54	1	0.26	0.5190	1.0000	2.07	0.10	69.30
B2713	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B3501	16	8.60	37	9.61	0.7502	1.0000	0.90	0.47	1.55
B3502	4	2.15	16	4.16	0.3040	1.0000	0.52	0.14	1.46
B3503	15	8.06	22	5.71	0.2655	1.0000	1.41	0.66	2.67
B3505	0	0.00	3	0.78	0.3538	1.0000	0.00	0.00	3.10
B3508	3	1.61	6	1.56	1.0000	1.0000	1.03	0.17	4.33
B3512	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B3515	1	0.54	0	0.00	0.2818	1.0000	.	.	.
B3541	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B3542	1	0.54	0	0.00	0.2818	1.0000	.	.	.
B3543	1	0.54	2	0.52	0.6664	1.0000	1.03	0.05	11.52
B3701	5	2.69	6	1.56	0.3195	1.0000	1.72	0.50	6.54
B3801	8	4.30	20	5.19	0.8268	1.0000	0.83	0.29	1.81
B3802	2	1.08	2	0.52	0.5809	1.0000	2.07	0.17	30.95
B3901	4	2.15	10	2.60	1.0000	1.0000	0.83	0.17	2.51
B3902	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B3905	0	0.00	4	1.04	0.2971	1.0000	0.00	0.00	2.05
B3906	0	0.00	4	1.04	0.2971	1.0000	0.00	0.00	2.05
B3910	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B3913	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4001	21	11.29	39	10.13	0.6519	1.0000	1.11	0.63	1.83
B4002	5	2.69	14	3.64	0.6121	1.0000	0.74	0.17	1.97
B4003	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4006	1	0.54	7	1.82	0.3810	1.0000	0.30	0.01	1.86
B4101	2	1.08	3	0.78	0.6523	1.0000	1.38	0.16	8.57
B4102	5	2.69	5	1.30	0.2952	1.0000	2.07	0.57	7.51
B4201	0	0.00	4	1.04	0.2971	1.0000	0.00	0.00	2.05

CL = confidence limit

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[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=B

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
B4202	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4402	24	12.90	46	11.95	0.7774	1.0000	1.08	0.63	1.71
B4403	16	8.60	31	8.05	0.8659	1.0000	1.07	0.56	1.90
B4405	1	0.54	5	1.30	0.6141	1.0000	0.41	0.02	2.86
B4427	2	1.08	2	0.52	0.5809	1.0000	2.07	0.17	30.95
B4501	4	2.15	8	2.08	1.0000	1.0000	1.03	0.18	3.40
B4504	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4601	3	1.61	4	1.04	0.6812	1.0000	1.55	0.19	7.23
B4603	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4612	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4701	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4801	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4802	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B4901	5	2.69	13	3.38	0.7883	1.0000	0.80	0.18	2.14
B5001	4	2.15	6	1.56	0.7133	1.0000	1.38	0.29	5.28
B5101	17	9.14	32	8.31	0.7408	1.0000	1.10	0.59	1.92
B5102	0	0.00	2	0.52	1.0000	1.0000	0.00	0.00	5.61
B5107	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B5109	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B5201	5	2.69	16	4.16	0.4569	1.0000	0.65	0.17	1.68
B5301	2	1.08	13	3.38	0.1357	1.0000	0.32	0.03	1.25
B5401	1	0.54	1	0.26	0.5190	1.0000	2.07	0.10	69.30
B5501	4	2.15	6	1.56	0.7133	1.0000	1.38	0.29	5.28
B5502	0	0.00	3	0.78	0.3538	1.0000	0.00	0.00	3.10
B5601	2	1.08	2	0.52	0.5809	1.0000	2.07	0.17	30.95
B5701	11	5.91	22	5.71	1.0000	1.0000	1.03	0.47	2.08
B5702	0	0.00	2	0.52	1.0000	1.0000	0.00	0.00	5.61
B5703	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B5704	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30

CL = confidence limit

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Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=B

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
B5801	5	2.69	15	3.90	0.6071	1.0000	0.69	0.17	1.80
B5901	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30
B6702	0	0.00	4	1.04	0.2971	1.0000	0.00	0.00	2.05
B8101	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	30.30

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

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Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=C

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
C0102	9	4.69	36	9.16	0.0604	0.6555	0.51	0.17	1.03
C0103	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.98
C0202	10	5.21	35	8.91	0.1242	0.6555	0.58	0.20	1.14
C0210	1	0.52	6	1.53	0.3988	0.9686	0.34	0.01	2.27
C0302	4	2.08	12	3.05	0.5759	1.0000	0.68	0.16	2.02
C0303	14	7.29	33	8.40	0.7352	1.0000	0.87	0.44	1.57
C0304	35	18.23	53	13.49	0.1297	0.6555	1.35	0.88	2.00
C0305	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.56
C0401	49	25.52	106	26.97	0.7561	1.0000	0.95	0.66	1.26
C0501	20	10.42	49	12.47	0.4846	1.0000	0.84	0.47	1.35
C0602	35	18.23	56	14.25	0.2122	0.8015	1.28	0.82	1.88
C0701	51	26.56	83	21.12	0.1350	0.6555	1.26	0.90	1.70
C0702	50	26.04	80	20.36	0.1284	0.6555	1.28	0.91	1.74
C0704	3	1.56	14	3.56	0.1923	0.8015	0.44	0.09	1.41
C0706	0	0.00	3	0.76	0.3245	0.8487	0.00	0.00	3.07
C0718	1	0.52	1	0.25	0.5217	1.0000	2.05	0.10	68.48
C0727	1	0.52	3	0.76	1.0000	1.0000	0.68	0.03	6.74
C0801	2	1.04	10	2.54	0.3165	0.8487	0.41	0.05	1.65
C0802	16	8.33	31	7.89	0.8665	1.0000	1.06	0.55	1.88
C1202	6	3.13	17	4.33	0.6326	1.0000	0.72	0.18	1.75
C1203	19	9.90	48	12.21	0.4722	1.0000	0.81	0.46	1.33
C1402	8	4.17	14	3.56	0.8060	1.0000	1.17	0.46	2.73
C1403	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.56
C1502	8	4.17	15	3.82	0.8146	1.0000	1.09	0.42	2.51
C1505	4	2.08	2	0.51	0.0871	0.6555	4.09	0.73	30.92
C1506	1	0.52	0	0.00	0.2845	0.8487	.	.	.
C1509	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.98
C1601	10	5.21	22	5.60	0.8892	1.0000	0.93	0.39	1.91
C1602	1	0.52	2	0.51	0.9978	1.0000	1.02	0.05	11.40

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=C

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
C1604	1	0.52	0	0.00	0.2845	0.8487	.	.	.
C1701	5	2.60	11	2.80	0.8496	1.0000	0.93	0.19	2.58
C1703	2	1.04	0	0.00	0.0840	0.6555	.	.	.
C1801	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.98
C1802	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.56

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DPA1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DPA10103	185	95.85	351	89.31	0.0073	0.0799	1.07	1.02	1.12
DPA10104	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPA10105	2	1.04	2	0.51	0.5819	1.0000	2.04	0.17	30.42
DPA10109	1	0.52	0	0.00	0.2856	0.6941	.	.	.
DPA10111	0	0.00	3	0.76	0.3155	0.6941	0.00	0.00	3.05
DPA10201	51	26.42	124	31.55	0.2015	0.6941	0.84	0.61	1.10
DPA10202	18	9.33	50	12.72	0.2563	0.6941	0.73	0.40	1.21
DPA10301	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPA10302	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPA10303	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPA10401	2	1.04	4	1.02	1.0000	1.0000	1.02	0.14	5.70

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DPB1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DPB10101	21	10.88	44	11.20	1.0000	1.0000	0.97	0.56	1.58
DPB10201	44	22.80	87	22.14	0.9121	1.0000	1.03	0.71	1.41
DPB10202	1	0.52	8	2.04	0.2398	1.0000	0.25	0.01	1.57
DPB10301	24	12.44	48	12.21	1.0000	1.0000	1.02	0.61	1.60
DPB10401	128	66.32	221	56.23	0.0192	0.5007	1.18	1.01	1.34
DPB10402	36	18.65	76	19.34	0.9073	1.0000	0.96	0.62	1.37
DPB10501	13	6.74	37	9.41	0.3263	1.0000	0.72	0.34	1.30
DPB10601	10	5.18	8	2.04	0.0402	0.5007	2.55	0.97	6.75
DPB10901	1	0.52	12	3.05	0.0527	0.5007	0.17	0.01	1.03
DPB11001	3	1.55	10	2.54	0.5327	1.0000	0.61	0.13	2.07
DPB110401	12	6.22	13	3.31	0.1166	0.8527	1.88	0.79	4.26
DPB110501	5	2.59	17	4.33	0.3391	1.0000	0.60	0.16	1.55
DPB110701	10	5.18	23	5.85	0.8419	1.0000	0.89	0.37	1.81
DPB11101	6	3.11	13	3.31	1.0000	1.0000	0.94	0.26	2.40
DPB112401	1	0.52	1	0.25	0.5231	1.0000	2.04	0.10	68.10
DPB112601	4	2.07	6	1.53	0.7303	1.0000	1.36	0.29	5.20
DPB113101	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB113501	1	0.52	6	1.53	0.3931	1.0000	0.34	0.01	2.26
DPB113801	1	0.52	1	0.25	0.5231	1.0000	2.04	0.10	68.10
DPB11401	3	1.55	19	4.83	0.0519	0.5007	0.32	0.05	1.02
DPB11501	0	0.00	6	1.53	0.1346	0.8527	0.00	0.00	1.31
DPB11601	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB11701	10	5.18	14	3.56	0.3607	1.0000	1.45	0.62	3.26
DPB11801	0	0.00	3	0.76	0.3155	1.0000	0.00	0.00	3.05
DPB11901	4	2.07	4	1.02	0.3960	1.0000	2.04	0.46	9.05
DPB12001	2	1.04	2	0.51	0.5819	1.0000	2.04	0.17	30.42
DPB12101	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB12201	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB12301	2	1.04	4	1.02	1.0000	1.0000	1.02	0.14	5.70

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DPB1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DPB12601	1	0.52	0	0.00	0.2856	1.0000	.	.	.
DPB12701	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB13301	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB13601	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB13901	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DPB14601	1	0.52	1	0.25	0.5231	1.0000	2.04	0.10	68.10
DPB15001	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB18101	0	0.00	1	0.25	1.0000	1.0000	0.00	0.00	29.84
DPB18501	0	0.00	3	0.76	0.3155	1.0000	0.00	0.00	3.05

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DQA1

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value***[1]	***FDR Adjusted p-value***[2]	***Relative Risk***	***Lower CL***[3]	***Upper CL***[3]
DQA10101	35	18.32	71	18.02	0.9060	1.0000	1.02	0.65	1.46
DQA10102	75	39.27	132	33.50	0.1855	0.7321	1.17	0.91	1.46
DQA10103	21	10.99	54	13.71	0.4119	0.7321	0.80	0.46	1.28
DQA10104	11	5.76	22	5.58	1.0000	1.0000	1.03	0.46	2.06
DQA10105	2	1.05	5	1.27	1.0000	1.0000	0.83	0.09	4.15
DQA10106	1	0.52	0	0.00	0.2829	0.7321	.	.	.
DQA10107	1	0.52	1	0.25	0.5199	0.7321	2.06	0.10	69.03
DQA10110	0	0.00	3	0.76	0.3432	0.7321	0.00	0.00	3.09
DQA10201	25	13.09	44	11.17	0.4814	0.7321	1.17	0.68	1.85
DQA10301	44	23.04	74	18.78	0.2169	0.7321	1.23	0.84	1.71
DQA10302	5	2.62	16	4.06	0.4578	0.7321	0.64	0.17	1.67
DQA10303	18	9.42	50	12.69	0.2586	0.7321	0.74	0.40	1.23
DQA10401	7	3.66	31	7.87	0.0629	0.7321	0.47	0.16	1.03
DQA10402	1	0.52	1	0.25	0.5199	0.7321	2.06	0.10	69.03
DQA10501	35	18.32	74	18.78	1.0000	1.0000	0.98	0.63	1.40
DQA10503	2	1.05	3	0.76	0.6534	0.8455	1.38	0.16	8.54
DQA10505	52	27.23	98	24.87	0.5324	0.7321	1.09	0.78	1.46
DQA10507	0	0.00	1	0.25	0.4489	0.7321	0.00	0.00	30.21
DQA10508	0	0.00	1	0.25	0.4489	0.7321	0.00	0.00	30.21
DQA10509	1	0.52	1	0.25	0.5199	0.7321	2.06	0.10	69.03
DQA10510	1	0.52	1	0.25	0.5199	0.7321	2.06	0.10	69.03
DQA10601	7	3.66	12	3.05	0.7906	0.9662	1.20	0.44	3.09

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DQB1

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DQB10201	35	19.02	73	19.57	0.9064	1.0000	0.97	0.62	1.39
DQB10202	37	20.11	74	19.84	1.0000	1.0000	1.01	0.66	1.44
DQB10301	38	20.65	86	23.06	0.5744	1.0000	0.90	0.61	1.25
DQB10302	22	11.96	43	11.53	0.8841	1.0000	1.04	0.61	1.68
DQB10303	9	4.89	18	4.83	1.0000	1.0000	1.01	0.42	2.21
DQB10304	0	0.00	2	0.54	0.7195	1.0000	0.00	0.00	5.50
DQB10319	2	1.09	4	1.07	1.0000	1.0000	1.01	0.14	5.68
DQB10402	6	3.26	19	5.09	0.3675	1.0000	0.64	0.16	1.53
DQB10501	38	20.65	81	21.72	0.8194	1.0000	0.95	0.62	1.34
DQB10502	7	3.80	22	5.90	0.3954	1.0000	0.65	0.18	1.45
DQB10503	11	5.98	21	5.63	0.8412	1.0000	1.06	0.48	2.16
DQB10601	8	4.35	15	4.02	0.8152	1.0000	1.08	0.42	2.48
DQB10602	52	28.26	85	22.79	0.1635	1.0000	1.24	0.89	1.67
DQB10603	16	8.70	40	10.72	0.5324	1.0000	0.81	0.43	1.40
DQB10604	11	5.98	25	6.70	0.8481	1.0000	0.89	0.40	1.75
DQB10609	8	4.35	12	3.22	0.4588	1.0000	1.35	0.52	3.31
DQB10688	0	0.00	1	0.27	1.0000	1.0000	0.00	0.00	29.70

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DRB1

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value*** [1]	***FDR Adjusted p-value*** [2]	***Relative Risk***	***Lower CL*** [3]	***Upper CL*** [3]
DRB10101	25	13.09	56	14.40	0.6941	1.0000	0.91	0.56	1.40
DRB10102	8	4.19	13	3.34	0.6254	1.0000	1.25	0.49	3.06
DRB10103	4	2.09	5	1.29	0.4598	1.0000	1.63	0.37	6.72
DRB10301	33	17.28	74	19.02	0.6378	1.0000	0.91	0.60	1.31
DRB10302	0	0.00	4	1.03	0.2930	1.0000	0.00	0.00	2.03
DRB10317	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB10342	0	0.00	3	0.77	0.3157	1.0000	0.00	0.00	3.06
DRB10401	22	11.52	37	9.51	0.4508	1.0000	1.21	0.67	1.99
DRB10402	6	3.14	14	3.60	1.0000	1.0000	0.87	0.23	2.21
DRB10403	2	1.05	11	2.83	0.2070	1.0000	0.37	0.05	1.48
DRB10404	12	6.28	21	5.40	0.6930	1.0000	1.16	0.55	2.31
DRB10405	3	1.57	9	2.31	0.7405	1.0000	0.68	0.14	2.35
DRB10406	1	0.52	1	0.26	0.5230	1.0000	2.04	0.10	68.15
DRB10407	1	0.52	6	1.54	0.3935	1.0000	0.34	0.01	2.26
DRB10408	2	1.05	6	1.54	1.0000	1.0000	0.68	0.09	3.17
DRB10410	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB10414	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB10415	1	0.52	0	0.00	0.2854	1.0000	.	.	.
DRB10442	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB10701	55	28.80	97	24.94	0.3508	1.0000	1.15	0.84	1.53
DRB10801	9	4.71	19	4.88	1.0000	1.0000	0.96	0.38	2.08
DRB10802	1	0.52	7	1.80	0.2693	1.0000	0.29	0.01	1.82
DRB10803	3	1.57	3	0.77	0.3630	1.0000	2.04	0.34	12.26
DRB10806	1	0.52	1	0.26	0.5230	1.0000	2.04	0.10	68.15
DRB10810	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB10813	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB10901	6	3.14	17	4.37	0.6322	1.0000	0.72	0.18	1.74
DRB10902	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB11001	3	1.57	6	1.54	1.0000	1.0000	1.02	0.17	4.26

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DRB1

	Cases n=195		**Controls n=395**		**Comparison of Proportions Cases vs. Controls**		**Relative Risk Cases vs. Controls**		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value***[1]	***FDR Adjusted p-value***[2]	***Relative Risk***	***Lower CL***[3]	***Upper CL***[3]
DRB11101	21	10.99	43	11.05	1.0000	1.0000	0.99	0.58	1.62
DRB11102	1	0.52	2	0.51	0.6805	1.0000	1.02	0.05	11.34
DRB11103	3	1.57	3	0.77	0.3630	1.0000	2.04	0.34	12.26
DRB11104	14	7.33	26	6.68	0.8546	1.0000	1.10	0.55	2.05
DRB11201	9	4.71	17	4.37	0.8251	1.0000	1.08	0.46	2.35
DRB11202	3	1.57	5	1.29	0.7007	1.0000	1.22	0.17	5.54
DRB11206	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB11301	12	6.28	40	10.28	0.1139	1.0000	0.61	0.25	1.12
DRB11302	20	10.47	33	8.48	0.4290	1.0000	1.23	0.66	2.09
DRB11303	4	2.09	6	1.54	0.7302	1.0000	1.36	0.29	5.20
DRB11304	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB11305	1	0.52	3	0.77	1.0000	1.0000	0.68	0.03	6.70
DRB11401	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB11403	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB11404	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB11405	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB11406	2	1.05	2	0.51	0.5818	1.0000	2.04	0.17	30.43
DRB114141	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB11425	0	0.00	2	0.51	1.0000	1.0000	0.00	0.00	5.53
DRB11430	1	0.52	0	0.00	0.2854	1.0000	.	.	.
DRB11454	15	7.85	21	5.40	0.2577	1.0000	1.45	0.70	2.79
DRB11457	1	0.52	1	0.26	0.5230	1.0000	2.04	0.10	68.15
DRB11501	46	24.08	67	17.22	0.0552	1.0000	1.40	0.97	1.95
DRB11502	5	2.62	13	3.34	0.7884	1.0000	0.78	0.18	2.11
DRB11503	1	0.52	6	1.54	0.3935	1.0000	0.34	0.01	2.26
DRB11596	0	0.00	1	0.26	1.0000	1.0000	0.00	0.00	29.82
DRB11601	4	2.09	8	2.06	1.0000	1.0000	1.02	0.18	3.34
DRB11602	1	0.52	6	1.54	0.3935	1.0000	0.34	0.01	2.26
DRB11609	2	1.05	4	1.03	1.0000	1.0000	1.02	0.14	5.70

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

GENE=DRBo

	Cases n=195		Controls n=395		Comparison of Proportions Cases vs. Controls		Relative Risk Cases vs. Controls		
Allele	***n***	**%**	***n***	**%**	***Boschloo's Method p-value***^{1}	***FDR Adjusted p-value***^{2}	***Relative Risk***	***Lower CL***^{3}	***Upper CL***^{3}
DRB30101	49	27.84	109	32.06	0.3504	1.0000	0.87	0.61	1.15
DRB30114	1	0.57	2	0.59	0.6366	1.0000	0.97	0.04	10.75
DRB30201	2	1.14	2	0.59	0.5844	1.0000	1.93	0.15	28.87
DRB30202	67	38.07	141	41.47	0.4939	1.0000	0.92	0.70	1.15
DRB30224	3	1.70	0	0.00	0.0283	0.3964	.	.	.
DRB30301	23	13.07	44	12.94	1.0000	1.0000	1.01	0.59	1.61
DRB40101	12	6.82	17	5.00	0.4057	1.0000	1.36	0.59	2.90
DRB40103	32	18.18	62	18.24	1.0000	1.0000	1.00	0.62	1.46
DRB50101	46	26.14	81	23.82	0.5768	1.0000	1.10	0.76	1.49
DRB50102	9	5.11	15	4.41	0.8153	1.0000	1.16	0.47	2.61
DRB50108	0	0.00	1	0.29	1.0000	1.0000	0.00	0.00	28.35
DRB50111	0	0.00	1	0.29	1.0000	1.0000	0.00	0.00	28.35
DRB50202	5	2.84	11	3.24	1.0000	1.0000	0.88	0.18	2.43
DRB50206	0	0.00	2	0.59	0.5218	1.0000	0.00	0.00	5.24

CL = confidence limit

[1] Boschloo, R. D. (1970). Raised conditional level of significance for the 2 x 2 table when testing the equality of probabilities. Statistica Neerlandica, 24, 1-35.

[2] Benjamini, Y., Krieger, A. M., & Yekutieli, D. (2006). Adaptive linear step-up procedures that control the false discovery rate. Biometrika, 93, 491-507.

[3] Chan, I. S. F. and Zhang, Z. (1999), Test-based exact confidence intervals for the difference of two binomial proportions, Biometrics, 55, 1202–1209.

Note 1. Percentages reported are the result of available data for the specific allele. Not all alleles have complete data due to possibly poor quality sequencing reads for specific genes.

Note 2. Relative risk is not calculated if control condition allele frequency (denominator) is equal to 0.

stim=IFNa

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
B Cells	IkB	5.73	7.87	4.59	6.86	1.00	63.20	4.82	6.44	4.16	5.47	1.00	42.30
B Cells	pERK	39.78	109.6	23.97	55.59	1.00	1073.00	36.85	115.8	25.03	48.67	1.00	1298.00
B Cells	pP38	2.34	2.78	1.94	2.74	1.00	16.30	1.97	2.28	1.74	2.21	1.00	17.20
B Cells	pPLCg2	10.61	19.46	7.81	13.42	1.00	218.00	8.15	11.80	6.94	9.35	1.00	93.20
B Cells	pS6	3.29	4.73	2.61	3.97	1.00	43.50	2.60	3.28	2.26	2.93	1.00	25.70
B Cells	pSTAT1	9.98	13.67	8.01	11.96	1.00	83.10	8.57	12.07	7.34	9.80	1.00	75.60
B Cells	pSTAT3	7.97	10.35	6.47	9.46	1.00	84.10	6.39	8.16	5.55	7.22	1.00	67.80
B Cells	pSTAT5	3.29	5.03	2.56	4.01	1.00	35.30	2.87	4.80	2.38	3.36	1.00	50.80
CD16+ NK Cells	IkB	6.22	7.71	5.08	7.35	1.00	43.70	5.79	8.36	4.91	6.67	1.00	59.40
CD16+ NK Cells	pERK	55.17	116.4	38.00	72.34	1.00	1115.00	54.12	132.9	40.12	68.11	1.00	1196.00
CD16+ NK Cells	pP38	2.20	3.02	1.75	2.64	1.00	18.50	2.01	2.70	1.73	2.30	1.00	19.70
CD16+ NK Cells	pPLCg2	11.58	18.95	8.79	14.38	1.00	186.00	11.00	18.35	9.06	12.93	1.00	192.00
CD16+ NK Cells	pS6	3.40	4.57	2.72	4.07	1.00	44.80	2.79	4.04	2.36	3.21	1.00	57.60
CD16+ NK Cells	pSTAT1	7.65	13.16	5.71	9.59	1.00	89.40	6.74	11.76	5.50	7.98	1.00	79.80
CD16+ NK Cells	pSTAT3	5.23	7.20	4.17	6.30	1.00	55.50	4.43	6.47	3.75	5.12	1.00	44.90
CD16+ NK Cells	pSTAT5	2.60	4.21	1.98	3.23	1.00	31.30	2.31	4.17	1.87	2.75	1.00	47.10
CD16+ Monocytes	IkB	10.98	13.12	9.09	12.87	1.00	95.30	9.29	11.16	8.15	10.43	1.00	57.20
CD16+ Monocytes	pERK	79.71	149.1	58.20	101.2	1.34	1388.00	74.50	163.6	57.78	91.23	1.00	1809.00
CD16+ Monocytes	pP38	5.45	6.93	4.45	6.45	1.00	41.30	4.46	5.24	3.93	5.00	1.00	36.50
CD16+ Monocytes	pPLCg2	16.81	33.24	12.02	21.61	1.00	394.00	13.83	19.62	11.82	15.84	1.00	172.00
CD16+ Monocytes	pS6	5.07	6.05	4.20	5.95	1.00	54.00	4.16	5.12	3.64	4.69	1.00	50.80
CD16+ Monocytes	pSTAT1	20.42	31.91	15.82	25.03	1.00	242.00	17.73	29.10	14.75	20.70	1.00	347.00
CD16+ Monocytes	pSTAT3	11.97	15.79	9.70	14.25	1.00	118.00	9.23	11.02	8.11	10.36	1.00	65.60
CD16+ Monocytes	pSTAT5	5.11	8.17	3.93	6.29	1.00	70.30	4.29	7.52	3.52	5.06	1.00	88.20
CD16- NK Cells	IkB	4.87	6.70	3.91	5.84	1.00	50.60	4.06	6.02	3.45	4.68	1.00	53.80
CD16- NK Cells	pERK	39.44	103.2	24.56	54.33	1.00	1064.00	34.92	95.55	25.16	44.67	1.00	1073.00
CD16- NK Cells	pP38	1.90	2.15	1.59	2.21	1.00	14.70	1.66	1.84	1.47	1.85	1.00	16.00
CD16- NK Cells	pPLCg2	7.05	14.79	4.92	9.19	1.00	176.00	5.51	8.75	4.62	6.40	1.00	68.50
CD16- NK Cells	pS6	2.77	3.22	2.31	3.24	1.00	27.80	2.34	3.00	2.03	2.64	1.00	40.80
CD16- NK Cells	pSTAT1	7.25	12.11	5.50	9.00	1.00	81.30	6.22	10.23	5.18	7.27	1.00	75.20
CD16- NK Cells	pSTAT3	4.28	7.16	3.25	5.32	1.00	69.00	3.38	5.73	2.80	3.97	1.00	63.30
CD16- NK Cells	pSTAT5	2.38	3.23	1.92	2.85	1.00	26.90	2.11	3.54	1.75	2.47	1.00	40.70
CD16- Monocytes	IkB	10.35	13.26	8.44	12.26	1.00	82.20	8.89	12.05	7.66	10.12	1.00	75.90

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	61.10	147.4	39.84	82.35	1.00	1452.00	53.56	135.8	39.69	67.43	1.00	1485.00
CD16- Monocytes	pP38	5.56	6.51	4.62	6.50	1.00	50.60	4.54	5.03	4.02	5.05	1.00	38.20
CD16- Monocytes	pPLCg2	10.71	22.58	7.45	13.97	1.00	269.00	8.24	12.64	6.95	9.53	1.00	94.80
CD16- Monocytes	pS6	4.08	5.77	3.24	4.91	1.00	55.40	3.30	4.73	2.81	3.78	1.00	59.10
CD16- Monocytes	pSTAT1	27.03	39.09	21.39	32.67	1.00	302.00	24.05	35.83	20.39	27.71	1.00	256.00
CD16- Monocytes	pSTAT3	11.53	16.96	9.08	13.98	1.00	152.00	8.61	12.00	7.39	9.84	1.00	112.00
CD16- Monocytes	pSTAT5	5.45	7.54	4.37	6.54	1.00	50.50	4.66	7.40	3.90	5.41	1.00	72.60
CD4+ T Cells	IkB	9.42	13.37	7.49	11.35	1.00	70.80	8.36	12.48	7.09	9.63	1.00	86.20
CD4+ T Cells	pERK	42.82	114.7	26.27	59.37	1.00	1180.00	37.56	111.0	26.22	48.90	1.00	1305.00
CD4+ T Cells	pP38	2.69	3.40	2.20	3.18	1.00	22.10	2.27	2.83	1.98	2.56	1.00	21.70
CD4+ T Cells	pPLCg2	6.83	16.65	4.43	9.24	1.00	196.00	5.12	9.43	4.16	6.09	1.00	76.70
CD4+ T Cells	pS6	2.98	4.70	2.30	3.66	1.00	47.60	2.50	3.89	2.10	2.89	1.00	52.20
CD4+ T Cells	pSTAT1	27.62	40.32	21.80	33.44	1.00	332.00	24.40	38.23	20.50	28.30	1.00	307.00
CD4+ T Cells	pSTAT3	10.81	16.43	8.44	13.18	1.00	152.00	7.75	12.12	6.51	8.99	1.00	128.00
CD4+ T Cells	pSTAT5	5.13	7.21	4.09	6.17	1.00	54.40	4.45	6.78	3.76	5.14	1.00	60.10
CD4-CD8- T Cells	IkB	5.29	8.06	4.13	6.45	1.00	59.40	4.41	6.89	3.70	5.11	1.00	49.40
CD4-CD8- T Cells	pERK	38.31	104.5	23.22	53.39	1.00	1131.00	32.41	97.38	22.47	42.36	1.00	1063.00
CD4-CD8- T Cells	pP38	2.25	2.82	1.84	2.65	1.00	18.20	1.86	2.29	1.62	2.09	1.00	18.90
CD4-CD8- T Cells	pPLCg2	6.66	15.58	4.41	8.90	1.00	183.00	4.94	9.49	3.97	5.90	1.00	91.90
CD4-CD8- T Cells	pS6	2.63	3.97	2.06	3.20	1.00	39.90	2.20	3.40	1.86	2.55	1.00	44.60
CD4-CD8- T Cells	pSTAT1	12.05	19.08	9.30	14.80	1.00	129.00	10.76	18.27	8.89	12.62	1.00	168.00
CD4-CD8- T Cells	pSTAT3	6.61	10.84	5.04	8.17	1.00	93.70	4.72	8.65	3.84	5.60	1.00	91.00
CD4-CD8- T Cells	pSTAT5	2.85	3.83	2.30	3.40	1.00	25.00	2.47	4.24	2.04	2.90	1.00	54.70
CD8+ T Cells	IkB	8.15	11.49	6.49	9.81	1.00	63.50	7.01	10.58	5.92	8.09	1.00	75.00
CD8+ T Cells	pERK	47.77	127.1	29.43	66.12	1.00	1305.00	39.46	109.6	28.27	50.64	1.00	1220.00
CD8+ T Cells	pP38	2.49	3.08	2.04	2.93	1.00	20.40	2.08	2.50	1.83	2.34	1.00	18.10
CD8+ T Cells	pPLCg2	7.18	17.11	4.71	9.64	1.00	203.00	5.37	9.84	4.36	6.37	1.00	84.80
CD8+ T Cells	pS6	3.09	4.61	2.43	3.76	1.00	44.50	2.55	3.91	2.15	2.95	1.00	51.20
CD8+ T Cells	pSTAT1	21.51	32.77	16.79	26.24	1.00	280.00	18.34	28.91	15.39	21.29	1.00	222.00
CD8+ T Cells	pSTAT3	8.38	13.85	6.38	10.38	1.00	122.00	5.95	10.22	4.91	7.00	1.00	111.00
CD8+ T Cells	pSTAT5	3.89	5.59	3.08	4.70	1.00	38.20	3.27	5.36	2.72	3.82	1.00	55.60
Dendritic Cells	IkB	4.34	6.89	3.35	5.33	1.00	64.40	3.45	5.48	2.89	4.01	1.00	51.30
Dendritic Cells	pERK	39.20	123.1	21.45	56.96	1.00	1416.00	29.09	72.73	21.67	36.52	1.00	894.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	4.73	6.16	3.84	5.62	1.00	40.10	3.86	5.69	3.28	4.44	1.00	46.10
Dendritic Cells	pPLCg2	6.76	16.77	4.34	9.18	1.00	204.00	5.17	9.68	4.18	6.16	1.00	81.50
Dendritic Cells	pS6	2.28	3.34	1.80	2.76	1.00	34.50	2.05	3.23	1.72	2.38	1.00	46.30
Dendritic Cells	pSTAT1	8.21	18.18	5.59	10.83	1.00	173.00	6.76	12.86	5.45	8.07	1.00	116.00
Dendritic Cells	pSTAT3	4.32	6.78	3.34	5.30	1.00	64.60	3.38	6.36	2.73	4.03	1.00	76.40
Dendritic Cells	pSTAT5	2.41	3.25	1.94	2.88	1.00	20.00	2.16	3.55	1.80	2.52	1.00	48.20
HLADR+ NK Cells	IkB	6.21	8.63	4.97	7.46	1.00	76.90	5.07	6.71	4.39	5.76	1.00	41.60
HLADR+ NK Cells	pERK	48.35	113.9	31.87	64.82	1.00	1163.00	42.73	101.5	32.35	53.12	1.00	1122.00
HLADR+ NK Cells	pP38	2.74	4.12	2.14	3.33	1.00	35.10	2.04	2.35	1.80	2.28	1.00	18.50
HLADR+ NK Cells	pPLCg2	10.39	17.62	7.84	12.94	1.00	182.00	8.37	12.39	7.10	9.64	1.00	103.00
HLADR+ NK Cells	pS6	3.46	5.26	2.70	4.22	1.00	62.30	2.75	2.81	2.46	3.04	1.00	21.70
HLADR+ NK Cells	pSTAT1	8.79	14.00	6.77	10.82	1.00	90.40	7.37	11.51	6.19	8.55	1.00	83.10
HLADR+ NK Cells	pSTAT3	5.39	8.45	4.17	6.61	1.00	71.40	4.20	6.49	3.53	4.86	1.00	52.90
HLADR+ NK Cells	pSTAT5	2.70	3.58	2.18	3.22	1.00	24.20	2.40	3.66	2.02	2.77	1.00	44.20
HLADR+CD38+ CD4+ T Cells	IkB	10.60	13.27	8.68	12.51	1.00	74.80	9.44	13.10	8.11	10.78	1.00	111.00
HLADR+CD38+ CD4+ T Cells	pERK	54.16	125.3	36.09	72.24	1.00	1298.00	48.65	118.8	36.52	60.78	1.00	1313.00
HLADR+CD38+ CD4+ T Cells	pP38	3.87	4.76	3.19	4.56	1.00	29.80	3.20	4.10	2.78	3.62	1.00	29.10
HLADR+CD38+ CD4+ T Cells	pPLCg2	11.73	31.94	7.12	16.34	1.00	405.00	9.53	20.00	7.48	11.57	1.00	213.00
HLADR+CD38+ CD4+ T Cells	pS6	4.23	6.04	3.36	5.10	1.00	57.10	3.56	5.63	2.98	4.13	1.00	77.40
HLADR+CD38+ CD4+ T Cells	pSTAT1	27.81	37.16	22.45	33.17	1.00	274.00	24.65	37.10	20.86	28.44	1.00	263.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	12.78	16.09	10.46	15.11	1.00	112.00	9.69	13.11	8.35	11.03	1.00	113.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	6.02	8.38	4.81	7.23	1.00	55.20	5.23	8.32	4.38	6.08	1.00	83.60
HLADR+CD38+ CD8+ T Cells	IkB	9.08	11.43	7.44	10.73	1.00	80.90	7.70	10.58	6.62	8.78	1.00	106.00
HLADR+CD38+ CD8+ T Cells	pERK	54.08	130.6	35.23	72.93	1.00	1346.00	46.38	110.2	35.11	57.64	1.00	1203.00
HLADR+CD38+ CD8+ T Cells	pP38	3.55	4.40	2.92	4.19	1.00	27.50	2.91	3.61	2.54	3.27	1.00	25.00
HLADR+CD38+ CD8+ T Cells	pPLCg2	12.20	30.45	7.81	16.59	1.00	378.00	9.12	15.82	7.51	10.74	1.00	128.00
HLADR+CD38+ CD8+ T Cells	pS6	4.19	6.17	3.30	5.08	1.00	58.60	3.35	4.54	2.89	3.81	1.00	43.70

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	20.70	27.59	16.72	24.68	1.00	166.00	16.95	24.24	14.47	19.43	1.00	186.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	10.34	13.77	8.35	12.33	1.00	97.70	7.87	10.90	6.76	8.99	1.00	91.50
HLADR+CD38+ CD8+ T Cells	pSTAT5	4.66	6.52	3.72	5.60	1.00	41.20	3.92	6.47	3.26	4.58	1.00	65.50
IgD+CD27+ B Cells	IkB	6.26	8.18	5.08	7.45	1.00	64.00	5.30	6.80	4.60	5.99	1.00	39.90
IgD+CD27+ B Cells	pERK	43.21	112.7	26.95	59.47	1.30	1091.00	39.85	118.0	27.80	51.90	1.00	1328.00
IgD+CD27+ B Cells	pP38	2.54	2.99	2.11	2.97	1.00	18.20	2.30	4.11	1.88	2.72	1.00	65.40
IgD+CD27+ B Cells	pPLCg2	11.54	20.20	8.63	14.46	1.00	224.00	8.95	12.59	7.66	10.23	1.00	105.00
IgD+CD27+ B Cells	pS6	3.62	5.09	2.88	4.35	1.00	44.40	2.77	3.34	2.43	3.11	1.00	26.90
IgD+CD27+ B Cells	pSTAT1	11.05	14.90	8.90	13.20	1.00	88.90	9.43	13.07	8.09	10.76	1.00	79.00
IgD+CD27+ B Cells	pSTAT3	8.93	10.94	7.35	10.50	1.00	87.70	7.19	8.61	6.31	8.07	1.00	70.00
IgD+CD27+ B Cells	pSTAT5	3.59	5.40	2.81	4.37	1.00	38.80	3.13	5.08	2.61	3.65	1.00	51.30
IgD+CD27- B Cells	IkB	5.09	6.94	4.09	6.10	1.00	59.60	4.20	5.75	3.62	4.79	1.00	53.80
IgD+CD27- B Cells	pERK	35.04	91.90	21.79	48.30	1.00	867.00	28.63	86.01	19.83	37.42	1.00	1204.00
IgD+CD27- B Cells	pP38	2.13	2.52	1.77	2.49	1.00	16.50	1.77	1.96	1.57	1.98	1.00	15.60
IgD+CD27- B Cells	pPLCg2	9.57	16.97	7.12	12.02	1.00	188.00	7.11	10.15	6.07	8.15	1.00	89.40
IgD+CD27- B Cells	pS6	2.93	4.06	2.35	3.52	1.00	37.30	2.35	2.92	2.05	2.64	1.00	24.20
IgD+CD27- B Cells	pSTAT1	8.80	12.04	7.06	10.54	1.00	69.80	7.47	10.88	6.35	8.58	1.00	73.80
IgD+CD27- B Cells	pSTAT3	7.39	9.03	6.08	8.69	1.00	73.40	5.92	7.18	5.19	6.65	1.00	60.40
IgD+CD27- B Cells	pSTAT5	2.84	4.28	2.22	3.46	1.00	33.60	2.51	4.64	2.03	2.98	1.00	64.60
IgD-CD27+ B Cells	IkB	4.98	6.65	4.02	5.94	1.00	40.50	4.40	7.63	3.62	5.18	1.00	96.60
IgD-CD27+ B Cells	pERK	35.24	107.0	19.80	50.67	1.00	1313.00	28.20	73.79	20.66	35.75	1.00	782.00
IgD-CD27+ B Cells	pP38	2.19	2.88	1.77	2.61	1.00	24.20	1.86	2.62	1.59	2.12	1.00	36.10
IgD-CD27+ B Cells	pPLCg2	10.29	18.75	7.58	12.99	1.00	190.00	7.91	11.34	6.75	9.07	1.00	96.10
IgD-CD27+ B Cells	pS6	3.65	5.58	2.85	4.46	1.00	51.00	2.61	3.22	2.28	2.94	1.00	28.80
IgD-CD27+ B Cells	pSTAT1	10.22	15.14	8.04	12.40	1.00	109.00	9.01	13.89	7.59	10.43	1.00	90.70
IgD-CD27+ B Cells	pSTAT3	7.00	11.15	5.39	8.60	1.00	101.00	5.67	8.98	4.75	6.59	1.00	80.60
IgD-CD27+ B Cells	pSTAT5	3.43	6.52	2.48	4.37	1.00	58.50	2.85	6.32	2.20	3.49	1.00	93.20

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	4.15	7.01	3.13	5.16	1.00	69.40	3.20	4.80	2.71	3.69	1.00	36.80
IgD-CD27- B Cells	pERK	24.45	61.97	15.48	33.41	1.00	749.00	21.31	69.42	14.19	28.42	1.00	1070.00
IgD-CD27- B Cells	pP38	1.93	2.51	1.56	2.29	1.00	24.40	1.69	2.29	1.46	1.93	1.00	33.60
IgD-CD27- B Cells	pPLCg2	8.01	13.89	6.00	10.02	1.00	145.00	6.18	9.00	5.25	7.10	1.00	83.90
IgD-CD27- B Cells	pS6	2.75	3.92	2.19	3.32	1.00	32.90	2.39	4.57	1.92	2.86	1.00	62.80
IgD-CD27- B Cells	pSTAT1	7.66	12.29	5.88	9.44	1.00	91.40	6.77	10.89	5.66	7.89	1.00	76.30
IgD-CD27- B Cells	pSTAT3	5.56	7.80	4.43	6.68	1.00	69.00	4.59	7.22	3.85	5.33	1.00	72.00
IgD-CD27- B Cells	pSTAT5	2.33	3.39	1.84	2.82	1.00	29.20	2.29	3.49	1.93	2.65	1.00	28.70
NK Cells	IkB	5.05	6.75	4.08	6.03	1.00	50.60	4.20	5.71	3.62	4.79	1.00	40.50
NK Cells	pERK	41.99	104.7	26.85	57.14	1.00	1064.00	37.41	98.19	27.37	47.44	1.00	1112.00
NK Cells	pP38	1.90	2.20	1.58	2.22	1.00	15.70	1.67	1.85	1.48	1.86	1.00	16.40
NK Cells	pPLCg2	7.85	15.59	5.59	10.10	1.00	179.00	6.27	9.76	5.27	7.27	1.00	79.20
NK Cells	pS6	2.75	2.99	2.32	3.19	1.00	27.80	2.29	2.28	2.06	2.53	1.00	17.90
NK Cells	pSTAT1	6.92	11.68	5.23	8.61	1.00	82.00	5.96	9.59	4.98	6.94	1.00	75.00
NK Cells	pSTAT3	4.41	7.02	3.39	5.42	1.00	62.50	3.46	5.53	2.89	4.02	1.00	51.60
NK Cells	pSTAT5	2.20	2.66	1.82	2.59	1.00	17.60	1.99	2.90	1.70	2.29	1.00	36.90
NKT Cells	IkB	10.95	14.12	8.90	13.01	1.00	67.60	10.61	15.98	8.98	12.25	1.00	130.00
NKT Cells	pERK	63.27	165.6	39.18	87.37	1.00	1680.00	65.56	195.5	45.51	85.60	1.00	2166.00
NKT Cells	pP38	3.83	5.08	3.09	4.56	1.00	32.70	3.49	5.43	2.93	4.05	1.00	45.70
NKT Cells	pPLCg2	8.77	21.07	5.70	11.83	1.00	250.00	7.20	14.15	5.75	8.65	1.00	117.00
NKT Cells	pS6	5.31	12.93	3.43	7.19	1.00	123.00	4.43	10.40	3.36	5.50	1.00	127.00
NKT Cells	pSTAT1	28.22	34.44	23.21	33.23	1.00	243.00	25.17	35.69	21.51	28.83	1.00	232.00
NKT Cells	pSTAT3	11.80	18.00	9.18	14.42	1.00	146.00	9.57	16.11	7.92	11.23	1.00	148.00
NKT Cells	pSTAT5	5.23	7.18	4.19	6.28	1.00	48.30	4.74	7.36	3.99	5.49	1.00	64.60
Regulatory T Cells	IkB	11.62	15.41	9.40	13.84	1.00	71.60	10.46	15.40	8.89	12.04	1.00	115.00
Regulatory T Cells	pERK	51.24	129.6	32.54	69.94	1.00	1354.00	44.06	117.9	32.01	56.11	1.00	1354.00
Regulatory T Cells	pP38	3.11	4.00	2.53	3.69	1.00	30.30	2.68	3.66	2.30	3.05	1.00	33.50
Regulatory T Cells	pPLCg2	7.25	17.45	4.73	9.76	1.00	209.00	5.53	9.34	4.58	6.49	1.00	78.80
Regulatory T Cells	pS6	3.26	4.21	2.65	3.87	1.00	40.50	2.79	3.82	2.40	3.18	1.00	44.50
Regulatory T Cells	pSTAT1	34.21	52.40	26.65	41.77	1.00	416.00	31.63	56.85	25.82	37.45	1.00	446.00
Regulatory T Cells	pSTAT3	12.45	18.20	9.82	15.07	1.00	174.00	9.24	14.38	7.77	10.71	1.00	135.00
Regulatory T Cells	pSTAT5	6.01	8.09	4.84	7.17	1.00	54.80	5.29	8.84	4.39	6.20	1.00	99.90

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	10.29	14.63	8.17	12.40	1.00	75.40	8.99	13.16	7.65	10.33	1.00	83.80
Central Memory CD4+ T Cells	pERK	45.26	114.8	28.70	61.82	1.00	1106.00	38.99	109.3	27.83	50.16	1.00	1196.00
Central Memory CD4+ T Cells	pP38	2.98	3.93	2.42	3.55	1.00	27.50	2.46	3.11	2.15	2.78	1.00	26.10
Central Memory CD4+ T Cells	pPLCg2	6.71	15.73	4.44	8.98	1.00	184.00	4.92	8.44	4.05	5.78	1.00	74.20
Central Memory CD4+ T Cells	pS6	2.97	4.86	2.27	3.67	1.00	50.70	2.46	3.76	2.07	2.84	1.00	51.50
Central Memory CD4+ T Cells	pSTAT1	34.91	52.32	27.36	42.46	1.00	406.00	30.29	47.47	25.44	35.13	1.00	358.00
Central Memory CD4+ T Cells	pSTAT3	11.65	18.75	8.95	14.36	1.00	186.00	8.04	13.07	6.70	9.37	1.00	143.00
Central Memory CD4+ T Cells	pSTAT5	5.99	8.35	4.79	7.20	1.00	65.30	5.00	7.15	4.27	5.73	1.00	49.20
Central Memory CD8+ T Cells	IkB	8.37	11.91	6.66	10.09	1.00	70.00	7.04	10.66	5.95	8.13	1.00	84.50
Central Memory CD8+ T Cells	pERK	46.75	110.7	30.78	62.72	1.00	1073.00	38.75	99.07	28.64	48.86	1.00	1042.00
Central Memory CD8+ T Cells	pP38	2.81	3.68	2.28	3.34	1.00	22.80	2.31	2.83	2.02	2.60	1.00	20.70
Central Memory CD8+ T Cells	pPLCg2	6.62	15.99	4.31	8.92	1.00	191.00	4.82	8.97	3.90	5.73	1.00	90.60
Central Memory CD8+ T Cells	pS6	3.43	4.87	2.72	4.13	1.00	45.00	2.75	3.82	2.36	3.14	1.00	47.10
Central Memory CD8+ T Cells	pSTAT1	23.78	40.20	17.98	29.57	1.00	383.00	19.87	32.80	16.52	23.22	1.00	270.00
Central Memory CD8+ T Cells	pSTAT3	8.69	14.90	6.54	10.84	1.00	142.00	6.07	10.90	4.95	7.18	1.00	125.00
Central Memory CD8+ T Cells	pSTAT5	4.04	6.09	3.16	4.92	1.00	47.50	3.35	5.59	2.77	3.92	1.00	65.10
Effector CD4+ T Cells	IkB	6.75	9.70	5.35	8.15	1.00	58.30	6.03	9.83	5.03	7.04	1.00	91.70
Effector CD4+ T Cells	pERK	35.29	82.66	23.36	47.21	1.00	845.00	28.74	76.33	20.94	36.54	1.00	1076.00
Effector CD4+ T Cells	pP38	2.24	2.73	1.85	2.63	1.00	19.20	1.90	2.24	1.67	2.13	1.00	19.90
Effector CD4+ T Cells	pPLCg2	6.05	14.23	3.99	8.10	1.00	165.00	4.43	8.37	3.57	5.28	1.00	83.80
Effector CD4+ T Cells	pS6	2.63	4.03	2.05	3.22	1.00	41.50	2.18	3.44	1.83	2.54	1.00	44.50
Effector CD4+ T Cells	pSTAT1	19.85	30.07	15.51	24.19	1.00	270.00	17.84	31.12	14.66	21.02	1.00	263.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	8.77	11.83	7.06	10.48	1.00	100.00	6.33	9.09	5.40	7.26	1.00	95.30
Effector CD4+ T Cells	pSTAT5	3.59	5.04	2.86	4.31	1.00	38.90	3.09	5.13	2.57	3.62	1.00	61.40
Effector CD8+ T Cells	IkB	5.90	8.51	4.67	7.13	1.00	56.50	5.04	7.88	4.24	5.85	1.00	68.50
Effector CD8+ T Cells	pERK	40.22	86.14	27.80	52.65	1.00	857.00	30.05	72.28	22.65	37.45	1.00	1025.00
Effector CD8+ T Cells	pP38	2.07	2.49	1.72	2.43	1.00	19.10	1.78	2.02	1.57	1.98	1.00	17.30
Effector CD8+ T Cells	pPLCg2	6.41	14.53	4.32	8.51	1.00	170.00	4.75	8.73	3.86	5.65	1.00	83.50
Effector CD8+ T Cells	pS6	2.61	4.02	2.03	3.20	1.00	41.10	2.23	3.68	1.85	2.61	1.00	49.70
Effector CD8+ T Cells	pSTAT1	15.73	24.89	12.14	19.32	1.00	222.00	13.65	23.46	11.25	16.05	1.00	198.00
Effector CD8+ T Cells	pSTAT3	6.73	10.36	5.23	8.22	1.00	82.50	4.83	8.11	4.00	5.67	1.00	85.10
Effector CD8+ T Cells	pSTAT5	2.90	4.05	2.31	3.48	1.00	29.20	2.45	4.09	2.03	2.87	1.00	46.70
Effector Memory CD4+ T Cells	IkB	6.80	10.88	5.23	8.37	1.00	74.60	5.62	9.01	4.70	6.54	1.00	64.90
Effector Memory CD4+ T Cells	pERK	36.07	90.89	22.96	49.18	1.00	961.00	26.85	66.73	20.03	33.67	1.00	904.00
Effector Memory CD4+ T Cells	pP38	2.40	3.26	1.93	2.87	1.00	23.10	1.92	2.28	1.69	2.16	1.00	22.90
Effector Memory CD4+ T Cells	pPLCg2	5.38	13.53	3.43	7.33	1.00	162.00	3.66	6.40	3.01	4.32	1.00	72.00
Effector Memory CD4+ T Cells	pS6	2.34	4.02	1.76	2.92	1.00	45.60	2.13	4.92	1.63	2.63	1.00	78.00
Effector Memory CD4+ T Cells	pSTAT1	23.77	42.76	17.60	29.94	1.00	408.00	20.51	39.46	16.48	24.55	1.00	345.00
Effector Memory CD4+ T Cells	pSTAT3	8.18	13.19	6.28	10.08	1.00	125.00	5.59	10.21	4.54	6.63	1.00	125.00
Effector Memory CD4+ T Cells	pSTAT5	3.78	5.90	2.93	4.64	1.00	55.90	3.05	4.92	2.55	3.55	1.00	52.50
Effector Memory CD8+ T Cells	IkB	5.84	9.44	4.48	7.20	1.00	68.10	4.74	8.02	3.92	5.56	1.00	71.00
Effector Memory CD8+ T Cells	pERK	34.60	66.18	25.05	44.15	1.00	674.00	26.47	57.19	20.61	32.32	1.00	799.00
Effector Memory CD8+ T Cells	pP38	2.25	2.89	1.83	2.66	1.00	20.80	1.94	2.50	1.69	2.20	1.00	22.60
Effector Memory CD8+ T Cells	pPLCg2	5.20	11.44	3.55	6.85	1.00	129.00	3.86	7.85	3.05	4.66	1.00	83.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	2.54	4.17	1.94	3.14	1.00	46.20	2.10	3.00	1.80	2.41	1.00	33.20
Effector Memory CD8+ T Cells	pSTAT1	15.85	31.07	11.37	20.34	1.00	313.00	13.81	26.52	11.09	16.52	1.00	221.00
Effector Memory CD8+ T Cells	pSTAT3	6.29	11.40	4.65	7.94	1.00	104.00	4.39	9.00	3.47	5.31	1.00	110.00
Effector Memory CD8+ T Cells	pSTAT5	2.88	4.10	2.28	3.47	1.00	35.00	2.34	4.10	1.92	2.76	1.00	54.70
Myeloid Dendritic Cells	IkB	4.54	7.06	3.52	5.56	1.00	70.60	3.64	5.75	3.06	4.23	1.00	57.30
Myeloid Dendritic Cells	pERK	42.21	127.3	23.85	60.57	1.00	1377.00	31.66	74.61	24.05	39.28	1.00	943.00
Myeloid Dendritic Cells	pP38	6.55	7.61	5.45	7.65	1.00	42.70	5.48	7.38	4.73	6.23	1.00	59.90
Myeloid Dendritic Cells	pPLCg2	7.31	17.63	4.77	9.85	1.00	215.00	5.62	10.61	4.54	6.70	1.00	91.00
Myeloid Dendritic Cells	pS6	2.48	3.67	1.95	3.01	1.00	35.60	2.14	3.51	1.78	2.50	1.00	52.90
Myeloid Dendritic Cells	pSTAT1	8.70	17.85	6.13	11.28	1.00	142.00	7.40	14.70	5.90	8.90	1.00	146.00
Myeloid Dendritic Cells	pSTAT3	4.54	7.66	3.44	5.65	1.00	78.40	3.54	6.73	2.85	4.22	1.00	81.50
Myeloid Dendritic Cells	pSTAT5	2.52	3.40	2.03	3.01	1.00	23.00	2.27	4.02	1.86	2.68	1.00	58.00
Monocytes	IkB	15.92	12.57	9.67	22.18	1.06	43.30	13.27	11.32	9.44	17.10	1.26	45.20
Monocytes	pERK	153.0	420.1	-55.9	361.9	3.29	1448.00	140.0	387.5	8.83	271.1	2.09	1485.00
Monocytes	pP38	2.67	4.65	0.36	4.99	1.00	16.60	2.87	5.64	0.96	4.77	1.00	27.30
Monocytes	pPLCg2	5.43	5.38	2.75	8.10	1.00	20.00	5.70	5.64	3.79	7.60	1.00	23.80
Monocytes	pS6	3.81	2.38	2.62	4.99	1.09	9.60	3.77	2.44	2.94	4.59	1.00	10.10
Monocytes	pSTAT1	22.37	22.77	11.05	33.69	1.00	77.40	20.31	16.54	14.72	25.91	1.51	66.00
Monocytes	pSTAT3	4.23	5.55	1.47	6.99	1.00	24.40	3.40	3.71	2.14	4.65	1.00	18.80
Monocytes	pSTAT5	4.99	4.98	2.51	7.46	1.00	17.80	4.47	3.55	3.27	5.67	1.00	14.00
Naive CD4+ T Cells	IkB	10.24	14.16	8.20	12.28	1.00	73.60	9.09	13.42	7.72	10.46	1.00	91.90
Naive CD4+ T Cells	pERK	44.68	116.4	27.89	61.48	1.00	1193.00	39.32	113.4	27.75	50.90	1.00	1339.00
Naive CD4+ T Cells	pP38	2.79	3.50	2.29	3.30	1.00	23.60	2.35	2.90	2.05	2.64	1.00	21.00
Naive CD4+ T Cells	pPLCg2	7.53	17.35	5.03	10.04	1.00	202.00	5.72	10.19	4.69	6.76	1.00	89.10
Naive CD4+ T Cells	pS6	3.30	4.88	2.60	4.01	1.00	46.70	2.80	4.54	2.33	3.26	1.00	65.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	28.95	38.73	23.37	34.54	1.00	295.00	25.57	38.22	21.66	29.47	1.00	300.00
Naive CD4+ T Cells	pSTAT3	12.18	16.61	9.78	14.57	1.00	148.00	8.88	12.40	7.61	10.14	1.00	123.00
Naive CD4+ T Cells	pSTAT5	5.47	7.36	4.41	6.53	1.00	52.50	4.80	7.25	4.06	5.54	1.00	67.30
Naive CD8+ T Cells	IkB	9.07	12.72	7.24	10.91	1.00	70.00	7.94	11.90	6.73	9.16	1.00	80.60
Naive CD8+ T Cells	pERK	49.87	132.0	30.82	68.91	1.00	1346.00	41.63	113.0	30.10	53.16	1.00	1241.00
Naive CD8+ T Cells	pP38	2.58	3.17	2.12	3.03	1.00	21.30	2.19	2.61	1.92	2.45	1.00	19.30
Naive CD8+ T Cells	pPLCg2	7.92	17.67	5.38	10.47	1.00	207.00	5.99	10.52	4.91	7.06	1.00	91.10
Naive CD8+ T Cells	pS6	3.36	4.82	2.67	4.06	1.00	44.50	2.75	4.24	2.32	3.19	1.00	56.10
Naive CD8+ T Cells	pSTAT1	24.47	34.67	19.47	29.47	1.00	287.00	21.09	31.66	17.85	24.32	1.00	255.00
Naive CD8+ T Cells	pSTAT3	9.53	14.68	7.41	11.64	1.00	128.00	6.83	10.70	5.73	7.92	1.00	109.00
Naive CD8+ T Cells	pSTAT5	4.35	6.19	3.46	5.24	1.00	41.10	3.65	6.05	3.04	4.27	1.00	61.10
Plasmoid Dendritic Cells	IkB	5.42	8.54	4.18	6.65	1.00	68.50	4.13	6.00	3.52	4.74	1.00	48.20
Plasmoid Dendritic Cells	pERK	44.67	130.6	25.82	63.51	1.00	1514.00	33.77	82.76	25.32	42.22	1.00	917.00
Plasmoid Dendritic Cells	pP38	2.93	3.96	2.36	3.51	1.00	25.00	2.57	3.63	2.20	2.94	1.00	25.50
Plasmoid Dendritic Cells	pPLCg2	7.82	18.03	5.22	10.42	1.00	211.00	5.95	10.24	4.90	6.99	1.00	77.60
Plasmoid Dendritic Cells	pS6	2.89	3.90	2.33	3.46	1.00	26.60	2.55	3.76	2.17	2.94	1.00	33.50
Plasmoid Dendritic Cells	pSTAT1	11.02	27.38	7.07	14.97	1.00	332.00	8.15	13.99	6.72	9.58	1.00	93.70
Plasmoid Dendritic Cells	pSTAT3	5.32	8.22	4.14	6.51	1.00	64.60	4.07	7.21	3.34	4.81	1.00	78.70
Plasmoid Dendritic Cells	pSTAT5	2.91	4.15	2.31	3.51	1.00	27.30	2.55	4.44	2.09	3.00	1.00	56.40
Plasmablasts	IkB	7.86	9.98	6.41	9.30	1.00	70.40	6.77	9.06	5.84	7.70	1.00	57.50
Plasmablasts	pERK	53.17	116.1	36.33	70.01	1.00	1006.00	53.92	153.8	38.11	69.73	1.00	1871.00
Plasmablasts	pP38	3.33	4.41	2.69	3.97	1.00	29.00	2.99	5.69	2.41	3.58	1.00	85.80
Plasmablasts	pPLCg2	10.90	22.01	7.71	14.09	1.00	259.00	8.79	13.59	7.39	10.18	1.00	106.00
Plasmablasts	pS6	4.70	6.22	3.80	5.61	1.00	41.10	3.54	4.14	3.11	3.96	1.00	31.30

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	10.59	14.36	8.50	12.67	1.00	75.20	9.31	13.32	7.94	10.68	1.00	75.40
Plasmablasts	pSTAT3	8.76	11.44	7.10	10.42	1.00	72.00	7.14	9.80	6.13	8.14	1.00	75.20
Plasmablasts	pSTAT5	3.71	5.65	2.89	4.53	1.00	41.90	3.41	5.84	2.81	4.01	1.00	54.10
Transitional B Cells	IkB	7.66	9.04	6.34	8.98	1.00	57.80	6.53	7.92	5.72	7.35	1.00	41.40
Transitional B Cells	pERK	54.50	142.7	33.70	75.31	1.00	1580.00	47.03	128.5	33.81	60.24	1.00	1576.00
Transitional B Cells	pP38	4.11	5.18	3.36	4.87	1.00	41.70	3.39	3.91	2.99	3.79	1.00	25.20
Transitional B Cells	pPLCg2	11.64	24.51	8.06	15.21	1.00	291.00	9.57	14.62	8.07	11.07	1.00	97.90
Transitional B Cells	pS6	5.12	7.59	4.01	6.22	1.00	77.40	4.10	4.80	3.60	4.59	1.00	32.60
Transitional B Cells	pSTAT1	10.86	15.79	8.56	13.16	1.00	93.50	9.16	13.49	7.77	10.54	1.00	103.00
Transitional B Cells	pSTAT3	11.48	11.42	9.82	13.15	1.00	92.70	9.98	11.06	8.84	11.12	1.00	85.60
Transitional B Cells	pSTAT5	3.74	5.72	2.91	4.58	1.00	35.70	3.09	5.07	2.57	3.61	1.00	61.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	**Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	**Minimum***	***Maximum***
B Cells	IkB	5.35	8.25	4.15	6.55	1.00	71.40	4.52	5.97	3.91	5.13	1.00	35.40
B Cells	pERK	39.00	127.0	20.58	57.42	1.00	1335.00	35.97	132.0	22.45	49.48	1.00	1563.00
B Cells	pP38	2.01	2.38	1.67	2.36	1.00	16.50	1.78	2.07	1.57	1.99	1.00	20.30
B Cells	pPLCg2	8.54	11.52	6.86	10.21	1.00	86.50	7.45	11.13	6.31	8.59	1.00	89.90
B Cells	pS6	2.94	5.07	2.21	3.68	1.00	51.30	2.61	4.16	2.19	3.04	1.00	40.10
B Cells	pSTAT1	5.46	8.46	4.23	6.69	1.00	50.90	4.98	8.56	4.11	5.86	1.00	61.30
B Cells	pSTAT3	9.13	12.77	7.28	10.98	1.00	119.00	7.59	8.77	6.69	8.48	1.00	71.60
B Cells	pSTAT5	2.19	3.80	1.64	2.74	1.00	36.30	2.08	3.86	1.68	2.47	1.00	40.60
CD16+ NK Cells	IkB	5.82	7.88	4.63	7.00	1.00	53.60	5.51	8.79	4.58	6.43	1.00	97.70
CD16+ NK Cells	pERK	51.55	131.4	31.78	71.32	1.00	1328.00	48.84	134.1	34.68	63.01	1.00	1511.00
CD16+ NK Cells	pP38	2.16	5.15	1.39	2.94	1.00	61.80	1.60	1.80	1.41	1.79	1.00	15.80
CD16+ NK Cells	pPLCg2	9.08	11.83	7.30	10.86	1.00	80.00	9.54	14.47	8.02	11.07	1.00	110.00
CD16+ NK Cells	pS6	2.91	3.99	2.31	3.51	1.00	33.10	2.95	5.72	2.35	3.55	1.00	75.00
CD16+ NK Cells	pSTAT1	5.72	10.88	4.09	7.36	1.00	69.00	4.50	9.06	3.54	5.46	1.00	58.00
CD16+ NK Cells	pSTAT3	10.61	14.06	8.49	12.72	1.00	105.00	9.36	10.98	8.20	10.52	1.00	57.10
CD16+ NK Cells	pSTAT5	2.21	4.20	1.58	2.84	1.00	38.30	2.13	4.14	1.69	2.57	1.00	43.60
CD16+ Monocytes	IkB	10.40	13.37	8.46	12.34	1.00	109.00	8.84	10.96	7.71	9.96	1.00	65.30
CD16+ Monocytes	pERK	76.09	159.2	52.99	99.19	2.10	1653.00	70.32	170.3	52.89	87.76	1.00	2002.00
CD16+ Monocytes	pP38	5.74	17.74	3.17	8.31	1.00	233.00	3.82	4.62	3.35	4.30	1.00	41.60
CD16+ Monocytes	pPLCg2	14.38	19.40	11.56	17.19	1.00	146.00	12.89	18.03	11.04	14.73	1.00	147.00
CD16+ Monocytes	pS6	4.70	7.06	3.68	5.73	1.00	70.60	4.16	6.31	3.52	4.81	1.00	62.00
CD16+ Monocytes	pSTAT1	11.96	19.99	9.06	14.86	1.00	134.00	11.27	19.85	9.24	13.30	1.00	150.00
CD16+ Monocytes	pSTAT3	23.03	24.99	19.41	26.66	1.16	227.00	20.07	20.02	18.02	22.12	1.00	117.00
CD16+ Monocytes	pSTAT5	3.78	6.34	2.86	4.70	1.00	44.60	3.46	6.29	2.81	4.10	1.00	63.70
CD16- NK Cells	IkB	4.60	7.49	3.52	5.69	1.00	70.00	3.93	5.52	3.37	4.50	1.00	33.80
CD16- NK Cells	pERK	38.46	106.9	22.96	53.96	1.00	1147.00	34.73	112.2	23.25	46.21	1.00	1346.00
CD16- NK Cells	pP38	1.68	2.07	1.38	1.98	1.00	18.70	1.48	1.43	1.33	1.62	1.00	14.50
CD16- NK Cells	pPLCg2	5.71	8.68	4.45	6.97	1.00	79.10	5.08	8.47	4.22	5.95	1.00	67.10
CD16- NK Cells	pS6	2.61	3.83	2.06	3.17	1.00	34.40	2.34	3.60	1.98	2.71	1.00	42.70
CD16- NK Cells	pSTAT1	5.18	8.67	3.92	6.44	1.00	51.60	4.49	7.85	3.68	5.29	1.00	53.40
CD16- NK Cells	pSTAT3	7.09	10.81	5.52	8.65	1.00	93.50	5.69	7.28	4.95	6.44	1.00	56.70
CD16- NK Cells	pSTAT5	1.95	3.06	1.51	2.40	1.00	27.70	1.82	3.09	1.51	2.14	1.00	33.10
CD16- Monocytes	IkB	9.54	13.43	7.59	11.48	1.00	100.00	8.25	11.20	7.10	9.40	1.00	64.70

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	58.77	160.2	35.53	82.02	1.50	1672.00	51.55	153.4	35.85	67.25	1.00	1828.00
CD16- Monocytes	pP38	4.65	5.23	3.89	5.41	1.00	30.40	3.87	4.01	3.46	4.28	1.00	24.60
CD16- Monocytes	pPLCg2	8.80	13.10	6.90	10.70	1.00	112.00	7.79	12.43	6.52	9.06	1.00	95.30
CD16- Monocytes	pS6	3.69	6.60	2.74	4.65	1.00	72.00	3.26	5.32	2.71	3.80	1.00	52.30
CD16- Monocytes	pSTAT1	15.39	22.77	12.09	18.70	1.00	157.00	14.10	21.99	11.85	16.35	1.00	143.00
CD16- Monocytes	pSTAT3	20.53	25.34	16.86	24.21	1.00	212.00	16.86	17.84	15.03	18.68	1.00	140.00
CD16- Monocytes	pSTAT5	3.34	5.40	2.55	4.12	1.00	40.30	3.09	5.45	2.53	3.64	1.00	53.80
CD4+ T Cells	IkB	8.61	12.78	6.75	10.46	1.00	78.40	7.52	10.92	6.40	8.63	1.00	58.60
CD4+ T Cells	pERK	41.70	131.6	22.61	60.79	1.00	1389.00	36.06	124.5	23.32	48.81	1.00	1615.00
CD4+ T Cells	pP38	2.26	2.90	1.84	2.68	1.00	22.00	1.96	2.32	1.72	2.20	1.00	18.80
CD4+ T Cells	pPLCg2	5.22	9.06	3.91	6.54	1.00	82.70	4.71	8.80	3.81	5.61	1.00	76.90
CD4+ T Cells	pS6	2.68	5.23	1.92	3.44	1.00	58.10	2.48	4.43	2.02	2.93	1.00	44.70
CD4+ T Cells	pSTAT1	14.44	22.33	11.20	17.68	1.00	153.00	12.58	20.56	10.48	14.69	1.00	153.00
CD4+ T Cells	pSTAT3	15.06	20.12	12.14	17.98	1.00	164.00	11.60	14.68	10.10	13.10	1.00	145.00
CD4+ T Cells	pSTAT5	2.57	4.19	1.96	3.18	1.00	37.80	2.42	4.29	1.98	2.86	1.00	47.60
CD4-CD8- T Cells	IkB	4.81	8.11	3.64	5.99	1.00	74.00	4.09	6.08	3.47	4.72	1.00	39.30
CD4-CD8- T Cells	pERK	38.12	120.8	20.61	55.64	1.00	1252.00	31.46	109.0	20.30	42.62	1.00	1221.00
CD4-CD8- T Cells	pP38	1.89	2.30	1.56	2.23	1.00	20.50	1.72	2.49	1.46	1.97	1.00	27.80
CD4-CD8- T Cells	pPLCg2	5.14	8.72	3.87	6.40	1.00	72.80	4.50	8.96	3.59	5.42	1.00	91.40
CD4-CD8- T Cells	pS6	2.35	4.35	1.72	2.98	1.00	48.70	2.21	3.96	1.81	2.62	1.00	39.00
CD4-CD8- T Cells	pSTAT1	7.44	11.93	5.71	9.17	1.00	64.80	6.58	11.85	5.37	7.79	1.00	98.00
CD4-CD8- T Cells	pSTAT3	9.94	15.03	7.76	12.12	1.00	123.00	7.17	10.11	6.14	8.21	1.00	103.00
CD4-CD8- T Cells	pSTAT5	1.99	3.34	1.50	2.47	1.00	31.60	1.89	3.60	1.52	2.26	1.00	42.40
CD8+ T Cells	IkB	7.47	11.30	5.83	9.10	1.00	77.70	6.40	9.52	5.43	7.38	1.00	63.50
CD8+ T Cells	pERK	45.95	139.9	25.66	66.24	1.00	1473.00	37.92	122.8	25.35	50.49	1.00	1510.00
CD8+ T Cells	pP38	2.09	2.61	1.72	2.47	1.00	20.40	1.84	2.19	1.62	2.07	1.00	17.50
CD8+ T Cells	pPLCg2	5.44	9.10	4.12	6.76	1.00	83.10	4.89	9.11	3.95	5.82	1.00	84.80
CD8+ T Cells	pS6	2.78	5.12	2.04	3.53	1.00	57.00	2.52	4.43	2.07	2.97	1.00	46.20
CD8+ T Cells	pSTAT1	12.29	18.86	9.55	15.02	1.00	140.00	10.77	17.52	8.98	12.56	1.00	125.00
CD8+ T Cells	pSTAT3	13.61	18.38	10.94	16.28	1.00	144.00	10.31	13.21	8.96	11.67	1.00	128.00
CD8+ T Cells	pSTAT5	2.34	3.83	1.79	2.90	1.00	33.90	2.22	4.04	1.81	2.64	1.00	42.30
Dendritic Cells	IkB	4.03	6.40	3.10	4.96	1.00	47.30	3.37	4.91	2.86	3.87	1.00	38.20
Dendritic Cells	pERK	39.35	132.9	20.07	58.64	1.00	1445.00	29.74	85.44	20.99	38.48	1.00	992.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	4.10	5.81	3.25	4.94	1.00	39.20	3.25	4.75	2.76	3.74	1.00	38.80
Dendritic Cells	pPLCg2	5.47	9.23	4.13	6.81	1.00	80.00	4.69	8.11	3.86	5.52	1.00	58.50
Dendritic Cells	pS6	2.19	4.33	1.56	2.82	1.00	52.10	2.04	3.51	1.69	2.40	1.00	35.40
Dendritic Cells	pSTAT1	5.99	11.75	4.28	7.69	1.00	87.70	5.04	10.05	4.01	6.07	1.00	84.60
Dendritic Cells	pSTAT3	6.80	11.09	5.19	8.40	1.00	76.10	5.14	8.04	4.32	5.96	1.00	91.70
Dendritic Cells	pSTAT5	1.92	2.64	1.54	2.31	1.00	21.10	1.88	3.41	1.53	2.23	1.00	44.30
HLADR+ NK Cells	IkB	5.91	10.10	4.44	7.38	1.00	107.00	4.89	6.29	4.25	5.54	1.00	36.20
HLADR+ NK Cells	pERK	45.62	121.7	27.91	63.33	1.00	1339.00	41.91	120.9	29.49	54.34	1.00	1400.00
HLADR+ NK Cells	pP38	2.06	2.62	1.68	2.44	1.00	20.00	1.83	2.01	1.62	2.04	1.00	17.00
HLADR+ NK Cells	pPLCg2	8.24	10.92	6.66	9.83	1.00	82.20	7.48	11.36	6.32	8.65	1.00	90.10
HLADR+ NK Cells	pS6	2.93	3.35	2.44	3.41	1.00	27.40	2.65	3.04	2.33	2.96	1.00	34.10
HLADR+ NK Cells	pSTAT1	5.87	9.55	4.48	7.25	1.00	66.40	5.10	8.33	4.24	5.95	1.00	56.20
HLADR+ NK Cells	pSTAT3	9.98	15.28	7.76	12.20	1.00	149.00	8.41	9.96	7.38	9.43	1.00	65.80
HLADR+ NK Cells	pSTAT5	2.12	2.73	1.72	2.52	1.00	23.10	1.98	2.84	1.69	2.27	1.00	31.30
HLADR+CD38+ CD4+ T Cells	IkB	9.96	13.84	7.95	11.97	1.00	91.90	8.81	12.00	7.58	10.04	1.00	66.40
HLADR+CD38+ CD4+ T Cells	pERK	52.09	135.6	32.43	71.76	1.00	1409.00	47.04	135.1	33.21	60.87	1.00	1615.00
HLADR+CD38+ CD4+ T Cells	pP38	3.29	4.07	2.70	3.88	1.00	27.30	2.89	3.58	2.53	3.26	1.00	25.70
HLADR+CD38+ CD4+ T Cells	pPLCg2	10.66	28.79	6.48	14.83	1.00	358.00	20.28	167.3	3.15	37.40	1.00	2531.00
HLADR+CD38+ CD4+ T Cells	pS6	3.91	6.71	2.94	4.89	1.00	67.40	3.50	5.63	2.93	4.08	1.00	60.90
HLADR+CD38+ CD4+ T Cells	pSTAT1	15.58	22.90	12.26	18.91	1.00	138.00	14.12	22.72	11.79	16.44	1.00	170.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	17.64	21.70	14.49	20.79	1.00	195.00	14.54	16.42	12.86	16.22	1.00	145.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	3.50	5.88	2.64	4.35	1.00	50.60	3.38	6.53	2.72	4.05	1.00	62.50
HLADR+CD38+ CD8+ T Cells	IkB	8.57	12.17	6.81	10.34	1.00	96.60	7.33	9.90	6.32	8.34	1.00	66.80
HLADR+CD38+ CD8+ T Cells	pERK	52.25	137.3	32.33	72.17	1.32	1457.00	44.59	122.6	32.04	57.15	1.00	1456.00
HLADR+CD38+ CD8+ T Cells	pP38	3.02	3.73	2.48	3.56	1.00	25.10	2.66	3.65	2.28	3.03	1.00	37.60
HLADR+CD38+ CD8+ T Cells	pPLCg2	9.65	16.19	7.30	12.00	1.00	144.00	15.54	125.8	2.67	28.42	1.00	2393.00
HLADR+CD38+ CD8+ T Cells	pS6	3.92	6.89	2.92	4.92	1.00	68.10	3.34	5.07	2.82	3.86	1.00	44.90

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	12.35	17.98	9.74	14.95	1.00	106.00	20.60	191.1	1.04	40.16	1.00	3667.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	14.68	16.91	12.22	17.13	1.00	144.00	12.10	13.52	10.71	13.48	1.00	103.00
HLADR+CD38+ CD8+ T Cells	pSTAT5	3.01	5.25	2.25	3.77	1.00	45.50	2.93	5.81	2.33	3.52	1.00	55.90
IgD+CD27+ B Cells	IkB	5.93	8.67	4.67	7.18	1.00	73.80	4.96	6.33	4.31	5.61	1.00	37.50
IgD+CD27+ B Cells	pERK	42.21	130.3	23.30	61.11	1.00	1374.00	39.05	135.4	25.19	52.91	1.00	1640.00
IgD+CD27+ B Cells	pP38	2.20	2.62	1.82	2.58	1.00	17.00	1.95	2.24	1.72	2.18	1.00	20.40
IgD+CD27+ B Cells	pPLCg2	9.37	12.32	7.58	11.16	1.00	91.40	8.17	11.82	6.96	9.38	1.00	96.40
IgD+CD27+ B Cells	pS6	3.22	5.29	2.45	3.99	1.00	52.30	2.79	4.32	2.35	3.23	1.00	40.10
IgD+CD27+ B Cells	pSTAT1	6.11	9.41	4.74	7.47	1.00	63.20	5.41	9.10	4.48	6.34	1.00	65.50
IgD+CD27+ B Cells	pSTAT3	10.14	13.30	8.22	12.07	1.00	122.00	8.49	9.32	7.53	9.44	1.00	74.40
IgD+CD27+ B Cells	pSTAT5	2.39	4.15	1.79	2.99	1.00	40.40	2.20	3.91	1.80	2.60	1.00	36.30
IgD+CD27- B Cells	IkB	4.88	7.53	3.79	5.98	1.00	64.70	4.09	5.67	3.51	4.67	1.00	40.70
IgD+CD27- B Cells	pERK	34.54	106.2	19.14	49.94	1.00	1014.00	28.05	98.03	18.00	38.10	1.00	1339.00
IgD+CD27- B Cells	pP38	1.82	2.07	1.51	2.12	1.00	15.10	1.57	1.70	1.40	1.74	1.00	16.90
IgD+CD27- B Cells	pPLCg2	7.78	10.32	6.29	9.28	1.00	74.00	6.65	10.14	5.61	7.69	1.00	89.40
IgD+CD27- B Cells	pS6	2.71	4.65	2.03	3.38	1.00	46.50	2.42	4.16	2.00	2.85	1.00	45.70
IgD+CD27- B Cells	pSTAT1	4.86	7.67	3.75	5.98	1.00	49.00	4.41	8.04	3.59	5.24	1.00	73.20
IgD+CD27- B Cells	pSTAT3	8.11	11.62	6.43	9.80	1.00	106.00	6.66	8.10	5.83	7.49	1.00	64.00
IgD+CD27- B Cells	pSTAT5	1.91	2.90	1.49	2.33	1.00	25.00	1.83	3.18	1.50	2.15	1.00	33.80
IgD-CD27+ B Cells	IkB	4.76	7.54	3.66	5.85	1.00	56.20	3.93	5.11	3.41	4.46	1.00	26.00
IgD-CD27+ B Cells	pERK	36.39	135.3	16.76	56.02	1.00	1653.00	27.37	78.52	19.32	35.42	1.00	817.00
IgD-CD27+ B Cells	pP38	1.90	1.99	1.61	2.19	1.00	13.10	1.61	1.66	1.43	1.78	1.00	19.80
IgD-CD27+ B Cells	pPLCg2	8.34	10.73	6.78	9.89	1.00	71.40	7.17	10.33	6.11	8.23	1.00	87.40
IgD-CD27+ B Cells	pS6	2.96	4.50	2.31	3.61	1.00	44.10	2.66	4.42	2.20	3.11	1.00	45.60
IgD-CD27+ B Cells	pSTAT1	5.86	9.12	4.53	7.18	1.00	54.80	5.49	9.67	4.50	6.48	1.00	64.80
IgD-CD27+ B Cells	pSTAT3	9.88	13.02	7.99	11.76	1.00	98.80	8.32	9.92	7.30	9.34	1.00	86.90
IgD-CD27+ B Cells	pSTAT5	2.17	3.96	1.60	2.75	1.00	38.60	2.02	4.18	1.59	2.45	1.00	59.30

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	4.05	7.80	2.92	5.18	1.00	71.40	2.97	3.84	2.58	3.37	1.00	24.60
IgD-CD27- B Cells	pERK	28.68	96.36	14.71	42.66	1.00	938.00	20.16	78.16	12.13	28.18	1.00	1424.00
IgD-CD27- B Cells	pP38	1.76	1.83	1.49	2.02	1.00	11.60	1.43	1.48	1.28	1.58	1.00	15.40
IgD-CD27- B Cells	pPLCg2	6.98	9.32	5.63	8.33	1.00	61.60	5.68	8.68	4.79	6.57	1.00	81.50
IgD-CD27- B Cells	pS6	2.88	4.92	2.17	3.60	1.00	40.30	2.33	4.56	1.86	2.80	1.00	67.70
IgD-CD27- B Cells	pSTAT1	5.01	8.06	3.84	6.18	1.00	51.00	4.65	9.90	3.63	5.66	1.00	125.00
IgD-CD27- B Cells	pSTAT3	7.78	9.84	6.36	9.21	1.00	79.20	6.27	7.75	5.48	7.07	1.00	68.60
IgD-CD27- B Cells	pSTAT5	1.98	3.47	1.48	2.48	1.00	33.70	1.82	4.58	1.35	2.29	1.00	79.30
NK Cells	IkB	4.64	7.29	3.58	5.70	1.00	70.00	3.96	5.19	3.43	4.49	1.00	33.60
NK Cells	pERK	40.44	112.7	24.05	56.83	1.00	1231.00	36.59	113.9	24.89	48.28	1.00	1365.00
NK Cells	pP38	1.66	2.04	1.36	1.95	1.00	18.70	1.48	1.46	1.33	1.63	1.00	15.00
NK Cells	pPLCg2	6.22	9.21	4.88	7.56	1.00	79.10	5.50	8.64	4.61	6.39	1.00	78.00
NK Cells	pS6	2.47	3.19	2.00	2.93	1.00	34.40	2.20	2.55	1.93	2.46	1.00	28.90
NK Cells	pSTAT1	4.79	7.98	3.63	5.95	1.00	44.20	4.09	7.14	3.36	4.83	1.00	52.20
NK Cells	pSTAT3	7.72	11.48	6.05	9.39	1.00	93.50	6.27	7.72	5.48	7.07	1.00	49.20
NK Cells	pSTAT5	1.80	2.38	1.46	2.15	1.00	23.10	1.66	2.28	1.43	1.90	1.00	27.20
NKT Cells	IkB	11.32	21.69	8.15	14.49	1.00	241.00	9.69	14.02	8.25	11.14	1.00	86.00
NKT Cells	pERK	59.76	168.1	35.16	84.35	1.00	1759.00	60.48	186.3	41.31	79.65	1.00	1923.00
NKT Cells	pP38	3.09	3.81	2.54	3.65	1.00	21.40	3.37	6.87	2.66	4.07	1.00	97.70
NKT Cells	pPLCg2	7.09	12.95	5.20	8.98	1.00	124.00	7.20	16.42	5.51	8.89	1.00	151.00
NKT Cells	pS6	5.15	16.58	2.72	7.57	1.00	211.00	5.04	16.26	3.36	6.71	1.00	209.00
NKT Cells	pSTAT1	18.49	32.26	13.77	23.21	1.00	269.00	15.29	25.79	12.64	17.94	1.00	199.00
NKT Cells	pSTAT3	18.03	28.46	13.87	22.19	1.00	286.00	14.73	22.53	12.41	17.05	1.00	283.00
NKT Cells	pSTAT5	3.30	5.87	2.45	4.16	1.00	61.40	3.05	4.92	2.54	3.56	1.00	43.00
Regulatory T Cells	IkB	10.76	14.84	8.60	12.91	1.00	71.20	9.45	13.56	8.06	10.84	1.00	69.00
Regulatory T Cells	pERK	49.04	141.8	28.48	69.60	1.00	1533.00	42.51	133.1	28.87	56.16	1.00	1652.00
Regulatory T Cells	pP38	2.63	3.45	2.13	3.13	1.00	23.10	2.24	2.72	1.96	2.52	1.00	22.50
Regulatory T Cells	pPLCg2	5.86	9.99	4.41	7.30	1.00	81.50	5.10	9.01	4.18	6.02	1.00	76.50
Regulatory T Cells	pS6	3.02	5.52	2.22	3.82	1.00	53.90	2.80	4.96	2.29	3.31	1.00	53.80
Regulatory T Cells	pSTAT1	19.34	33.67	14.45	24.22	1.00	273.00	17.00	29.62	13.96	20.03	1.00	242.00
Regulatory T Cells	pSTAT3	17.96	22.14	14.75	21.17	1.00	196.00	14.19	17.01	12.44	15.93	1.00	162.00
Regulatory T Cells	pSTAT5	3.06	5.42	2.28	3.85	1.00	55.30	2.96	7.58	2.18	3.74	1.00	126.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	9.36	13.58	7.40	11.33	1.00	81.20	8.05	11.47	6.88	9.23	1.00	57.50
Central Memory CD4+ T Cells	pERK	43.87	133.6	24.49	63.24	1.00	1381.00	37.29	123.1	24.69	49.89	1.00	1549.00
Central Memory CD4+ T Cells	pP38	2.47	3.28	2.00	2.95	1.00	26.30	2.07	2.36	1.83	2.31	1.00	15.80
Central Memory CD4+ T Cells	pPLCg2	5.13	8.64	3.88	6.38	1.00	83.10	4.51	7.92	3.70	5.32	1.00	73.20
Central Memory CD4+ T Cells	pS6	2.66	5.21	1.91	3.42	1.00	59.60	2.41	3.99	2.00	2.82	1.00	36.90
Central Memory CD4+ T Cells	pSTAT1	19.42	29.69	15.11	23.72	1.00	203.00	16.82	27.19	14.04	19.60	1.00	181.00
Central Memory CD4+ T Cells	pSTAT3	18.10	23.67	14.67	21.54	1.00	210.00	13.40	16.38	11.73	15.08	1.00	162.00
Central Memory CD4+ T Cells	pSTAT5	2.83	4.25	2.21	3.44	1.00	32.00	2.62	4.23	2.18	3.05	1.00	45.70
Central Memory CD8+ T Cells	IkB	7.85	11.81	6.14	9.56	1.00	82.10	6.50	9.62	5.52	7.49	1.00	65.10
Central Memory CD8+ T Cells	pERK	45.51	131.8	26.39	64.63	1.00	1389.00	37.22	110.9	25.86	48.57	1.00	1291.00
Central Memory CD8+ T Cells	pP38	2.30	2.86	1.89	2.72	1.00	23.60	2.02	2.38	1.77	2.26	1.00	19.00
Central Memory CD8+ T Cells	pPLCg2	4.97	8.44	3.75	6.20	1.00	83.40	4.39	7.76	3.60	5.19	1.00	71.00
Central Memory CD8+ T Cells	pS6	3.02	5.25	2.26	3.78	1.00	57.00	2.63	4.03	2.22	3.04	1.00	37.70
Central Memory CD8+ T Cells	pSTAT1	14.28	24.12	10.79	17.78	1.00	205.00	12.62	21.24	10.45	14.80	1.00	149.00
Central Memory CD8+ T Cells	pSTAT3	15.40	20.21	12.47	18.33	1.00	155.00	11.17	14.49	9.68	12.65	1.00	145.00
Central Memory CD8+ T Cells	pSTAT5	2.47	4.09	1.88	3.06	1.00	35.20	2.26	3.63	1.88	2.63	1.00	35.90
Effector CD4+ T Cells	IkB	6.43	9.79	5.01	7.85	1.00	67.90	5.51	8.27	4.67	6.36	1.00	50.30
Effector CD4+ T Cells	pERK	34.25	91.40	20.99	47.50	1.00	896.00	27.87	86.18	19.04	36.69	1.00	1273.00
Effector CD4+ T Cells	pP38	1.92	2.29	1.59	2.26	1.00	16.50	1.69	1.96	1.48	1.89	1.00	20.40
Effector CD4+ T Cells	pPLCg2	4.70	7.99	3.54	5.86	1.00	72.40	4.12	7.87	3.31	4.92	1.00	76.50
Effector CD4+ T Cells	pS6	2.38	4.47	1.73	3.03	1.00	49.60	2.26	4.20	1.83	2.69	1.00	43.50
Effector CD4+ T Cells	pSTAT1	10.97	16.88	8.52	13.42	1.00	122.00	9.26	15.87	7.64	10.89	1.00	121.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	11.86	15.44	9.62	14.10	1.00	121.00	8.96	11.47	7.78	10.13	1.00	121.00
Effector CD4+ T Cells	pSTAT5	2.09	3.18	1.63	2.55	1.00	28.50	1.98	3.65	1.61	2.36	1.00	45.00
Effector CD8+ T Cells	IkB	5.79	9.40	4.42	7.15	1.00	81.00	4.74	7.10	4.02	5.47	1.00	49.50
Effector CD8+ T Cells	pERK	36.29	76.80	25.15	47.43	1.00	790.00	28.02	72.65	20.58	35.47	1.00	1144.00
Effector CD8+ T Cells	pP38	1.85	2.34	1.51	2.19	1.00	18.00	1.67	2.35	1.43	1.91	1.00	33.10
Effector CD8+ T Cells	pPLCg2	5.02	8.09	3.85	6.20	1.00	74.20	4.44	8.35	3.59	5.30	1.00	85.30
Effector CD8+ T Cells	pS6	2.48	4.79	1.78	3.17	1.00	56.60	2.24	4.14	1.81	2.66	1.00	45.10
Effector CD8+ T Cells	pSTAT1	10.12	16.43	7.73	12.50	1.00	115.00	8.39	14.38	6.91	9.86	1.00	110.00
Effector CD8+ T Cells	pSTAT3	11.21	15.12	9.01	13.40	1.00	122.00	8.38	10.83	7.27	9.49	1.00	102.00
Effector CD8+ T Cells	pSTAT5	1.98	2.92	1.56	2.40	1.00	23.90	1.89	3.48	1.54	2.25	1.00	42.40
Effector Memory CD4+ T Cells	IkB	6.52	10.32	5.02	8.01	1.00	74.80	5.27	8.02	4.45	6.09	1.00	50.10
Effector Memory CD4+ T Cells	pERK	34.46	96.69	20.43	48.48	1.00	927.00	26.63	79.14	18.53	34.73	1.00	1196.00
Effector Memory CD4+ T Cells	pP38	2.00	2.68	1.61	2.39	1.00	24.60	1.68	1.76	1.50	1.86	1.00	13.40
Effector Memory CD4+ T Cells	pPLCg2	4.12	7.47	3.04	5.20	1.00	77.10	3.54	6.68	2.85	4.22	1.00	67.90
Effector Memory CD4+ T Cells	pS6	2.16	4.53	1.51	2.82	1.00	56.00	2.05	3.75	1.67	2.44	1.00	38.60
Effector Memory CD4+ T Cells	pSTAT1	14.31	23.60	10.88	17.73	1.00	179.00	11.79	21.31	9.61	13.97	1.00	170.00
Effector Memory CD4+ T Cells	pSTAT3	12.62	17.99	10.01	15.23	1.00	155.00	9.00	12.70	7.70	10.30	1.00	145.00
Effector Memory CD4+ T Cells	pSTAT5	2.23	3.53	1.72	2.74	1.00	31.60	2.00	2.98	1.69	2.30	1.00	33.10
Effector Memory CD8+ T Cells	IkB	5.40	8.72	4.14	6.67	1.00	75.00	4.44	7.12	3.71	5.17	1.00	57.00
Effector Memory CD8+ T Cells	pERK	38.35	114.5	21.74	54.96	1.00	1313.00	26.32	72.64	18.86	33.77	1.00	1112.00
Effector Memory CD8+ T Cells	pP38	1.93	2.59	1.56	2.31	1.00	22.60	1.76	3.28	1.42	2.10	1.00	55.00
Effector Memory CD8+ T Cells	pPLCg2	4.06	7.19	3.02	5.10	1.00	75.90	3.58	7.11	2.85	4.31	1.00	73.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	2.44	5.18	1.69	3.19	1.00	64.70	2.11	3.71	1.73	2.49	1.00	42.70
Effector Memory CD8+ T Cells	pSTAT1	10.51	18.51	7.82	13.19	1.00	163.00	8.99	16.64	7.28	10.70	1.00	130.00
Effector Memory CD8+ T Cells	pSTAT3	11.07	16.11	8.73	13.40	1.00	123.00	8.00	11.67	6.80	9.19	1.00	133.00
Effector Memory CD8+ T Cells	pSTAT5	1.95	2.92	1.53	2.38	1.00	24.50	1.81	3.00	1.51	2.12	1.00	39.10
Myeloid Dendritic Cells	IkB	4.29	6.68	3.32	5.25	1.00	47.30	3.63	5.37	3.09	4.18	1.00	37.50
Myeloid Dendritic Cells	pERK	42.86	138.7	22.74	62.97	1.00	1437.00	33.44	94.98	23.72	43.16	1.00	1061.00
Myeloid Dendritic Cells	pP38	5.73	7.11	4.70	6.77	1.00	42.10	4.64	6.31	3.99	5.28	1.00	45.10
Myeloid Dendritic Cells	pPLCg2	6.01	9.90	4.58	7.45	1.00	80.00	5.13	8.62	4.25	6.01	1.00	58.90
Myeloid Dendritic Cells	pS6	2.35	4.48	1.70	3.00	1.00	52.10	2.19	3.76	1.81	2.58	1.00	39.40
Myeloid Dendritic Cells	pSTAT1	6.76	13.78	4.76	8.76	1.00	107.00	5.60	11.16	4.46	6.74	1.00	109.00
Myeloid Dendritic Cells	pSTAT3	7.59	13.10	5.69	9.49	1.00	93.70	5.87	9.02	4.95	6.80	1.00	96.10
Myeloid Dendritic Cells	pSTAT5	2.10	2.85	1.69	2.51	1.00	21.10	2.00	3.79	1.61	2.39	1.00	54.40
Monocytes	IkB	14.99	14.01	8.02	21.95	1.00	46.70	12.62	11.16	8.85	16.40	1.53	44.50
Monocytes	pERK	169.3	472.6	-65.7	404.3	3.29	1672.00	160.7	455.6	6.56	314.9	2.18	1828.00
Monocytes	pP38	3.04	5.89	0.11	5.97	1.00	20.30	3.02	5.80	1.06	4.98	1.00	24.40
Monocytes	pPLCg2	4.90	5.08	2.37	7.43	1.00	16.30	5.63	5.98	3.60	7.65	1.00	24.20
Monocytes	pS6	3.62	2.28	2.49	4.76	1.07	7.98	3.63	2.29	2.85	4.40	1.00	9.18
Monocytes	pSTAT1	11.95	13.97	5.00	18.89	1.00	53.60	13.41	15.27	8.24	18.58	1.00	67.80
Monocytes	pSTAT3	8.27	11.47	2.57	13.97	1.00	45.20	8.79	10.02	5.40	12.18	1.13	49.00
Monocytes	pSTAT5	2.28	1.83	1.37	3.19	1.00	7.83	2.36	1.75	1.77	2.96	1.00	7.83
Naive CD4+ T Cells	IkB	9.50	13.72	7.51	11.49	1.00	77.50	8.33	11.90	7.11	9.55	1.00	62.60
Naive CD4+ T Cells	pERK	43.57	133.1	24.27	62.87	1.00	1405.00	37.96	126.7	24.99	50.94	1.00	1643.00
Naive CD4+ T Cells	pP38	2.38	2.95	1.95	2.81	1.00	19.80	2.07	2.44	1.82	2.32	1.00	19.50
Naive CD4+ T Cells	pPLCg2	5.91	9.78	4.49	7.33	1.00	83.80	5.31	9.53	4.34	6.29	1.00	79.80
Naive CD4+ T Cells	pS6	3.00	5.51	2.20	3.80	1.00	58.30	2.76	4.84	2.26	3.26	1.00	49.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	14.35	21.46	11.24	17.47	1.00	145.00	12.48	20.17	10.42	14.54	1.00	160.00
Naive CD4+ T Cells	pSTAT3	16.21	20.10	13.30	19.13	1.00	155.00	12.72	15.02	11.18	14.26	1.00	141.00
Naive CD4+ T Cells	pSTAT5	2.71	4.51	2.06	3.37	1.00	43.50	2.52	4.49	2.06	2.98	1.00	49.20
Naive CD8+ T Cells	IkB	8.42	12.61	6.59	10.25	1.00	76.00	7.29	10.81	6.18	8.39	1.00	67.70
Naive CD8+ T Cells	pERK	48.01	143.0	27.27	68.76	1.00	1507.00	39.99	125.5	27.15	52.84	1.00	1536.00
Naive CD8+ T Cells	pP38	2.19	2.71	1.80	2.58	1.00	19.50	1.94	2.28	1.70	2.17	1.00	17.60
Naive CD8+ T Cells	pPLCg2	6.10	9.76	4.68	7.51	1.00	84.30	5.52	9.87	4.51	6.53	1.00	86.50
Naive CD8+ T Cells	pS6	3.01	5.38	2.23	3.79	1.00	57.00	2.72	4.81	2.23	3.22	1.00	48.30
Naive CD8+ T Cells	pSTAT1	13.28	19.42	10.46	16.09	1.00	135.00	11.64	18.32	9.76	13.51	1.00	131.00
Naive CD8+ T Cells	pSTAT3	14.94	19.20	12.16	17.73	1.00	144.00	11.53	13.88	10.11	12.95	1.00	128.00
Naive CD8+ T Cells	pSTAT5	2.52	4.18	1.91	3.12	1.00	39.00	2.38	4.39	1.93	2.83	1.00	45.10
Plasmoid Dendritic Cells	IkB	4.66	6.99	3.64	5.68	1.00	54.50	3.77	5.23	3.24	4.31	1.00	39.20
Plasmoid Dendritic Cells	pERK	43.01	141.0	22.51	63.52	1.00	1541.00	33.34	91.42	23.98	42.70	1.00	1025.00
Plasmoid Dendritic Cells	pP38	2.62	3.86	2.06	3.19	1.00	24.00	2.23	3.28	1.89	2.56	1.00	29.70
Plasmoid Dendritic Cells	pPLCg2	5.91	8.23	4.71	7.11	1.00	58.00	5.32	9.70	4.33	6.32	1.00	81.10
Plasmoid Dendritic Cells	pS6	2.46	3.11	2.01	2.91	1.00	20.20	2.46	4.87	1.96	2.96	1.00	58.00
Plasmoid Dendritic Cells	pSTAT1	5.94	10.55	4.40	7.47	1.00	80.00	5.21	10.30	4.16	6.26	1.00	91.90
Plasmoid Dendritic Cells	pSTAT3	7.08	9.46	5.71	8.46	1.00	70.80	5.45	8.12	4.61	6.28	1.00	95.60
Plasmoid Dendritic Cells	pSTAT5	2.00	2.61	1.62	2.38	1.00	24.80	1.99	3.83	1.60	2.38	1.00	50.80
Plasmablasts	IkB	7.58	11.41	5.92	9.25	1.00	108.00	6.50	8.42	5.63	7.37	1.00	41.60
Plasmablasts	pERK	50.94	135.6	31.17	70.72	1.00	1397.00	48.91	159.4	32.46	65.36	1.00	2172.00
Plasmablasts	pP38	2.71	3.74	2.16	3.26	1.00	24.70	2.69	4.11	2.27	3.11	1.00	55.30
Plasmablasts	pPLCg2	8.79	12.62	6.95	10.63	1.00	107.00	8.02	13.93	6.59	9.46	1.00	122.00
Plasmablasts	pS6	3.75	5.40	2.96	4.53	1.00	58.10	3.44	4.43	2.99	3.90	1.00	37.30

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-10

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	6.79	10.30	5.28	8.29	1.00	64.00	6.12	10.16	5.07	7.17	1.00	67.00
Plasmablasts	pSTAT3	9.67	13.69	7.68	11.67	1.00	138.00	8.33	10.64	7.23	9.43	1.00	83.20
Plasmablasts	pSTAT5	2.69	4.54	2.03	3.35	1.00	46.20	2.73	5.40	2.17	3.28	1.00	70.20
Transitional B Cells	IkB	8.53	15.41	6.29	10.77	1.00	152.00	6.28	8.36	5.43	7.14	1.00	48.60
Transitional B Cells	pERK	53.18	140.2	32.79	73.57	1.00	1385.00	48.87	156.4	32.82	64.92	1.00	2172.00
Transitional B Cells	pP38	3.44	4.37	2.80	4.07	1.00	28.00	3.38	4.54	2.91	3.84	1.00	50.20
Transitional B Cells	pPLCg2	9.72	14.38	7.63	11.81	1.00	101.00	8.70	13.51	7.31	10.09	1.00	111.00
Transitional B Cells	pS6	4.12	5.96	3.25	4.98	1.00	58.10	3.95	5.19	3.42	4.48	1.00	40.30
Transitional B Cells	pSTAT1	7.13	10.90	5.55	8.72	1.00	71.80	6.45	12.07	5.21	7.69	1.00	117.00
Transitional B Cells	pSTAT3	11.80	14.49	9.70	13.91	1.00	150.00	10.61	12.76	9.30	11.92	1.00	134.00
Transitional B Cells	pSTAT5	3.08	5.14	2.33	3.83	1.00	38.80	2.65	4.14	2.23	3.08	1.00	42.20

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
B Cells	IkB	5.32	7.06	4.30	6.35	1.00	38.30	4.74	6.48	4.08	5.40	1.00	44.60
B Cells	pERK	39.77	121.8	22.06	57.49	1.00	1180.00	36.67	133.5	23.04	50.30	1.00	1617.00
B Cells	pP38	2.07	2.45	1.72	2.43	1.00	16.60	1.89	2.28	1.66	2.12	1.00	21.90
B Cells	pPLCg2	8.56	10.42	7.05	10.08	1.00	62.80	7.84	12.13	6.60	9.07	1.00	94.50
B Cells	pS6	2.79	3.58	2.27	3.31	1.00	24.70	2.77	4.89	2.27	3.27	1.00	48.70
B Cells	pSTAT1	5.95	9.45	4.58	7.32	1.00	61.40	5.45	9.51	4.48	6.42	1.00	75.40
B Cells	pSTAT3	8.80	8.84	7.52	10.09	1.00	68.10	7.75	8.58	6.87	8.62	1.00	83.50
B Cells	pSTAT5	2.31	3.32	1.83	2.80	1.00	29.10	2.34	4.32	1.90	2.78	1.00	40.60
CD16+ NK Cells	IkB	6.02	7.95	4.83	7.21	1.00	45.10	5.62	7.69	4.82	6.43	1.00	51.60
CD16+ NK Cells	pERK	51.07	122.3	32.77	69.37	1.00	1200.00	50.16	148.1	34.64	65.69	1.00	1996.00
CD16+ NK Cells	pP38	1.85	2.24	1.52	2.19	1.00	16.70	1.76	2.22	1.53	2.00	1.00	26.30
CD16+ NK Cells	pPLCg2	10.44	13.53	8.42	12.47	1.00	80.00	9.94	14.87	8.38	11.50	1.00	140.00
CD16+ NK Cells	pS6	2.84	3.81	2.27	3.41	1.00	33.10	2.95	4.80	2.45	3.45	1.00	58.30
CD16+ NK Cells	pSTAT1	5.04	9.39	3.63	6.44	1.00	60.40	4.66	8.93	3.72	5.59	1.00	64.00
CD16+ NK Cells	pSTAT3	13.10	15.44	10.79	15.41	1.00	125.00	11.13	12.85	9.78	12.48	1.00	110.00
CD16+ NK Cells	pSTAT5	2.58	4.17	1.96	3.21	1.00	27.80	2.08	3.61	1.71	2.46	1.00	47.90
CD16+ Monocytes	IkB	10.11	11.46	8.44	11.78	1.00	56.90	8.91	11.04	7.79	10.04	1.00	62.30
CD16+ Monocytes	pERK	79.00	162.1	55.42	102.6	2.04	1494.00	70.20	162.0	53.66	86.73	1.00	1859.00
CD16+ Monocytes	pP38	4.48	5.38	3.69	5.26	1.00	37.90	4.17	5.10	3.65	4.69	1.00	34.30
CD16+ Monocytes	pPLCg2	14.36	18.06	11.73	16.98	1.00	128.00	13.81	21.89	11.58	16.05	1.00	182.00
CD16+ Monocytes	pS6	4.21	4.68	3.53	4.89	1.00	37.80	4.29	7.36	3.54	5.04	1.00	96.60
CD16+ Monocytes	pSTAT1	11.82	19.43	9.00	14.65	1.00	147.00	11.14	19.61	9.14	13.14	1.00	154.00
CD16+ Monocytes	pSTAT3	16.81	15.66	14.54	19.09	1.00	88.40	15.19	15.47	13.61	16.77	1.00	121.00
CD16+ Monocytes	pSTAT5	3.83	5.97	2.96	4.70	1.00	41.70	3.84	7.31	3.10	4.59	1.00	73.40
CD16- NK Cells	IkB	4.66	6.16	3.76	5.55	1.00	30.90	4.23	6.17	3.60	4.86	1.00	48.80
CD16- NK Cells	pERK	39.44	107.1	23.86	55.02	1.00	1064.00	35.22	117.4	23.24	47.21	1.00	1527.00
CD16- NK Cells	pP38	1.73	2.05	1.43	2.03	1.00	14.90	1.58	1.64	1.41	1.75	1.00	16.70
CD16- NK Cells	pPLCg2	5.67	7.43	4.59	6.75	1.00	44.00	5.44	9.06	4.52	6.37	1.00	67.10
CD16- NK Cells	pS6	2.50	2.82	2.09	2.91	1.00	23.90	2.47	4.24	2.04	2.90	1.00	48.80
CD16- NK Cells	pSTAT1	5.44	9.07	4.12	6.76	1.00	60.40	4.86	8.49	3.99	5.73	1.00	61.30
CD16- NK Cells	pSTAT3	6.85	7.71	5.72	7.97	1.00	53.60	6.03	7.18	5.30	6.76	1.00	50.10
CD16- NK Cells	pSTAT5	2.08	2.80	1.68	2.49	1.00	23.10	2.13	4.08	1.71	2.55	1.00	55.80
CD16- Monocytes	IkB	9.58	12.42	7.78	11.39	1.00	62.80	8.68	12.03	7.45	9.90	1.00	70.60

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	60.02	157.5	37.11	82.92	1.85	1511.00	52.37	152.6	36.79	67.95	1.00	1880.00
CD16- Monocytes	pP38	4.79	5.80	3.94	5.63	1.00	44.80	4.16	4.60	3.69	4.63	1.00	35.60
CD16- Monocytes	pPLCg2	8.69	11.36	7.04	10.34	1.00	79.90	8.41	15.23	6.86	9.97	1.00	162.00
CD16- Monocytes	pS6	3.41	4.17	2.80	4.01	1.00	32.10	3.43	6.28	2.78	4.07	1.00	76.90
CD16- Monocytes	pSTAT1	15.30	24.31	11.76	18.83	1.00	192.00	14.08	23.64	11.66	16.49	1.00	185.00
CD16- Monocytes	pSTAT3	12.24	14.55	10.13	14.36	1.00	123.00	10.37	13.13	9.03	11.71	1.00	114.00
CD16- Monocytes	pSTAT5	3.46	4.83	2.76	4.17	1.00	33.80	3.40	6.06	2.78	4.01	1.00	67.90
CD4+ T Cells	IkB	8.68	12.53	6.86	10.50	1.00	68.30	7.95	11.84	6.74	9.16	1.00	66.00
CD4+ T Cells	pERK	42.31	127.3	23.79	60.83	1.00	1273.00	36.83	125.1	24.06	49.60	1.00	1648.00
CD4+ T Cells	pP38	2.32	2.90	1.90	2.75	1.00	19.20	2.12	2.67	1.85	2.40	1.00	21.40
CD4+ T Cells	pPLCg2	5.04	7.30	3.98	6.11	1.00	46.30	5.02	9.68	4.03	6.01	1.00	75.90
CD4+ T Cells	pS6	2.46	3.40	1.97	2.96	1.00	29.90	2.62	5.37	2.07	3.17	1.00	68.80
CD4+ T Cells	pSTAT1	14.63	23.22	11.25	18.00	1.00	185.00	12.98	22.00	10.73	15.22	1.00	192.00
CD4+ T Cells	pSTAT3	13.52	15.61	11.25	15.79	1.00	136.00	11.14	13.61	9.75	12.53	1.00	116.00
CD4+ T Cells	pSTAT5	2.74	3.67	2.21	3.27	1.00	27.80	2.74	4.82	2.25	3.24	1.00	57.30
CD4-CD8- T Cells	IkB	4.87	6.97	3.85	5.88	1.00	45.80	4.24	6.27	3.60	4.88	1.00	42.20
CD4-CD8- T Cells	pERK	38.27	118.1	21.09	55.45	1.00	1113.00	31.07	101.0	20.76	41.38	1.00	1103.00
CD4-CD8- T Cells	pP38	1.96	2.34	1.62	2.30	1.00	16.90	1.80	2.50	1.55	2.06	1.00	27.50
CD4-CD8- T Cells	pPLCg2	4.95	7.13	3.91	5.98	1.00	47.80	4.73	9.55	3.75	5.70	1.00	92.20
CD4-CD8- T Cells	pS6	2.20	2.80	1.79	2.60	1.00	22.40	2.34	4.67	1.86	2.81	1.00	54.20
CD4-CD8- T Cells	pSTAT1	7.69	13.12	5.78	9.60	1.00	79.30	6.93	12.24	5.68	8.18	1.00	76.30
CD4-CD8- T Cells	pSTAT3	9.16	11.64	7.47	10.86	1.00	81.10	7.10	9.25	6.16	8.04	1.00	75.40
CD4-CD8- T Cells	pSTAT5	2.08	2.83	1.67	2.49	1.00	25.00	2.13	4.11	1.71	2.54	1.00	54.70
CD8+ T Cells	IkB	7.55	10.86	5.97	9.13	1.00	60.90	6.75	10.23	5.70	7.79	1.00	64.80
CD8+ T Cells	pERK	46.60	137.5	26.60	66.60	1.00	1381.00	38.40	122.1	25.93	50.87	1.00	1553.00
CD8+ T Cells	pP38	2.17	2.64	1.79	2.56	1.00	18.00	1.97	2.39	1.73	2.21	1.00	18.90
CD8+ T Cells	pPLCg2	5.34	7.55	4.25	6.44	1.00	43.40	5.21	10.02	4.19	6.23	1.00	82.90
CD8+ T Cells	pS6	2.57	3.34	2.08	3.05	1.00	26.80	2.70	5.51	2.13	3.26	1.00	71.60
CD8+ T Cells	pSTAT1	12.86	20.97	9.81	15.91	1.00	180.00	11.35	19.26	9.38	13.31	1.00	162.00
CD8+ T Cells	pSTAT3	13.03	14.57	10.91	15.15	1.00	107.00	10.32	12.12	9.08	11.55	1.00	94.60
CD8+ T Cells	pSTAT5	2.54	3.48	2.04	3.05	1.00	26.90	2.55	4.80	2.06	3.04	1.00	60.40
Dendritic Cells	IkB	4.02	5.63	3.20	4.84	1.00	34.30	3.62	5.48	3.06	4.18	1.00	35.70
Dendritic Cells	pERK	37.97	109.4	22.06	53.88	1.00	983.00	30.48	90.19	21.27	39.69	1.00	1073.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	4.24	5.98	3.37	5.11	1.00	41.40	3.40	4.76	2.92	3.89	1.00	35.00
Dendritic Cells	pPLCg2	5.34	7.98	4.18	6.50	1.00	58.50	5.01	9.43	4.05	5.97	1.00	97.40
Dendritic Cells	pS6	2.00	2.39	1.65	2.35	1.00	18.50	2.18	4.71	1.70	2.66	1.00	64.20
Dendritic Cells	pSTAT1	6.23	13.33	4.29	8.17	1.00	99.30	5.27	10.99	4.15	6.39	1.00	118.00
Dendritic Cells	pSTAT3	4.43	6.20	3.53	5.33	1.00	56.10	3.84	5.99	3.23	4.45	1.00	69.50
Dendritic Cells	pSTAT5	1.91	2.25	1.58	2.23	1.00	14.90	1.98	3.65	1.61	2.36	1.00	49.70
HLADR+ NK Cells	IkB	5.73	7.19	4.68	6.78	1.00	36.40	5.11	6.71	4.43	5.80	1.00	39.40
HLADR+ NK Cells	pERK	49.09	125.7	30.75	67.42	1.00	1288.00	43.13	119.5	30.90	55.37	1.00	1536.00
HLADR+ NK Cells	pP38	2.26	3.02	1.82	2.70	1.00	17.40	2.04	2.35	1.79	2.28	1.00	18.20
HLADR+ NK Cells	pPLCg2	8.48	10.74	6.92	10.05	1.00	78.20	8.29	13.03	6.96	9.63	1.00	104.00
HLADR+ NK Cells	pS6	2.92	2.93	2.49	3.34	1.00	21.60	2.72	3.30	2.38	3.06	1.00	29.40
HLADR+ NK Cells	pSTAT1	6.22	9.96	4.77	7.68	1.00	68.50	5.52	9.25	4.57	6.46	1.00	68.60
HLADR+ NK Cells	pSTAT3	9.49	10.41	7.97	11.01	1.00	65.70	8.97	11.80	7.76	10.17	1.00	140.00
HLADR+ NK Cells	pSTAT5	2.32	2.93	1.89	2.75	1.00	19.10	2.26	3.26	1.92	2.59	1.00	30.10
HLADR+CD38+ CD4+ T Cells	IkB	10.12	13.49	8.16	12.08	1.00	75.20	9.17	12.64	7.88	10.46	1.00	71.20
HLADR+CD38+ CD4+ T Cells	pERK	53.10	129.2	34.30	71.89	1.09	1221.00	47.10	128.6	33.97	60.23	1.00	1634.00
HLADR+CD38+ CD4+ T Cells	pP38	3.42	4.16	2.82	4.03	1.00	26.70	3.13	3.90	2.73	3.53	1.00	22.10
HLADR+CD38+ CD4+ T Cells	pPLCg2	15.39	85.06	3.01	27.76	1.00	1145.00	18.76	176.0	0.79	36.73	1.00	3362.00
HLADR+CD38+ CD4+ T Cells	pS6	3.61	4.55	2.94	4.27	1.00	33.90	3.69	6.50	3.03	4.36	1.00	75.20
HLADR+CD38+ CD4+ T Cells	pSTAT1	16.07	24.17	12.56	19.59	1.00	174.00	14.35	23.79	11.93	16.78	1.00	210.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	15.26	14.83	13.10	17.41	1.00	88.40	13.12	14.10	11.68	14.56	1.00	123.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	3.70	5.21	2.94	4.45	1.00	32.00	3.78	7.08	3.05	4.50	1.00	66.30
HLADR+CD38+ CD8+ T Cells	IkB	8.54	11.29	6.90	10.18	1.00	68.10	7.62	9.94	6.60	8.63	1.00	58.50
HLADR+CD38+ CD8+ T Cells	pERK	53.28	133.6	33.84	72.71	1.76	1280.00	45.42	122.8	32.88	57.96	1.00	1562.00
HLADR+CD38+ CD8+ T Cells	pP38	3.11	3.78	2.56	3.66	1.00	26.40	2.83	3.44	2.48	3.18	1.00	22.60
HLADR+CD38+ CD8+ T Cells	pPLCg2	10.64	21.00	7.58	13.69	1.00	216.00	16.13	135.8	2.27	29.99	1.00	2599.00
HLADR+CD38+ CD8+ T Cells	pS6	3.66	4.85	2.95	4.36	1.00	39.10	3.58	6.39	2.93	4.23	1.00	67.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	13.05	19.19	10.26	15.84	1.00	116.00	11.35	17.98	9.51	13.18	1.00	133.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	13.55	13.15	11.63	15.46	1.00	84.80	11.63	12.81	10.32	12.94	1.00	122.00
HLADR+CD38+ CD8+ T Cells	pSTAT5	3.40	4.93	2.68	4.12	1.00	32.60	3.37	6.50	2.70	4.03	1.00	72.80
IgD+CD27+ B Cells	IkB	5.85	7.53	4.76	6.95	1.00	40.60	5.23	6.95	4.52	5.94	1.00	47.00
IgD+CD27+ B Cells	pERK	42.91	125.0	24.74	61.09	1.16	1210.00	39.71	136.2	25.81	53.62	1.00	1672.00
IgD+CD27+ B Cells	pP38	2.26	2.68	1.87	2.65	1.00	17.30	2.04	2.42	1.79	2.29	1.00	22.20
IgD+CD27+ B Cells	pPLCg2	9.40	10.98	7.80	10.99	1.00	64.20	8.60	12.80	7.30	9.91	1.00	98.80
IgD+CD27+ B Cells	pS6	3.07	3.80	2.52	3.62	1.00	27.20	3.02	5.40	2.47	3.57	1.00	53.80
IgD+CD27+ B Cells	pSTAT1	6.57	10.46	5.05	8.09	1.00	71.40	5.98	10.17	4.94	7.02	1.00	76.50
IgD+CD27+ B Cells	pSTAT3	9.90	9.53	8.51	11.28	1.00	70.00	8.73	9.10	7.80	9.66	1.00	88.40
IgD+CD27+ B Cells	pSTAT5	2.50	3.60	1.98	3.02	1.00	31.50	2.51	4.70	2.03	2.99	1.00	44.80
IgD+CD27- B Cells	IkB	4.81	6.25	3.90	5.72	1.00	35.70	4.14	5.74	3.55	4.72	1.00	54.70
IgD+CD27- B Cells	pERK	34.93	99.98	20.39	49.48	1.00	1028.00	28.70	104.3	18.04	39.36	1.00	1420.00
IgD+CD27- B Cells	pP38	1.94	2.28	1.60	2.27	1.00	15.60	1.73	2.04	1.52	1.94	1.00	20.10
IgD+CD27- B Cells	pPLCg2	7.80	9.50	6.41	9.18	1.00	59.40	7.02	10.92	5.91	8.14	1.00	95.60
IgD+CD27- B Cells	pS6	2.53	3.17	2.07	2.99	1.00	21.80	2.52	4.44	2.06	2.97	1.00	48.70
IgD+CD27- B Cells	pSTAT1	5.35	8.62	4.10	6.60	1.00	61.60	4.90	8.95	3.99	5.82	1.00	79.30
IgD+CD27- B Cells	pSTAT3	8.33	8.24	7.13	9.53	1.00	61.60	7.38	7.87	6.58	8.19	1.00	76.00
IgD+CD27- B Cells	pSTAT5	2.14	3.05	1.69	2.58	1.00	29.10	2.05	3.43	1.70	2.40	1.00	33.10
IgD-CD27+ B Cells	IkB	4.89	6.71	3.91	5.86	1.00	42.40	4.18	6.18	3.55	4.81	1.00	59.10
IgD-CD27+ B Cells	pERK	31.13	78.21	19.76	42.51	1.00	938.00	27.30	71.17	20.03	34.56	1.00	741.00
IgD-CD27+ B Cells	pP38	2.03	2.89	1.61	2.45	1.00	27.80	1.71	1.85	1.53	1.90	1.00	15.50
IgD-CD27+ B Cells	pPLCg2	8.09	9.83	6.66	9.52	1.00	62.10	7.56	11.32	6.41	8.72	1.00	86.00
IgD-CD27+ B Cells	pS6	2.72	2.96	2.29	3.15	1.00	23.30	2.74	4.27	2.30	3.17	1.00	42.40
IgD-CD27+ B Cells	pSTAT1	6.34	10.42	4.82	7.85	1.00	62.80	5.57	9.39	4.61	6.53	1.00	52.50
IgD-CD27+ B Cells	pSTAT3	7.81	10.56	6.27	9.34	1.00	74.60	6.38	8.26	5.54	7.22	1.00	71.20
IgD-CD27+ B Cells	pSTAT5	2.07	2.48	1.71	2.43	1.00	19.00	2.18	3.57	1.82	2.54	1.00	37.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	**Mean**	**SD**	**Lower CL**	**Upper CL**	**Minimum***	**Maximum**	**Mean**	**SD**	**Lower CL**	**Upper CL**	**Minimum***	**Maximum**
IgD-CD27- B Cells	IkB	3.84	5.96	2.97	4.71	1.00	47.40	3.27	5.28	2.73	3.81	1.00	53.10
IgD-CD27- B Cells	pERK	26.15	68.31	16.21	36.08	1.00	666.00	20.58	69.84	13.42	27.74	1.00	1144.00
IgD-CD27- B Cells	pP38	1.96	4.06	1.37	2.55	1.00	51.00	1.56	1.74	1.38	1.74	1.00	20.90
IgD-CD27- B Cells	pPLCg2	6.66	8.48	5.42	7.89	1.00	56.20	6.28	10.85	5.17	7.40	1.00	109.00
IgD-CD27- B Cells	pS6	2.92	5.87	2.07	3.77	1.00	54.70	2.46	4.16	2.03	2.88	1.00	39.00
IgD-CD27- B Cells	pSTAT1	5.47	9.61	4.07	6.87	1.00	66.00	4.64	8.94	3.72	5.55	1.00	74.40
IgD-CD27- B Cells	pSTAT3	6.27	7.72	5.15	7.39	1.00	64.60	5.26	6.62	4.59	5.94	1.00	57.20
IgD-CD27- B Cells	pSTAT5	1.90	2.16	1.58	2.21	1.00	12.80	1.93	4.40	1.47	2.38	1.00	67.50
NK Cells	IkB	4.69	6.04	3.81	5.57	1.00	34.50	4.20	5.60	3.63	4.77	1.00	34.90
NK Cells	pERK	41.40	109.9	25.37	57.43	1.00	1088.00	37.20	118.6	25.06	49.34	1.00	1519.00
NK Cells	pP38	1.72	2.05	1.42	2.02	1.00	15.50	1.59	1.65	1.42	1.76	1.00	16.30
NK Cells	pPLCg2	6.27	8.31	5.06	7.49	1.00	58.50	5.97	9.61	4.99	6.96	1.00	69.80
NK Cells	pS6	2.39	2.33	2.05	2.73	1.00	18.60	2.25	2.78	1.97	2.54	1.00	28.80
NK Cells	pSTAT1	5.06	8.59	3.81	6.31	1.00	60.60	4.46	7.65	3.67	5.24	1.00	59.30
NK Cells	pSTAT3	7.77	8.69	6.50	9.03	1.00	53.10	6.79	7.76	6.00	7.59	1.00	52.90
NK Cells	pSTAT5	1.97	2.38	1.62	2.31	1.00	17.50	1.91	2.68	1.63	2.18	1.00	27.40
NKT Cells	IkB	10.77	15.04	8.57	12.98	1.00	82.20	10.15	15.38	8.57	11.73	1.00	141.00
NKT Cells	pERK	62.86	178.0	36.76	88.96	1.00	1789.00	61.21	191.6	41.55	80.88	1.00	1919.00
NKT Cells	pP38	3.27	4.25	2.65	3.89	1.00	23.10	3.23	4.92	2.72	3.73	1.00	35.10
NKT Cells	pPLCg2	7.38	11.96	5.62	9.13	1.00	86.50	8.67	27.47	5.85	11.49	1.00	375.00
NKT Cells	pS6	7.51	30.73	3.00	12.02	1.00	356.00	5.16	14.88	3.63	6.68	1.00	170.00
NKT Cells	pSTAT1	17.33	24.78	13.69	20.96	1.00	149.00	17.45	40.34	13.31	21.59	1.00	595.00
NKT Cells	pSTAT3	15.74	17.31	13.20	18.28	1.00	129.00	14.09	18.86	12.16	16.03	1.00	163.00
NKT Cells	pSTAT5	3.58	5.25	2.81	4.34	1.00	40.80	3.64	7.03	2.92	4.36	1.00	67.50
Regulatory T Cells	IkB	11.17	15.57	8.90	13.43	1.00	81.30	9.96	14.61	8.47	11.45	1.00	74.60
Regulatory T Cells	pERK	49.54	132.7	30.24	68.84	1.00	1317.00	43.89	134.6	30.14	57.63	1.00	1714.00
Regulatory T Cells	pP38	2.63	3.29	2.15	3.11	1.00	24.00	2.46	3.20	2.13	2.78	1.00	24.20
Regulatory T Cells	pPLCg2	5.63	9.15	4.30	6.96	1.00	85.30	5.43	10.23	4.39	6.48	1.00	75.70
Regulatory T Cells	pS6	2.80	3.67	2.27	3.33	1.00	34.30	3.07	5.75	2.48	3.65	1.00	78.00
Regulatory T Cells	pSTAT1	19.15	35.55	13.98	24.32	1.00	329.00	17.54	35.86	13.87	21.20	1.00	359.00
Regulatory T Cells	pSTAT3	15.18	17.51	12.64	17.73	1.00	151.00	12.79	15.25	11.23	14.35	1.00	138.00
Regulatory T Cells	pSTAT5	3.05	4.36	2.41	3.68	1.00	35.80	2.95	5.01	2.44	3.46	1.00	55.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	9.44	13.57	7.46	11.41	1.00	72.20	8.40	12.30	7.14	9.65	1.00	69.60
Central Memory CD4+ T Cells	pERK	44.62	130.2	25.68	63.55	1.00	1248.00	38.25	125.5	25.44	51.07	1.00	1597.00
Central Memory CD4+ T Cells	pP38	2.56	3.29	2.08	3.03	1.00	23.50	2.26	2.77	1.98	2.54	1.00	18.90
Central Memory CD4+ T Cells	pPLCg2	5.02	7.20	3.97	6.07	1.00	48.80	4.87	9.13	3.93	5.80	1.00	72.00
Central Memory CD4+ T Cells	pS6	2.44	3.32	1.96	2.92	1.00	29.10	2.51	4.49	2.05	2.97	1.00	46.90
Central Memory CD4+ T Cells	pSTAT1	18.42	30.11	14.04	22.80	1.00	225.00	16.02	27.11	13.25	18.79	1.00	207.00
Central Memory CD4+ T Cells	pSTAT3	14.41	17.85	11.81	17.00	1.00	169.00	11.40	14.21	9.95	12.85	1.00	125.00
Central Memory CD4+ T Cells	pSTAT5	2.76	3.69	2.22	3.30	1.00	26.40	2.74	4.62	2.27	3.22	1.00	52.00
Central Memory CD8+ T Cells	IkB	7.81	11.35	6.16	9.46	1.00	63.50	6.80	10.45	5.74	7.87	1.00	91.40
Central Memory CD8+ T Cells	pERK	46.75	134.5	27.19	66.31	1.00	1259.00	37.86	112.5	26.37	49.34	1.00	1428.00
Central Memory CD8+ T Cells	pP38	2.44	3.08	2.00	2.89	1.00	20.00	2.15	2.61	1.89	2.42	1.00	19.20
Central Memory CD8+ T Cells	pPLCg2	4.95	7.15	3.91	5.98	1.00	46.50	4.75	9.32	3.80	5.70	1.00	73.60
Central Memory CD8+ T Cells	pS6	2.83	3.50	2.32	3.34	1.00	27.50	2.78	4.72	2.30	3.26	1.00	51.00
Central Memory CD8+ T Cells	pSTAT1	14.66	26.28	10.83	18.48	1.00	250.00	12.79	22.64	10.48	15.10	1.00	176.00
Central Memory CD8+ T Cells	pSTAT3	13.54	15.58	11.28	15.81	1.00	132.00	10.45	12.46	9.17	11.72	1.00	106.00
Central Memory CD8+ T Cells	pSTAT5	2.52	3.29	2.04	3.00	1.00	22.40	2.46	4.36	2.01	2.90	1.00	45.60
Effector CD4+ T Cells	IkB	6.49	9.69	5.08	7.90	1.00	59.30	5.86	9.16	4.92	6.80	1.00	61.80
Effector CD4+ T Cells	pERK	34.99	91.98	21.61	48.36	1.00	860.00	27.29	84.26	18.68	35.90	1.00	1404.00
Effector CD4+ T Cells	pP38	2.01	2.43	1.66	2.36	1.00	16.90	1.83	2.12	1.61	2.04	1.00	17.80
Effector CD4+ T Cells	pPLCg2	4.53	6.61	3.57	5.49	1.00	42.60	4.36	8.36	3.50	5.21	1.00	76.30
Effector CD4+ T Cells	pS6	2.18	2.90	1.76	2.61	1.00	24.30	2.37	4.95	1.87	2.88	1.00	60.30
Effector CD4+ T Cells	pSTAT1	11.39	18.27	8.73	14.05	1.00	156.00	10.04	17.66	8.23	11.84	1.00	160.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	11.31	12.17	9.54	13.08	1.00	94.20	9.44	10.90	8.33	10.56	1.00	84.60
Effector CD4+ T Cells	pSTAT5	2.31	2.99	1.88	2.75	1.00	25.30	2.31	4.03	1.89	2.72	1.00	48.00
Effector CD8+ T Cells	IkB	5.74	8.18	4.55	6.93	1.00	48.00	5.13	7.98	4.31	5.94	1.00	57.80
Effector CD8+ T Cells	pERK	39.52	98.05	25.25	53.78	1.00	919.00	30.19	85.65	21.43	38.94	1.00	1309.00
Effector CD8+ T Cells	pP38	1.88	2.20	1.56	2.20	1.00	17.10	1.77	2.07	1.56	1.98	1.00	16.00
Effector CD8+ T Cells	pPLCg2	4.91	6.81	3.93	5.90	1.00	42.00	4.67	9.04	3.75	5.60	1.00	85.50
Effector CD8+ T Cells	pS6	2.23	2.81	1.82	2.64	1.00	22.70	2.39	5.08	1.87	2.91	1.00	63.70
Effector CD8+ T Cells	pSTAT1	10.43	17.32	7.91	12.95	1.00	149.00	9.14	16.30	7.47	10.80	1.00	143.00
Effector CD8+ T Cells	pSTAT3	11.12	12.28	9.33	12.91	1.00	72.20	8.79	10.29	7.74	9.84	1.00	76.60
Effector CD8+ T Cells	pSTAT5	2.19	2.83	1.77	2.60	1.00	20.70	2.19	4.32	1.75	2.63	1.00	57.60
Effector Memory CD4+ T Cells	IkB	6.25	9.56	4.86	7.64	1.00	61.40	5.62	9.01	4.69	6.54	1.00	60.80
Effector Memory CD4+ T Cells	pERK	33.85	89.45	20.84	46.86	1.00	929.00	26.81	84.90	18.13	35.49	1.00	1365.00
Effector Memory CD4+ T Cells	pP38	2.08	2.61	1.70	2.46	1.00	19.40	1.81	2.03	1.60	2.02	1.00	16.40
Effector Memory CD4+ T Cells	pPLCg2	3.84	5.52	3.04	4.64	1.00	32.40	3.75	7.30	3.00	4.49	1.00	66.40
Effector Memory CD4+ T Cells	pS6	1.93	2.33	1.59	2.27	1.00	21.20	2.14	4.33	1.70	2.58	1.00	48.80
Effector Memory CD4+ T Cells	pSTAT1	13.33	23.48	9.92	16.75	1.00	211.00	11.79	22.24	9.51	14.06	1.00	175.00
Effector Memory CD4+ T Cells	pSTAT3	10.13	13.20	8.21	12.05	1.00	119.00	7.83	10.65	6.75	8.92	1.00	102.00
Effector Memory CD4+ T Cells	pSTAT5	2.16	2.66	1.77	2.55	1.00	20.70	2.12	3.80	1.74	2.51	1.00	48.40
Effector Memory CD8+ T Cells	IkB	5.56	8.45	4.33	6.79	1.00	66.00	4.65	7.60	3.87	5.42	1.00	54.40
Effector Memory CD8+ T Cells	pERK	33.66	68.74	23.66	43.66	1.00	626.00	30.10	104.7	19.39	40.80	1.00	1597.00
Effector Memory CD8+ T Cells	pP38	2.02	2.44	1.66	2.37	1.00	18.10	1.82	2.19	1.60	2.05	1.00	15.90
Effector Memory CD8+ T Cells	pPLCg2	3.91	5.48	3.12	4.71	1.00	32.60	3.74	7.26	3.00	4.48	1.00	68.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	2.17	2.65	1.78	2.55	1.00	20.50	2.31	4.35	1.87	2.76	1.00	40.60
Effector Memory CD8+ T Cells	pSTAT1	10.64	20.24	7.70	13.58	1.00	199.00	9.21	17.90	7.38	11.04	1.00	151.00
Effector Memory CD8+ T Cells	pSTAT3	9.89	13.07	7.99	11.79	1.00	102.00	7.52	9.98	6.50	8.54	1.00	93.30
Effector Memory CD8+ T Cells	pSTAT5	2.00	2.37	1.66	2.35	1.00	15.60	2.01	3.82	1.62	2.40	1.00	47.20
Myeloid Dendritic Cells	IkB	4.39	6.07	3.51	5.27	1.00	33.10	3.84	5.84	3.25	4.44	1.00	41.80
Myeloid Dendritic Cells	pERK	41.47	116.5	24.52	58.41	1.00	1119.00	33.31	92.91	23.83	42.80	1.00	1183.00
Myeloid Dendritic Cells	pP38	5.91	7.41	4.83	6.99	1.00	43.90	4.87	6.24	4.23	5.51	1.00	41.80
Myeloid Dendritic Cells	pPLCg2	5.84	8.74	4.57	7.11	1.00	63.00	5.56	10.53	4.49	6.64	1.00	114.00
Myeloid Dendritic Cells	pS6	2.11	2.50	1.74	2.47	1.00	18.70	2.35	5.54	1.78	2.91	1.00	81.30
Myeloid Dendritic Cells	pSTAT1	6.90	15.03	4.72	9.09	1.00	114.00	5.91	12.85	4.60	7.23	1.00	137.00
Myeloid Dendritic Cells	pSTAT3	4.51	6.92	3.51	5.52	1.00	68.50	3.89	6.51	3.23	4.56	1.00	74.00
Myeloid Dendritic Cells	pSTAT5	2.05	2.58	1.68	2.43	1.00	20.10	2.12	4.09	1.70	2.54	1.00	52.90
Monocytes	IkB	16.15	14.82	8.52	23.77	1.17	44.10	12.79	11.31	8.96	16.61	1.25	45.10
Monocytes	pERK	174.1	464.7	-64.8	413.0	2.29	1511.00	159.5	453.8	5.95	313.1	2.10	1880.00
Monocytes	pP38	3.17	6.04	0.06	6.27	1.00	22.90	3.03	6.02	0.99	5.07	1.00	26.10
Monocytes	pPLCg2	6.01	6.20	2.82	9.20	1.00	23.10	5.72	6.42	3.54	7.89	1.00	27.20
Monocytes	pS6	3.86	2.49	2.58	5.15	1.00	8.56	3.47	2.20	2.73	4.21	1.00	8.50
Monocytes	pSTAT1	13.15	15.62	5.12	21.19	1.00	63.20	11.04	10.82	7.38	14.70	1.00	40.80
Monocytes	pSTAT3	5.81	7.22	2.10	9.53	1.00	28.20	5.18	6.58	2.95	7.41	1.00	34.40
Monocytes	pSTAT5	2.64	2.21	1.51	3.78	1.00	9.16	2.44	2.14	1.71	3.16	1.00	9.62
Naive CD4+ T Cells	IkB	9.59	13.60	7.61	11.56	1.00	73.20	8.78	12.88	7.46	10.09	1.00	70.20
Naive CD4+ T Cells	pERK	44.34	129.6	25.50	63.19	1.00	1291.00	38.74	127.7	25.70	51.78	1.00	1676.00
Naive CD4+ T Cells	pP38	2.42	3.02	1.98	2.86	1.00	20.70	2.22	2.77	1.94	2.50	1.00	22.10
Naive CD4+ T Cells	pPLCg2	5.73	7.93	4.58	6.88	1.00	49.50	5.66	10.51	4.59	6.74	1.00	78.20
Naive CD4+ T Cells	pS6	2.79	3.85	2.23	3.35	1.00	34.90	2.90	5.71	2.31	3.48	1.00	71.60

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	15.16	23.12	11.80	18.52	1.00	171.00	13.26	22.18	10.99	15.52	1.00	202.00
Naive CD4+ T Cells	pSTAT3	15.61	16.14	13.26	17.95	1.00	129.00	13.12	14.51	11.64	14.60	1.00	125.00
Naive CD4+ T Cells	pSTAT5	3.01	4.05	2.43	3.60	1.00	31.30	2.96	5.13	2.44	3.49	1.00	60.10
Naive CD8+ T Cells	IkB	8.53	12.36	6.74	10.33	1.00	65.70	7.68	11.54	6.50	8.86	1.00	70.20
Naive CD8+ T Cells	pERK	48.79	141.5	28.21	69.37	1.00	1417.00	40.62	125.9	27.76	53.47	1.00	1580.00
Naive CD8+ T Cells	pP38	2.26	2.78	1.86	2.66	1.00	18.80	2.06	2.50	1.81	2.32	1.00	19.00
Naive CD8+ T Cells	pPLCg2	6.07	8.16	4.88	7.26	1.00	48.00	5.88	10.90	4.76	6.99	1.00	83.40
Naive CD8+ T Cells	pS6	2.79	3.69	2.26	3.33	1.00	30.50	2.92	5.91	2.31	3.52	1.00	76.70
Naive CD8+ T Cells	pSTAT1	14.14	21.77	10.97	17.31	1.00	179.00	12.40	20.21	10.34	14.47	1.00	174.00
Naive CD8+ T Cells	pSTAT3	14.66	15.40	12.42	16.90	1.00	110.00	11.85	13.02	10.52	13.18	1.00	98.80
Naive CD8+ T Cells	pSTAT5	2.78	3.87	2.22	3.35	1.00	31.00	2.77	5.11	2.25	3.29	1.00	61.40
Plasmoid Dendritic Cells	IkB	5.22	8.56	3.98	6.47	1.00	73.20	4.22	6.36	3.58	4.87	1.00	41.70
Plasmoid Dendritic Cells	pERK	42.73	115.2	25.98	59.48	1.00	1017.00	35.38	105.8	24.59	46.18	1.00	1273.00
Plasmoid Dendritic Cells	pP38	2.87	4.10	2.28	3.47	1.00	24.40	2.29	3.13	1.97	2.61	1.00	27.10
Plasmoid Dendritic Cells	pPLCg2	6.44	9.13	5.12	7.77	1.00	67.70	5.73	10.37	4.67	6.79	1.00	103.00
Plasmoid Dendritic Cells	pS6	2.72	3.69	2.18	3.26	1.00	31.30	2.56	5.01	2.05	3.07	1.00	57.60
Plasmoid Dendritic Cells	pSTAT1	6.47	11.91	4.74	8.20	1.00	93.50	5.79	11.82	4.59	7.00	1.00	95.80
Plasmoid Dendritic Cells	pSTAT3	5.88	7.24	4.83	6.94	1.00	55.60	4.50	6.58	3.82	5.17	1.00	67.50
Plasmoid Dendritic Cells	pSTAT5	2.15	2.74	1.75	2.55	1.00	17.90	2.14	5.06	1.62	2.65	1.00	84.30
Plasmablasts	IkB	7.02	8.68	5.75	8.29	1.00	42.60	6.52	8.82	5.61	7.42	1.00	42.90
Plasmablasts	pERK	54.21	139.2	33.84	74.57	1.00	1328.00	49.79	152.8	34.11	65.47	1.00	1925.00
Plasmablasts	pP38	3.10	4.24	2.48	3.72	1.00	28.30	2.66	3.65	2.28	3.03	1.00	35.00
Plasmablasts	pPLCg2	8.12	9.51	6.73	9.51	1.00	62.10	8.35	14.37	6.87	9.82	1.00	133.00
Plasmablasts	pS6	3.69	4.05	3.09	4.28	1.00	22.60	3.60	5.14	3.07	4.13	1.00	47.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-21

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	7.38	11.52	5.69	9.06	1.00	67.50	6.52	10.04	5.49	7.55	1.00	68.80
Plasmablasts	pSTAT3	9.47	9.12	8.14	10.80	1.00	64.80	8.27	9.24	7.32	9.22	1.00	77.50
Plasmablasts	pSTAT5	2.97	4.29	2.35	3.60	1.00	25.90	2.79	4.49	2.33	3.25	1.00	39.80
Transitional B Cells	IkB	7.25	8.77	5.97	8.54	1.00	45.50	6.68	9.22	5.74	7.62	1.00	62.60
Transitional B Cells	pERK	51.01	128.8	32.17	69.85	1.21	1058.00	46.51	136.7	32.51	60.51	1.00	1774.00
Transitional B Cells	pP38	3.47	4.04	2.88	4.06	1.00	23.30	3.56	4.60	3.09	4.03	1.00	39.00
Transitional B Cells	pPLCg2	9.93	12.05	8.16	11.69	1.00	70.70	9.56	16.13	7.91	11.21	1.00	142.00
Transitional B Cells	pS6	4.20	5.15	3.45	4.95	1.00	39.50	4.55	10.18	3.51	5.59	1.00	139.00
Transitional B Cells	pSTAT1	8.03	14.20	5.95	10.10	1.00	125.00	7.13	12.92	5.81	8.45	1.00	121.00
Transitional B Cells	pSTAT3	11.09	9.22	9.74	12.44	1.00	51.20	10.61	10.92	9.49	11.73	1.00	85.30
Transitional B Cells	pSTAT5	2.82	3.99	2.23	3.40	1.00	26.40	2.95	5.12	2.42	3.47	1.00	45.20

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
B Cells	IkB	5.55	7.50	4.46	6.64	1.00	44.40	4.92	7.35	4.17	5.66	1.00	73.20
B Cells	pERK	39.46	112.5	23.10	55.83	1.00	1141.00	36.60	111.7	25.24	47.96	1.00	1203.00
B Cells	pP38	2.31	2.83	1.90	2.73	1.00	17.20	1.90	2.15	1.68	2.12	1.00	17.60
B Cells	pPLCg2	9.06	11.26	7.42	10.69	1.00	73.20	8.01	12.14	6.77	9.24	1.00	97.20
B Cells	pS6	3.07	4.54	2.41	3.74	1.00	35.50	2.88	5.62	2.31	3.45	1.00	81.20
B Cells	pSTAT1	5.54	8.74	4.27	6.81	1.00	55.80	5.14	9.12	4.21	6.06	1.00	83.60
B Cells	pSTAT3	5.70	9.16	4.37	7.04	1.00	75.80	4.60	7.94	3.80	5.41	1.00	71.00
B Cells	pSTAT5	2.18	3.16	1.72	2.64	1.00	26.40	2.30	5.36	1.75	2.84	1.00	82.00
CD16+ NK Cells	IkB	5.75	7.39	4.64	6.86	1.00	43.70	5.74	9.28	4.77	6.71	1.00	91.30
CD16+ NK Cells	pERK	50.37	115.6	33.07	67.67	1.00	1170.00	48.18	109.8	36.73	59.63	1.00	1258.00
CD16+ NK Cells	pP38	2.11	2.81	1.69	2.53	1.00	18.30	1.93	2.77	1.64	2.22	1.00	25.20
CD16+ NK Cells	pPLCg2	10.06	12.89	8.13	11.99	1.00	94.80	10.63	17.32	8.82	12.43	1.00	159.00
CD16+ NK Cells	pS6	2.91	3.34	2.41	3.41	1.00	29.60	3.14	5.92	2.53	3.76	1.00	82.80
CD16+ NK Cells	pSTAT1	5.08	10.43	3.52	6.64	1.00	67.70	4.21	8.23	3.35	5.07	1.00	70.60
CD16+ NK Cells	pSTAT3	4.19	7.43	3.08	5.30	1.00	61.30	3.57	6.00	2.94	4.19	1.00	52.00
CD16+ NK Cells	pSTAT5	2.00	2.49	1.63	2.37	1.00	16.00	2.05	4.25	1.61	2.50	1.00	62.30
CD16+ Monocytes	IkB	10.86	12.94	8.98	12.75	1.00	68.90	9.34	12.18	8.10	10.58	1.00	116.00
CD16+ Monocytes	pERK	78.09	151.2	56.09	100.1	1.41	1457.00	73.80	156.9	57.85	89.76	1.00	1580.00
CD16+ Monocytes	pP38	5.20	6.71	4.23	6.18	1.00	43.50	4.41	5.04	3.90	4.93	1.00	36.80
CD16+ Monocytes	pPLCg2	14.14	17.58	11.58	16.69	1.00	115.00	13.54	19.18	11.59	15.49	1.00	173.00
CD16+ Monocytes	pS6	4.77	6.01	3.90	5.64	1.00	45.20	4.41	8.21	3.57	5.24	1.00	124.00
CD16+ Monocytes	pSTAT1	12.65	21.56	9.52	15.79	1.00	131.00	11.24	18.63	9.35	13.14	1.00	132.00
CD16+ Monocytes	pSTAT3	10.51	14.59	8.39	12.64	1.00	91.00	8.55	11.35	7.40	9.71	1.00	75.00
CD16+ Monocytes	pSTAT5	3.78	6.10	2.89	4.67	1.00	53.90	3.82	8.55	2.95	4.69	1.00	121.00
CD16- NK Cells	IkB	4.54	5.94	3.68	5.41	1.00	33.40	4.14	6.60	3.47	4.81	1.00	69.00
CD16- NK Cells	pERK	39.01	102.8	24.05	53.96	1.00	1055.00	35.23	98.34	25.23	45.23	1.00	1043.00
CD16- NK Cells	pP38	1.95	2.32	1.61	2.28	1.00	16.00	1.59	1.64	1.42	1.75	1.00	18.00
CD16- NK Cells	pPLCg2	5.96	7.99	4.80	7.13	1.00	54.50	5.44	9.36	4.49	6.40	1.00	80.60
CD16- NK Cells	pS6	2.64	3.34	2.16	3.13	1.00	30.20	2.53	4.59	2.06	2.99	1.00	64.70
CD16- NK Cells	pSTAT1	5.00	8.67	3.74	6.26	1.00	57.50	4.64	8.34	3.79	5.49	1.00	68.60
CD16- NK Cells	pSTAT3	3.68	6.64	2.71	4.65	1.00	59.40	3.04	5.78	2.45	3.63	1.00	61.10
CD16- NK Cells	pSTAT5	1.92	2.43	1.56	2.27	1.00	19.30	2.00	4.32	1.56	2.44	1.00	65.30
CD16- Monocytes	IkB	9.92	12.65	8.08	11.76	1.00	65.90	8.77	12.76	7.47	10.07	1.00	112.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	60.26	153.3	37.96	82.57	1.00	1576.00	52.94	134.8	39.24	66.64	1.00	1489.00
CD16- Monocytes	pP38	5.32	6.27	4.41	6.24	1.00	43.50	4.34	4.66	3.87	4.82	1.00	37.40
CD16- Monocytes	pPLCg2	8.77	11.39	7.11	10.43	1.00	74.60	8.01	13.05	6.68	9.34	1.00	121.00
CD16- Monocytes	pS6	3.84	5.59	3.02	4.65	1.00	46.00	3.54	7.29	2.80	4.28	1.00	108.00
CD16- Monocytes	pSTAT1	17.25	26.96	13.33	21.17	1.00	188.00	16.07	26.29	13.40	18.74	1.00	220.00
CD16- Monocytes	pSTAT3	10.82	15.83	8.52	13.12	1.00	135.00	8.85	12.50	7.58	10.13	1.00	119.00
CD16- Monocytes	pSTAT5	3.36	5.01	2.63	4.09	1.00	39.70	3.38	7.26	2.64	4.12	1.00	102.00
CD4+ T Cells	IkB	8.82	12.24	7.04	10.60	1.00	64.90	7.98	12.45	6.72	9.25	1.00	106.00
CD4+ T Cells	pERK	42.57	121.8	24.86	60.29	1.00	1266.00	37.17	111.1	25.88	48.46	1.00	1291.00
CD4+ T Cells	pP38	2.67	3.41	2.18	3.17	1.00	23.60	2.17	2.53	1.92	2.43	1.00	22.70
CD4+ T Cells	pPLCg2	5.32	8.40	4.10	6.54	1.00	58.30	5.02	10.34	3.97	6.07	1.00	115.00
CD4+ T Cells	pS6	2.79	4.40	2.15	3.43	1.00	37.60	2.75	6.48	2.09	3.41	1.00	102.00
CD4+ T Cells	pSTAT1	19.50	28.50	15.35	23.64	1.00	200.00	18.20	29.04	15.25	21.15	1.00	227.00
CD4+ T Cells	pSTAT3	14.18	17.94	11.57	16.79	1.00	153.00	11.54	14.56	10.06	13.02	1.00	147.00
CD4+ T Cells	pSTAT5	2.77	3.98	2.19	3.35	1.00	29.90	2.86	6.27	2.23	3.50	1.00	94.80
CD4-CD8- T Cells	IkB	5.13	7.83	3.99	6.27	1.00	51.00	4.32	7.47	3.56	5.08	1.00	77.00
CD4-CD8- T Cells	pERK	39.19	117.0	22.17	56.21	1.00	1190.00	32.55	104.5	21.92	43.18	1.00	1082.00
CD4-CD8- T Cells	pP38	2.21	2.70	1.81	2.60	1.00	19.40	1.79	2.23	1.56	2.02	1.00	23.30
CD4-CD8- T Cells	pPLCg2	5.28	7.93	4.13	6.44	1.00	54.40	4.71	10.02	3.69	5.73	1.00	95.00
CD4-CD8- T Cells	pS6	2.50	3.93	1.93	3.07	1.00	31.50	2.38	5.59	1.81	2.95	1.00	82.80
CD4-CD8- T Cells	pSTAT1	7.57	12.17	5.80	9.34	1.00	62.60	7.01	12.71	5.72	8.30	1.00	87.70
CD4-CD8- T Cells	pSTAT3	5.46	9.46	4.09	6.84	1.00	82.30	4.43	8.63	3.56	5.31	1.00	94.20
CD4-CD8- T Cells	pSTAT5	1.93	2.69	1.54	2.32	1.00	18.90	2.04	5.03	1.53	2.56	1.00	78.40
CD8+ T Cells	IkB	7.72	10.77	6.15	9.28	1.00	55.80	6.85	11.11	5.72	7.98	1.00	99.30
CD8+ T Cells	pERK	47.01	130.4	28.04	65.97	1.00	1377.00	39.30	113.2	27.79	50.81	1.00	1280.00
CD8+ T Cells	pP38	2.47	3.11	2.02	2.92	1.00	21.70	2.01	2.27	1.78	2.24	1.00	19.30
CD8+ T Cells	pPLCg2	5.66	8.58	4.41	6.91	1.00	55.60	5.23	10.65	4.15	6.32	1.00	114.00
CD8+ T Cells	pS6	2.88	4.33	2.25	3.51	1.00	35.10	2.80	6.51	2.14	3.46	1.00	101.00
CD8+ T Cells	pSTAT1	13.10	20.35	10.14	16.06	1.00	142.00	11.95	19.65	9.95	13.95	1.00	150.00
CD8+ T Cells	pSTAT3	7.71	13.03	5.81	9.60	1.00	115.00	6.07	10.80	4.97	7.17	1.00	123.00
CD8+ T Cells	pSTAT5	2.22	3.28	1.75	2.70	1.00	25.60	2.37	5.84	1.78	2.96	1.00	89.90
Dendritic Cells	IkB	4.06	5.81	3.21	4.90	1.00	32.50	3.55	6.15	2.93	4.18	1.00	57.70
Dendritic Cells	pERK	40.74	133.2	21.37	60.11	1.00	1524.00	31.09	88.93	22.05	40.14	1.00	1202.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	4.48	5.98	3.61	5.34	1.00	42.30	3.56	5.08	3.05	4.08	1.00	35.10
Dendritic Cells	pPLCg2	5.71	9.02	4.40	7.02	1.00	76.70	4.87	8.65	3.99	5.74	1.00	81.80
Dendritic Cells	pS6	2.20	3.21	1.73	2.67	1.00	27.70	2.21	4.93	1.70	2.71	1.00	74.20
Dendritic Cells	pSTAT1	5.75	10.53	4.22	7.28	1.00	58.00	5.06	10.41	4.00	6.12	1.00	87.20
Dendritic Cells	pSTAT3	3.76	6.71	2.79	4.74	1.00	58.80	3.13	6.81	2.43	3.82	1.00	80.50
Dendritic Cells	pSTAT5	1.82	2.24	1.49	2.14	1.00	15.50	1.97	4.40	1.52	2.41	1.00	69.20
HLADR+ NK Cells	IkB	5.68	6.72	4.70	6.66	1.00	34.30	4.96	6.41	4.31	5.61	1.00	41.40
HLADR+ NK Cells	pERK	48.08	117.6	30.87	65.29	1.00	1210.00	44.07	108.8	32.97	55.16	1.00	1160.00
HLADR+ NK Cells	pP38	2.43	3.17	1.96	2.89	1.00	19.90	1.99	2.16	1.77	2.21	1.00	20.40
HLADR+ NK Cells	pPLCg2	8.87	11.50	7.18	10.55	1.00	91.40	7.99	12.18	6.75	9.23	1.00	123.00
HLADR+ NK Cells	pS6	3.11	3.21	2.64	3.57	1.00	25.00	2.77	3.09	2.45	3.08	1.00	27.60
HLADR+ NK Cells	pSTAT1	5.42	8.71	4.15	6.69	1.00	58.10	5.07	8.69	4.18	5.95	1.00	72.40
HLADR+ NK Cells	pSTAT3	4.22	6.99	3.20	5.24	1.00	58.90	3.53	6.21	2.90	4.16	1.00	52.60
HLADR+ NK Cells	pSTAT5	2.19	2.66	1.80	2.58	1.00	19.60	2.04	2.91	1.74	2.34	1.00	32.10
HLADR+CD38+ CD4+ T Cells	IkB	10.19	12.85	8.32	12.06	1.00	69.80	9.21	13.02	7.88	10.53	1.00	110.00
HLADR+CD38+ CD4+ T Cells	pERK	53.68	129.3	34.88	72.48	1.00	1317.00	48.15	117.8	36.17	60.12	1.00	1294.00
HLADR+CD38+ CD4+ T Cells	pP38	3.79	4.87	3.09	4.50	1.00	32.00	3.16	3.72	2.79	3.54	1.00	32.20
HLADR+CD38+ CD4+ T Cells	pPLCg2	9.29	13.68	7.30	11.28	1.00	81.30	8.83	16.03	7.20	10.46	1.00	128.00
HLADR+CD38+ CD4+ T Cells	pS6	4.00	5.82	3.16	4.85	1.00	51.00	3.79	7.70	3.01	4.58	1.00	116.00
HLADR+CD38+ CD4+ T Cells	pSTAT1	18.95	26.69	15.06	22.83	1.00	155.00	17.39	26.87	14.66	20.12	1.00	203.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	14.27	16.00	11.94	16.60	1.00	104.00	11.82	13.70	10.43	13.22	1.00	104.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	3.45	4.88	2.74	4.16	1.00	35.90	3.56	7.70	2.78	4.35	1.00	105.00
HLADR+CD38+ CD8+ T Cells	IkB	8.71	10.88	7.13	10.29	1.00	64.00	7.60	10.69	6.51	8.68	1.00	107.00
HLADR+CD38+ CD8+ T Cells	pERK	53.47	129.0	34.71	72.23	1.00	1343.00	46.80	114.3	35.17	58.42	1.00	1291.00
HLADR+CD38+ CD8+ T Cells	pP38	3.42	4.45	2.78	4.07	1.00	29.50	2.91	3.44	2.56	3.26	1.00	28.70
HLADR+CD38+ CD8+ T Cells	pPLCg2	9.69	13.90	7.67	11.71	1.00	92.90	8.96	15.54	7.38	10.54	1.00	129.00
HLADR+CD38+ CD8+ T Cells	pS6	3.98	6.21	3.08	4.89	1.00	52.30	3.67	7.34	2.92	4.42	1.00	108.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	12.62	18.32	9.95	15.28	1.00	120.00	11.10	17.41	9.33	12.87	1.00	121.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	8.43	12.10	6.67	10.19	1.00	88.40	6.87	11.01	5.75	7.99	1.00	97.40
HLADR+CD38+ CD8+ T Cells	pSTAT5	2.86	4.22	2.25	3.48	1.00	29.90	3.04	7.11	2.32	3.77	1.00	104.00
IgD+CD27+ B Cells	IkB	6.16	8.03	4.99	7.32	1.00	51.90	5.40	7.81	4.61	6.19	1.00	76.40
IgD+CD27+ B Cells	pERK	42.96	116.0	26.08	59.83	1.00	1174.00	40.09	116.2	28.27	51.91	1.00	1217.00
IgD+CD27+ B Cells	pP38	2.53	3.07	2.09	2.98	1.00	19.10	2.09	2.35	1.85	2.33	1.00	19.90
IgD+CD27+ B Cells	pPLCg2	9.93	12.01	8.18	11.68	1.00	75.70	8.79	12.83	7.48	10.09	1.00	108.00
IgD+CD27+ B Cells	pS6	3.39	4.85	2.68	4.09	1.00	39.70	3.12	5.93	2.52	3.72	1.00	85.10
IgD+CD27+ B Cells	pSTAT1	6.18	9.83	4.75	7.61	1.00	66.60	5.61	9.78	4.61	6.60	1.00	93.20
IgD+CD27+ B Cells	pSTAT3	6.44	9.63	5.04	7.84	1.00	80.30	5.23	8.38	4.37	6.08	1.00	72.40
IgD+CD27+ B Cells	pSTAT5	2.38	3.40	1.89	2.88	1.00	27.40	2.43	5.70	1.86	3.01	1.00	88.60
IgD+CD27- B Cells	IkB	4.85	6.59	3.89	5.81	1.00	46.00	4.28	6.51	3.61	4.94	1.00	66.80
IgD+CD27- B Cells	pERK	34.80	95.69	20.89	48.72	1.00	896.00	32.04	100.1	21.87	42.22	1.00	1243.00
IgD+CD27- B Cells	pP38	2.14	2.64	1.76	2.53	1.00	17.20	1.71	1.89	1.51	1.90	1.00	18.50
IgD+CD27- B Cells	pPLCg2	8.21	10.27	6.72	9.70	1.00	66.60	6.99	10.75	5.90	8.08	1.00	90.40
IgD+CD27- B Cells	pS6	2.82	4.17	2.22	3.43	1.00	30.00	2.61	5.20	2.08	3.14	1.00	74.80
IgD+CD27- B Cells	pSTAT1	4.92	7.60	3.81	6.03	1.00	40.20	4.56	8.14	3.74	5.39	1.00	67.00
IgD+CD27- B Cells	pSTAT3	5.28	8.25	4.08	6.48	1.00	66.50	4.25	7.05	3.53	4.96	1.00	66.30
IgD+CD27- B Cells	pSTAT5	1.94	2.56	1.57	2.32	1.00	18.90	2.04	4.52	1.58	2.50	1.00	65.10
IgD-CD27+ B Cells	IkB	4.98	7.12	3.95	6.02	1.00	40.90	4.34	6.78	3.65	5.03	1.00	60.90
IgD-CD27+ B Cells	pERK	32.78	75.76	21.76	43.80	1.00	701.00	28.52	73.21	21.07	35.96	1.00	879.00
IgD-CD27+ B Cells	pP38	2.39	3.94	1.82	2.96	1.00	36.30	1.68	1.74	1.51	1.86	1.00	14.70
IgD-CD27+ B Cells	pPLCg2	8.76	10.98	7.16	10.36	1.00	76.10	7.65	11.73	6.46	8.85	1.00	98.80
IgD-CD27+ B Cells	pS6	3.14	4.21	2.53	3.75	1.00	35.70	2.98	6.05	2.36	3.59	1.00	90.40
IgD-CD27+ B Cells	pSTAT1	6.07	11.28	4.43	7.71	1.00	95.30	5.43	10.07	4.40	6.45	1.00	99.40
IgD-CD27+ B Cells	pSTAT3	5.70	14.70	3.56	7.84	1.00	164.00	4.29	8.34	3.44	5.13	1.00	84.60
IgD-CD27+ B Cells	pSTAT5	2.08	3.18	1.62	2.55	1.00	25.30	2.50	10.08	1.48	3.53	1.00	186.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	3.74	5.15	2.99	4.49	1.00	31.00	3.41	5.64	2.83	3.98	1.00	58.60
IgD-CD27- B Cells	pERK	28.59	83.69	16.42	40.77	1.00	894.00	19.58	44.32	15.06	24.10	1.00	676.00
IgD-CD27- B Cells	pP38	1.98	2.55	1.61	2.36	1.00	18.80	1.55	1.83	1.36	1.73	1.00	24.60
IgD-CD27- B Cells	pPLCg2	6.98	8.49	5.74	8.21	1.00	59.80	6.06	9.49	5.10	7.03	1.00	76.90
IgD-CD27- B Cells	pS6	2.59	3.51	2.08	3.10	1.00	28.80	2.72	5.55	2.15	3.28	1.00	61.20
IgD-CD27- B Cells	pSTAT1	4.82	8.12	3.64	6.00	1.00	49.80	4.38	7.99	3.57	5.20	1.00	52.00
IgD-CD27- B Cells	pSTAT3	4.20	6.44	3.26	5.13	1.00	50.30	3.57	6.74	2.88	4.25	1.00	73.20
IgD-CD27- B Cells	pSTAT5	1.81	2.54	1.44	2.18	1.00	20.90	2.05	5.04	1.54	2.57	1.00	61.80
NK Cells	IkB	4.62	5.76	3.78	5.46	1.00	32.90	4.10	5.38	3.55	4.65	1.00	37.60
NK Cells	pERK	41.65	107.4	25.99	57.32	1.00	1116.00	37.59	101.3	27.27	47.92	1.00	1131.00
NK Cells	pP38	1.94	2.37	1.60	2.29	1.00	16.80	1.59	1.67	1.42	1.76	1.00	18.60
NK Cells	pPLCg2	6.62	8.78	5.34	7.90	1.00	70.40	5.88	8.89	4.97	6.79	1.00	71.40
NK Cells	pS6	2.52	2.62	2.14	2.90	1.00	20.70	2.30	2.55	2.04	2.56	1.00	23.40
NK Cells	pSTAT1	4.80	8.82	3.52	6.09	1.00	64.80	4.18	7.34	3.43	4.93	1.00	66.00
NK Cells	pSTAT3	3.68	6.49	2.73	4.63	1.00	54.50	2.96	5.18	2.43	3.49	1.00	47.50
NK Cells	pSTAT5	1.85	2.19	1.53	2.17	1.00	17.60	1.75	2.31	1.51	1.99	1.00	28.30
NKT Cells	IkB	10.09	12.18	8.30	11.89	1.00	53.10	10.15	14.14	8.71	11.60	1.00	90.30
NKT Cells	pERK	62.84	169.0	37.98	87.70	1.00	1784.00	62.42	184.0	43.61	81.23	1.00	1686.00
NKT Cells	pP38	3.71	5.11	2.96	4.46	1.00	33.00	3.26	4.49	2.80	3.72	1.00	31.90
NKT Cells	pPLCg2	6.46	9.27	5.10	7.82	1.00	77.40	6.56	12.63	5.26	7.85	1.00	138.00
NKT Cells	pS6	5.27	18.56	2.54	8.00	1.00	242.00	4.45	10.87	3.34	5.56	1.00	137.00
NKT Cells	pSTAT1	19.84	26.61	15.93	23.76	1.00	154.00	18.17	27.00	15.41	20.93	1.00	199.00
NKT Cells	pSTAT3	13.16	17.11	10.64	15.67	1.00	141.00	11.45	16.91	9.72	13.18	1.00	159.00
NKT Cells	pSTAT5	2.99	4.13	2.39	3.60	1.00	34.60	3.03	4.68	2.55	3.51	1.00	47.00
Regulatory T Cells	IkB	10.76	13.96	8.73	12.79	1.00	72.00	10.19	16.51	8.51	11.87	1.00	159.00
Regulatory T Cells	pERK	49.53	131.1	30.46	68.59	1.00	1393.00	43.14	115.5	31.40	54.89	1.00	1320.00
Regulatory T Cells	pP38	3.03	3.93	2.46	3.60	1.00	31.50	2.50	3.02	2.20	2.81	1.00	25.30
Regulatory T Cells	pPLCg2	5.81	8.99	4.50	7.11	1.00	76.70	5.39	10.42	4.33	6.45	1.00	107.00
Regulatory T Cells	pS6	3.12	4.60	2.45	3.79	1.00	44.70	3.23	8.42	2.37	4.08	1.00	128.00
Regulatory T Cells	pSTAT1	23.40	39.84	17.61	29.20	1.00	312.00	21.13	36.93	17.37	24.88	1.00	313.00
Regulatory T Cells	pSTAT3	16.00	18.87	13.25	18.74	1.00	166.00	12.80	15.37	11.24	14.36	1.00	153.00
Regulatory T Cells	pSTAT5	2.86	4.34	2.23	3.49	1.00	35.00	2.92	6.68	2.24	3.60	1.00	101.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	9.64	13.21	7.72	11.56	1.00	68.80	8.44	12.59	7.16	9.72	1.00	90.30
Central Memory CD4+ T Cells	pERK	44.80	122.8	26.94	62.66	1.00	1270.00	38.78	112.6	27.32	50.23	1.00	1248.00
Central Memory CD4+ T Cells	pP38	2.92	3.84	2.36	3.48	1.00	28.10	2.33	2.67	2.05	2.60	1.00	24.60
Central Memory CD4+ T Cells	pPLCg2	5.22	7.93	4.07	6.37	1.00	57.00	4.73	8.95	3.82	5.64	1.00	82.50
Central Memory CD4+ T Cells	pS6	2.71	4.23	2.10	3.33	1.00	35.60	2.60	5.25	2.07	3.13	1.00	74.20
Central Memory CD4+ T Cells	pSTAT1	21.61	32.57	16.87	26.35	1.00	229.00	19.59	32.20	16.32	22.86	1.00	246.00
Central Memory CD4+ T Cells	pSTAT3	14.65	19.40	11.82	17.47	1.00	184.00	11.45	14.54	9.98	12.93	1.00	157.00
Central Memory CD4+ T Cells	pSTAT5	2.64	3.87	2.08	3.20	1.00	31.40	2.64	5.36	2.10	3.19	1.00	72.80
Central Memory CD8+ T Cells	IkB	8.05	11.27	6.41	9.69	1.00	62.90	6.78	10.64	5.69	7.86	1.00	81.70
Central Memory CD8+ T Cells	pERK	46.39	121.1	28.78	64.00	1.00	1207.00	38.89	105.2	28.18	49.59	1.00	1157.00
Central Memory CD8+ T Cells	pP38	2.82	3.71	2.28	3.36	1.00	24.80	2.19	2.42	1.94	2.44	1.00	19.10
Central Memory CD8+ T Cells	pPLCg2	5.14	7.89	3.99	6.29	1.00	55.30	4.51	8.41	3.66	5.37	1.00	81.80
Central Memory CD8+ T Cells	pS6	3.18	4.37	2.55	3.82	1.00	36.30	2.93	6.08	2.31	3.54	1.00	88.90
Central Memory CD8+ T Cells	pSTAT1	13.40	22.84	10.08	16.72	1.00	196.00	12.31	20.74	10.20	14.42	1.00	156.00
Central Memory CD8+ T Cells	pSTAT3	7.03	13.51	5.06	8.99	1.00	132.00	5.21	10.59	4.13	6.28	1.00	131.00
Central Memory CD8+ T Cells	pSTAT5	2.16	3.25	1.69	2.63	1.00	25.50	2.19	4.72	1.71	2.67	1.00	63.20
Effector CD4+ T Cells	IkB	6.31	9.06	4.99	7.62	1.00	53.60	5.70	9.76	4.71	6.70	1.00	93.30
Effector CD4+ T Cells	pERK	33.74	74.46	22.91	44.57	1.00	676.00	26.86	72.98	19.42	34.30	1.00	1170.00
Effector CD4+ T Cells	pP38	2.28	2.82	1.87	2.69	1.00	21.60	1.84	2.12	1.62	2.06	1.00	21.70
Effector CD4+ T Cells	pPLCg2	4.79	7.58	3.69	5.89	1.00	55.80	4.35	9.36	3.39	5.30	1.00	105.00
Effector CD4+ T Cells	pS6	2.50	4.12	1.90	3.10	1.00	35.50	2.45	6.04	1.83	3.06	1.00	94.80
Effector CD4+ T Cells	pSTAT1	14.96	22.17	11.73	18.18	1.00	170.00	14.07	23.67	11.65	16.48	1.00	187.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	11.64	13.09	9.74	13.55	1.00	91.90	9.55	11.85	8.35	10.76	1.00	116.00
Effector CD4+ T Cells	pSTAT5	2.32	3.27	1.84	2.79	1.00	26.70	2.40	5.62	1.82	2.97	1.00	89.10
Effector CD8+ T Cells	IkB	5.78	8.19	4.59	6.97	1.00	43.70	5.01	8.73	4.12	5.90	1.00	85.30
Effector CD8+ T Cells	pERK	39.92	96.10	25.95	53.90	1.00	1040.00	28.94	69.16	21.90	35.98	1.00	1128.00
Effector CD8+ T Cells	pP38	2.11	2.60	1.73	2.49	1.00	20.60	1.74	1.93	1.54	1.94	1.00	18.80
Effector CD8+ T Cells	pPLCg2	5.18	7.73	4.06	6.31	1.00	51.90	4.66	9.76	3.67	5.66	1.00	106.00
Effector CD8+ T Cells	pS6	2.44	3.86	1.88	3.00	1.00	33.10	2.64	7.18	1.91	3.37	1.00	91.70
Effector CD8+ T Cells	pSTAT1	10.17	15.82	7.87	12.48	1.00	112.00	9.35	16.51	7.67	11.03	1.00	131.00
Effector CD8+ T Cells	pSTAT3	6.29	9.71	4.88	7.71	1.00	73.80	5.06	8.70	4.18	5.95	1.00	95.80
Effector CD8+ T Cells	pSTAT5	1.89	2.65	1.50	2.27	1.00	21.60	2.04	5.08	1.52	2.55	1.00	81.10
Effector Memory CD4+ T Cells	IkB	6.45	9.83	5.02	7.87	1.00	64.50	5.32	8.90	4.42	6.23	1.00	63.30
Effector Memory CD4+ T Cells	pERK	35.57	95.75	21.65	49.50	1.00	901.00	27.15	75.05	19.51	34.80	1.00	1131.00
Effector Memory CD4+ T Cells	pP38	2.31	3.00	1.87	2.75	1.00	22.90	1.84	2.08	1.62	2.05	1.00	21.20
Effector Memory CD4+ T Cells	pPLCg2	4.06	6.32	3.14	4.98	1.00	43.90	3.54	7.02	2.83	4.26	1.00	68.60
Effector Memory CD4+ T Cells	pS6	2.16	3.49	1.65	2.66	1.00	30.00	2.08	4.22	1.65	2.51	1.00	61.40
Effector Memory CD4+ T Cells	pSTAT1	14.49	24.61	10.91	18.07	1.00	217.00	13.09	24.11	10.63	15.54	1.00	199.00
Effector Memory CD4+ T Cells	pSTAT3	9.40	12.84	7.53	11.27	1.00	114.00	7.27	11.18	6.13	8.41	1.00	142.00
Effector Memory CD4+ T Cells	pSTAT5	2.02	2.70	1.63	2.42	1.00	19.10	2.02	4.41	1.57	2.47	1.00	70.60
Effector Memory CD8+ T Cells	IkB	5.75	8.87	4.46	7.04	1.00	58.60	4.76	8.56	3.89	5.63	1.00	73.20
Effector Memory CD8+ T Cells	pERK	36.56	86.07	24.04	49.08	1.00	894.00	26.61	61.14	20.37	32.84	1.00	899.00
Effector Memory CD8+ T Cells	pP38	2.30	2.82	1.89	2.71	1.00	20.30	1.79	2.01	1.59	2.00	1.00	19.10
Effector Memory CD8+ T Cells	pPLCg2	3.93	5.78	3.09	4.77	1.00	42.00	3.72	7.63	2.94	4.50	1.00	73.60

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	2.46	3.55	1.94	2.98	1.00	31.50	2.25	4.74	1.77	2.73	1.00	64.70
Effector Memory CD8+ T Cells	pSTAT1	9.84	18.08	7.21	12.47	1.00	166.00	8.86	16.59	7.17	10.55	1.00	132.00
Effector Memory CD8+ T Cells	pSTAT3	4.82	9.13	3.49	6.14	1.00	84.60	3.89	8.64	3.01	4.77	1.00	115.00
Effector Memory CD8+ T Cells	pSTAT5	1.71	2.12	1.41	2.02	1.00	14.40	1.90	4.34	1.46	2.34	1.00	59.30
Myeloid Dendritic Cells	IkB	4.31	5.96	3.44	5.17	1.00	33.70	3.73	6.22	3.10	4.36	1.00	55.10
Myeloid Dendritic Cells	pERK	43.42	135.8	23.67	63.17	1.00	1554.00	33.74	89.38	24.66	42.83	1.00	1232.00
Myeloid Dendritic Cells	pP38	6.25	7.52	5.16	7.34	1.00	44.40	5.09	6.63	4.42	5.76	1.00	48.20
Myeloid Dendritic Cells	pPLCg2	6.19	9.49	4.81	7.57	1.00	80.00	5.32	9.20	4.38	6.25	1.00	82.00
Myeloid Dendritic Cells	pS6	2.44	3.88	1.87	3.00	1.00	32.90	2.35	5.18	1.82	2.88	1.00	74.60
Myeloid Dendritic Cells	pSTAT1	6.35	12.00	4.60	8.09	1.00	69.40	5.61	11.47	4.45	6.78	1.00	107.00
Myeloid Dendritic Cells	pSTAT3	3.95	7.32	2.88	5.01	1.00	67.60	3.32	7.44	2.57	4.08	1.00	88.40
Myeloid Dendritic Cells	pSTAT5	1.97	2.64	1.59	2.36	1.00	22.90	2.06	4.06	1.64	2.47	1.00	53.10
Monocytes	IkB	15.59	13.03	9.11	22.07	1.14	45.50	12.56	10.64	8.96	16.16	1.32	39.70
Monocytes	pERK	159.0	440.9	-60.2	378.3	3.58	1567.00	140.2	384.9	9.95	270.4	1.91	1489.00
Monocytes	pP38	2.81	5.19	0.23	5.39	1.00	17.80	2.77	5.11	1.04	4.50	1.00	21.40
Monocytes	pPLCg2	5.16	4.87	2.74	7.58	1.00	18.40	5.53	5.97	3.51	7.54	1.00	21.90
Monocytes	pS6	3.85	2.30	2.70	4.99	1.00	9.01	3.62	2.36	2.82	4.42	1.00	10.10
Monocytes	pSTAT1	13.50	16.64	5.22	21.77	1.00	62.20	11.94	10.88	8.26	15.63	1.00	40.50
Monocytes	pSTAT3	3.77	5.29	1.14	6.40	1.00	23.50	2.81	2.29	2.04	3.58	1.00	10.50
Monocytes	pSTAT5	2.21	1.80	1.32	3.10	1.00	7.87	2.36	2.15	1.64	3.09	1.00	12.20
Naive CD4+ T Cells	IkB	9.65	13.11	7.74	11.55	1.00	66.80	8.79	13.56	7.41	10.17	1.00	112.00
Naive CD4+ T Cells	pERK	44.39	123.4	26.45	62.34	1.00	1277.00	38.95	112.6	27.50	50.40	1.00	1309.00
Naive CD4+ T Cells	pP38	2.81	3.59	2.28	3.33	1.00	25.70	2.29	2.68	2.02	2.56	1.00	24.80
Naive CD4+ T Cells	pPLCg2	5.94	8.93	4.64	7.24	1.00	62.60	5.61	10.98	4.50	6.73	1.00	121.00
Naive CD4+ T Cells	pS6	3.12	4.66	2.45	3.80	1.00	40.30	3.04	6.95	2.34	3.75	1.00	108.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	22.10	29.66	17.78	26.41	1.00	192.00	20.83	31.15	17.66	24.00	1.00	244.00
Naive CD4+ T Cells	pSTAT3	17.01	19.03	14.24	19.77	1.00	151.00	14.37	15.95	12.75	15.99	1.00	146.00
Naive CD4+ T Cells	pSTAT5	3.11	4.36	2.48	3.75	1.00	30.90	3.22	6.69	2.54	3.90	1.00	98.50
Naive CD8+ T Cells	IkB	8.61	11.96	6.87	10.35	1.00	59.10	7.74	12.44	6.47	9.00	1.00	110.00
Naive CD8+ T Cells	pERK	49.11	135.7	29.38	68.85	1.00	1441.00	41.46	115.6	29.71	53.21	1.00	1298.00
Naive CD8+ T Cells	pP38	2.58	3.29	2.10	3.05	1.00	23.80	2.12	2.44	1.87	2.37	1.00	22.50
Naive CD8+ T Cells	pPLCg2	6.33	9.23	4.99	7.67	1.00	61.10	5.89	11.38	4.73	7.05	1.00	118.00
Naive CD8+ T Cells	pS6	3.10	4.52	2.44	3.76	1.00	37.80	3.01	6.88	2.31	3.71	1.00	106.00
Naive CD8+ T Cells	pSTAT1	14.94	21.85	11.76	18.12	1.00	141.00	13.69	21.24	11.53	15.85	1.00	158.00
Naive CD8+ T Cells	pSTAT3	9.98	14.85	7.82	12.14	1.00	121.00	7.97	11.88	6.76	9.18	1.00	124.00
Naive CD8+ T Cells	pSTAT5	2.42	3.55	1.91	2.94	1.00	26.70	2.59	6.34	1.95	3.24	1.00	95.00
Plasmoid Dendritic Cells	IkB	5.16	7.47	4.07	6.25	1.00	49.00	4.24	7.38	3.49	4.99	1.00	76.60
Plasmoid Dendritic Cells	pERK	46.81	150.3	24.95	68.67	1.00	1663.00	35.12	92.41	25.72	44.52	1.00	1022.00
Plasmoid Dendritic Cells	pP38	3.09	4.75	2.40	3.78	1.00	38.00	2.33	3.23	2.01	2.66	1.00	30.40
Plasmoid Dendritic Cells	pPLCg2	6.71	9.86	5.27	8.14	1.00	81.50	5.52	9.76	4.53	6.52	1.00	87.90
Plasmoid Dendritic Cells	pS6	2.81	3.70	2.27	3.35	1.00	24.30	2.72	6.56	2.06	3.39	1.00	90.40
Plasmoid Dendritic Cells	pSTAT1	6.51	10.92	4.92	8.09	1.00	66.80	5.53	11.97	4.31	6.75	1.00	132.00
Plasmoid Dendritic Cells	pSTAT3	4.42	7.12	3.38	5.45	1.00	57.50	3.54	7.07	2.83	4.26	1.00	77.10
Plasmoid Dendritic Cells	pSTAT5	2.04	2.60	1.66	2.41	1.00	24.90	2.16	5.87	1.56	2.76	1.00	86.70
Plasmablasts	IkB	7.49	9.07	6.16	8.82	1.00	55.80	6.76	8.78	5.86	7.66	1.00	48.70
Plasmablasts	pERK	56.28	141.6	35.51	77.05	1.00	1385.00	48.34	129.1	35.08	61.60	1.00	1331.00
Plasmablasts	pP38	3.19	4.97	2.46	3.92	1.00	46.30	2.62	3.26	2.29	2.96	1.00	26.30
Plasmablasts	pPLCg2	9.16	11.52	7.47	10.85	1.00	74.60	7.88	12.03	6.65	9.12	1.00	104.00
Plasmablasts	pS6	4.08	4.51	3.42	4.74	1.00	37.30	3.64	5.13	3.12	4.17	1.00	55.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-6

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	7.09	11.66	5.38	8.80	1.00	95.30	6.03	9.68	5.04	7.02	1.00	60.60
Plasmablasts	pSTAT3	7.22	11.12	5.59	8.85	1.00	82.70	5.57	9.04	4.64	6.50	1.00	76.00
Plasmablasts	pSTAT5	2.87	4.47	2.21	3.52	1.00	36.80	2.77	4.49	2.31	3.23	1.00	41.90
Transitional B Cells	IkB	7.18	8.78	5.89	8.47	1.00	47.10	6.87	9.98	5.85	7.89	1.00	110.00
Transitional B Cells	pERK	51.62	113.6	34.96	68.28	1.00	935.00	47.06	112.0	35.62	58.49	1.00	1020.00
Transitional B Cells	pP38	4.02	4.90	3.30	4.74	1.00	28.10	3.35	3.75	2.97	3.73	1.00	27.30
Transitional B Cells	pPLCg2	10.20	11.99	8.44	11.96	1.00	74.60	9.44	15.50	7.85	11.02	1.00	123.00
Transitional B Cells	pS6	4.48	5.46	3.68	5.28	1.00	36.20	4.42	9.34	3.47	5.38	1.00	153.00
Transitional B Cells	pSTAT1	6.85	9.89	5.40	8.30	1.00	51.60	6.66	11.45	5.49	7.82	1.00	87.90
Transitional B Cells	pSTAT3	9.57	10.43	8.04	11.10	1.00	74.00	8.83	12.79	7.53	10.14	1.00	134.00
Transitional B Cells	pSTAT5	2.91	4.44	2.26	3.56	1.00	29.90	3.02	7.18	2.28	3.75	1.00	114.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
B Cells	IkB	5.55	7.56	4.46	6.64	1.00	50.50	4.75	7.24	4.01	5.49	1.00	72.40
B Cells	pERK	40.25	123.7	22.36	58.14	1.00	1244.00	35.40	120.8	23.10	47.70	1.00	1320.00
B Cells	pP38	2.26	2.65	1.88	2.64	1.00	13.80	1.81	2.02	1.60	2.01	1.00	18.70
B Cells	pPLCg2	9.23	12.41	7.44	11.03	1.00	79.30	7.67	11.31	6.52	8.82	1.00	82.60
B Cells	pS6	2.96	4.42	2.32	3.60	1.00	36.00	2.71	5.44	2.15	3.26	1.00	78.20
B Cells	pSTAT1	5.66	11.07	4.06	7.26	1.00	113.00	4.83	8.58	3.96	5.71	1.00	64.80
B Cells	pSTAT3	5.94	10.28	4.45	7.43	1.00	69.80	4.22	7.18	3.49	4.95	1.00	61.20
B Cells	pSTAT5	2.57	4.41	1.93	3.20	1.00	33.40	2.23	4.76	1.74	2.71	1.00	58.50
CD16+ NK Cells	IkB	6.54	9.76	5.09	8.00	1.00	72.60	5.68	8.45	4.80	6.57	1.00	63.60
CD16+ NK Cells	pERK	54.78	130.1	35.36	74.19	1.00	1273.00	50.62	142.1	35.71	65.54	1.00	1823.00
CD16+ NK Cells	pP38	2.14	2.90	1.71	2.57	1.00	19.30	1.84	2.65	1.56	2.12	1.00	26.90
CD16+ NK Cells	pPLCg2	10.39	14.18	8.27	12.50	1.00	99.10	10.27	15.67	8.63	11.92	1.00	139.00
CD16+ NK Cells	pS6	3.14	5.99	2.25	4.04	1.00	68.80	3.27	6.73	2.56	3.97	1.00	78.70
CD16+ NK Cells	pSTAT1	8.35	40.26	2.34	14.35	1.00	514.00	4.16	7.94	3.33	5.00	1.00	64.40
CD16+ NK Cells	pSTAT3	4.45	7.65	3.31	5.59	1.00	45.50	3.34	5.65	2.75	3.93	1.00	46.00
CD16+ NK Cells	pSTAT5	2.50	5.05	1.75	3.26	1.00	52.60	2.27	5.41	1.70	2.84	1.00	79.90
CD16+ Monocytes	IkB	10.56	12.70	8.72	12.39	1.00	78.70	9.07	11.28	7.92	10.22	1.00	79.90
CD16+ Monocytes	pERK	79.57	168.0	55.27	103.9	1.57	1584.00	70.92	165.9	54.02	87.81	1.00	1875.00
CD16+ Monocytes	pP38	5.32	6.54	4.37	6.26	1.00	40.80	4.22	5.00	3.71	4.73	1.00	35.00
CD16+ Monocytes	pPLCg2	14.69	18.92	11.95	17.43	1.00	116.00	13.45	19.63	11.45	15.45	1.00	165.00
CD16+ Monocytes	pS6	4.74	6.23	3.84	5.64	1.00	54.30	4.28	6.71	3.59	4.96	1.00	74.80
CD16+ Monocytes	pSTAT1	12.49	25.45	8.81	16.17	1.00	255.00	10.32	18.99	8.39	12.26	1.00	167.00
CD16+ Monocytes	pSTAT3	9.47	15.61	7.21	11.72	1.00	102.00	6.78	9.92	5.77	7.79	1.00	70.20
CD16+ Monocytes	pSTAT5	5.29	9.09	3.97	6.60	1.00	65.50	4.39	8.67	3.51	5.27	1.00	91.70
CD16- NK Cells	IkB	4.68	6.17	3.79	5.57	1.00	37.20	3.97	5.88	3.37	4.57	1.00	45.30
CD16- NK Cells	pERK	39.87	115.6	23.14	56.60	1.00	1255.00	34.35	106.5	23.51	45.19	1.00	1180.00
CD16- NK Cells	pP38	1.87	2.13	1.56	2.18	1.00	12.50	1.53	1.51	1.37	1.68	1.00	13.40
CD16- NK Cells	pPLCg2	6.28	8.87	5.00	7.56	1.00	67.30	5.31	8.94	4.40	6.22	1.00	77.20
CD16- NK Cells	pS6	2.66	3.63	2.14	3.19	1.00	32.40	2.38	3.92	1.98	2.78	1.00	58.00
CD16- NK Cells	pSTAT1	5.18	9.49	3.80	6.55	1.00	76.20	4.34	7.95	3.53	5.15	1.00	59.10
CD16- NK Cells	pSTAT3	3.75	6.73	2.78	4.73	1.00	54.30	2.82	5.11	2.30	3.34	1.00	47.40
CD16- NK Cells	pSTAT5	2.57	3.87	2.01	3.13	1.00	31.10	2.22	3.87	1.83	2.62	1.00	43.70
CD16- Monocytes	IkB	10.00	12.91	8.13	11.86	1.00	74.40	8.45	11.97	7.23	9.67	1.00	82.20

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	61.99	166.6	37.89	86.10	1.00	1671.00	51.88	143.2	37.30	66.46	1.00	1611.00
CD16- Monocytes	pP38	5.36	6.32	4.44	6.27	1.00	50.80	4.11	4.33	3.67	4.55	1.00	29.90
CD16- Monocytes	pPLCg2	9.67	13.46	7.73	11.62	1.00	87.90	8.19	13.02	6.87	9.52	1.00	115.00
CD16- Monocytes	pS6	3.74	5.54	2.94	4.54	1.00	52.40	3.33	6.20	2.70	3.96	1.00	79.10
CD16- Monocytes	pSTAT1	14.68	25.06	11.05	18.30	1.00	212.00	12.71	20.68	10.60	14.81	1.00	133.00
CD16- Monocytes	pSTAT3	8.25	15.44	6.02	10.48	1.00	108.00	5.57	10.09	4.54	6.59	1.00	94.80
CD16- Monocytes	pSTAT5	6.46	9.47	5.09	7.83	1.00	55.90	5.43	9.52	4.47	6.40	1.00	84.10
CD4+ T Cells	IkB	8.93	12.42	7.13	10.73	1.00	64.40	7.75	11.87	6.54	8.95	1.00	81.50
CD4+ T Cells	pERK	43.76	133.0	24.52	63.00	1.00	1381.00	36.40	118.9	24.30	48.50	1.00	1448.00
CD4+ T Cells	pP38	2.57	3.14	2.12	3.03	1.00	16.30	2.04	2.37	1.80	2.28	1.00	18.20
CD4+ T Cells	pPLCg2	6.24	10.23	4.76	7.72	1.00	81.30	5.26	9.54	4.29	6.23	1.00	75.70
CD4+ T Cells	pS6	2.73	4.39	2.10	3.37	1.00	39.50	2.58	5.45	2.03	3.14	1.00	73.40
CD4+ T Cells	pSTAT1	13.71	22.41	10.47	16.95	1.00	167.00	11.65	19.14	9.70	13.60	1.00	135.00
CD4+ T Cells	pSTAT3	8.12	15.36	5.89	10.34	1.00	125.00	5.22	10.47	4.15	6.28	1.00	115.00
CD4+ T Cells	pSTAT5	9.79	14.64	7.67	11.91	1.00	129.00	8.59	14.41	7.13	10.06	1.00	114.00
CD4-CD8- T Cells	IkB	5.11	8.02	3.95	6.27	1.00	54.70	4.07	6.47	3.41	4.73	1.00	50.60
CD4-CD8- T Cells	pERK	37.75	107.9	22.14	53.37	1.00	1020.00	31.61	105.4	20.88	42.33	1.00	1168.00
CD4-CD8- T Cells	pP38	2.14	2.55	1.77	2.51	1.00	13.80	1.70	2.11	1.49	1.92	1.00	22.60
CD4-CD8- T Cells	pPLCg2	5.85	9.82	4.43	7.27	1.00	74.40	4.94	10.35	3.89	5.99	1.00	103.00
CD4-CD8- T Cells	pS6	2.36	3.58	1.84	2.88	1.00	33.70	2.22	4.45	1.76	2.67	1.00	60.80
CD4-CD8- T Cells	pSTAT1	7.52	15.22	5.32	9.72	1.00	142.00	6.12	11.18	4.98	7.26	1.00	73.00
CD4-CD8- T Cells	pSTAT3	5.05	10.02	3.60	6.50	1.00	73.40	3.40	7.35	2.65	4.15	1.00	79.40
CD4-CD8- T Cells	pSTAT5	3.57	5.65	2.75	4.39	1.00	42.40	2.78	5.02	2.27	3.29	1.00	57.20
CD8+ T Cells	IkB	7.77	11.02	6.17	9.36	1.00	59.40	6.60	10.43	5.53	7.66	1.00	74.40
CD8+ T Cells	pERK	48.60	145.1	27.61	69.58	1.00	1481.00	38.24	118.5	26.18	50.31	1.00	1377.00
CD8+ T Cells	pP38	2.38	2.87	1.97	2.80	1.00	15.00	1.90	2.13	1.68	2.11	1.00	16.10
CD8+ T Cells	pPLCg2	6.40	10.40	4.90	7.91	1.00	79.80	5.33	9.81	4.33	6.33	1.00	83.20
CD8+ T Cells	pS6	2.81	4.27	2.19	3.43	1.00	37.40	2.62	5.48	2.06	3.18	1.00	78.20
CD8+ T Cells	pSTAT1	12.01	20.98	8.97	15.04	1.00	167.00	10.08	16.75	8.37	11.78	1.00	123.00
CD8+ T Cells	pSTAT3	6.15	12.75	4.31	8.00	1.00	97.40	4.07	8.76	3.17	4.96	1.00	97.70
CD8+ T Cells	pSTAT5	6.26	9.34	4.91	7.61	1.00	58.60	5.00	8.59	4.12	5.87	1.00	77.10
Dendritic Cells	IkB	4.33	6.46	3.39	5.26	1.00	36.90	3.47	5.42	2.92	4.02	1.00	39.70
Dendritic Cells	pERK	39.69	126.6	21.38	58.00	1.00	1183.00	29.93	88.26	20.94	38.92	1.00	1052.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	4.46	6.07	3.59	5.34	1.00	41.60	3.39	4.97	2.89	3.90	1.00	40.30
Dendritic Cells	pPLCg2	5.93	9.44	4.57	7.30	1.00	73.60	5.16	11.74	3.96	6.35	1.00	171.00
Dendritic Cells	pS6	2.14	3.19	1.68	2.60	1.00	29.50	2.07	3.97	1.66	2.47	1.00	53.60
Dendritic Cells	pSTAT1	5.99	13.18	4.08	7.90	1.00	105.00	4.89	9.86	3.88	5.89	1.00	70.20
Dendritic Cells	pSTAT3	3.67	6.89	2.68	4.67	1.00	53.00	2.71	5.66	2.13	3.28	1.00	72.00
Dendritic Cells	pSTAT5	2.43	3.67	1.90	2.96	1.00	23.70	2.10	4.16	1.68	2.52	1.00	54.10
HLADR+ NK Cells	IkB	5.97	7.90	4.83	7.12	1.00	53.10	4.99	6.46	4.33	5.65	1.00	37.00
HLADR+ NK Cells	pERK	47.93	124.4	29.89	65.97	1.00	1339.00	42.30	115.9	30.46	54.13	1.00	1357.00
HLADR+ NK Cells	pP38	2.37	2.88	1.95	2.79	1.00	15.70	1.95	2.22	1.73	2.18	1.00	17.60
HLADR+ NK Cells	pPLCg2	9.50	14.09	7.46	11.54	1.00	107.00	8.04	12.09	6.80	9.27	1.00	105.00
HLADR+ NK Cells	pS6	3.07	3.66	2.54	3.60	1.00	33.50	2.67	2.74	2.39	2.95	1.00	20.00
HLADR+ NK Cells	pSTAT1	5.73	11.06	4.12	7.33	1.00	109.00	4.78	8.12	3.95	5.61	1.00	68.10
HLADR+ NK Cells	pSTAT3	4.41	7.83	3.27	5.54	1.00	54.90	3.41	5.95	2.80	4.02	1.00	49.10
HLADR+ NK Cells	pSTAT5	2.74	3.90	2.17	3.30	1.00	27.10	2.29	3.07	1.98	2.60	1.00	26.80
HLADR+CD38+ CD4+ T Cells	IkB	10.47	13.40	8.53	12.40	1.00	67.40	8.91	12.70	7.61	10.20	1.00	92.70
HLADR+CD38+ CD4+ T Cells	pERK	54.32	139.4	34.15	74.48	1.00	1460.00	46.50	123.8	33.90	59.10	1.00	1456.00
HLADR+CD38+ CD4+ T Cells	pP38	3.73	4.57	3.07	4.39	1.00	23.70	2.89	3.50	2.54	3.25	1.00	28.30
HLADR+CD38+ CD4+ T Cells	pPLCg2	10.32	15.52	8.07	12.56	1.00	98.60	14.83	120.1	2.60	27.06	1.00	2311.00
HLADR+CD38+ CD4+ T Cells	pS6	3.89	5.64	3.08	4.71	1.00	50.40	3.60	6.85	2.90	4.29	1.00	93.50
HLADR+CD38+ CD4+ T Cells	pSTAT1	14.88	23.67	11.46	18.30	1.00	187.00	12.70	20.44	10.62	14.78	1.00	144.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	9.74	15.86	7.45	12.04	1.00	97.20	6.68	11.51	5.51	7.85	1.00	106.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	8.89	12.65	7.06	10.72	1.00	74.80	7.77	13.59	6.38	9.15	1.00	122.00
HLADR+CD38+ CD8+ T Cells	IkB	8.91	11.75	7.22	10.61	1.00	69.40	7.36	9.87	6.36	8.37	1.00	67.30
HLADR+CD38+ CD8+ T Cells	pERK	56.56	156.9	33.86	79.26	1.06	1629.00	45.43	122.6	32.94	57.91	1.00	1373.00
HLADR+CD38+ CD8+ T Cells	pP38	3.35	4.03	2.77	3.93	1.00	20.60	2.63	3.10	2.31	2.95	1.00	22.20
HLADR+CD38+ CD8+ T Cells	pPLCg2	10.55	15.83	8.26	12.84	1.00	97.20	9.77	27.69	6.95	12.59	1.00	470.00
HLADR+CD38+ CD8+ T Cells	pS6	3.81	5.65	2.99	4.62	1.00	48.60	3.45	6.58	2.78	4.12	1.00	88.40

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	11.81	20.28	8.87	14.74	1.00	198.00	9.98	16.29	8.32	11.64	1.00	105.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	7.80	13.61	5.83	9.77	1.00	83.00	5.45	9.86	4.45	6.45	1.00	84.60
HLADR+CD38+ CD8+ T Cells	pSTAT5	5.30	8.27	4.10	6.50	1.00	66.20	4.25	7.68	3.47	5.03	1.00	72.20
IgD+CD27+ B Cells	IkB	6.09	8.03	4.93	7.25	1.00	51.70	5.23	7.86	4.43	6.03	1.00	84.80
IgD+CD27+ B Cells	pERK	43.73	127.5	25.29	62.18	1.00	1273.00	38.23	122.1	25.80	50.67	1.00	1331.00
IgD+CD27+ B Cells	pP38	2.46	2.89	2.04	2.88	1.00	15.20	1.96	2.17	1.74	2.18	1.00	18.90
IgD+CD27+ B Cells	pPLCg2	9.98	12.99	8.11	11.86	1.00	79.50	8.39	11.95	7.17	9.60	1.00	83.80
IgD+CD27+ B Cells	pS6	3.23	4.59	2.56	3.89	1.00	36.70	2.94	6.19	2.31	3.58	1.00	90.60
IgD+CD27+ B Cells	pSTAT1	6.22	12.06	4.48	7.97	1.00	122.00	5.30	9.40	4.34	6.26	1.00	80.40
IgD+CD27+ B Cells	pSTAT3	6.66	10.93	5.08	8.24	1.00	72.80	4.76	7.63	3.98	5.53	1.00	62.90
IgD+CD27+ B Cells	pSTAT5	2.77	4.71	2.09	3.45	1.00	33.60	2.40	5.56	1.84	2.97	1.00	74.80
IgD+CD27- B Cells	IkB	4.96	6.96	3.95	5.97	1.00	46.00	4.22	6.59	3.55	4.89	1.00	58.80
IgD+CD27- B Cells	pERK	36.08	108.7	20.35	51.81	1.00	1014.00	31.93	115.1	20.21	43.65	1.00	1262.00
IgD+CD27- B Cells	pP38	2.06	2.34	1.72	2.40	1.00	12.40	1.66	1.80	1.47	1.84	1.00	15.70
IgD+CD27- B Cells	pPLCg2	8.34	11.32	6.70	9.98	1.00	75.90	6.77	9.81	5.77	7.77	1.00	70.00
IgD+CD27- B Cells	pS6	2.70	4.21	2.09	3.31	1.00	36.60	2.52	4.96	2.02	3.03	1.00	72.80
IgD+CD27- B Cells	pSTAT1	5.12	10.61	3.59	6.66	1.00	114.00	4.28	7.41	3.52	5.03	1.00	51.60
IgD+CD27- B Cells	pSTAT3	5.62	9.58	4.23	7.00	1.00	63.80	3.89	6.38	3.24	4.54	1.00	56.90
IgD+CD27- B Cells	pSTAT5	2.28	4.00	1.70	2.86	1.00	29.50	1.87	3.32	1.53	2.21	1.00	41.30
IgD-CD27+ B Cells	IkB	5.05	7.02	4.03	6.06	1.00	37.00	4.26	7.63	3.49	5.04	1.00	99.10
IgD-CD27+ B Cells	pERK	33.19	98.69	18.91	47.47	1.00	1183.00	26.95	76.85	19.13	34.78	1.00	891.00
IgD-CD27+ B Cells	pP38	2.06	2.34	1.72	2.40	1.00	12.50	1.65	2.33	1.41	1.88	1.00	37.10
IgD-CD27+ B Cells	pPLCg2	8.86	11.87	7.15	10.58	1.00	82.70	7.41	11.04	6.29	8.54	1.00	102.00
IgD-CD27+ B Cells	pS6	3.07	4.32	2.45	3.70	1.00	31.40	2.70	5.19	2.17	3.23	1.00	72.60
IgD-CD27+ B Cells	pSTAT1	6.29	12.46	4.49	8.10	1.00	113.00	4.95	8.56	4.07	5.82	1.00	59.40
IgD-CD27+ B Cells	pSTAT3	5.35	10.58	3.82	6.88	1.00	81.40	3.67	6.84	2.97	4.37	1.00	66.50
IgD-CD27+ B Cells	pSTAT5	2.54	4.34	1.91	3.17	1.00	33.80	2.18	4.03	1.77	2.59	1.00	45.60

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	4.18	6.58	3.23	5.13	1.00	50.90	3.25	6.92	2.54	3.96	1.00	83.40
IgD-CD27- B Cells	pERK	25.55	74.95	14.71	36.39	1.00	909.00	15.70	22.52	13.40	18.01	1.00	167.00
IgD-CD27- B Cells	pP38	2.17	3.43	1.68	2.67	1.00	35.70	1.57	2.84	1.28	1.86	1.00	44.10
IgD-CD27- B Cells	pPLCg2	7.42	10.86	5.84	8.99	1.00	81.30	6.00	11.84	4.78	7.21	1.00	150.00
IgD-CD27- B Cells	pS6	2.60	3.56	2.08	3.11	1.00	28.20	2.30	4.98	1.79	2.81	1.00	69.60
IgD-CD27- B Cells	pSTAT1	4.92	9.69	3.52	6.32	1.00	90.60	4.07	7.86	3.26	4.88	1.00	57.80
IgD-CD27- B Cells	pSTAT3	4.76	9.45	3.40	6.13	1.00	67.80	3.36	7.33	2.61	4.11	1.00	94.90
IgD-CD27- B Cells	pSTAT5	2.25	3.33	1.77	2.73	1.00	24.40	1.91	4.13	1.48	2.33	1.00	49.80
NK Cells	IkB	4.81	6.24	3.91	5.72	1.00	37.20	3.99	5.24	3.45	4.52	1.00	32.40
NK Cells	pERK	42.32	118.5	25.13	59.52	1.00	1258.00	36.74	110.0	25.51	47.97	1.00	1234.00
NK Cells	pP38	1.82	2.10	1.52	2.13	1.00	12.90	1.53	1.52	1.38	1.69	1.00	13.10
NK Cells	pPLCg2	6.97	10.06	5.51	8.43	1.00	72.60	5.81	9.18	4.87	6.74	1.00	84.80
NK Cells	pS6	2.49	3.01	2.05	2.93	1.00	32.40	2.18	2.11	1.96	2.40	1.00	14.30
NK Cells	pSTAT1	4.98	10.26	3.49	6.47	1.00	93.50	3.91	6.90	3.20	4.61	1.00	60.90
NK Cells	pSTAT3	3.80	6.73	2.83	4.78	1.00	49.00	2.83	4.92	2.32	3.33	1.00	38.70
NK Cells	pSTAT5	2.35	3.34	1.87	2.83	1.00	21.70	1.93	2.50	1.67	2.18	1.00	26.30
NKT Cells	IkB	10.96	14.01	8.92	13.00	1.00	72.80	9.87	14.08	8.43	11.32	1.00	89.40
NKT Cells	pERK	66.93	183.9	40.18	93.67	1.00	1833.00	58.80	175.0	40.88	76.72	1.00	1685.00
NKT Cells	pP38	3.86	5.19	3.11	4.62	1.00	34.20	3.07	4.13	2.64	3.49	1.00	24.20
NKT Cells	pPLCg2	8.42	15.42	6.18	10.67	1.00	144.00	7.25	13.98	5.82	8.68	1.00	114.00
NKT Cells	pS6	6.43	25.07	2.79	10.08	1.00	305.00	5.95	24.59	3.44	8.47	1.00	302.00
NKT Cells	pSTAT1	18.50	38.49	12.90	24.10	1.00	398.00	14.15	22.35	11.87	16.44	1.00	162.00
NKT Cells	pSTAT3	10.08	22.94	6.74	13.42	1.00	248.00	6.74	14.57	5.25	8.23	1.00	141.00
NKT Cells	pSTAT5	9.42	12.55	7.59	11.24	1.00	73.00	7.62	11.41	6.45	8.79	1.00	89.90
Regulatory T Cells	IkB	11.53	15.25	9.32	13.74	1.00	71.80	9.82	14.88	8.31	11.34	1.00	85.70
Regulatory T Cells	pERK	51.59	143.0	30.90	72.28	1.00	1444.00	42.28	122.9	29.75	54.81	1.00	1424.00
Regulatory T Cells	pP38	3.02	3.81	2.47	3.57	1.00	22.30	2.32	2.72	2.04	2.60	1.00	19.20
Regulatory T Cells	pPLCg2	6.58	10.13	5.11	8.04	1.00	88.90	5.83	10.86	4.72	6.94	1.00	104.00
Regulatory T Cells	pS6	3.03	4.28	2.41	3.65	1.00	35.20	2.92	6.01	2.31	3.54	1.00	81.10
Regulatory T Cells	pSTAT1	18.43	37.07	13.07	23.79	1.00	303.00	15.15	26.91	12.41	17.89	1.00	244.00
Regulatory T Cells	pSTAT3	9.29	17.42	6.77	11.81	1.00	146.00	6.11	12.13	4.88	7.35	1.00	125.00
Regulatory T Cells	pSTAT5	12.63	18.55	9.94	15.31	1.00	154.00	10.85	19.86	8.83	12.88	1.00	191.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	9.86	13.78	7.87	11.85	1.00	71.40	8.26	12.31	7.00	9.51	1.00	78.00
Central Memory CD4+ T Cells	pERK	45.54	133.1	26.29	64.79	1.00	1381.00	37.88	118.8	25.79	49.98	1.00	1400.00
Central Memory CD4+ T Cells	pP38	2.79	3.51	2.28	3.30	1.00	19.10	2.21	2.57	1.95	2.47	1.00	19.30
Central Memory CD4+ T Cells	pPLCg2	6.28	10.03	4.82	7.73	1.00	82.20	5.11	8.46	4.25	5.97	1.00	69.30
Central Memory CD4+ T Cells	pS6	2.70	4.21	2.09	3.30	1.00	40.40	2.51	4.79	2.02	3.00	1.00	63.90
Central Memory CD4+ T Cells	pSTAT1	17.67	29.37	13.42	21.92	1.00	208.00	15.17	24.90	12.64	17.71	1.00	156.00
Central Memory CD4+ T Cells	pSTAT3	8.33	17.10	5.86	10.80	1.00	154.00	5.27	11.26	4.12	6.42	1.00	130.00
Central Memory CD4+ T Cells	pSTAT5	12.65	17.95	10.05	15.24	1.00	147.00	10.50	16.77	8.79	12.21	1.00	127.00
Central Memory CD8+ T Cells	IkB	8.19	11.83	6.48	9.90	1.00	65.10	6.65	10.38	5.60	7.71	1.00	73.40
Central Memory CD8+ T Cells	pERK	47.17	133.9	27.80	66.55	1.00	1342.00	37.44	107.4	26.49	48.40	1.00	1234.00
Central Memory CD8+ T Cells	pP38	2.64	3.18	2.18	3.10	1.00	17.60	2.12	2.38	1.87	2.36	1.00	16.70
Central Memory CD8+ T Cells	pPLCg2	5.94	9.57	4.56	7.32	1.00	79.10	4.93	9.10	4.00	5.86	1.00	80.20
Central Memory CD8+ T Cells	pS6	3.13	4.50	2.48	3.78	1.00	38.80	2.80	5.57	2.23	3.37	1.00	80.90
Central Memory CD8+ T Cells	pSTAT1	13.41	24.24	9.90	16.91	1.00	188.00	11.49	19.59	9.49	13.48	1.00	142.00
Central Memory CD8+ T Cells	pSTAT3	6.25	13.54	4.29	8.21	1.00	116.00	4.18	9.60	3.20	5.16	1.00	114.00
Central Memory CD8+ T Cells	pSTAT5	7.73	12.68	5.89	9.56	1.00	104.00	5.94	10.32	4.89	6.99	1.00	105.00
Effector CD4+ T Cells	IkB	6.67	9.68	5.27	8.07	1.00	54.20	5.52	8.98	4.60	6.43	1.00	66.40
Effector CD4+ T Cells	pERK	36.66	100.1	22.18	51.15	1.00	899.00	27.85	79.61	19.74	35.95	1.00	1220.00
Effector CD4+ T Cells	pP38	2.20	2.61	1.82	2.58	1.00	15.70	1.71	1.76	1.53	1.89	1.00	13.20
Effector CD4+ T Cells	pPLCg2	5.54	9.29	4.19	6.88	1.00	77.40	4.49	8.49	3.62	5.35	1.00	71.40
Effector CD4+ T Cells	pS6	2.42	3.94	1.85	2.99	1.00	37.60	2.30	5.03	1.79	2.82	1.00	68.10
Effector CD4+ T Cells	pSTAT1	10.69	18.79	7.97	13.41	1.00	158.00	8.80	15.17	7.25	10.34	1.00	119.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	7.03	12.21	5.26	8.80	1.00	89.40	4.50	8.22	3.66	5.33	1.00	93.70
Effector CD4+ T Cells	pSTAT5	6.46	10.96	4.88	8.05	1.00	99.60	5.43	10.37	4.37	6.49	1.00	89.90
Effector CD8+ T Cells	IkB	5.89	8.73	4.62	7.15	1.00	52.00	4.91	8.29	4.06	5.75	1.00	62.60
Effector CD8+ T Cells	pERK	39.92	95.33	26.13	53.71	1.00	804.00	29.38	79.17	21.31	37.45	1.00	1128.00
Effector CD8+ T Cells	pP38	2.11	2.59	1.73	2.49	1.00	15.00	1.63	1.64	1.47	1.80	1.00	14.60
Effector CD8+ T Cells	pPLCg2	5.77	9.63	4.38	7.16	1.00	76.70	4.75	9.01	3.84	5.67	1.00	90.50
Effector CD8+ T Cells	pS6	2.45	3.93	1.88	3.02	1.00	37.40	2.24	4.66	1.76	2.71	1.00	63.50
Effector CD8+ T Cells	pSTAT1	9.61	18.01	7.00	12.21	1.00	161.00	7.92	13.99	6.49	9.35	1.00	111.00
Effector CD8+ T Cells	pSTAT3	5.22	10.30	3.73	6.71	1.00	74.20	3.53	7.13	2.81	4.26	1.00	75.60
Effector CD8+ T Cells	pSTAT5	4.21	6.47	3.27	5.14	1.00	53.60	3.40	6.30	2.76	4.04	1.00	59.90
Effector Memory CD4+ T Cells	IkB	6.63	10.43	5.12	8.14	1.00	65.70	5.19	8.66	4.30	6.07	1.00	56.90
Effector Memory CD4+ T Cells	pERK	37.48	115.1	20.83	54.14	1.00	1103.00	26.38	78.77	18.33	34.42	1.00	1082.00
Effector Memory CD4+ T Cells	pP38	2.30	2.89	1.88	2.72	1.00	17.00	1.76	1.86	1.57	1.95	1.00	16.30
Effector Memory CD4+ T Cells	pPLCg2	4.80	8.31	3.60	6.01	1.00	75.90	3.88	7.40	3.12	4.63	1.00	73.80
Effector Memory CD4+ T Cells	pS6	2.07	3.20	1.61	2.53	1.00	32.70	2.03	4.34	1.59	2.48	1.00	54.80
Effector Memory CD4+ T Cells	pSTAT1	13.12	24.99	9.51	16.74	1.00	193.00	10.69	19.91	8.66	12.72	1.00	145.00
Effector Memory CD4+ T Cells	pSTAT3	6.06	12.75	4.21	7.90	1.00	115.00	3.82	8.66	2.94	4.70	1.00	115.00
Effector Memory CD4+ T Cells	pSTAT5	7.39	13.57	5.43	9.35	1.00	130.00	5.71	11.57	4.53	6.89	1.00	105.00
Effector Memory CD8+ T Cells	IkB	5.84	9.53	4.47	7.22	1.00	59.30	4.60	8.06	3.78	5.43	1.00	63.80
Effector Memory CD8+ T Cells	pERK	40.67	120.2	23.28	58.07	1.00	1061.00	27.77	79.78	19.61	35.93	1.00	1103.00
Effector Memory CD8+ T Cells	pP38	2.36	3.82	1.81	2.92	1.00	40.30	1.67	1.77	1.49	1.85	1.00	16.00
Effector Memory CD8+ T Cells	pPLCg2	4.68	8.11	3.51	5.86	1.00	72.00	3.75	7.36	3.00	4.50	1.00	78.90

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	2.29	3.27	1.81	2.76	1.00	32.10	2.13	4.14	1.71	2.56	1.00	63.70
Effector Memory CD8+ T Cells	pSTAT1	10.27	20.93	7.24	13.29	1.00	164.00	8.02	15.38	6.45	9.59	1.00	119.00
Effector Memory CD8+ T Cells	pSTAT3	4.80	10.53	3.28	6.32	1.00	89.90	3.19	7.83	2.39	3.99	1.00	107.00
Effector Memory CD8+ T Cells	pSTAT5	4.96	9.52	3.59	6.34	1.00	84.30	3.56	6.85	2.86	4.26	1.00	56.10
Myeloid Dendritic Cells	IkB	4.50	6.68	3.53	5.47	1.00	43.20	3.69	5.99	3.08	4.30	1.00	53.70
Myeloid Dendritic Cells	pERK	42.24	129.0	23.58	60.91	1.00	1190.00	33.19	98.32	23.18	43.20	1.00	1365.00
Myeloid Dendritic Cells	pP38	6.15	7.46	5.07	7.23	1.00	46.50	4.88	6.70	4.20	5.57	1.00	60.90
Myeloid Dendritic Cells	pPLCg2	6.37	9.99	4.93	7.81	1.00	77.60	5.38	10.51	4.31	6.45	1.00	134.00
Myeloid Dendritic Cells	pS6	2.26	3.54	1.75	2.78	1.00	34.10	2.18	4.06	1.76	2.59	1.00	54.40
Myeloid Dendritic Cells	pSTAT1	6.56	14.05	4.53	8.59	1.00	109.00	5.32	10.72	4.23	6.41	1.00	79.00
Myeloid Dendritic Cells	pSTAT3	3.80	7.42	2.73	4.87	1.00	62.10	2.88	6.11	2.25	3.50	1.00	75.40
Myeloid Dendritic Cells	pSTAT5	2.52	4.01	1.94	3.10	1.00	27.80	2.12	4.21	1.69	2.55	1.00	63.90
Monocytes	IkB	15.99	13.90	9.08	22.91	1.18	47.00	12.65	11.00	8.93	16.37	1.22	42.50
Monocytes	pERK	167.8	467.2	-64.5	400.2	3.10	1661.00	150.7	417.6	9.39	292.0	1.73	1611.00
Monocytes	pP38	2.94	5.58	0.16	5.72	1.00	20.30	2.89	5.48	1.04	4.75	1.00	22.40
Monocytes	pPLCg2	5.49	5.10	2.95	8.02	1.00	17.20	5.91	5.82	3.94	7.87	1.00	25.70
Monocytes	pS6	3.80	2.35	2.63	4.97	1.03	8.26	3.59	2.31	2.80	4.37	1.00	9.81
Monocytes	pSTAT1	10.53	12.46	4.34	16.73	1.00	48.40	9.77	10.37	6.26	13.28	1.00	39.70
Monocytes	pSTAT3	2.09	1.77	1.20	2.97	1.00	7.38	2.03	1.77	1.43	2.63	1.00	7.10
Monocytes	pSTAT5	5.93	6.86	2.53	9.34	1.00	26.40	4.56	3.80	3.27	5.84	1.00	16.90
Naive CD4+ T Cells	IkB	9.81	13.36	7.88	11.75	1.00	64.40	8.53	12.82	7.23	9.84	1.00	87.90
Naive CD4+ T Cells	pERK	45.69	133.9	26.32	65.06	1.00	1384.00	38.18	120.4	25.92	50.44	1.00	1468.00
Naive CD4+ T Cells	pP38	2.69	3.27	2.21	3.16	1.00	17.20	2.14	2.49	1.89	2.39	1.00	18.50
Naive CD4+ T Cells	pPLCg2	6.99	10.92	5.41	8.57	1.00	85.70	5.91	10.27	4.86	6.95	1.00	81.10
Naive CD4+ T Cells	pS6	3.07	4.70	2.39	3.75	1.00	39.30	2.86	5.95	2.26	3.47	1.00	81.10

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	13.93	21.86	10.76	17.09	1.00	161.00	11.69	18.83	9.77	13.61	1.00	132.00
Naive CD4+ T Cells	pSTAT3	9.45	16.04	7.13	11.77	1.00	122.00	6.06	10.78	4.96	7.15	1.00	111.00
Naive CD4+ T Cells	pSTAT5	10.47	14.71	8.34	12.60	1.00	127.00	9.41	15.21	7.86	10.96	1.00	119.00
Naive CD8+ T Cells	IkB	8.73	12.27	6.95	10.50	1.00	63.70	7.44	11.59	6.26	8.62	1.00	80.90
Naive CD8+ T Cells	pERK	50.63	147.6	29.27	71.98	1.00	1498.00	40.19	120.9	27.87	52.50	1.00	1392.00
Naive CD8+ T Cells	pP38	2.49	3.02	2.05	2.92	1.00	17.10	1.97	2.24	1.75	2.20	1.00	16.40
Naive CD8+ T Cells	pPLCg2	7.16	11.09	5.56	8.77	1.00	84.30	5.99	10.53	4.92	7.06	1.00	87.20
Naive CD8+ T Cells	pS6	3.05	4.49	2.40	3.70	1.00	37.20	2.81	5.87	2.22	3.41	1.00	82.20
Naive CD8+ T Cells	pSTAT1	13.04	21.84	9.88	16.20	1.00	174.00	10.92	17.51	9.14	12.70	1.00	131.00
Naive CD8+ T Cells	pSTAT3	7.01	13.67	5.03	8.98	1.00	102.00	4.58	9.12	3.65	5.51	1.00	96.10
Naive CD8+ T Cells	pSTAT5	7.15	10.24	5.67	8.63	1.00	60.40	5.79	9.55	4.82	6.77	1.00	83.40
Plasmoid Dendritic Cells	IkB	5.46	8.98	4.16	6.76	1.00	66.40	4.14	6.88	3.44	4.84	1.00	67.90
Plasmoid Dendritic Cells	pERK	45.85	144.3	24.98	66.71	1.00	1428.00	35.39	104.2	24.78	46.00	1.00	1190.00
Plasmoid Dendritic Cells	pP38	2.92	4.08	2.33	3.51	1.00	22.70	2.36	3.14	2.04	2.68	1.00	26.60
Plasmoid Dendritic Cells	pPLCg2	6.84	9.95	5.40	8.28	1.00	79.80	6.07	12.67	4.78	7.36	1.00	144.00
Plasmoid Dendritic Cells	pS6	2.72	3.67	2.19	3.25	1.00	31.60	2.89	7.82	2.09	3.68	1.00	111.00
Plasmoid Dendritic Cells	pSTAT1	5.95	10.37	4.45	7.45	1.00	79.00	5.64	12.42	4.38	6.91	1.00	128.00
Plasmoid Dendritic Cells	pSTAT3	3.97	6.96	2.97	4.98	1.00	48.50	3.04	6.41	2.39	3.69	1.00	79.90
Plasmoid Dendritic Cells	pSTAT5	2.80	4.90	2.09	3.50	1.00	50.20	2.42	5.23	1.88	2.95	1.00	66.20
Plasmablasts	IkB	8.13	10.38	6.61	9.64	1.00	66.10	7.19	17.95	5.34	9.04	1.00	309.00
Plasmablasts	pERK	52.06	120.8	34.48	69.63	1.00	1131.00	47.49	140.6	33.00	61.98	1.00	1620.00
Plasmablasts	pP38	3.41	4.80	2.71	4.10	1.00	25.10	2.70	4.16	2.27	3.13	1.00	49.00
Plasmablasts	pPLCg2	9.61	12.73	7.76	11.46	1.00	82.90	8.03	12.27	6.77	9.30	1.00	89.40
Plasmablasts	pS6	4.74	7.50	3.65	5.83	1.00	74.40	7.20	72.78	-0.30	14.70	1.00	1390.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IL-7

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	7.53	14.99	5.35	9.71	1.00	138.00	5.71	9.60	4.72	6.70	1.00	63.20
Plasmablasts	pSTAT3	6.76	10.46	5.24	8.28	1.00	66.70	5.25	8.97	4.32	6.17	1.00	75.20
Plasmablasts	pSTAT5	3.42	5.63	2.60	4.24	1.00	41.70	2.68	4.19	2.25	3.11	1.00	42.90
Transitional B Cells	IkB	7.96	10.41	6.45	9.48	1.00	79.90	6.41	9.33	5.46	7.37	1.00	96.40
Transitional B Cells	pERK	51.91	119.4	34.55	69.27	1.07	975.00	45.93	135.1	32.07	59.78	1.00	1671.00
Transitional B Cells	pP38	3.94	4.69	3.26	4.62	1.00	30.00	3.34	4.25	2.90	3.77	1.00	39.00
Transitional B Cells	pPLCg2	10.03	12.59	8.20	11.86	1.00	82.70	8.63	12.47	7.35	9.91	1.00	103.00
Transitional B Cells	pS6	4.59	5.55	3.79	5.40	1.00	40.50	4.29	7.93	3.48	5.11	1.00	109.00
Transitional B Cells	pSTAT1	7.91	14.97	5.73	10.09	1.00	143.00	6.53	12.43	5.25	7.80	1.00	114.00
Transitional B Cells	pSTAT3	10.07	11.68	8.37	11.77	1.00	77.40	7.74	10.01	6.71	8.76	1.00	89.20
Transitional B Cells	pSTAT5	3.19	5.60	2.37	4.00	1.00	50.80	2.90	6.70	2.21	3.58	1.00	106.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
B Cells	IkB	5.31	7.56	4.20	6.43	1.00	60.10	4.70	6.43	4.04	5.36	1.00	45.50
B Cells	pERK	38.68	131.7	19.25	58.10	1.00	1384.00	35.83	131.9	22.31	49.35	1.00	1597.00
B Cells	pP38	2.06	2.52	1.69	2.43	1.00	20.20	1.84	2.17	1.61	2.06	1.00	21.20
B Cells	pPLCg2	8.53	10.65	6.96	10.11	1.00	73.40	7.69	11.07	6.56	8.83	1.00	86.50
B Cells	pS6	2.96	5.40	2.16	3.75	1.00	59.90	2.68	4.68	2.20	3.16	1.00	59.30
B Cells	pSTAT1	5.64	9.78	4.20	7.08	1.00	71.60	4.99	8.96	4.08	5.91	1.00	78.00
B Cells	pSTAT3	5.43	9.32	4.06	6.81	1.00	82.70	4.38	7.56	3.60	5.16	1.00	89.10
B Cells	pSTAT5	2.21	4.16	1.59	2.82	1.00	47.60	2.13	4.43	1.67	2.58	1.00	47.20
CD16+ NK Cells	IkB	6.59	9.04	5.23	7.95	1.00	54.40	5.59	8.00	4.75	6.43	1.00	58.50
CD16+ NK Cells	pERK	51.96	124.5	33.21	70.70	1.00	1248.00	54.00	162.8	36.85	71.14	1.00	2068.00
CD16+ NK Cells	pP38	2.04	2.89	1.61	2.48	1.00	21.30	1.76	2.12	1.53	1.98	1.00	19.30
CD16+ NK Cells	pPLCg2	10.92	14.35	8.76	13.08	1.00	104.00	10.23	15.56	8.59	11.86	1.00	150.00
CD16+ NK Cells	pS6	3.03	4.61	2.33	3.72	1.00	50.20	2.99	5.04	2.46	3.52	1.00	62.80
CD16+ NK Cells	pSTAT1	5.44	10.59	3.85	7.04	1.00	64.40	4.59	9.79	3.56	5.62	1.00	72.60
CD16+ NK Cells	pSTAT3	4.37	8.72	3.05	5.68	1.00	74.20	3.41	5.86	2.79	4.03	1.00	65.90
CD16+ NK Cells	pSTAT5	2.16	3.76	1.60	2.73	1.00	34.60	2.09	3.87	1.68	2.50	1.00	39.30
CD16+ Monocytes	IkB	9.60	12.68	7.73	11.47	1.00	105.00	8.78	10.93	7.66	9.90	1.00	64.80
CD16+ Monocytes	pERK	70.28	152.6	47.77	92.78	1.75	1553.00	67.28	158.6	51.03	83.53	1.00	1807.00
CD16+ Monocytes	pP38	5.43	7.00	4.40	6.46	1.00	43.40	5.37	6.61	4.69	6.04	1.00	54.20
CD16+ Monocytes	pPLCg2	13.62	18.84	10.84	16.40	1.00	185.00	12.86	18.08	11.01	14.71	1.00	176.00
CD16+ Monocytes	pS6	4.66	6.30	3.73	5.59	1.00	67.30	4.55	6.56	3.87	5.22	1.00	74.00
CD16+ Monocytes	pSTAT1	10.52	18.76	7.75	13.28	1.00	107.00	9.18	16.28	7.51	10.85	1.00	114.00
CD16+ Monocytes	pSTAT3	8.62	14.97	6.41	10.82	1.00	136.00	6.93	10.18	5.88	7.97	1.00	99.60
CD16+ Monocytes	pSTAT5	3.32	5.61	2.50	4.15	1.00	46.50	3.31	6.69	2.62	3.99	1.00	85.50
CD16- NK Cells	IkB	4.76	7.28	3.68	5.83	1.00	55.50	4.12	5.85	3.52	4.72	1.00	42.00
CD16- NK Cells	pERK	38.82	119.8	21.15	56.50	1.00	1309.00	35.14	117.0	23.14	47.14	1.00	1510.00
CD16- NK Cells	pP38	1.74	2.15	1.42	2.05	1.00	18.30	1.58	1.69	1.40	1.75	1.00	17.80
CD16- NK Cells	pPLCg2	5.56	7.32	4.48	6.64	1.00	65.70	5.48	8.65	4.59	6.37	1.00	65.90
CD16- NK Cells	pS6	2.57	4.47	1.91	3.23	1.00	54.70	2.38	3.99	1.97	2.79	1.00	56.10
CD16- NK Cells	pSTAT1	5.20	9.84	3.75	6.65	1.00	68.50	4.55	9.25	3.60	5.50	1.00	94.80
CD16- NK Cells	pSTAT3	3.89	10.78	2.30	5.48	1.00	132.00	2.86	5.14	2.34	3.39	1.00	50.40
CD16- NK Cells	pSTAT5	2.03	4.14	1.42	2.64	1.00	50.20	1.91	4.01	1.50	2.33	1.00	44.00
CD16- Monocytes	IkB	8.82	11.70	7.10	10.55	1.00	89.40	7.87	10.56	6.79	8.95	1.00	80.40

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	57.57	158.0	34.26	80.88	1.36	1606.00	52.47	150.0	37.09	67.84	1.00	1828.00
CD16- Monocytes	pP38	6.54	7.70	5.41	7.68	1.00	52.30	6.35	7.38	5.59	7.11	1.00	51.80
CD16- Monocytes	pPLCg2	8.27	11.21	6.61	9.92	1.00	91.10	7.80	12.47	6.52	9.08	1.00	98.30
CD16- Monocytes	pS6	3.92	6.45	2.97	4.87	1.00	74.60	3.67	6.27	3.02	4.31	1.00	85.00
CD16- Monocytes	pSTAT1	13.71	22.55	10.38	17.03	1.00	138.00	11.92	19.74	9.89	13.94	1.00	158.00
CD16- Monocytes	pSTAT3	7.55	15.57	5.26	9.85	1.00	160.00	5.79	11.43	4.62	6.96	1.00	119.00
CD16- Monocytes	pSTAT5	2.98	5.78	2.12	3.83	1.00	64.40	2.81	5.97	2.20	3.42	1.00	68.50
CD4+ T Cells	IkB	8.90	13.29	6.94	10.86	1.00	82.70	7.97	11.93	6.75	9.20	1.00	77.80
CD4+ T Cells	pERK	41.93	136.8	21.76	62.10	1.00	1424.00	36.33	123.2	23.70	48.96	1.00	1666.00
CD4+ T Cells	pP38	2.35	3.06	1.90	2.80	1.00	24.60	2.04	2.44	1.79	2.29	1.00	19.90
CD4+ T Cells	pPLCg2	5.12	8.38	3.89	6.36	1.00	82.00	4.87	8.92	3.95	5.78	1.00	81.80
CD4+ T Cells	pS6	2.62	5.45	1.81	3.42	1.00	67.10	2.54	5.12	2.02	3.07	1.00	70.60
CD4+ T Cells	pSTAT1	12.82	21.74	9.61	16.03	1.00	146.00	10.99	19.00	9.05	12.94	1.00	148.00
CD4+ T Cells	pSTAT3	7.19	15.69	4.87	9.50	1.00	164.00	4.98	10.47	3.91	6.05	1.00	109.00
CD4+ T Cells	pSTAT5	2.29	4.83	1.57	3.00	1.00	58.50	2.15	4.65	1.67	2.63	1.00	59.10
CD4-CD8- T Cells	IkB	5.12	8.27	3.90	6.34	1.00	58.30	4.30	6.68	3.62	4.99	1.00	47.60
CD4-CD8- T Cells	pERK	37.89	124.1	19.59	56.20	1.00	1213.00	31.17	103.5	20.56	41.79	1.00	1276.00
CD4-CD8- T Cells	pP38	1.97	2.46	1.61	2.34	1.00	21.70	1.77	2.22	1.54	2.00	1.00	20.90
CD4-CD8- T Cells	pPLCg2	4.98	7.58	3.86	6.10	1.00	68.60	4.45	8.39	3.59	5.31	1.00	71.80
CD4-CD8- T Cells	pS6	2.38	4.34	1.74	3.02	1.00	51.20	2.28	4.42	1.83	2.73	1.00	58.50
CD4-CD8- T Cells	pSTAT1	7.36	13.41	5.38	9.33	1.00	77.40	6.28	11.91	5.06	7.50	1.00	99.60
CD4-CD8- T Cells	pSTAT3	4.68	10.84	3.08	6.28	1.00	115.00	3.42	7.37	2.67	4.18	1.00	68.40
CD4-CD8- T Cells	pSTAT5	1.92	3.81	1.36	2.48	1.00	46.90	1.85	3.88	1.45	2.24	1.00	51.00
CD8+ T Cells	IkB	7.76	11.58	6.05	9.47	1.00	76.10	6.76	10.35	5.70	7.82	1.00	69.20
CD8+ T Cells	pERK	46.05	145.6	24.57	67.53	1.00	1514.00	38.10	121.3	25.66	50.53	1.00	1571.00
CD8+ T Cells	pP38	2.19	2.85	1.77	2.61	1.00	23.10	1.90	2.21	1.67	2.13	1.00	18.20
CD8+ T Cells	pPLCg2	5.39	8.42	4.15	6.63	1.00	78.40	5.06	9.20	4.12	6.01	1.00	83.10
CD8+ T Cells	pS6	2.74	5.40	1.94	3.54	1.00	64.80	2.60	5.17	2.07	3.13	1.00	72.80
CD8+ T Cells	pSTAT1	11.65	19.97	8.71	14.60	1.00	139.00	9.85	16.83	8.12	11.57	1.00	126.00
CD8+ T Cells	pSTAT3	5.51	12.29	3.70	7.33	1.00	119.00	4.01	8.75	3.11	4.91	1.00	81.50
CD8+ T Cells	pSTAT5	2.16	4.54	1.49	2.83	1.00	55.30	2.08	4.59	1.61	2.55	1.00	57.60
Dendritic Cells	IkB	3.88	6.53	2.92	4.84	1.00	50.40	3.44	5.09	2.92	3.96	1.00	42.20
Dendritic Cells	pERK	37.60	123.7	19.35	55.85	1.00	1248.00	30.65	99.24	20.48	40.83	1.00	1408.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	5.33	7.22	4.27	6.40	1.00	38.40	4.61	6.80	3.92	5.31	1.00	48.60
Dendritic Cells	pPLCg2	5.02	7.14	3.96	6.07	1.00	55.60	4.72	7.91	3.91	5.54	1.00	69.20
Dendritic Cells	pS6	2.26	3.92	1.68	2.83	1.00	45.20	2.22	4.19	1.79	2.65	1.00	53.90
Dendritic Cells	pSTAT1	5.74	11.57	4.04	7.45	1.00	76.90	4.82	10.01	3.80	5.85	1.00	88.20
Dendritic Cells	pSTAT3	3.27	6.40	2.32	4.21	1.00	63.00	2.79	6.12	2.17	3.42	1.00	77.40
Dendritic Cells	pSTAT5	1.88	3.47	1.36	2.39	1.00	42.00	1.85	3.83	1.46	2.24	1.00	49.90
HLADR+ NK Cells	IkB	5.74	7.44	4.64	6.84	1.00	50.30	5.07	6.48	4.41	5.74	1.00	39.50
HLADR+ NK Cells	pERK	46.11	126.3	27.43	64.80	1.00	1365.00	42.12	122.0	29.58	54.66	1.00	1571.00
HLADR+ NK Cells	pP38	2.24	2.94	1.81	2.67	1.00	21.50	2.05	2.48	1.79	2.30	1.00	21.90
HLADR+ NK Cells	pPLCg2	8.13	9.03	6.79	9.46	1.00	60.30	8.00	11.59	6.81	9.19	1.00	116.00
HLADR+ NK Cells	pS6	3.06	3.81	2.49	3.62	1.00	29.10	2.69	2.91	2.39	2.99	1.00	28.10
HLADR+ NK Cells	pSTAT1	5.89	10.68	4.31	7.47	1.00	69.40	4.96	8.80	4.05	5.86	1.00	74.40
HLADR+ NK Cells	pSTAT3	4.57	11.72	2.84	6.31	1.00	139.00	3.55	6.13	2.92	4.18	1.00	62.80
HLADR+ NK Cells	pSTAT5	2.11	2.61	1.73	2.50	1.00	16.30	2.13	3.64	1.75	2.50	1.00	47.40
HLADR+CD38+ CD4+ T Cells	IkB	10.50	16.23	8.11	12.90	1.00	135.00	8.99	12.36	7.72	10.26	1.00	72.00
HLADR+CD38+ CD4+ T Cells	pERK	52.44	145.6	30.96	73.92	1.00	1493.00	46.49	131.0	33.06	59.92	1.00	1690.00
HLADR+CD38+ CD4+ T Cells	pP38	3.51	4.60	2.83	4.19	1.00	34.80	3.09	3.74	2.71	3.47	1.00	25.60
HLADR+CD38+ CD4+ T Cells	pPLCg2	9.52	16.32	7.11	11.92	1.00	134.00	10.13	27.40	7.32	12.94	1.00	382.00
HLADR+CD38+ CD4+ T Cells	pS6	3.91	7.09	2.86	4.95	1.00	79.10	3.63	6.08	3.01	4.25	1.00	78.40
HLADR+CD38+ CD4+ T Cells	pSTAT1	14.57	24.06	11.02	18.12	1.00	148.00	12.32	20.51	10.21	14.42	1.00	146.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	9.39	22.04	6.14	12.64	1.00	256.00	6.66	12.26	5.41	7.92	1.00	123.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	3.06	5.99	2.17	3.94	1.00	68.60	2.92	5.93	2.31	3.53	1.00	64.00
HLADR+CD38+ CD8+ T Cells	IkB	8.63	12.05	6.85	10.41	1.00	93.50	7.42	9.69	6.42	8.41	1.00	64.60
HLADR+CD38+ CD8+ T Cells	pERK	51.66	147.9	29.85	73.47	1.20	1566.00	44.82	122.6	32.26	57.39	1.00	1549.00
HLADR+CD38+ CD8+ T Cells	pP38	3.10	4.12	2.49	3.71	1.00	33.20	2.75	3.20	2.42	3.07	1.00	22.20
HLADR+CD38+ CD8+ T Cells	pPLCg2	9.41	14.02	7.35	11.48	1.00	100.00	9.06	16.37	7.38	10.74	1.00	133.00
HLADR+CD38+ CD8+ T Cells	pS6	3.72	6.73	2.72	4.71	1.00	77.40	3.47	6.16	2.84	4.10	1.00	82.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	12.10	19.84	9.18	15.03	1.00	109.00	9.95	16.17	8.29	11.60	1.00	118.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	7.44	17.55	4.85	10.03	1.00	199.00	5.63	10.71	4.53	6.73	1.00	126.00
HLADR+CD38+ CD8+ T Cells	pSTAT5	2.91	5.71	2.07	3.75	1.00	64.90	2.83	6.19	2.20	3.46	1.00	69.40
IgD+CD27+ B Cells	IkB	5.84	8.03	4.65	7.02	1.00	66.00	5.20	6.81	4.50	5.90	1.00	47.50
IgD+CD27+ B Cells	pERK	41.78	134.5	21.95	61.62	1.33	1408.00	38.75	133.7	25.05	52.45	1.00	1615.00
IgD+CD27+ B Cells	pP38	2.26	2.82	1.84	2.67	1.00	22.80	1.99	2.31	1.76	2.23	1.00	21.50
IgD+CD27+ B Cells	pPLCg2	9.34	11.32	7.67	11.01	1.00	78.40	8.57	11.83	7.35	9.78	1.00	89.40
IgD+CD27+ B Cells	pS6	3.25	5.75	2.40	4.09	1.00	63.30	2.96	4.95	2.45	3.47	1.00	61.60
IgD+CD27+ B Cells	pSTAT1	6.19	10.48	4.65	7.74	1.00	76.90	5.52	9.53	4.54	6.50	1.00	76.50
IgD+CD27+ B Cells	pSTAT3	6.43	12.50	4.58	8.27	1.00	134.00	4.96	8.06	4.14	5.79	1.00	91.30
IgD+CD27+ B Cells	pSTAT5	2.40	4.43	1.74	3.05	1.00	49.50	2.31	4.71	1.82	2.79	1.00	52.50
IgD+CD27- B Cells	IkB	4.78	6.50	3.83	5.74	1.00	46.10	4.19	5.61	3.61	4.76	1.00	37.50
IgD+CD27- B Cells	pERK	34.48	113.1	17.80	51.16	1.00	1119.00	29.38	106.0	18.50	40.27	1.00	1436.00
IgD+CD27- B Cells	pP38	1.89	2.28	1.55	2.23	1.00	20.20	1.76	2.48	1.51	2.02	1.00	33.00
IgD+CD27- B Cells	pPLCg2	7.69	9.45	6.29	9.08	1.00	58.50	7.00	10.16	5.96	8.04	1.00	78.80
IgD+CD27- B Cells	pS6	2.71	5.08	1.96	3.46	1.00	56.70	2.47	3.91	2.07	2.87	1.00	40.30
IgD+CD27- B Cells	pSTAT1	5.10	8.90	3.79	6.42	1.00	60.80	4.50	8.36	3.64	5.35	1.00	80.60
IgD+CD27- B Cells	pSTAT3	5.11	7.80	3.96	6.26	1.00	58.00	4.15	6.94	3.44	4.86	1.00	85.60
IgD+CD27- B Cells	pSTAT5	1.98	3.27	1.50	2.46	1.00	36.30	1.91	3.43	1.56	2.26	1.00	36.80
IgD-CD27+ B Cells	IkB	5.00	7.30	3.92	6.08	1.00	45.60	4.19	5.92	3.58	4.80	1.00	48.70
IgD-CD27+ B Cells	pERK	33.42	107.0	17.64	49.20	1.00	1091.00	27.05	78.13	19.04	35.06	1.00	1028.00
IgD-CD27+ B Cells	pP38	2.00	2.67	1.61	2.39	1.00	22.60	1.70	1.70	1.53	1.88	1.00	15.20
IgD-CD27+ B Cells	pPLCg2	8.30	10.13	6.81	9.79	1.00	74.00	7.44	11.02	6.31	8.57	1.00	90.90
IgD-CD27+ B Cells	pS6	2.95	4.30	2.31	3.58	1.00	41.10	2.78	5.01	2.26	3.29	1.00	73.20
IgD-CD27+ B Cells	pSTAT1	6.05	11.15	4.41	7.70	1.00	70.00	5.38	10.18	4.33	6.42	1.00	99.60
IgD-CD27+ B Cells	pSTAT3	4.93	10.16	3.43	6.43	1.00	102.00	3.93	7.37	3.17	4.68	1.00	69.90
IgD-CD27+ B Cells	pSTAT5	2.10	3.30	1.61	2.59	1.00	31.10	2.09	4.70	1.61	2.57	1.00	50.20

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	3.92	5.95	3.04	4.79	1.00	39.60	3.64	6.11	3.01	4.27	1.00	54.30
IgD-CD27- B Cells	pERK	30.25	118.5	12.78	47.72	1.00	1388.00	25.21	123.0	12.58	37.84	1.00	1961.00
IgD-CD27- B Cells	pP38	1.83	2.11	1.52	2.14	1.00	15.30	1.63	2.37	1.39	1.87	1.00	34.10
IgD-CD27- B Cells	pPLCg2	6.40	7.67	5.27	7.53	1.00	49.20	5.98	8.92	5.06	6.90	1.00	84.50
IgD-CD27- B Cells	pS6	2.51	3.96	1.92	3.09	1.00	39.20	2.47	4.76	1.98	2.96	1.00	52.80
IgD-CD27- B Cells	pSTAT1	5.70	12.92	3.79	7.60	1.00	130.00	4.68	9.72	3.68	5.68	1.00	103.00
IgD-CD27- B Cells	pSTAT3	4.25	7.54	3.14	5.36	1.00	50.70	3.44	5.94	2.83	4.05	1.00	53.00
IgD-CD27- B Cells	pSTAT5	1.63	1.86	1.35	1.90	1.00	15.50	1.89	4.16	1.47	2.32	1.00	44.70
NK Cells	IkB	4.65	6.17	3.74	5.56	1.00	36.30	4.11	5.36	3.56	4.66	1.00	36.40
NK Cells	pERK	40.37	118.5	22.84	57.90	1.00	1262.00	37.17	120.6	24.78	49.56	1.00	1536.00
NK Cells	pP38	1.70	2.13	1.39	2.02	1.00	19.30	1.56	1.65	1.39	1.73	1.00	16.90
NK Cells	pPLCg2	5.96	6.79	4.96	6.97	1.00	42.20	5.93	8.77	5.03	6.83	1.00	77.70
NK Cells	pS6	2.30	2.18	1.98	2.63	1.00	17.40	2.18	2.35	1.94	2.43	1.00	24.10
NK Cells	pSTAT1	4.80	8.88	3.49	6.12	1.00	62.30	4.03	7.52	3.26	4.81	1.00	66.10
NK Cells	pSTAT3	3.80	10.15	2.30	5.31	1.00	122.00	2.83	4.98	2.31	3.34	1.00	53.30
NK Cells	pSTAT5	1.78	2.12	1.46	2.09	1.00	14.20	1.71	2.85	1.41	2.00	1.00	43.70
NKT Cells	IkB	10.60	17.19	8.04	13.17	1.00	169.00	9.87	14.01	8.43	11.32	1.00	86.50
NKT Cells	pERK	60.47	198.1	30.92	90.03	1.00	2206.00	58.11	181.8	39.35	76.88	1.00	1977.00
NKT Cells	pP38	3.26	4.34	2.62	3.91	1.00	29.50	3.02	4.42	2.57	3.48	1.00	42.60
NKT Cells	pPLCg2	6.00	7.54	4.88	7.13	1.00	44.80	6.85	13.67	5.44	8.26	1.00	136.00
NKT Cells	pS6	4.30	10.90	2.67	5.93	1.00	138.00	4.93	14.28	3.45	6.40	1.00	211.00
NKT Cells	pSTAT1	20.16	78.20	8.50	31.83	1.00	1012.00	13.31	22.05	11.03	15.58	1.00	205.00
NKT Cells	pSTAT3	7.37	12.34	5.53	9.21	1.00	82.80	6.99	17.54	5.18	8.80	1.00	206.00
NKT Cells	pSTAT5	2.48	3.25	1.99	2.96	1.00	25.40	2.69	5.19	2.15	3.23	1.00	65.80
Regulatory T Cells	IkB	11.10	15.71	8.79	13.42	1.00	104.00	10.15	15.22	8.59	11.71	1.00	89.10
Regulatory T Cells	pERK	49.29	144.8	27.94	70.65	1.00	1519.00	43.51	132.7	29.91	57.11	1.00	1638.00
Regulatory T Cells	pP38	2.70	3.50	2.18	3.21	1.00	28.20	2.34	2.92	2.04	2.64	1.00	27.40
Regulatory T Cells	pPLCg2	5.71	9.78	4.27	7.15	1.00	96.10	5.45	9.89	4.43	6.46	1.00	104.00
Regulatory T Cells	pS6	3.03	6.77	2.03	4.03	1.00	84.80	2.85	4.71	2.36	3.33	1.00	65.10
Regulatory T Cells	pSTAT1	16.22	30.20	11.77	20.68	1.00	246.00	14.38	26.33	11.68	17.07	1.00	240.00
Regulatory T Cells	pSTAT3	8.20	19.24	5.36	11.04	1.00	211.00	5.75	11.54	4.56	6.93	1.00	126.00
Regulatory T Cells	pSTAT5	2.46	5.10	1.70	3.21	1.00	61.10	2.35	5.42	1.79	2.90	1.00	76.30

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	9.76	14.36	7.64	11.87	1.00	76.70	8.56	12.86	7.24	9.87	1.00	84.80
Central Memory CD4+ T Cells	pERK	44.29	138.3	23.89	64.68	1.00	1420.00	38.07	125.8	25.18	50.97	1.00	1671.00
Central Memory CD4+ T Cells	pP38	2.57	3.43	2.07	3.08	1.00	27.50	2.19	2.58	1.93	2.46	1.00	19.00
Central Memory CD4+ T Cells	pPLCg2	5.00	7.40	3.91	6.10	1.00	68.50	4.76	8.47	3.89	5.63	1.00	80.00
Central Memory CD4+ T Cells	pS6	2.57	4.80	1.86	3.28	1.00	56.90	2.52	5.15	1.99	3.05	1.00	73.80
Central Memory CD4+ T Cells	pSTAT1	16.60	28.41	12.41	20.79	1.00	182.00	14.13	24.47	11.62	16.64	1.00	171.00
Central Memory CD4+ T Cells	pSTAT3	7.33	17.92	4.69	9.98	1.00	196.00	5.01	11.24	3.86	6.16	1.00	118.00
Central Memory CD4+ T Cells	pSTAT5	2.27	4.24	1.65	2.90	1.00	48.00	2.18	4.69	1.70	2.66	1.00	60.30
Central Memory CD8+ T Cells	IkB	7.99	11.73	6.26	9.72	1.00	64.00	6.86	10.82	5.76	7.97	1.00	86.00
Central Memory CD8+ T Cells	pERK	46.45	143.9	25.22	67.68	1.00	1502.00	37.65	111.8	26.19	49.11	1.00	1473.00
Central Memory CD8+ T Cells	pP38	2.48	3.28	2.00	2.96	1.00	26.50	2.06	2.39	1.82	2.31	1.00	19.00
Central Memory CD8+ T Cells	pPLCg2	4.94	7.55	3.82	6.05	1.00	59.60	4.64	8.41	3.78	5.50	1.00	87.70
Central Memory CD8+ T Cells	pS6	3.01	5.22	2.24	3.78	1.00	59.10	2.83	5.83	2.23	3.42	1.00	86.50
Central Memory CD8+ T Cells	pSTAT1	13.42	24.35	9.83	17.02	1.00	198.00	11.19	19.60	9.19	13.20	1.00	152.00
Central Memory CD8+ T Cells	pSTAT3	5.54	13.04	3.61	7.46	1.00	134.00	4.12	9.30	3.17	5.07	1.00	93.00
Central Memory CD8+ T Cells	pSTAT5	2.07	3.80	1.51	2.63	1.00	43.40	2.09	4.79	1.59	2.58	1.00	65.10
Effector CD4+ T Cells	IkB	6.61	10.29	5.09	8.13	1.00	69.20	5.89	9.24	4.95	6.84	1.00	64.80
Effector CD4+ T Cells	pERK	34.65	98.51	20.12	49.18	1.00	930.00	27.96	89.90	18.73	37.19	1.00	1468.00
Effector CD4+ T Cells	pP38	2.03	2.53	1.65	2.40	1.00	22.40	1.75	1.88	1.55	1.94	1.00	15.00
Effector CD4+ T Cells	pPLCg2	4.58	7.33	3.50	5.66	1.00	73.80	4.25	7.62	3.47	5.04	1.00	73.20
Effector CD4+ T Cells	pS6	2.39	5.19	1.63	3.16	1.00	64.60	2.31	4.69	1.83	2.79	1.00	64.20
Effector CD4+ T Cells	pSTAT1	10.29	18.10	7.62	12.96	1.00	123.00	8.47	15.04	6.93	10.02	1.00	128.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	6.33	11.98	4.56	8.09	1.00	117.00	4.42	8.02	3.60	5.25	1.00	72.20
Effector CD4+ T Cells	pSTAT5	2.04	4.44	1.38	2.69	1.00	55.60	1.91	3.98	1.50	2.32	1.00	53.50
Effector CD8+ T Cells	IkB	6.03	9.43	4.64	7.42	1.00	61.10	5.12	8.20	4.27	5.96	1.00	64.90
Effector CD8+ T Cells	pERK	40.62	120.8	22.81	58.44	1.00	1324.00	30.45	86.31	21.59	39.31	1.00	1305.00
Effector CD8+ T Cells	pP38	1.98	2.76	1.58	2.39	1.00	21.90	1.71	1.91	1.51	1.91	1.00	18.60
Effector CD8+ T Cells	pPLCg2	4.99	7.62	3.87	6.12	1.00	69.40	4.51	8.08	3.68	5.34	1.00	72.00
Effector CD8+ T Cells	pS6	2.41	4.93	1.68	3.14	1.00	59.40	2.27	4.54	1.80	2.74	1.00	64.90
Effector CD8+ T Cells	pSTAT1	9.62	16.69	7.16	12.08	1.00	112.00	7.90	14.16	6.45	9.35	1.00	106.00
Effector CD8+ T Cells	pSTAT3	4.69	9.04	3.36	6.02	1.00	71.80	3.50	6.97	2.78	4.21	1.00	63.80
Effector CD8+ T Cells	pSTAT5	1.98	4.06	1.39	2.58	1.00	49.70	1.87	4.10	1.45	2.29	1.00	51.80
Effector Memory CD4+ T Cells	IkB	6.66	10.76	5.07	8.25	1.00	59.40	5.62	9.33	4.67	6.58	1.00	70.60
Effector Memory CD4+ T Cells	pERK	34.57	101.1	19.65	49.49	1.00	1014.00	26.30	80.78	18.01	34.59	1.00	1335.00
Effector Memory CD4+ T Cells	pP38	2.15	2.92	1.72	2.58	1.00	25.90	1.77	2.01	1.57	1.98	1.00	18.00
Effector Memory CD4+ T Cells	pPLCg2	3.96	6.54	2.99	4.92	1.00	60.10	3.64	6.76	2.94	4.33	1.00	73.00
Effector Memory CD4+ T Cells	pS6	2.09	4.02	1.50	2.69	1.00	47.90	2.08	4.31	1.63	2.52	1.00	62.00
Effector Memory CD4+ T Cells	pSTAT1	12.59	23.22	9.16	16.01	1.00	170.00	10.52	19.65	8.50	12.54	1.00	135.00
Effector Memory CD4+ T Cells	pSTAT3	5.57	14.38	3.44	7.69	1.00	164.00	3.79	8.19	2.95	4.63	1.00	92.30
Effector Memory CD4+ T Cells	pSTAT5	1.88	3.52	1.36	2.40	1.00	42.80	1.77	3.68	1.39	2.15	1.00	55.60
Effector Memory CD8+ T Cells	IkB	6.29	11.69	4.56	8.01	1.00	105.00	4.74	8.03	3.92	5.57	1.00	63.20
Effector Memory CD8+ T Cells	pERK	38.86	120.3	21.11	56.61	1.00	1167.00	27.33	71.57	19.98	34.67	1.00	1031.00
Effector Memory CD8+ T Cells	pP38	2.12	3.12	1.66	2.58	1.00	26.50	1.79	2.16	1.56	2.01	1.00	21.80
Effector Memory CD8+ T Cells	pPLCg2	4.29	7.46	3.19	5.39	1.00	60.30	3.62	6.57	2.94	4.29	1.00	63.50

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	2.41	4.16	1.79	3.02	1.00	39.90	2.20	4.20	1.77	2.63	1.00	55.60
Effector Memory CD8+ T Cells	pSTAT1	10.66	21.31	7.52	13.80	1.00	162.00	8.07	15.38	6.49	9.65	1.00	110.00
Effector Memory CD8+ T Cells	pSTAT3	4.70	13.19	2.75	6.65	1.00	154.00	3.32	7.44	2.56	4.09	1.00	81.30
Effector Memory CD8+ T Cells	pSTAT5	1.92	3.65	1.39	2.46	1.00	41.60	1.80	3.58	1.44	2.17	1.00	44.80
Myeloid Dendritic Cells	IkB	4.07	6.46	3.12	5.03	1.00	48.00	3.55	5.06	3.03	4.07	1.00	42.80
Myeloid Dendritic Cells	pERK	41.18	134.4	21.35	61.01	1.00	1444.00	32.71	92.20	23.26	42.16	1.00	1255.00
Myeloid Dendritic Cells	pP38	8.70	11.36	7.02	10.37	1.00	85.80	7.94	10.45	6.87	9.02	1.00	69.80
Myeloid Dendritic Cells	pPLCg2	5.59	8.66	4.32	6.87	1.00	78.00	5.12	8.63	4.24	6.01	1.00	75.20
Myeloid Dendritic Cells	pS6	2.47	4.17	1.85	3.08	1.00	46.90	2.40	4.41	1.95	2.85	1.00	53.90
Myeloid Dendritic Cells	pSTAT1	6.14	11.93	4.38	7.90	1.00	79.10	5.33	11.07	4.19	6.46	1.00	93.20
Myeloid Dendritic Cells	pSTAT3	3.58	8.27	2.36	4.80	1.00	91.70	2.98	6.56	2.31	3.65	1.00	81.70
Myeloid Dendritic Cells	pSTAT5	1.98	3.69	1.43	2.52	1.00	44.10	1.91	3.78	1.53	2.30	1.00	46.00
Monocytes	IkB	14.19	13.74	7.12	21.25	1.34	47.50	11.63	10.89	7.94	15.31	1.09	45.50
Monocytes	pERK	174.7	469.5	-66.6	416.1	3.68	1606.00	154.3	440.6	5.21	303.3	1.89	1828.00
Monocytes	pP38	3.31	5.64	0.41	6.22	1.00	19.00	3.24	6.05	1.20	5.29	1.00	25.10
Monocytes	pPLCg2	5.55	5.91	2.51	8.59	1.00	21.80	5.53	6.53	3.32	7.74	1.00	27.50
Monocytes	pS6	3.91	2.55	2.60	5.22	1.02	9.51	3.83	2.64	2.93	4.72	1.00	11.00
Monocytes	pSTAT1	10.22	12.74	3.67	16.77	1.00	51.80	9.03	9.76	5.73	12.33	1.00	36.70
Monocytes	pSTAT3	1.74	1.21	1.12	2.36	1.00	5.06	1.72	1.26	1.30	2.15	1.00	5.96
Monocytes	pSTAT5	1.86	1.27	1.20	2.51	1.00	5.33	1.88	1.93	1.23	2.54	1.00	10.30
Naive CD4+ T Cells	IkB	9.78	14.40	7.65	11.90	1.00	87.70	8.74	12.86	7.43	10.06	1.00	81.80
Naive CD4+ T Cells	pERK	43.48	137.6	23.19	63.78	1.00	1428.00	38.19	126.2	25.25	51.13	1.00	1690.00
Naive CD4+ T Cells	pP38	2.44	3.18	1.97	2.91	1.00	25.60	2.15	2.55	1.89	2.41	1.00	20.50
Naive CD4+ T Cells	pPLCg2	5.82	9.18	4.47	7.18	1.00	86.00	5.52	9.69	4.52	6.51	1.00	86.70
Naive CD4+ T Cells	pS6	2.91	5.78	2.06	3.77	1.00	70.60	2.83	5.39	2.28	3.38	1.00	72.40

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	12.84	21.24	9.71	15.97	1.00	131.00	10.87	18.48	8.97	12.76	1.00	145.00
Naive CD4+ T Cells	pSTAT3	8.34	15.93	5.99	10.69	1.00	158.00	5.82	10.89	4.71	6.94	1.00	113.00
Naive CD4+ T Cells	pSTAT5	2.43	5.09	1.68	3.19	1.00	61.10	2.29	4.96	1.78	2.80	1.00	60.10
Naive CD8+ T Cells	IkB	8.75	13.14	6.82	10.69	1.00	82.90	7.72	11.78	6.51	8.93	1.00	75.20
Naive CD8+ T Cells	pERK	47.91	148.2	26.05	69.76	1.00	1527.00	40.24	124.7	27.46	53.02	1.00	1593.00
Naive CD8+ T Cells	pP38	2.28	3.05	1.83	2.73	1.00	25.40	1.99	2.30	1.75	2.23	1.00	18.30
Naive CD8+ T Cells	pPLCg2	6.04	8.96	4.72	7.36	1.00	82.70	5.73	10.02	4.70	6.76	1.00	86.90
Naive CD8+ T Cells	pS6	2.96	5.68	2.12	3.79	1.00	67.90	2.82	5.42	2.26	3.38	1.00	75.00
Naive CD8+ T Cells	pSTAT1	12.47	20.64	9.42	15.51	1.00	135.00	10.59	17.47	8.80	12.38	1.00	127.00
Naive CD8+ T Cells	pSTAT3	6.27	13.08	4.34	8.20	1.00	121.00	4.50	9.19	3.56	5.44	1.00	86.70
Naive CD8+ T Cells	pSTAT5	2.33	4.84	1.62	3.05	1.00	58.30	2.25	5.06	1.73	2.76	1.00	59.60
Plasmoid Dendritic Cells	IkB	4.91	8.32	3.68	6.14	1.00	65.90	4.21	6.13	3.58	4.84	1.00	42.30
Plasmoid Dendritic Cells	pERK	44.85	146.7	23.15	66.55	1.00	1634.00	36.28	114.5	24.54	48.02	1.00	1648.00
Plasmoid Dendritic Cells	pP38	2.88	4.02	2.29	3.48	1.00	21.40	2.45	3.30	2.11	2.79	1.00	25.10
Plasmoid Dendritic Cells	pPLCg2	6.08	9.31	4.70	7.45	1.00	82.00	5.67	9.46	4.70	6.64	1.00	80.60
Plasmoid Dendritic Cells	pS6	3.05	5.77	2.19	3.90	1.00	57.30	2.61	4.99	2.10	3.12	1.00	63.70
Plasmoid Dendritic Cells	pSTAT1	6.89	15.98	4.53	9.26	1.00	155.00	5.19	10.24	4.14	6.24	1.00	88.20
Plasmoid Dendritic Cells	pSTAT3	3.66	6.03	2.77	4.55	1.00	33.60	3.14	7.07	2.41	3.86	1.00	86.50
Plasmoid Dendritic Cells	pSTAT5	2.33	4.82	1.61	3.04	1.00	56.20	2.16	5.23	1.62	2.69	1.00	65.80
Plasmablasts	IkB	6.95	8.10	5.75	8.16	1.00	43.70	6.77	12.04	5.53	8.01	1.00	161.00
Plasmablasts	pERK	47.18	128.8	27.96	66.41	1.00	1320.00	49.67	151.8	34.00	65.35	1.00	1652.00
Plasmablasts	pP38	2.81	3.98	2.22	3.41	1.00	32.90	2.64	3.59	2.27	3.02	1.00	27.20
Plasmablasts	pPLCg2	7.96	8.27	6.73	9.20	1.00	42.40	7.97	11.93	6.74	9.20	1.00	90.90
Plasmablasts	pS6	3.89	4.63	3.20	4.58	1.00	30.10	3.75	5.09	3.22	4.27	1.00	42.60

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=LPS

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	6.38	10.55	4.80	7.95	1.00	72.20	6.70	13.21	5.33	8.06	1.00	127.00
Plasmablasts	pSTAT3	5.65	7.82	4.48	6.82	1.00	49.80	5.31	8.75	4.41	6.22	1.00	81.70
Plasmablasts	pSTAT5	2.62	3.93	2.03	3.20	1.00	30.50	2.51	4.60	2.04	2.99	1.00	56.40
Transitional B Cells	IkB	7.20	9.24	5.81	8.58	1.00	71.40	7.51	17.68	5.69	9.34	1.00	272.00
Transitional B Cells	pERK	48.42	124.9	29.73	67.10	1.50	1237.00	47.46	142.8	32.73	62.20	1.00	1838.00
Transitional B Cells	pP38	3.73	4.84	3.01	4.46	1.00	33.20	3.58	5.98	2.96	4.19	1.00	80.40
Transitional B Cells	pPLCg2	9.28	10.98	7.63	10.92	1.00	62.90	10.19	19.43	8.18	12.19	1.00	229.00
Transitional B Cells	pS6	3.82	4.15	3.20	4.44	1.00	22.50	5.25	23.03	2.87	7.62	1.00	430.00
Transitional B Cells	pSTAT1	7.03	11.21	5.36	8.71	1.00	63.10	7.76	15.29	6.19	9.34	1.00	124.00
Transitional B Cells	pSTAT3	8.58	10.67	6.98	10.17	1.00	99.40	8.24	11.41	7.07	9.42	1.00	104.00
Transitional B Cells	pSTAT5	2.62	3.56	2.09	3.16	1.00	25.00	3.17	11.40	1.99	4.35	1.00	195.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
B Cells	IkB	5.45	6.60	4.48	6.43	1.00	35.20	5.04	6.18	4.40	5.68	1.00	34.70
B Cells	pERK	53.53	135.5	33.53	73.52	1.00	1361.00	48.73	128.9	35.48	61.97	1.00	1510.00
B Cells	pP38	3.38	4.39	2.73	4.03	1.00	27.10	3.22	4.24	2.78	3.66	1.00	31.20
B Cells	pPLCg2	8.26	9.69	6.83	9.68	1.00	66.60	8.06	11.06	6.92	9.20	1.00	90.20
B Cells	pS6	9.01	25.80	5.21	12.82	1.00	321.00	6.83	9.83	5.82	7.84	1.00	84.60
B Cells	pSTAT1	5.61	8.99	4.29	6.94	1.00	60.60	4.94	7.91	4.13	5.75	1.00	63.70
B Cells	pSTAT3	6.25	13.26	4.29	8.20	1.00	121.00	5.32	12.62	4.02	6.62	1.00	178.00
B Cells	pSTAT5	2.03	2.86	1.61	2.45	1.00	29.80	2.05	3.18	1.73	2.38	1.00	33.30
CD16+ NK Cells	IkB	6.25	8.41	4.96	7.53	1.00	46.90	5.95	8.26	5.08	6.83	1.00	53.80
CD16+ NK Cells	pERK	60.23	141.2	38.65	81.80	1.00	1196.00	56.69	139.5	41.90	71.48	1.00	1676.00
CD16+ NK Cells	pP38	2.45	3.96	1.84	3.05	1.00	39.10	2.45	4.43	1.98	2.92	1.00	44.10
CD16+ NK Cells	pPLCg2	9.18	11.60	7.41	10.95	1.00	71.80	9.16	12.60	7.82	10.49	1.00	104.00
CD16+ NK Cells	pS6	4.96	6.54	3.96	5.96	1.00	52.30	4.79	6.18	4.13	5.44	1.00	41.70
CD16+ NK Cells	pSTAT1	5.35	10.56	3.74	6.97	1.00	67.00	4.45	9.27	3.46	5.43	1.00	83.30
CD16+ NK Cells	pSTAT3	4.27	10.00	2.74	5.80	1.00	87.40	4.02	8.31	3.14	4.90	1.00	101.00
CD16+ NK Cells	pSTAT5	2.18	3.13	1.70	2.66	1.00	25.60	1.89	2.71	1.60	2.17	1.00	28.40
CD16+ Monocytes	IkB	10.53	12.60	8.67	12.39	1.00	84.40	9.63	11.44	8.45	10.80	1.00	60.40
CD16+ Monocytes	pERK	80.37	151.0	58.11	102.6	1.00	1440.00	84.27	186.1	65.11	103.4	1.00	2022.00
CD16+ Monocytes	pP38	5.96	7.84	4.80	7.12	1.00	60.60	6.29	8.56	5.41	7.17	1.00	66.60
CD16+ Monocytes	pPLCg2	12.01	13.57	10.01	14.01	1.00	90.40	15.23	52.66	9.80	20.65	1.00	959.00
CD16+ Monocytes	pS6	10.16	14.90	7.96	12.36	1.00	106.00	9.29	13.09	7.95	10.64	1.00	83.90
CD16+ Monocytes	pSTAT1	10.15	16.17	7.76	12.54	1.00	102.00	10.43	22.30	8.13	12.72	1.00	234.00
CD16+ Monocytes	pSTAT3	9.44	19.37	6.59	12.30	1.00	149.00	8.62	18.35	6.73	10.51	1.00	191.00
CD16+ Monocytes	pSTAT5	3.04	4.30	2.41	3.68	1.00	31.20	4.23	19.35	2.24	6.22	1.00	351.00
CD16- NK Cells	IkB	5.02	6.48	4.06	5.97	1.00	43.30	4.62	6.48	3.95	5.28	1.00	49.10
CD16- NK Cells	pERK	49.57	130.4	30.34	68.80	1.00	1408.00	42.53	110.3	31.20	53.87	1.00	1244.00
CD16- NK Cells	pP38	2.27	3.28	1.79	2.76	1.00	31.10	2.14	2.89	1.84	2.44	1.00	26.70
CD16- NK Cells	pPLCg2	5.48	6.39	4.53	6.42	1.00	46.70	5.69	8.68	4.79	6.58	1.00	81.90
CD16- NK Cells	pS6	4.69	7.08	3.65	5.74	1.00	71.80	4.24	5.94	3.62	4.85	1.00	54.00
CD16- NK Cells	pSTAT1	5.24	8.97	3.92	6.56	1.00	62.30	4.56	8.16	3.72	5.40	1.00	77.80
CD16- NK Cells	pSTAT3	4.07	11.06	2.44	5.70	1.00	127.00	3.26	8.94	2.34	4.18	1.00	133.00
CD16- NK Cells	pSTAT5	1.81	2.43	1.46	2.17	1.00	25.70	1.85	2.70	1.57	2.13	1.00	33.20
CD16- Monocytes	IkB	9.26	11.14	7.61	10.90	1.00	62.00	8.58	10.92	7.46	9.71	1.00	64.70

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	76.55	177.4	50.38	102.7	1.00	1767.00	68.08	154.7	52.18	83.98	1.00	1549.00
CD16- Monocytes	pP38	7.01	7.91	5.84	8.17	1.00	45.50	6.58	7.44	5.82	7.35	1.00	55.50
CD16- Monocytes	pPLCg2	7.45	8.45	6.20	8.69	1.00	49.60	7.96	13.41	6.58	9.34	1.00	136.00
CD16- Monocytes	pS6	10.03	16.24	7.64	12.43	1.00	130.00	8.57	13.25	7.21	9.93	1.00	102.00
CD16- Monocytes	pSTAT1	11.56	16.08	9.19	13.93	1.00	90.60	10.94	16.36	9.26	12.62	1.00	113.00
CD16- Monocytes	pSTAT3	8.68	22.43	5.37	11.99	1.00	222.00	7.00	20.25	4.92	9.08	1.00	287.00
CD16- Monocytes	pSTAT5	2.67	3.90	2.09	3.24	1.00	37.50	2.74	4.45	2.28	3.20	1.00	44.40
CD4+ T Cells	IkB	8.65	10.78	7.06	10.24	1.00	50.80	8.13	10.37	7.06	9.20	1.00	59.90
CD4+ T Cells	pERK	67.34	157.0	44.19	90.50	1.00	1519.00	57.26	132.4	43.65	70.87	1.00	1404.00
CD4+ T Cells	pP38	4.29	5.16	3.53	5.05	1.00	24.50	3.95	5.11	3.42	4.47	1.00	42.00
CD4+ T Cells	pPLCg2	4.73	6.19	3.82	5.65	1.00	38.90	5.08	9.22	4.14	6.03	1.00	93.70
CD4+ T Cells	pS6	8.84	14.59	6.69	10.99	1.00	100.00	7.65	12.02	6.41	8.88	1.00	87.90
CD4+ T Cells	pSTAT1	11.67	17.13	9.14	14.20	1.00	126.00	10.34	15.68	8.73	11.95	1.00	111.00
CD4+ T Cells	pSTAT3	8.23	19.64	5.34	11.13	1.00	175.00	6.04	16.54	4.34	7.74	1.00	213.00
CD4+ T Cells	pSTAT5	2.08	2.90	1.65	2.51	1.00	28.50	2.12	3.21	1.79	2.45	1.00	32.30
CD4-CD8- T Cells	IkB	5.31	6.80	4.31	6.32	1.00	33.00	4.69	6.29	4.05	5.34	1.00	35.90
CD4-CD8- T Cells	pERK	49.48	115.5	32.44	66.52	1.00	1067.00	41.08	97.83	31.02	51.13	1.00	953.00
CD4-CD8- T Cells	pP38	3.28	4.20	2.66	3.90	1.00	32.50	2.91	3.94	2.51	3.32	1.00	29.30
CD4-CD8- T Cells	pPLCg2	4.68	6.13	3.77	5.58	1.00	42.60	4.61	7.89	3.80	5.42	1.00	72.00
CD4-CD8- T Cells	pS6	6.26	10.03	4.78	7.74	1.00	83.80	5.30	8.26	4.45	6.15	1.00	67.20
CD4-CD8- T Cells	pSTAT1	7.20	11.80	5.46	8.95	1.00	75.20	6.49	11.43	5.32	7.67	1.00	97.20
CD4-CD8- T Cells	pSTAT3	5.38	14.17	3.29	7.47	1.00	148.00	4.06	10.91	2.94	5.18	1.00	130.00
CD4-CD8- T Cells	pSTAT5	1.77	2.29	1.43	2.11	1.00	24.00	1.76	2.41	1.51	2.01	1.00	23.20
CD8+ T Cells	IkB	7.60	9.39	6.22	8.99	1.00	43.80	6.89	8.75	5.99	7.79	1.00	44.60
CD8+ T Cells	pERK	63.78	151.9	41.37	86.18	1.00	1536.00	52.61	121.1	40.16	65.06	1.00	1291.00
CD8+ T Cells	pP38	3.93	4.76	3.23	4.63	1.00	26.40	3.47	4.48	3.01	3.93	1.00	34.80
CD8+ T Cells	pPLCg2	4.93	6.25	4.00	5.85	1.00	39.30	5.15	8.80	4.25	6.06	1.00	75.40
CD8+ T Cells	pS6	9.51	17.40	6.94	12.08	1.00	129.00	7.35	11.93	6.12	8.57	1.00	96.60
CD8+ T Cells	pSTAT1	10.85	15.67	8.54	13.16	1.00	103.00	9.73	14.90	8.20	11.26	1.00	102.00
CD8+ T Cells	pSTAT3	6.38	16.82	3.90	8.86	1.00	158.00	4.70	13.21	3.34	6.05	1.00	163.00
CD8+ T Cells	pSTAT5	1.96	2.60	1.58	2.34	1.00	26.60	2.02	3.08	1.70	2.34	1.00	33.60
Dendritic Cells	IkB	3.79	5.38	2.99	4.58	1.00	39.90	3.56	5.56	2.99	4.13	1.00	51.90
Dendritic Cells	pERK	39.60	133.7	19.88	59.32	1.00	1485.00	29.92	75.10	22.20	37.64	1.00	766.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	5.73	7.90	4.56	6.89	1.00	48.70	5.10	7.16	4.36	5.83	1.00	39.60
Dendritic Cells	pPLCg2	4.34	5.70	3.50	5.18	1.00	47.40	4.54	7.80	3.73	5.34	1.00	77.50
Dendritic Cells	pS6	3.44	6.23	2.52	4.36	1.00	66.60	3.25	5.50	2.69	3.82	1.00	43.40
Dendritic Cells	pSTAT1	5.08	8.95	3.76	6.40	1.00	63.70	4.64	8.85	3.73	5.55	1.00	72.00
Dendritic Cells	pSTAT3	3.51	10.94	1.90	5.13	1.00	135.00	2.78	7.41	2.02	3.54	1.00	104.00
Dendritic Cells	pSTAT5	1.68	2.20	1.35	2.00	1.00	24.00	1.77	2.58	1.50	2.03	1.00	22.20
HLADR+ NK Cells	IkB	6.12	7.21	5.05	7.19	1.00	43.10	5.67	7.32	4.91	6.42	1.00	47.40
HLADR+ NK Cells	pERK	54.53	120.7	36.67	72.38	1.00	1180.00	50.99	119.2	38.70	63.27	1.00	1305.00
HLADR+ NK Cells	pP38	2.95	4.50	2.28	3.62	1.00	35.40	2.86	4.10	2.44	3.28	1.00	37.60
HLADR+ NK Cells	pPLCg2	7.92	9.12	6.57	9.27	1.00	71.00	8.33	12.38	7.05	9.61	1.00	122.00
HLADR+ NK Cells	pS6	5.59	8.41	4.35	6.84	1.00	71.80	5.29	7.62	4.50	6.07	1.00	63.10
HLADR+ NK Cells	pSTAT1	5.75	9.88	4.29	7.21	1.00	71.20	5.20	9.09	4.26	6.14	1.00	85.60
HLADR+ NK Cells	pSTAT3	4.59	11.31	2.92	6.27	1.00	126.00	4.16	11.91	2.93	5.38	1.00	171.00
HLADR+ NK Cells	pSTAT5	2.17	2.92	1.74	2.60	1.00	27.60	2.16	3.34	1.81	2.50	1.00	38.00
HLADR+CD38+ CD4+ T Cells	IkB	9.87	11.27	8.21	11.53	1.00	50.10	9.49	11.97	8.26	10.72	1.00	72.20
HLADR+CD38+ CD4+ T Cells	pERK	73.51	157.4	50.29	96.74	1.00	1536.00	67.42	139.4	53.09	81.75	1.00	1408.00
HLADR+CD38+ CD4+ T Cells	pP38	5.66	6.56	4.69	6.62	1.00	38.10	5.62	7.55	4.84	6.39	1.00	55.90
HLADR+CD38+ CD4+ T Cells	pPLCg2	31.12	218.4	-1.10	63.33	1.00	2149.00	62.87	538.9	7.48	118.3	1.00	6708.00
HLADR+CD38+ CD4+ T Cells	pS6	10.47	14.97	8.26	12.68	1.00	98.50	9.59	14.20	8.13	11.05	1.00	94.80
HLADR+CD38+ CD4+ T Cells	pSTAT1	13.44	19.13	10.62	16.26	1.00	130.00	12.31	19.47	10.31	14.31	1.00	144.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	9.42	17.49	6.84	12.00	1.00	132.00	7.64	16.52	5.94	9.33	1.00	169.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	3.31	6.42	2.37	4.26	1.00	60.40	3.80	10.35	2.74	4.87	1.00	146.00
HLADR+CD38+ CD8+ T Cells	IkB	8.75	10.12	7.26	10.25	1.00	48.70	8.10	10.07	7.06	9.13	1.00	59.40
HLADR+CD38+ CD8+ T Cells	pERK	66.54	140.1	45.88	87.21	1.04	1357.00	61.48	133.2	47.77	75.19	1.00	1456.00
HLADR+CD38+ CD8+ T Cells	pP38	5.06	5.76	4.21	5.91	1.00	31.70	4.91	6.23	4.27	5.55	1.00	39.80
HLADR+CD38+ CD8+ T Cells	pPLCg2	46.00	494.8	-27.0	119.0	1.00	6627.00	27.56	264.9	0.29	54.82	1.00	4867.00
HLADR+CD38+ CD8+ T Cells	pS6	11.00	20.36	7.99	14.00	1.00	203.00	8.92	12.52	7.63	10.20	1.00	88.90

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	11.52	16.44	9.09	13.94	1.00	89.10	10.43	16.90	8.69	12.17	1.00	138.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	7.47	14.10	5.39	9.55	1.00	105.00	6.47	15.50	4.88	8.07	1.00	202.00
HLADR+CD38+ CD8+ T Cells	pSTAT5	3.04	6.74	2.04	4.03	1.00	77.80	3.14	7.19	2.40	3.88	1.00	106.00
IgD+CD27+ B Cells	IkB	6.05	7.10	5.00	7.10	1.00	36.50	5.59	6.82	4.89	6.30	1.00	42.10
IgD+CD27+ B Cells	pERK	57.93	140.9	37.15	78.71	1.06	1404.00	53.19	132.2	39.61	66.78	1.00	1536.00
IgD+CD27+ B Cells	pP38	3.68	4.67	2.99	4.37	1.00	28.00	3.54	4.52	3.07	4.00	1.00	31.70
IgD+CD27+ B Cells	pPLCg2	9.07	10.34	7.55	10.59	1.00	69.00	8.91	11.79	7.70	10.12	1.00	92.20
IgD+CD27+ B Cells	pS6	9.88	26.85	5.92	13.84	1.00	331.00	7.42	10.31	6.36	8.48	1.00	90.80
IgD+CD27+ B Cells	pSTAT1	6.14	9.50	4.74	7.54	1.00	58.80	5.39	8.41	4.53	6.26	1.00	68.40
IgD+CD27+ B Cells	pSTAT3	7.11	14.24	5.01	9.21	1.00	129.00	6.02	13.26	4.66	7.38	1.00	184.00
IgD+CD27+ B Cells	pSTAT5	2.19	3.11	1.73	2.65	1.00	30.10	2.24	3.45	1.89	2.60	1.00	33.80
IgD+CD27- B Cells	IkB	4.93	5.72	4.08	5.77	1.00	28.20	4.44	5.29	3.89	4.98	1.00	32.00
IgD+CD27- B Cells	pERK	47.74	111.3	31.33	64.16	1.00	1025.00	41.55	103.0	30.95	52.14	1.00	1138.00
IgD+CD27- B Cells	pP38	3.20	4.21	2.58	3.82	1.00	26.60	3.03	3.97	2.62	3.44	1.00	31.70
IgD+CD27- B Cells	pPLCg2	7.77	9.27	6.40	9.13	1.00	66.00	7.24	9.69	6.25	8.24	1.00	90.90
IgD+CD27- B Cells	pS6	8.60	25.50	4.84	12.36	1.00	318.00	6.34	9.54	5.36	7.32	1.00	90.10
IgD+CD27- B Cells	pSTAT1	5.09	8.28	3.87	6.31	1.00	59.60	4.48	7.46	3.72	5.25	1.00	57.50
IgD+CD27- B Cells	pSTAT3	6.03	12.52	4.19	7.88	1.00	113.00	5.22	12.47	3.93	6.50	1.00	179.00
IgD+CD27- B Cells	pSTAT5	1.87	2.54	1.50	2.25	1.00	28.00	1.88	2.80	1.59	2.16	1.00	26.60
IgD-CD27+ B Cells	IkB	4.96	6.26	4.03	5.88	1.00	30.20	4.81	6.84	4.10	5.51	1.00	69.60
IgD-CD27+ B Cells	pERK	47.35	117.5	29.97	64.73	1.00	1291.00	37.34	78.14	29.29	45.40	1.00	884.00
IgD-CD27+ B Cells	pP38	3.04	4.12	2.43	3.65	1.00	26.90	2.82	3.69	2.44	3.20	1.00	31.60
IgD-CD27+ B Cells	pPLCg2	7.91	9.41	6.51	9.30	1.00	71.00	7.50	9.42	6.53	8.47	1.00	76.90
IgD-CD27+ B Cells	pS6	8.74	20.45	5.72	11.77	1.00	233.00	6.56	9.10	5.62	7.50	1.00	58.80
IgD-CD27+ B Cells	pSTAT1	6.61	11.63	4.89	8.33	1.00	71.00	5.28	9.09	4.34	6.21	1.00	62.10
IgD-CD27+ B Cells	pSTAT3	6.02	16.98	3.51	8.53	1.00	176.00	4.70	10.66	3.60	5.80	1.00	126.00
IgD-CD27+ B Cells	pSTAT5	2.02	2.89	1.59	2.45	1.00	30.40	1.89	2.78	1.60	2.17	1.00	36.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	4.04	5.78	3.18	4.89	1.00	50.70	3.79	5.78	3.19	4.38	1.00	49.80
IgD-CD27- B Cells	pERK	38.73	104.3	23.34	54.12	1.00	1138.00	30.21	105.2	19.35	41.06	1.00	1891.00
IgD-CD27- B Cells	pP38	2.70	3.37	2.20	3.20	1.00	24.60	2.82	6.60	2.14	3.51	1.00	105.00
IgD-CD27- B Cells	pPLCg2	7.56	11.46	5.87	9.26	1.00	90.40	6.24	8.78	5.33	7.14	1.00	81.00
IgD-CD27- B Cells	pS6	7.23	21.91	4.00	10.46	1.00	275.00	5.41	7.91	4.59	6.22	1.00	61.50
IgD-CD27- B Cells	pSTAT1	5.12	8.93	3.80	6.43	1.00	61.10	4.62	9.08	3.69	5.56	1.00	83.60
IgD-CD27- B Cells	pSTAT3	4.83	11.23	3.17	6.48	1.00	116.00	4.02	10.17	2.97	5.07	1.00	139.00
IgD-CD27- B Cells	pSTAT5	1.74	2.45	1.38	2.10	1.00	28.20	1.77	3.09	1.45	2.09	1.00	38.40
NK Cells	IkB	5.10	6.48	4.14	6.06	1.00	43.10	4.68	6.34	4.02	5.33	1.00	46.90
NK Cells	pERK	50.30	126.3	31.63	68.98	1.00	1335.00	44.15	110.3	32.78	55.51	1.00	1251.00
NK Cells	pP38	2.24	3.18	1.77	2.71	1.00	30.00	2.14	2.87	1.84	2.44	1.00	26.30
NK Cells	pPLCg2	5.90	6.84	4.89	6.91	1.00	47.20	6.12	8.98	5.19	7.04	1.00	82.10
NK Cells	pS6	4.64	6.80	3.64	5.65	1.00	67.70	4.22	5.72	3.63	4.81	1.00	50.20
NK Cells	pSTAT1	5.07	9.25	3.71	6.44	1.00	64.90	4.36	8.18	3.52	5.20	1.00	78.50
NK Cells	pSTAT3	4.16	10.93	2.54	5.78	1.00	122.00	3.33	8.86	2.42	4.25	1.00	131.00
NK Cells	pSTAT5	1.79	2.36	1.45	2.14	1.00	24.50	1.79	2.54	1.53	2.05	1.00	33.20
NKT Cells	IkB	10.91	16.73	8.41	13.40	1.00	149.00	10.13	13.73	8.70	11.55	1.00	94.30
NKT Cells	pERK	88.50	232.6	53.79	123.2	1.00	1823.00	79.63	208.9	57.97	101.3	1.00	2036.00
NKT Cells	pP38	5.40	8.15	4.19	6.62	1.00	78.40	5.23	8.98	4.29	6.16	1.00	119.00
NKT Cells	pPLCg2	9.68	53.04	1.76	17.59	1.00	700.00	7.61	17.16	5.83	9.39	1.00	153.00
NKT Cells	pS6	12.16	21.41	8.96	15.35	1.00	151.00	11.98	25.27	9.36	14.60	1.00	312.00
NKT Cells	pSTAT1	16.63	42.68	10.26	22.99	1.00	510.00	13.82	25.20	11.21	16.44	1.00	275.00
NKT Cells	pSTAT3	13.57	73.56	2.59	24.54	1.00	956.00	8.69	32.10	5.37	12.02	1.00	496.00
NKT Cells	pSTAT5	2.55	3.79	1.99	3.12	1.00	38.40	2.91	5.80	2.31	3.51	1.00	67.30
Regulatory T Cells	IkB	10.90	13.00	8.98	12.82	1.00	62.00	9.99	12.54	8.70	11.27	1.00	66.60
Regulatory T Cells	pERK	76.23	164.6	51.95	100.5	1.00	1620.00	64.79	135.2	50.89	78.69	1.00	1408.00
Regulatory T Cells	pP38	4.75	5.54	3.93	5.56	1.00	27.80	4.62	6.46	3.95	5.28	1.00	57.20
Regulatory T Cells	pPLCg2	5.05	6.26	4.12	5.97	1.00	39.80	5.74	11.79	4.53	6.95	1.00	129.00
Regulatory T Cells	pS6	11.04	26.22	7.17	14.91	1.00	313.00	8.54	14.36	7.07	10.02	1.00	145.00
Regulatory T Cells	pSTAT1	14.78	23.86	11.26	18.30	1.00	169.00	13.98	24.87	11.42	16.53	1.00	205.00
Regulatory T Cells	pSTAT3	8.87	19.76	5.96	11.78	1.00	166.00	6.75	16.33	5.07	8.43	1.00	177.00
Regulatory T Cells	pSTAT5	2.20	3.17	1.74	2.67	1.00	30.90	2.52	6.73	1.83	3.21	1.00	112.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	**Mean**	**SD**	**Lower CL**	**Upper CL**	**Minimum***	**Maximum**	**Mean**	**SD**	**Lower CL**	**Upper CL**	**Minimum***	**Maximum**
Central Memory CD4+ T Cells	IkB	9.58	12.07	7.80	11.36	1.00	53.10	8.87	11.22	7.71	10.02	1.00	67.60
Central Memory CD4+ T Cells	pERK	71.91	159.7	48.35	95.47	1.00	1532.00	59.06	130.8	45.61	72.50	1.00	1350.00
Central Memory CD4+ T Cells	pP38	4.83	5.78	3.98	5.68	1.00	28.00	4.25	5.22	3.71	4.79	1.00	38.40
Central Memory CD4+ T Cells	pPLCg2	4.64	5.82	3.79	5.50	1.00	36.70	4.88	8.35	4.02	5.74	1.00	83.10
Central Memory CD4+ T Cells	pS6	10.41	19.14	7.59	13.24	1.00	149.00	7.77	11.75	6.56	8.98	1.00	84.20
Central Memory CD4+ T Cells	pSTAT1	14.87	21.82	11.65	18.09	1.00	164.00	13.38	20.31	11.29	15.46	1.00	139.00
Central Memory CD4+ T Cells	pSTAT3	8.67	23.04	5.27	12.07	1.00	222.00	6.05	17.48	4.25	7.85	1.00	229.00
Central Memory CD4+ T Cells	pSTAT5	2.16	3.17	1.69	2.62	1.00	32.20	2.16	3.37	1.81	2.51	1.00	35.80
Central Memory CD8+ T Cells	IkB	8.16	10.60	6.60	9.73	1.00	50.30	7.25	9.33	6.29	8.20	1.00	55.80
Central Memory CD8+ T Cells	pERK	62.51	141.5	41.64	83.39	1.00	1420.00	51.77	108.7	40.59	62.94	1.00	1138.00
Central Memory CD8+ T Cells	pP38	4.36	5.24	3.58	5.13	1.00	28.90	3.73	4.65	3.25	4.20	1.00	31.60
Central Memory CD8+ T Cells	pPLCg2	4.48	5.65	3.65	5.31	1.00	38.90	4.67	7.59	3.89	5.45	1.00	57.20
Central Memory CD8+ T Cells	pS6	10.05	16.09	7.68	12.42	1.00	105.00	7.48	11.50	6.30	8.67	1.00	95.30
Central Memory CD8+ T Cells	pSTAT1	12.70	19.50	9.83	15.58	1.00	133.00	11.44	18.48	9.54	13.34	1.00	133.00
Central Memory CD8+ T Cells	pSTAT3	6.37	17.41	3.80	8.94	1.00	186.00	4.61	11.90	3.39	5.83	1.00	124.00
Central Memory CD8+ T Cells	pSTAT5	2.00	2.82	1.59	2.42	1.00	29.20	2.05	3.33	1.71	2.39	1.00	35.00
Effector CD4+ T Cells	IkB	6.55	8.17	5.35	7.76	1.00	44.00	6.14	8.19	5.30	6.99	1.00	59.60
Effector CD4+ T Cells	pERK	50.03	96.37	35.82	64.25	1.00	731.00	42.61	89.05	33.45	51.78	1.00	1070.00
Effector CD4+ T Cells	pP38	3.49	3.90	2.92	4.07	1.00	18.70	3.30	4.03	2.88	3.71	1.00	27.40
Effector CD4+ T Cells	pPLCg2	4.36	5.69	3.52	5.20	1.00	39.70	4.49	7.43	3.73	5.26	1.00	64.00
Effector CD4+ T Cells	pS6	6.46	9.20	5.10	7.81	1.00	68.60	6.15	9.62	5.16	7.14	1.00	84.60
Effector CD4+ T Cells	pSTAT1	9.60	14.32	7.48	11.71	1.00	92.90	8.36	13.28	6.99	9.72	1.00	108.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	6.74	12.59	4.88	8.59	1.00	101.00	5.09	11.16	3.94	6.24	1.00	106.00
Effector CD4+ T Cells	pSTAT5	1.83	2.32	1.49	2.17	1.00	23.50	1.81	2.48	1.56	2.07	1.00	24.90
Effector CD8+ T Cells	IkB	5.90	7.21	4.84	6.97	1.00	34.80	5.27	6.85	4.56	5.97	1.00	39.20
Effector CD8+ T Cells	pERK	51.75	109.4	35.62	67.89	1.00	1076.00	39.74	80.55	31.44	48.04	1.00	1067.00
Effector CD8+ T Cells	pP38	3.23	3.80	2.67	3.79	1.00	25.00	2.94	3.74	2.56	3.33	1.00	25.30
Effector CD8+ T Cells	pPLCg2	4.62	5.74	3.77	5.46	1.00	38.50	4.65	7.48	3.88	5.42	1.00	73.00
Effector CD8+ T Cells	pS6	6.84	11.29	5.17	8.50	1.00	94.30	5.77	9.12	4.83	6.71	1.00	87.70
Effector CD8+ T Cells	pSTAT1	9.07	13.58	7.06	11.07	1.00	83.50	7.94	12.76	6.62	9.25	1.00	94.10
Effector CD8+ T Cells	pSTAT3	5.14	11.71	3.41	6.87	1.00	115.00	3.95	9.58	2.96	4.94	1.00	93.70
Effector CD8+ T Cells	pSTAT5	1.72	2.03	1.42	2.02	1.00	21.10	1.78	2.52	1.52	2.04	1.00	30.70
Effector Memory CD4+ T Cells	IkB	6.56	8.67	5.28	7.84	1.00	42.70	5.98	8.12	5.14	6.81	1.00	51.10
Effector Memory CD4+ T Cells	pERK	48.06	102.6	32.92	63.19	1.00	1049.00	36.32	75.07	28.58	44.06	1.00	978.00
Effector Memory CD4+ T Cells	pP38	3.49	4.07	2.89	4.09	1.00	20.80	3.08	3.68	2.70	3.46	1.00	25.60
Effector Memory CD4+ T Cells	pPLCg2	3.58	4.64	2.90	4.26	1.00	35.10	3.64	5.63	3.06	4.22	1.00	44.50
Effector Memory CD4+ T Cells	pS6	5.83	8.76	4.54	7.13	1.00	64.50	5.03	7.75	4.24	5.83	1.00	66.70
Effector Memory CD4+ T Cells	pSTAT1	11.89	18.80	9.11	14.66	1.00	131.00	10.42	17.99	8.56	12.27	1.00	159.00
Effector Memory CD4+ T Cells	pSTAT3	5.55	12.60	3.69	7.41	1.00	124.00	4.11	10.15	3.06	5.16	1.00	98.80
Effector Memory CD4+ T Cells	pSTAT5	1.74	2.28	1.40	2.07	1.00	24.70	1.76	2.29	1.52	1.99	1.00	24.70
Effector Memory CD8+ T Cells	IkB	5.78	7.79	4.63	6.92	1.00	41.70	5.09	6.95	4.37	5.80	1.00	43.50
Effector Memory CD8+ T Cells	pERK	43.74	79.87	31.96	55.52	1.00	685.00	37.00	83.69	28.38	45.61	1.00	1196.00
Effector Memory CD8+ T Cells	pP38	3.32	3.89	2.74	3.89	1.00	20.00	2.83	3.72	2.45	3.22	1.00	40.60
Effector Memory CD8+ T Cells	pPLCg2	3.73	4.80	3.02	4.44	1.00	34.20	3.81	5.93	3.20	4.42	1.00	44.50

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	6.54	10.99	4.92	8.16	1.00	81.50	5.13	8.18	4.29	5.97	1.00	80.80
Effector Memory CD8+ T Cells	pSTAT1	9.51	15.28	7.26	11.77	1.00	94.80	8.72	15.55	7.12	10.32	1.00	120.00
Effector Memory CD8+ T Cells	pSTAT3	4.53	11.11	2.89	6.17	1.00	109.00	3.58	9.57	2.60	4.57	1.00	114.00
Effector Memory CD8+ T Cells	pSTAT5	1.82	2.90	1.39	2.24	1.00	29.00	1.74	2.31	1.50	1.98	1.00	22.00
Myeloid Dendritic Cells	IkB	3.99	5.52	3.17	4.80	1.00	37.80	3.78	5.89	3.17	4.38	1.00	44.60
Myeloid Dendritic Cells	pERK	41.53	139.4	20.96	62.10	1.00	1523.00	32.16	79.33	24.01	40.32	1.00	775.00
Myeloid Dendritic Cells	pP38	8.07	10.37	6.54	9.60	1.00	63.70	7.10	9.29	6.15	8.06	1.00	49.80
Myeloid Dendritic Cells	pPLCg2	4.67	6.25	3.75	5.59	1.00	52.60	5.00	8.97	4.08	5.92	1.00	89.20
Myeloid Dendritic Cells	pS6	3.69	6.94	2.66	4.71	1.00	75.70	3.48	6.09	2.85	4.10	1.00	51.60
Myeloid Dendritic Cells	pSTAT1	5.48	9.91	4.02	6.94	1.00	72.60	5.23	10.06	4.19	6.26	1.00	74.60
Myeloid Dendritic Cells	pSTAT3	3.83	12.73	1.95	5.71	1.00	156.00	3.17	9.11	2.23	4.11	1.00	122.00
Myeloid Dendritic Cells	pSTAT5	1.77	2.73	1.37	2.18	1.00	31.90	1.88	2.86	1.58	2.17	1.00	25.40
Monocytes	IkB	17.62	14.03	10.41	24.84	1.11	49.20	12.54	10.77	8.89	16.18	1.38	43.50
Monocytes	pERK	171.3	472.0	-71.4	414.0	3.06	1738.00	136.5	388.2	5.11	267.8	1.43	1553.00
Monocytes	pP38	2.98	5.52	0.14	5.82	1.00	18.90	2.68	5.05	0.97	4.39	1.00	21.40
Monocytes	pPLCg2	4.86	5.00	2.29	7.43	1.00	16.60	4.84	4.88	3.19	6.50	1.00	19.50
Monocytes	pS6	6.16	6.34	2.90	9.41	1.00	24.70	5.22	4.18	3.80	6.63	1.00	17.20
Monocytes	pSTAT1	8.96	8.67	4.50	13.42	1.00	32.40	8.69	7.82	6.04	11.34	1.00	29.70
Monocytes	pSTAT3	1.78	1.14	1.20	2.36	1.00	5.73	1.63	1.33	1.18	2.08	1.00	7.21
Monocytes	pSTAT5	2.00	1.92	1.02	2.99	1.00	8.88	1.85	1.72	1.26	2.43	1.00	8.56
Naive CD4+ T Cells	IkB	9.41	11.63	7.69	11.12	1.00	56.70	8.97	11.43	7.79	10.15	1.00	76.60
Naive CD4+ T Cells	pERK	72.76	162.3	48.82	96.70	1.00	1532.00	63.90	141.0	49.41	78.40	1.00	1424.00
Naive CD4+ T Cells	pP38	4.74	5.56	3.92	5.56	1.00	27.50	4.50	5.78	3.91	5.10	1.00	44.50
Naive CD4+ T Cells	pPLCg2	5.46	6.96	4.43	6.49	1.00	43.00	5.84	10.35	4.78	6.90	1.00	102.00
Naive CD4+ T Cells	pS6	10.62	17.29	8.07	13.17	1.00	114.00	9.30	14.59	7.80	10.80	1.00	112.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	11.63	16.25	9.23	14.03	1.00	112.00	10.11	14.88	8.58	11.64	1.00	101.00
Naive CD4+ T Cells	pSTAT3	9.76	20.99	6.67	12.86	1.00	174.00	7.29	19.17	5.32	9.26	1.00	266.00
Naive CD4+ T Cells	pSTAT5	2.24	3.07	1.79	2.70	1.00	28.30	2.27	3.47	1.92	2.63	1.00	33.30
Naive CD8+ T Cells	IkB	8.42	10.45	6.88	9.96	1.00	48.90	7.87	10.21	6.82	8.92	1.00	61.50
Naive CD8+ T Cells	pERK	69.83	160.3	46.19	93.47	1.00	1580.00	59.09	129.4	45.79	72.40	1.00	1309.00
Naive CD8+ T Cells	pP38	4.35	5.20	3.58	5.11	1.00	27.00	3.98	5.09	3.45	4.50	1.00	37.80
Naive CD8+ T Cells	pPLCg2	5.64	6.95	4.61	6.66	1.00	41.60	5.90	9.86	4.88	6.91	1.00	85.70
Naive CD8+ T Cells	pS6	11.51	21.15	8.39	14.63	1.00	151.00	9.18	14.87	7.65	10.71	1.00	115.00
Naive CD8+ T Cells	pSTAT1	11.55	16.11	9.17	13.92	1.00	106.00	10.38	15.31	8.80	11.95	1.00	103.00
Naive CD8+ T Cells	pSTAT3	7.42	18.76	4.66	10.19	1.00	166.00	5.58	16.30	3.91	7.26	1.00	228.00
Naive CD8+ T Cells	pSTAT5	2.13	2.79	1.72	2.54	1.00	27.00	2.18	3.51	1.82	2.55	1.00	37.70
Plasmoid Dendritic Cells	IkB	4.84	6.60	3.87	5.82	1.00	43.50	4.50	6.70	3.81	5.19	1.00	59.90
Plasmoid Dendritic Cells	pERK	44.73	131.9	25.28	64.18	1.00	1365.00	35.38	78.92	27.27	43.49	1.00	922.00
Plasmoid Dendritic Cells	pP38	4.25	9.16	2.90	5.60	1.00	105.00	3.31	4.76	2.82	3.80	1.00	35.40
Plasmoid Dendritic Cells	pPLCg2	5.31	6.50	4.35	6.27	1.00	42.00	5.65	9.29	4.70	6.61	1.00	74.40
Plasmoid Dendritic Cells	pS6	5.21	8.79	3.91	6.51	1.00	65.60	4.33	7.03	3.61	5.05	1.00	52.30
Plasmoid Dendritic Cells	pSTAT1	5.93	9.73	4.49	7.36	1.00	55.40	5.13	9.39	4.16	6.10	1.00	82.60
Plasmoid Dendritic Cells	pSTAT3	3.76	9.61	2.34	5.18	1.00	112.00	3.15	8.09	2.32	3.98	1.00	110.00
Plasmoid Dendritic Cells	pSTAT5	2.38	4.63	1.69	3.06	1.00	45.50	2.08	4.06	1.66	2.50	1.00	56.50
Plasmablasts	IkB	7.22	9.55	5.80	8.64	1.00	77.80	7.22	14.05	5.76	8.68	1.00	213.00
Plasmablasts	pERK	54.67	125.2	35.99	73.35	1.00	1020.00	56.74	159.2	40.19	73.28	1.00	2263.00
Plasmablasts	pP38	3.90	5.41	3.09	4.70	1.00	42.90	3.59	5.01	3.07	4.11	1.00	38.20
Plasmablasts	pPLCg2	8.21	9.90	6.73	9.69	1.00	63.30	8.54	13.77	7.11	9.97	1.00	111.00
Plasmablasts	pS6	8.80	23.70	5.26	12.33	1.00	293.00	7.27	11.62	6.07	8.48	1.00	118.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=PMA

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	7.00	11.32	5.31	8.68	1.00	65.70	6.25	10.14	5.19	7.30	1.00	73.00
Plasmablasts	pSTAT3	6.79	10.99	5.15	8.43	1.00	100.00	5.91	11.02	4.77	7.06	1.00	111.00
Plasmablasts	pSTAT5	2.60	4.52	1.93	3.27	1.00	41.60	2.67	4.64	2.18	3.15	1.00	44.40
Transitional B Cells	IkB	10.31	31.25	5.61	15.02	1.00	368.00	6.39	8.52	5.51	7.27	1.00	62.60
Transitional B Cells	pERK	55.75	118.3	37.94	73.56	1.21	1052.00	52.84	131.6	39.22	66.45	1.00	1694.00
Transitional B Cells	pP38	4.83	7.69	3.67	5.98	1.00	78.70	4.57	6.61	3.89	5.26	1.00	53.60
Transitional B Cells	pPLCg2	78.55	903.2	-57.4	214.5	1.00	11854.0	9.48	14.70	7.96	11.00	1.00	129.00
Transitional B Cells	pS6	7.83	9.53	6.40	9.26	1.00	54.40	8.40	14.30	6.92	9.88	1.00	116.00
Transitional B Cells	pSTAT1	8.14	14.13	6.01	10.26	1.00	120.00	6.56	11.51	5.37	7.75	1.00	104.00
Transitional B Cells	pSTAT3	10.09	16.17	7.66	12.53	1.00	175.00	9.00	16.10	7.33	10.67	1.00	242.00
Transitional B Cells	pSTAT5	7.86	63.33	-1.67	17.39	1.00	831.00	3.14	6.67	2.45	3.83	1.00	73.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	**Mean**	**SD**	**Lower CL**	**Upper CL**	**Minimum***	**Maximum**	**Mean**	**SD**	**Lower CL**	**Upper CL**	**Minimum***	**Maximum**
B Cells	IkB	6.42	10.10	4.97	7.88	1.00	94.80	5.28	7.54	4.51	6.05	1.00	71.40
B Cells	pERK	34.63	80.50	23.01	46.24	1.00	779.00	30.93	74.34	23.37	38.49	1.00	961.00
B Cells	pP38	2.30	2.91	1.88	2.71	1.00	20.10	1.81	1.88	1.62	2.01	1.00	17.50
B Cells	pPLCg2	9.96	13.51	8.01	11.91	1.00	117.00	8.23	11.73	7.04	9.42	1.00	82.90
B Cells	pS6	3.80	6.79	2.82	4.78	1.00	70.30	3.12	5.17	2.59	3.65	1.00	72.20
B Cells	pSTAT1	6.18	9.08	4.87	7.49	1.00	55.40	5.47	9.47	4.50	6.43	1.00	81.30
B Cells	pSTAT3	7.03	13.34	5.10	8.95	1.00	128.00	5.20	9.11	4.27	6.12	1.00	74.80
B Cells	pSTAT5	2.61	4.26	2.00	3.23	1.00	38.30	2.33	4.49	1.87	2.79	1.00	57.60
CD16+ NK Cells	IkB	6.57	8.47	5.31	7.83	1.00	49.70	6.18	8.99	5.24	7.12	1.00	77.10
CD16+ NK Cells	pERK	49.29	100.3	34.37	64.22	1.00	889.00	44.36	81.51	35.85	52.87	1.00	889.00
CD16+ NK Cells	pP38	2.11	3.05	1.65	2.56	1.00	22.30	1.83	2.44	1.57	2.08	1.00	23.00
CD16+ NK Cells	pPLCg2	11.68	14.26	9.55	13.80	1.00	108.00	10.54	15.73	8.90	12.18	1.00	174.00
CD16+ NK Cells	pS6	3.48	3.42	2.97	3.99	1.00	21.90	3.40	5.27	2.85	3.95	1.00	67.50
CD16+ NK Cells	pSTAT1	5.84	11.04	4.20	7.48	1.00	72.20	4.76	9.37	3.78	5.74	1.00	74.00
CD16+ NK Cells	pSTAT3	4.51	7.75	3.36	5.67	1.00	50.30	3.75	6.94	3.03	4.48	1.00	48.50
CD16+ NK Cells	pSTAT5	2.40	3.31	1.91	2.89	1.00	20.50	2.35	4.07	1.92	2.77	1.00	48.20
CD16+ Monocytes	IkB	11.89	15.58	9.64	14.14	1.00	130.00	9.90	12.46	8.63	11.17	1.00	80.40
CD16+ Monocytes	pERK	71.16	125.6	53.04	89.28	1.00	1170.00	65.94	119.8	53.75	78.12	1.00	1350.00
CD16+ Monocytes	pP38	5.11	6.11	4.23	5.99	1.00	37.70	4.12	4.77	3.63	4.60	1.00	34.40
CD16+ Monocytes	pPLCg2	16.41	20.77	13.41	19.41	1.00	160.00	14.79	21.32	12.62	16.96	1.00	237.00
CD16+ Monocytes	pS6	5.94	8.81	4.66	7.21	1.00	84.90	4.85	6.75	4.17	5.54	1.00	82.70
CD16+ Monocytes	pSTAT1	12.63	19.79	9.77	15.48	1.00	123.00	11.59	19.96	9.56	13.62	1.00	156.00
CD16+ Monocytes	pSTAT3	10.16	19.14	7.40	12.92	1.00	201.00	7.58	13.17	6.24	8.92	1.00	144.00
CD16+ Monocytes	pSTAT5	4.43	7.36	3.37	5.49	1.00	51.20	3.75	6.94	3.04	4.45	1.00	74.20
CD16- NK Cells	IkB	5.49	9.68	4.10	6.89	1.00	104.00	4.44	6.64	3.77	5.12	1.00	68.10
CD16- NK Cells	pERK	33.86	73.64	23.23	44.48	1.00	707.00	30.06	63.03	23.65	36.47	1.00	771.00
CD16- NK Cells	pP38	1.99	2.80	1.59	2.39	1.00	23.10	1.57	1.64	1.41	1.74	1.00	20.30
CD16- NK Cells	pPLCg2	6.89	9.65	5.50	8.28	1.00	76.50	5.82	8.88	4.92	6.73	1.00	70.60
CD16- NK Cells	pS6	3.33	5.19	2.58	4.08	1.00	54.70	2.77	4.53	2.31	3.23	1.00	69.60
CD16- NK Cells	pSTAT1	5.51	8.69	4.25	6.76	1.00	54.20	4.91	8.86	4.01	5.81	1.00	69.40
CD16- NK Cells	pSTAT3	4.30	9.07	2.99	5.61	1.00	82.50	3.19	6.21	2.56	3.83	1.00	56.90
CD16- NK Cells	pSTAT5	2.31	3.33	1.83	2.79	1.00	21.60	2.08	3.87	1.69	2.48	1.00	50.90
CD16- Monocytes	IkB	11.07	15.58	8.82	13.32	1.00	125.00	9.38	13.09	8.05	10.72	1.00	95.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
CD16- Monocytes	pERK	52.58	114.7	36.04	69.12	1.19	1128.00	46.26	91.17	36.99	55.53	1.00	1058.00
CD16- Monocytes	pP38	5.35	5.70	4.53	6.17	1.00	33.90	4.27	4.46	3.81	4.72	1.00	35.60
CD16- Monocytes	pPLCg2	10.31	14.64	8.20	12.42	1.00	132.00	8.69	13.21	7.34	10.03	1.00	117.00
CD16- Monocytes	pS6	4.85	8.48	3.62	6.07	1.00	89.60	3.89	6.25	3.26	4.53	1.00	83.40
CD16- Monocytes	pSTAT1	16.17	24.16	12.69	19.66	1.00	155.00	14.67	23.62	12.27	17.07	1.00	196.00
CD16- Monocytes	pSTAT3	9.02	18.22	6.39	11.65	1.00	174.00	6.40	12.67	5.11	7.68	1.00	121.00
CD16- Monocytes	pSTAT5	3.62	5.74	2.79	4.45	1.00	46.30	3.13	5.74	2.55	3.72	1.00	65.50
CD4+ T Cells	IkB	10.25	15.37	8.03	12.47	1.00	106.00	8.90	13.35	7.54	10.25	1.00	89.40
CD4+ T Cells	pERK	36.63	87.32	24.03	49.23	1.00	845.00	31.46	70.85	24.26	38.67	1.00	758.00
CD4+ T Cells	pP38	2.58	3.45	2.08	3.08	1.00	23.40	2.05	2.32	1.82	2.29	1.00	22.20
CD4+ T Cells	pPLCg2	6.31	11.18	4.69	7.92	1.00	108.00	5.18	9.47	4.22	6.14	1.00	83.40
CD4+ T Cells	pS6	3.55	7.00	2.54	4.56	1.00	76.60	2.90	5.12	2.38	3.43	1.00	73.80
CD4+ T Cells	pSTAT1	14.33	21.09	11.28	17.37	1.00	151.00	12.81	20.76	10.69	14.92	1.00	137.00
CD4+ T Cells	pSTAT3	8.51	17.03	6.05	10.96	1.00	141.00	5.60	11.62	4.42	6.78	1.00	99.60
CD4+ T Cells	pSTAT5	2.60	4.22	2.00	3.21	1.00	37.50	2.29	4.39	1.85	2.74	1.00	57.30
CD4-CD8- T Cells	IkB	6.08	11.10	4.48	7.68	1.00	111.00	4.80	7.37	4.05	5.55	1.00	55.90
CD4-CD8- T Cells	pERK	32.86	75.49	21.96	43.75	1.00	733.00	27.93	64.38	21.39	34.48	1.00	646.00
CD4-CD8- T Cells	pP38	2.27	3.23	1.81	2.74	1.00	26.10	1.76	2.02	1.55	1.97	1.00	19.90
CD4-CD8- T Cells	pPLCg2	7.59	20.33	4.66	10.52	1.00	238.00	4.96	8.75	4.07	5.85	1.00	63.20
CD4-CD8- T Cells	pS6	3.17	6.61	2.22	4.13	1.00	74.80	2.53	4.14	2.11	2.95	1.00	54.70
CD4-CD8- T Cells	pSTAT1	7.79	12.32	6.01	9.57	1.00	69.40	7.05	12.52	5.78	8.32	1.00	84.60
CD4-CD8- T Cells	pSTAT3	5.82	13.69	3.84	7.79	1.00	137.00	3.92	8.74	3.03	4.81	1.00	79.00
CD4-CD8- T Cells	pSTAT5	2.31	3.84	1.76	2.87	1.00	38.60	1.96	3.58	1.60	2.32	1.00	48.80
CD8+ T Cells	IkB	8.90	13.51	6.95	10.85	1.00	102.00	7.56	11.57	6.38	8.73	1.00	88.20
CD8+ T Cells	pERK	40.61	94.79	26.93	54.28	1.00	917.00	33.50	71.49	26.23	40.77	1.00	788.00
CD8+ T Cells	pP38	2.43	3.26	1.96	2.90	1.00	21.70	1.93	2.14	1.71	2.14	1.00	20.50
CD8+ T Cells	pPLCg2	6.72	11.39	5.07	8.36	1.00	107.00	5.47	9.74	4.48	6.46	1.00	80.60
CD8+ T Cells	pS6	3.70	6.94	2.70	4.70	1.00	74.60	3.00	5.20	2.47	3.53	1.00	73.00
CD8+ T Cells	pSTAT1	12.93	19.35	10.14	15.73	1.00	138.00	11.52	18.68	9.63	13.42	1.00	142.00
CD8+ T Cells	pSTAT3	6.65	14.97	4.49	8.81	1.00	129.00	4.55	10.28	3.51	5.60	1.00	95.80
CD8+ T Cells	pSTAT5	2.48	4.04	1.90	3.07	1.00	36.70	2.22	4.24	1.79	2.65	1.00	53.90
Dendritic Cells	IkB	4.69	8.57	3.45	5.92	1.00	83.80	3.78	5.88	3.18	4.38	1.00	51.00
Dendritic Cells	pERK	33.73	95.43	19.96	47.49	1.00	992.00	27.35	55.76	21.68	33.02	1.00	565.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases n = 187						**Controls n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Dendritic Cells	pP38	4.49	5.30	3.72	5.25	1.00	30.90	3.70	4.96	3.19	4.20	1.00	29.50
Dendritic Cells	pPLCg2	6.43	11.15	4.82	8.04	1.00	89.10	5.13	8.50	4.26	5.99	1.00	63.00
Dendritic Cells	pS6	2.59	4.23	1.98	3.20	1.00	40.90	2.33	4.10	1.91	2.74	1.00	57.80
Dendritic Cells	pSTAT1	6.03	10.27	4.55	7.51	1.00	60.70	5.38	11.12	4.25	6.51	1.00	103.00
Dendritic Cells	pSTAT3	4.25	9.59	2.87	5.63	1.00	98.30	3.18	7.04	2.46	3.89	1.00	74.40
Dendritic Cells	pSTAT5	2.13	3.09	1.69	2.58	1.00	25.10	1.95	3.24	1.62	2.28	1.00	42.20
HLADR+ NK Cells	IkB	6.34	7.85	5.20	7.48	1.00	38.80	5.44	6.94	4.73	6.14	1.00	41.90
HLADR+ NK Cells	pERK	41.11	88.51	28.27	53.94	1.00	899.00	37.19	70.13	30.04	44.34	1.00	777.00
HLADR+ NK Cells	pP38	2.36	3.10	1.91	2.81	1.00	21.40	1.97	2.17	1.75	2.19	1.00	23.40
HLADR+ NK Cells	pPLCg2	10.29	13.95	8.27	12.32	1.00	108.00	8.82	13.01	7.49	10.14	1.00	110.00
HLADR+ NK Cells	pS6	3.62	5.27	2.85	4.38	1.00	57.00	3.20	3.44	2.84	3.55	1.00	23.40
HLADR+ NK Cells	pSTAT1	5.95	9.74	4.54	7.37	1.00	67.00	5.36	9.13	4.43	6.29	1.00	75.90
HLADR+ NK Cells	pSTAT3	4.52	7.80	3.39	5.65	1.00	62.20	3.81	7.21	3.07	4.54	1.00	58.80
HLADR+ NK Cells	pSTAT5	2.55	3.52	2.03	3.06	1.00	22.90	2.26	3.31	1.93	2.60	1.00	37.60
HLADR+CD38+ CD4+ T Cells	IkB	11.73	16.83	9.30	14.16	1.00	131.00	10.02	14.01	8.60	11.45	1.00	95.80
HLADR+CD38+ CD4+ T Cells	pERK	47.15	95.54	33.37	60.93	1.00	912.00	41.89	80.49	33.71	50.08	1.00	826.00
HLADR+CD38+ CD4+ T Cells	pP38	3.71	4.61	3.05	4.38	1.00	28.20	2.99	3.50	2.63	3.35	1.00	27.60
HLADR+CD38+ CD4+ T Cells	pPLCg2	10.51	16.33	8.15	12.86	1.00	135.00	9.14	16.27	7.49	10.80	1.00	133.00
HLADR+CD38+ CD4+ T Cells	pS6	4.85	8.32	3.65	6.05	1.00	87.00	4.06	6.40	3.41	4.71	1.00	83.80
HLADR+CD38+ CD4+ T Cells	pSTAT1	15.89	22.35	12.67	19.12	1.00	143.00	14.33	23.18	11.97	16.68	1.00	159.00
HLADR+CD38+ CD4+ T Cells	pSTAT3	10.60	18.98	7.87	13.34	1.00	171.00	7.62	15.11	6.08	9.15	1.00	147.00
HLADR+CD38+ CD4+ T Cells	pSTAT5	3.49	5.43	2.71	4.28	1.00	44.20	3.09	5.74	2.51	3.67	1.00	67.50
HLADR+CD38+ CD8+ T Cells	IkB	10.02	14.15	7.98	12.06	1.00	104.00	8.35	11.37	7.20	9.51	1.00	87.20
HLADR+CD38+ CD8+ T Cells	pERK	46.91	96.15	33.04	60.78	1.03	951.00	40.77	76.40	33.00	48.54	1.00	808.00
HLADR+CD38+ CD8+ T Cells	pP38	3.37	4.22	2.76	3.98	1.00	26.40	2.75	3.16	2.43	3.07	1.00	25.70
HLADR+CD38+ CD8+ T Cells	pPLCg2	10.82	15.74	8.55	13.09	1.00	130.00	9.14	14.87	7.62	10.65	1.00	122.00
HLADR+CD38+ CD8+ T Cells	pS6	4.89	8.31	3.69	6.09	1.00	82.60	4.02	6.36	3.37	4.66	1.00	79.50

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
HLADR+CD38+ CD8+ T Cells	pSTAT1	12.73	17.55	10.19	15.26	1.00	95.50	11.49	18.38	9.62	13.36	1.00	143.00
HLADR+CD38+ CD8+ T Cells	pSTAT3	8.62	16.75	6.20	11.03	1.00	156.00	6.41	12.83	5.11	7.72	1.00	119.00
HLADR+CD38+ CD8+ T Cells	pSTAT5	3.20	4.90	2.50	3.91	1.00	39.30	2.89	5.21	2.36	3.42	1.00	56.70
IgD+CD27+ B Cells	IkB	7.02	10.51	5.50	8.53	1.00	97.20	5.77	8.04	4.95	6.59	1.00	77.10
IgD+CD27+ B Cells	pERK	37.82	82.59	25.91	49.74	1.32	790.00	33.78	77.37	25.91	41.65	1.00	1014.00
IgD+CD27+ B Cells	pP38	2.53	3.18	2.07	2.98	1.00	21.20	1.97	2.10	1.76	2.19	1.00	19.20
IgD+CD27+ B Cells	pPLCg2	10.95	14.16	8.91	12.99	1.00	119.00	9.09	12.46	7.82	10.36	1.00	89.40
IgD+CD27+ B Cells	pS6	4.16	7.05	3.14	5.17	1.00	71.40	3.37	5.42	2.81	3.92	1.00	74.00
IgD+CD27+ B Cells	pSTAT1	6.85	9.82	5.43	8.26	1.00	61.10	5.96	10.14	4.93	6.99	1.00	85.70
IgD+CD27+ B Cells	pSTAT3	7.87	13.99	5.86	9.89	1.00	131.00	5.84	9.65	4.86	6.82	1.00	78.40
IgD+CD27+ B Cells	pSTAT5	2.82	4.52	2.17	3.47	1.00	39.80	2.48	4.71	2.00	2.96	1.00	60.40
IgD+CD27- B Cells	IkB	5.78	9.18	4.46	7.10	1.00	87.20	4.66	6.37	4.01	5.31	1.00	58.60
IgD+CD27- B Cells	pERK	31.13	67.82	21.35	40.91	1.30	626.00	26.32	58.16	20.40	32.24	1.00	719.00
IgD+CD27- B Cells	pP38	2.12	2.62	1.74	2.50	1.00	17.20	1.72	2.23	1.49	1.95	1.00	30.10
IgD+CD27- B Cells	pPLCg2	8.96	12.30	7.19	10.74	1.00	110.00	7.30	10.25	6.26	8.34	1.00	70.60
IgD+CD27- B Cells	pS6	3.46	6.13	2.57	4.34	1.00	60.50	2.95	5.42	2.40	3.50	1.00	67.70
IgD+CD27- B Cells	pSTAT1	5.51	8.23	4.32	6.70	1.00	52.90	4.77	8.30	3.93	5.62	1.00	63.90
IgD+CD27- B Cells	pSTAT3	6.73	12.67	4.90	8.56	1.00	127.00	4.85	8.00	4.04	5.67	1.00	65.20
IgD+CD27- B Cells	pSTAT5	2.38	3.79	1.83	2.92	1.00	34.70	2.14	3.83	1.75	2.52	1.00	45.70
IgD-CD27+ B Cells	IkB	5.78	8.39	4.57	6.99	1.00	56.40	4.72	7.03	4.01	5.44	1.00	66.60
IgD-CD27+ B Cells	pERK	30.44	71.05	20.19	40.69	1.00	687.00	25.31	51.21	20.10	30.52	1.00	511.00
IgD-CD27+ B Cells	pP38	2.10	2.37	1.76	2.44	1.00	15.80	1.69	1.65	1.52	1.86	1.00	15.70
IgD-CD27+ B Cells	pPLCg2	9.55	11.42	7.90	11.19	1.00	79.90	8.15	11.20	7.02	9.29	1.00	82.20
IgD-CD27+ B Cells	pS6	3.83	5.71	3.00	4.65	1.00	54.00	3.11	4.70	2.63	3.59	1.00	65.70
IgD-CD27+ B Cells	pSTAT1	6.42	9.88	4.99	7.84	1.00	53.60	5.99	10.60	4.91	7.07	1.00	82.50
IgD-CD27+ B Cells	pSTAT3	5.81	11.22	4.19	7.42	1.00	85.60	4.54	9.00	3.63	5.46	1.00	79.00
IgD-CD27+ B Cells	pSTAT5	2.46	3.61	1.94	2.98	1.00	24.50	2.28	4.32	1.84	2.72	1.00	50.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
IgD-CD27- B Cells	IkB	4.69	7.66	3.59	5.80	1.00	65.70	3.63	5.70	3.05	4.21	1.00	44.70
IgD-CD27- B Cells	pERK	23.21	47.62	16.34	30.08	1.00	563.00	19.30	38.93	15.34	23.27	1.00	475.00
IgD-CD27- B Cells	pP38	1.95	2.32	1.61	2.28	1.00	18.50	1.59	1.73	1.41	1.77	1.00	16.10
IgD-CD27- B Cells	pPLCg2	8.34	12.00	6.61	10.07	1.00	90.90	6.51	10.05	5.49	7.54	1.00	86.80
IgD-CD27- B Cells	pS6	3.03	4.40	2.40	3.67	1.00	40.70	2.82	4.62	2.35	3.29	1.00	54.70
IgD-CD27- B Cells	pSTAT1	5.34	8.45	4.12	6.56	1.00	47.90	4.84	8.97	3.92	5.75	1.00	79.80
IgD-CD27- B Cells	pSTAT3	4.82	9.07	3.51	6.13	1.00	65.00	3.76	6.90	3.05	4.46	1.00	58.20
IgD-CD27- B Cells	pSTAT5	2.35	3.97	1.77	2.92	1.00	36.50	1.87	3.21	1.54	2.19	1.00	45.20
NK Cells	IkB	5.38	7.28	4.33	6.43	1.00	42.90	4.46	5.83	3.87	5.06	1.00	40.40
NK Cells	pERK	36.09	79.33	24.62	47.57	1.00	781.00	32.07	65.24	25.42	38.73	1.00	777.00
NK Cells	pP38	1.94	2.58	1.57	2.31	1.00	19.90	1.57	1.69	1.39	1.74	1.00	21.40
NK Cells	pPLCg2	7.58	10.14	6.11	9.05	1.00	84.20	6.44	9.39	5.48	7.39	1.00	81.00
NK Cells	pS6	3.12	3.78	2.57	3.67	1.00	29.20	2.59	2.70	2.31	2.86	1.00	24.20
NK Cells	pSTAT1	5.24	8.54	4.00	6.47	1.00	56.50	4.46	7.93	3.65	5.27	1.00	70.00
NK Cells	pSTAT3	4.42	9.18	3.09	5.75	1.00	82.50	3.14	5.92	2.54	3.74	1.00	50.90
NK Cells	pSTAT5	2.25	3.29	1.78	2.73	1.00	21.60	1.90	2.69	1.62	2.17	1.00	34.50
NKT Cells	IkB	12.99	20.53	10.00	15.98	1.00	188.00	11.04	15.50	9.46	12.63	1.00	84.30
NKT Cells	pERK	56.04	144.1	35.03	77.05	1.00	1536.00	50.77	115.9	38.93	62.62	1.00	1224.00
NKT Cells	pP38	3.76	5.07	3.02	4.50	1.00	29.30	3.22	4.56	2.75	3.68	1.00	43.50
NKT Cells	pPLCg2	8.45	12.88	6.58	10.33	1.00	86.20	7.41	13.99	5.98	8.84	1.00	144.00
NKT Cells	pS6	4.94	6.65	3.97	5.91	1.00	53.00	4.60	9.18	3.66	5.53	1.00	141.00
NKT Cells	pSTAT1	18.46	29.00	14.23	22.69	1.00	250.00	15.82	25.60	13.20	18.44	1.00	183.00
NKT Cells	pSTAT3	10.38	21.81	7.20	13.56	1.00	184.00	7.24	15.62	5.65	8.84	1.00	152.00
NKT Cells	pSTAT5	3.45	5.56	2.64	4.27	1.00	42.20	3.24	6.26	2.60	3.88	1.00	72.20
Regulatory T Cells	IkB	12.92	18.41	10.26	15.58	1.00	91.10	11.29	16.64	9.60	12.98	1.00	98.50
Regulatory T Cells	pERK	42.90	93.33	29.44	56.37	1.00	884.00	37.43	75.21	29.79	45.08	1.00	808.00
Regulatory T Cells	pP38	2.91	3.64	2.38	3.44	1.00	24.50	2.40	2.84	2.11	2.69	1.00	24.80
Regulatory T Cells	pPLCg2	6.76	11.10	5.16	8.36	1.00	93.50	5.82	10.02	4.81	6.84	1.00	83.60
Regulatory T Cells	pS6	3.80	6.42	2.87	4.73	1.00	70.30	3.24	5.06	2.72	3.75	1.00	73.80
Regulatory T Cells	pSTAT1	18.47	30.81	14.03	22.92	1.00	261.00	16.93	29.28	13.96	19.91	1.00	194.00
Regulatory T Cells	pSTAT3	9.15	16.86	6.72	11.58	1.00	120.00	6.37	12.59	5.09	7.65	1.00	104.00
Regulatory T Cells	pSTAT5	2.67	3.94	2.10	3.24	1.00	31.00	2.48	4.70	2.00	2.95	1.00	49.80

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Central Memory CD4+ T Cells	IkB	11.17	16.64	8.77	13.57	1.00	112.00	9.45	13.85	8.04	10.86	1.00	81.00
Central Memory CD4+ T Cells	pERK	37.84	87.62	25.20	50.48	1.00	838.00	31.66	67.47	24.80	38.52	1.00	741.00
Central Memory CD4+ T Cells	pP38	2.77	3.88	2.21	3.33	1.00	28.20	2.16	2.44	1.91	2.41	1.00	25.20
Central Memory CD4+ T Cells	pPLCg2	6.16	10.88	4.59	7.73	1.00	108.00	4.89	8.19	4.06	5.72	1.00	74.00
Central Memory CD4+ T Cells	pS6	3.47	7.01	2.45	4.48	1.00	78.30	2.77	4.45	2.31	3.22	1.00	57.50
Central Memory CD4+ T Cells	pSTAT1	18.47	27.78	14.46	22.48	1.00	187.00	16.43	26.69	13.71	19.14	1.00	210.00
Central Memory CD4+ T Cells	pSTAT3	8.42	18.18	5.80	11.04	1.00	153.00	5.40	11.32	4.24	6.55	1.00	100.00
Central Memory CD4+ T Cells	pSTAT5	2.62	4.36	2.00	3.25	1.00	39.50	2.21	3.83	1.82	2.59	1.00	40.10
Central Memory CD8+ T Cells	IkB	9.23	14.14	7.19	11.27	1.00	107.00	7.53	11.04	6.41	8.66	1.00	74.60
Central Memory CD8+ T Cells	pERK	40.02	93.12	26.58	53.45	1.00	855.00	31.91	60.75	25.74	38.09	1.00	591.00
Central Memory CD8+ T Cells	pP38	2.66	3.63	2.14	3.18	1.00	26.50	2.09	2.30	1.85	2.32	1.00	22.10
Central Memory CD8+ T Cells	pPLCg2	6.18	10.78	4.62	7.73	1.00	105.00	4.73	7.94	3.92	5.53	1.00	68.30
Central Memory CD8+ T Cells	pS6	4.05	7.33	3.00	5.11	1.00	78.90	3.17	4.98	2.66	3.67	1.00	62.00
Central Memory CD8+ T Cells	pSTAT1	15.01	24.13	11.52	18.49	1.00	190.00	13.20	22.18	10.94	15.45	1.00	192.00
Central Memory CD8+ T Cells	pSTAT3	6.65	15.94	4.35	8.95	1.00	145.00	4.50	10.22	3.46	5.54	1.00	101.00
Central Memory CD8+ T Cells	pSTAT5	2.43	4.17	1.83	3.03	1.00	39.20	2.11	3.89	1.71	2.50	1.00	44.50
Effector CD4+ T Cells	IkB	7.64	12.04	5.90	9.37	1.00	92.90	6.45	9.91	5.44	7.46	1.00	74.60
Effector CD4+ T Cells	pERK	31.31	66.89	21.66	40.96	1.00	641.00	26.58	55.16	20.97	32.19	1.00	606.00
Effector CD4+ T Cells	pP38	2.30	3.07	1.86	2.74	1.00	21.10	1.85	2.08	1.64	2.06	1.00	21.20
Effector CD4+ T Cells	pPLCg2	5.65	9.86	4.23	7.07	1.00	91.90	4.44	7.75	3.66	5.23	1.00	72.60
Effector CD4+ T Cells	pS6	3.12	6.27	2.22	4.03	1.00	67.90	2.61	4.70	2.14	3.09	1.00	66.40
Effector CD4+ T Cells	pSTAT1	11.56	17.59	9.03	14.10	1.00	132.00	9.86	16.80	8.16	11.57	1.00	119.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector CD4+ T Cells	pSTAT3	7.27	13.33	5.35	9.19	1.00	113.00	4.85	9.04	3.93	5.77	1.00	81.20
Effector CD4+ T Cells	pSTAT5	2.28	3.49	1.77	2.78	1.00	31.60	2.05	3.82	1.66	2.44	1.00	52.50
Effector CD8+ T Cells	IkB	6.75	10.95	5.17	8.32	1.00	89.90	5.46	8.53	4.59	6.33	1.00	66.80
Effector CD8+ T Cells	pERK	35.89	72.96	25.37	46.42	1.00	632.00	27.41	51.01	22.22	32.60	1.00	608.00
Effector CD8+ T Cells	pP38	2.20	2.99	1.77	2.63	1.00	20.50	1.70	1.87	1.51	1.89	1.00	20.30
Effector CD8+ T Cells	pPLCg2	6.28	10.60	4.75	7.81	1.00	95.80	4.85	8.27	4.01	5.70	1.00	67.30
Effector CD8+ T Cells	pS6	3.17	6.30	2.27	4.08	1.00	68.20	2.55	4.39	2.11	3.00	1.00	60.40
Effector CD8+ T Cells	pSTAT1	10.15	15.55	7.91	12.39	1.00	113.00	8.89	15.27	7.33	10.44	1.00	126.00
Effector CD8+ T Cells	pSTAT3	5.64	12.52	3.83	7.44	1.00	117.00	3.90	8.33	3.05	4.75	1.00	78.40
Effector CD8+ T Cells	pSTAT5	2.22	3.50	1.72	2.73	1.00	31.40	1.94	3.51	1.58	2.30	1.00	45.80
Effector Memory CD4+ T Cells	IkB	7.82	13.07	5.94	9.71	1.00	106.00	6.17	9.30	5.22	7.11	1.00	62.10
Effector Memory CD4+ T Cells	pERK	31.17	72.87	20.65	41.68	1.00	697.00	24.36	50.56	19.21	29.51	1.00	533.00
Effector Memory CD4+ T Cells	pP38	2.35	3.47	1.85	2.85	1.00	25.40	1.79	1.95	1.59	1.98	1.00	22.80
Effector Memory CD4+ T Cells	pPLCg2	4.94	9.83	3.53	6.36	1.00	105.00	3.64	5.91	3.04	4.24	1.00	50.30
Effector Memory CD4+ T Cells	pS6	2.81	6.59	1.86	3.76	1.00	77.40	2.17	3.31	1.83	2.51	1.00	39.20
Effector Memory CD4+ T Cells	pSTAT1	13.95	22.47	10.71	17.19	1.00	184.00	12.16	21.50	9.97	14.35	1.00	187.00
Effector Memory CD4+ T Cells	pSTAT3	6.39	14.63	4.28	8.50	1.00	137.00	4.10	8.85	3.20	5.00	1.00	84.20
Effector Memory CD4+ T Cells	pSTAT5	2.13	3.48	1.63	2.63	1.00	34.40	1.84	2.87	1.55	2.14	1.00	36.40
Effector Memory CD8+ T Cells	IkB	6.92	12.44	5.13	8.72	1.00	110.00	5.11	8.00	4.30	5.92	1.00	54.20
Effector Memory CD8+ T Cells	pERK	34.11	77.12	22.99	45.24	1.00	715.00	24.40	43.63	19.95	28.84	1.00	525.00
Effector Memory CD8+ T Cells	pP38	2.55	5.01	1.83	3.28	1.00	51.80	1.73	1.89	1.54	1.92	1.00	20.20
Effector Memory CD8+ T Cells	pPLCg2	5.36	11.96	3.63	7.08	1.00	105.00	3.74	6.27	3.10	4.38	1.00	49.00

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Effector Memory CD8+ T Cells	pS6	3.21	7.07	2.20	4.23	1.00	81.30	2.40	3.61	2.03	2.76	1.00	38.20
Effector Memory CD8+ T Cells	pSTAT1	11.24	19.53	8.43	14.06	1.00	156.00	9.45	17.61	7.66	11.24	1.00	170.00
Effector Memory CD8+ T Cells	pSTAT3	5.39	13.65	3.42	7.36	1.00	138.00	3.60	8.57	2.72	4.47	1.00	85.80
Effector Memory CD8+ T Cells	pSTAT5	2.03	3.34	1.55	2.51	1.00	35.50	1.82	3.32	1.48	2.15	1.00	46.70
Myeloid Dendritic Cells	IkB	4.86	8.49	3.64	6.09	1.00	80.20	3.95	6.11	3.33	4.57	1.00	53.50
Myeloid Dendritic Cells	pERK	36.73	107.2	21.27	52.19	1.00	1150.00	29.18	54.74	23.61	34.74	1.00	581.00
Myeloid Dendritic Cells	pP38	6.39	7.02	5.38	7.40	1.00	47.20	5.13	6.47	4.47	5.79	1.00	41.50
Myeloid Dendritic Cells	pPLCg2	6.69	10.58	5.16	8.21	1.00	85.80	5.60	9.08	4.67	6.52	1.00	71.40
Myeloid Dendritic Cells	pS6	2.67	3.86	2.12	3.23	1.00	29.20	2.45	4.14	2.03	2.87	1.00	58.00
Myeloid Dendritic Cells	pSTAT1	6.80	11.52	5.14	8.46	1.00	63.00	5.92	12.22	4.68	7.16	1.00	121.00
Myeloid Dendritic Cells	pSTAT3	4.38	8.70	3.13	5.64	1.00	72.20	3.32	7.28	2.58	4.06	1.00	79.20
Myeloid Dendritic Cells	pSTAT5	2.29	3.36	1.80	2.77	1.00	25.10	2.10	3.60	1.73	2.47	1.00	47.50
Monocytes	IkB	16.08	12.94	9.65	22.52	1.00	42.70	12.73	9.87	9.39	16.07	1.59	37.70
Monocytes	pERK	122.4	329.3	-41.3	286.2	2.40	1131.00	88.34	239.8	7.21	169.5	1.68	1058.00
Monocytes	pP38	2.64	4.55	0.38	4.90	1.00	15.70	2.28	3.94	0.94	3.61	1.00	19.90
Monocytes	pPLCg2	6.42	6.32	3.28	9.56	1.00	23.40	5.38	4.61	3.82	6.94	1.00	19.40
Monocytes	pS6	5.02	3.86	3.10	6.95	1.00	13.90	4.55	3.19	3.47	5.63	1.00	12.20
Monocytes	pSTAT1	14.11	19.20	4.56	23.66	1.00	76.40	11.42	11.93	7.38	15.46	1.00	47.00
Monocytes	pSTAT3	2.29	2.05	1.27	3.31	1.00	7.56	1.96	1.62	1.41	2.51	1.00	6.22
Monocytes	pSTAT5	2.50	1.86	1.58	3.42	1.00	6.63	2.21	1.88	1.57	2.84	1.00	9.52
Naive CD4+ T Cells	IkB	11.16	16.26	8.82	13.51	1.00	104.00	9.71	14.41	8.24	11.17	1.00	97.70
Naive CD4+ T Cells	pERK	38.09	88.00	25.39	50.78	1.00	852.00	33.07	72.88	25.66	40.48	1.00	792.00
Naive CD4+ T Cells	pP38	2.67	3.43	2.18	3.17	1.00	22.10	2.14	2.40	1.90	2.38	1.00	21.20
Naive CD4+ T Cells	pPLCg2	7.04	11.78	5.34	8.74	1.00	110.00	5.80	10.21	4.76	6.84	1.00	89.40
Naive CD4+ T Cells	pS6	3.93	7.29	2.88	4.98	1.00	76.60	3.20	5.45	2.64	3.75	1.00	78.40

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases **n = 187**						**Controls** **n = 374**					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Naive CD4+ T Cells	pSTAT1	14.53	20.99	11.50	17.56	1.00	144.00	12.74	20.62	10.64	14.83	1.00	133.00
Naive CD4+ T Cells	pSTAT3	9.83	17.43	7.31	12.34	1.00	135.00	6.46	12.23	5.22	7.70	1.00	102.00
Naive CD4+ T Cells	pSTAT5	2.76	4.36	2.13	3.39	1.00	36.90	2.43	4.68	1.96	2.91	1.00	61.40
Naive CD8+ T Cells	IkB	9.88	14.70	7.76	12.00	1.00	99.60	8.47	12.93	7.16	9.79	1.00	96.90
Naive CD8+ T Cells	pERK	41.94	95.72	28.13	55.75	1.00	927.00	35.17	74.02	27.64	42.70	1.00	826.00
Naive CD8+ T Cells	pP38	2.51	3.24	2.04	2.98	1.00	20.50	2.01	2.24	1.79	2.24	1.00	20.70
Naive CD8+ T Cells	pPLCg2	7.46	11.98	5.73	9.19	1.00	109.00	6.14	10.55	5.07	7.21	1.00	88.20
Naive CD8+ T Cells	pS6	3.97	7.06	2.95	4.99	1.00	72.80	3.21	5.50	2.66	3.77	1.00	77.60
Naive CD8+ T Cells	pSTAT1	13.91	20.06	11.02	16.81	1.00	140.00	12.36	19.36	10.39	14.33	1.00	144.00
Naive CD8+ T Cells	pSTAT3	7.45	15.40	5.23	9.67	1.00	123.00	5.07	10.83	3.97	6.17	1.00	98.50
Naive CD8+ T Cells	pSTAT5	2.64	4.18	2.03	3.24	1.00	35.60	2.38	4.61	1.91	2.84	1.00	57.80
Plasmoid Dendritic Cells	IkB	5.82	11.51	4.16	7.48	1.00	128.00	4.40	6.34	3.76	5.05	1.00	55.00
Plasmoid Dendritic Cells	pERK	38.62	99.49	24.27	52.98	1.00	1082.00	32.63	69.81	25.53	39.72	1.00	664.00
Plasmoid Dendritic Cells	pP38	2.75	3.73	2.21	3.29	1.00	23.20	2.32	3.01	2.01	2.62	1.00	22.20
Plasmoid Dendritic Cells	pPLCg2	7.60	13.44	5.66	9.54	1.00	137.00	5.92	9.45	4.96	6.88	1.00	70.80
Plasmoid Dendritic Cells	pS6	3.69	8.06	2.52	4.85	1.00	100.00	2.98	5.33	2.44	3.52	1.00	60.40
Plasmoid Dendritic Cells	pSTAT1	6.41	11.00	4.82	7.99	1.00	78.60	5.58	10.30	4.53	6.62	1.00	66.30
Plasmoid Dendritic Cells	pSTAT3	5.03	13.68	3.06	7.01	1.00	163.00	3.42	7.43	2.67	4.18	1.00	71.80
Plasmoid Dendritic Cells	pSTAT5	2.54	4.37	1.91	3.17	1.00	44.20	2.06	3.49	1.70	2.41	1.00	39.70
Plasmablasts	IkB	8.83	12.86	6.97	10.69	1.00	105.00	6.89	8.63	6.01	7.78	1.00	45.60
Plasmablasts	pERK	47.19	97.00	33.15	61.22	1.00	775.00	43.48	104.4	32.79	54.16	1.00	1464.00
Plasmablasts	pP38	3.06	4.67	2.38	3.73	1.00	37.80	2.61	3.40	2.26	2.95	1.00	34.30
Plasmablasts	pPLCg2	10.15	14.56	8.04	12.25	1.00	138.00	8.44	12.60	7.15	9.73	1.00	97.70
Plasmablasts	pS6	5.53	8.87	4.25	6.82	1.00	82.40	3.92	4.87	3.42	4.42	1.00	37.60

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=Unstim

		Cases n = 187						Controls n = 374					
Cell	**Phospho-Epitope**	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum****	***Maximum***
Plasmablasts	pSTAT1	7.33	10.75	5.78	8.89	1.00	68.10	6.62	10.93	5.50	7.74	1.00	73.20
Plasmablasts	pSTAT3	8.15	14.12	6.11	10.20	1.00	134.00	5.97	9.72	4.97	6.96	1.00	74.60
Plasmablasts	pSTAT5	3.33	5.55	2.52	4.13	1.00	46.20	2.75	4.54	2.28	3.21	1.00	45.20
Transitional B Cells	IkB	9.48	15.16	7.28	11.68	1.00	105.00	7.15	9.75	6.15	8.15	1.00	92.20
Transitional B Cells	pERK	46.93	91.20	33.70	60.16	1.00	725.00	40.60	87.96	31.61	49.59	1.00	1183.00
Transitional B Cells	pP38	3.95	5.03	3.22	4.68	1.00	29.60	3.22	3.71	2.84	3.60	1.00	29.30
Transitional B Cells	pPLCg2	11.17	14.55	9.06	13.28	1.00	128.00	9.40	13.69	8.00	10.80	1.00	102.00
Transitional B Cells	pS6	5.98	9.46	4.61	7.35	1.00	81.10	5.03	8.11	4.20	5.86	1.00	97.40
Transitional B Cells	pSTAT1	7.66	10.86	6.09	9.24	1.00	64.90	6.95	11.55	5.77	8.13	1.00	95.30
Transitional B Cells	pSTAT3	11.27	14.19	9.21	13.32	1.00	126.00	8.98	11.65	7.79	10.17	1.00	110.00
Transitional B Cells	pSTAT5	3.28	5.14	2.53	4.03	1.00	40.40	2.87	4.97	2.36	3.38	1.00	45.20

* Minimum staining intensity is 1.00.
Note. SD = standard deviation, CL = confidence limit

stim=IFNa

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	5.94	2.95	5.52	6.37	0.46	17.90	5.64	3.19	5.31	5.96	0.36	21.10
CD16+ NK Cells	1.22	1.54	0.99	1.44	0.00	9.44	1.20	1.38	1.06	1.34	0.00	8.45
CD16+ Monocytes	1.98	3.82	1.43	2.53	0.01	45.30	1.89	3.64	1.52	2.26	0.00	45.10
CD16- NK Cells	2.93	2.32	2.59	3.26	0.05	15.20	2.71	2.17	2.49	2.93	0.02	15.10
CD16- Monocytes	22.25	14.92	20.10	24.40	1.23	75.20	22.30	15.69	20.70	23.91	0.92	74.60
CD19+ Lymphocytes	7.88	3.44	7.38	8.37	1.22	23.90	7.93	3.87	7.54	8.33	2.06	28.90
CD4+ T Cells	30.48	10.13	29.01	31.94	4.62	63.50	30.45	10.42	29.39	31.51	7.22	63.20
CD4-CD8- T Cells	4.65	4.80	3.96	5.34	0.14	23.00	5.14	5.50	4.58	5.70	0.06	31.10
CD8+ T Cells	16.38	6.82	15.39	17.36	3.46	43.30	16.16	6.61	15.49	16.84	1.52	37.80
Dendritic Cells	3.53	3.09	3.08	3.98	0.04	19.20	4.14	4.44	3.69	4.59	0.20	36.20
HLADR+ NK Cells	1.01	0.99	0.87	1.16	0.01	7.29	0.97	1.03	0.87	1.08	0.00	8.87
HLADR+CD38+ CD4+ T Cells	3.31	5.52	2.51	4.11	0.07	35.50	2.83	4.22	2.40	3.26	0.06	28.50
HLADR+CD38+ CD8+ T Cells	1.63	2.35	1.29	1.97	0.05	15.20	1.50	2.33	1.26	1.73	0.00	19.90
IgD+CD27+ B Cells	2.43	2.02	2.14	2.72	0.08	11.10	2.28	2.20	2.06	2.51	0.06	15.50
IgD+CD27- B Cells	2.62	1.94	2.34	2.90	0.13	11.20	2.43	1.85	2.24	2.62	0.00	8.13
IgD-CD27+ B Cells	0.38	0.39	0.33	0.44	0.01	2.84	0.37	0.38	0.33	0.41	0.00	2.71
IgD-CD27- B Cells	0.52	0.56	0.44	0.60	0.00	3.37	0.56	0.59	0.50	0.62	0.00	3.61
NK Cells	4.28	3.08	3.83	4.72	0.05	16.10	4.07	2.90	3.77	4.36	0.03	16.90
NKT Cells	5.68	6.32	4.76	6.59	0.00	40.20	4.89	5.58	4.32	5.46	0.00	44.30
T Cells	52.74	13.17	50.84	54.64	10.30	76.60	53.07	14.38	51.61	54.54	12.80	82.40
Regulatory T Cells	1.83	2.22	1.51	2.15	0.01	16.70	1.64	2.01	1.44	1.85	0.00	16.90
Basophils	1.17	1.35	0.98	1.36	0.08	11.20	1.11	1.26	0.98	1.24	0.06	11.70
Central Memory CD4+ T Cells	4.52	2.48	4.16	4.88	0.43	14.40	4.64	2.52	4.38	4.90	0.21	15.50
Central Memory CD8+ T Cells	1.65	1.30	1.47	1.84	0.03	9.21	1.62	1.10	1.50	1.73	0.06	6.48
Effector CD4+ T Cells	8.01	5.61	7.20	8.82	0.16	26.30	8.06	5.92	7.45	8.66	0.00	28.50
Effector CD8+ T Cells	5.63	4.28	5.02	6.25	0.04	28.00	5.63	4.18	5.21	6.06	0.00	22.70
Effector Memory CD4+ T Cells	5.74	4.54	5.09	6.40	0.04	19.60	6.42	5.20	5.89	6.95	0.00	24.10
Effector Memory CD8+ T Cells	2.40	2.23	2.08	2.72	0.01	10.20	2.62	2.51	2.37	2.88	0.00	18.90
Lymphocytes	71.49	16.16	69.16	73.82	14.40	92.20	71.60	17.61	69.80	73.39	18.90	93.00
Myeloid Dendritic Cells	1.98	1.53	1.76	2.20	0.03	9.72	2.10	1.69	1.92	2.27	0.07	8.51
Monocytes	24.28	15.29	22.08	26.49	5.64	75.40	24.25	16.41	22.57	25.93	4.53	75.30
Naive CD4+ T Cells	12.20	7.87	11.06	13.34	1.27	38.20	11.34	7.56	10.57	12.12	0.64	44.60
Naive CD8+ T Cells	6.69	4.04	6.11	7.28	0.64	22.20	6.29	3.88	5.90	6.69	0.43	21.40

Note. SD = standard deviation, CL = confidence limit

stim=IFNa

	Cases **n = 187**						**Controls** **n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	8.31	4.96	7.60	9.03	0.09	25.70	8.67	5.80	8.08	9.26	0.63	41.10
Non-T Lymphocytes	15.33	6.40	14.40	16.25	1.54	34.40	15.33	7.32	14.59	16.08	2.80	47.30
Plasmoid Dendritic Cells	0.45	0.38	0.39	0.51	0.00	2.22	0.56	0.58	0.50	0.62	0.02	4.49
Plasmablasts	0.20	0.14	0.18	0.22	0.00	1.02	0.19	0.14	0.18	0.21	0.00	0.85
Transitional B Cells	0.21	0.17	0.18	0.23	0.00	0.95	0.17	0.14	0.16	0.19	0.00	0.94

Note. SD = standard deviation, CL = confidence limit

stim=IL-10

	Cases **n = 187**						**Controls** **n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	6.20	3.00	5.77	6.64	0.53	18.90	5.73	3.26	5.40	6.06	0.28	20.20
CD16+ NK Cells	1.21	1.58	0.99	1.44	0.00	10.00	1.17	1.37	1.03	1.31	0.00	7.98
CD16+ Monocytes	1.40	1.40	1.19	1.60	0.00	10.10	1.62	2.74	1.34	1.90	0.01	33.00
CD16- NK Cells	3.33	2.61	2.96	3.71	0.02	14.50	2.98	2.45	2.73	3.23	0.04	15.40
CD16- Monocytes	22.20	14.79	20.06	24.35	5.50	82.50	22.21	15.56	20.62	23.80	1.60	73.30
CD19+ Lymphocytes	8.32	3.56	7.80	8.84	0.83	24.40	8.25	3.94	7.85	8.66	1.74	28.00
CD4+ T Cells	29.67	10.26	28.18	31.16	4.70	65.00	29.46	10.29	28.41	30.52	5.98	58.30
CD4-CD8- T Cells	5.33	5.33	4.56	6.10	0.07	29.10	5.78	5.72	5.20	6.37	0.02	31.80
CD8+ T Cells	15.91	6.63	14.95	16.87	2.82	43.60	15.77	6.41	15.12	16.43	1.98	37.80
Dendritic Cells	4.18	3.59	3.66	4.70	0.02	23.40	4.84	4.82	4.35	5.33	0.15	39.30
HLADR+ NK Cells	1.13	1.34	0.93	1.32	0.00	9.41	1.06	1.34	0.93	1.20	0.00	9.90
HLADR+CD38+ CD4+ T Cells	2.97	5.20	2.21	3.72	0.10	31.70	2.60	4.02	2.19	3.01	0.11	28.20
HLADR+CD38+ CD8+ T Cells	1.46	2.37	1.12	1.81	0.06	15.00	1.35	2.18	1.13	1.58	0.06	18.60
IgD+CD27+ B Cells	2.46	2.18	2.14	2.77	0.06	11.80	2.27	2.31	2.04	2.51	0.04	16.60
IgD+CD27- B Cells	2.76	1.90	2.49	3.04	0.10	9.37	2.48	1.83	2.29	2.67	0.00	8.52
IgD-CD27+ B Cells	0.40	0.37	0.34	0.45	0.02	2.78	0.38	0.35	0.34	0.41	0.00	2.31
IgD-CD27- B Cells	0.59	0.61	0.50	0.68	0.01	3.12	0.60	0.62	0.54	0.67	0.00	4.41
NK Cells	4.71	3.37	4.22	5.20	0.02	15.90	4.30	3.11	3.98	4.62	0.05	18.10
NKT Cells	5.09	6.13	4.19	5.98	0.00	42.70	4.62	5.57	4.05	5.19	0.00	43.10
T Cells	52.14	13.47	50.18	54.09	8.08	78.20	52.37	14.36	50.90	53.84	10.20	77.70
Regulatory T Cells	1.63	2.02	1.34	1.93	0.01	16.30	1.44	1.63	1.27	1.61	0.00	10.60
Basophils	1.09	1.29	0.90	1.28	0.05	11.80	1.08	1.40	0.93	1.22	0.07	13.70
Central Memory CD4+ T Cells	4.47	2.58	4.09	4.84	0.52	14.20	4.50	2.60	4.24	4.77	0.13	14.80
Central Memory CD8+ T Cells	1.61	1.24	1.43	1.79	0.05	8.04	1.62	1.18	1.50	1.74	0.01	8.26
Effector CD4+ T Cells	8.20	5.65	7.38	9.02	0.20	28.40	8.10	5.75	7.51	8.69	0.00	25.10
Effector CD8+ T Cells	5.71	4.13	5.11	6.31	0.08	28.60	5.62	3.97	5.21	6.03	0.00	23.00
Effector Memory CD4+ T Cells	6.10	4.48	5.45	6.75	0.04	21.00	6.64	5.15	6.11	7.16	0.00	22.40
Effector Memory CD8+ T Cells	2.54	2.20	2.22	2.86	0.01	9.32	2.74	2.49	2.49	3.00	0.00	19.40
Lymphocytes	72.26	15.93	69.95	74.57	9.75	91.60	71.96	17.27	70.19	73.73	20.00	93.60
Myeloid Dendritic Cells	2.32	1.74	2.07	2.57	0.02	9.73	2.41	1.85	2.22	2.60	0.05	8.41
Monocytes	23.64	15.04	21.46	25.82	6.44	82.70	23.89	16.15	22.24	25.55	4.03	77.60
Naive CD4+ T Cells	10.92	7.60	9.82	12.02	0.98	41.40	10.23	7.20	9.50	10.97	0.45	40.10
Naive CD8+ T Cells	6.06	3.81	5.51	6.61	0.53	19.80	5.79	3.74	5.41	6.18	0.38	22.00

Note. SD = standard deviation, CL = confidence limit

stim=IL-10

	Cases **n = 187**						**Controls** **n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	9.47	5.41	8.68	10.25	0.04	29.80	9.66	6.16	9.03	10.29	0.61	44.20
Non-T Lymphocytes	16.71	6.66	15.75	17.68	0.96	36.00	16.46	7.61	15.68	17.24	2.68	52.00
Plasmoid Dendritic Cells	0.54	0.44	0.47	0.60	0.00	2.52	0.65	0.61	0.59	0.71	0.03	5.02
Plasmablasts	0.18	0.13	0.16	0.20	0.00	0.84	0.18	0.14	0.17	0.20	0.00	1.09
Transitional B Cells	0.20	0.17	0.17	0.22	0.00	0.96	0.16	0.14	0.15	0.18	0.00	0.97

Note. SD = standard deviation, CL = confidence limit

stim=IL-21

	Cases n = 187						**Controls n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	6.14	3.04	5.70	6.58	0.55	17.40	5.78	3.32	5.44	6.11	0.29	21.20
CD16+ NK Cells	1.19	1.59	0.96	1.42	0.00	9.68	1.18	1.37	1.04	1.32	0.00	7.33
CD16+ Monocytes	1.48	1.56	1.25	1.71	0.01	9.13	1.60	2.61	1.33	1.86	0.01	28.10
CD16- NK Cells	3.43	2.75	3.03	3.83	0.11	15.90	3.04	2.51	2.79	3.30	0.02	17.60
CD16- Monocytes	21.93	14.85	19.77	24.09	5.09	70.50	21.68	15.20	20.13	23.23	1.88	73.90
CD19+ Lymphocytes	8.29	3.61	7.76	8.81	1.83	23.60	8.23	4.07	7.81	8.64	1.70	29.70
CD4+ T Cells	29.82	10.37	28.31	31.32	6.11	63.50	29.86	10.48	28.79	30.93	6.11	60.30
CD4-CD8- T Cells	5.24	5.28	4.47	6.00	0.08	28.00	5.73	5.73	5.14	6.31	0.08	32.60
CD8+ T Cells	15.90	6.79	14.92	16.89	3.42	44.80	15.92	6.41	15.26	16.57	2.05	36.00
Dendritic Cells	4.19	3.48	3.68	4.70	0.14	22.90	4.75	4.59	4.28	5.22	0.12	40.80
HLADR+ NK Cells	1.15	1.39	0.95	1.36	0.01	10.30	1.08	1.41	0.94	1.23	0.01	12.20
HLADR+CD38+ CD4+ T Cells	2.87	5.05	2.14	3.61	0.10	30.70	2.67	4.28	2.23	3.10	0.10	28.70
HLADR+CD38+ CD8+ T Cells	1.42	2.23	1.10	1.75	0.06	14.70	1.39	2.28	1.16	1.62	0.04	18.70
IgD+CD27+ B Cells	2.45	2.20	2.13	2.77	0.07	11.60	2.29	2.36	2.05	2.53	0.04	20.50
IgD+CD27- B Cells	2.74	1.94	2.46	3.02	0.11	10.40	2.52	1.85	2.33	2.71	0.00	8.98
IgD-CD27+ B Cells	0.37	0.33	0.32	0.42	0.01	1.98	0.37	0.36	0.34	0.41	0.01	2.67
IgD-CD27- B Cells	0.58	0.62	0.49	0.67	0.00	3.60	0.60	0.61	0.54	0.66	0.00	4.50
NK Cells	4.78	3.42	4.28	5.28	0.11	17.10	4.39	3.13	4.07	4.71	0.03	19.60
NKT Cells	5.17	6.32	4.25	6.10	0.00	45.30	4.86	5.93	4.25	5.46	0.00	45.30
T Cells	52.18	13.61	50.20	54.16	11.30	75.70	52.85	14.41	51.38	54.32	11.70	78.60
Regulatory T Cells	1.71	2.26	1.38	2.04	0.02	15.90	1.52	1.89	1.33	1.71	0.01	15.20
Basophils	1.10	1.37	0.90	1.30	0.09	12.90	1.07	1.34	0.93	1.21	0.05	13.40
Central Memory CD4+ T Cells	4.54	2.66	4.16	4.93	0.49	14.00	4.60	2.72	4.32	4.88	0.30	14.70
Central Memory CD8+ T Cells	1.60	1.20	1.43	1.77	0.05	7.42	1.63	1.19	1.51	1.75	0.07	9.27
Effector CD4+ T Cells	8.06	5.57	7.25	8.87	0.29	25.30	8.20	5.89	7.60	8.80	0.00	32.10
Effector CD8+ T Cells	5.68	4.24	5.06	6.30	0.08	29.70	5.71	4.05	5.29	6.12	0.00	22.30
Effector Memory CD4+ T Cells	6.18	4.59	5.51	6.85	0.02	21.00	6.75	5.25	6.22	7.29	0.00	24.20
Effector Memory CD8+ T Cells	2.54	2.25	2.21	2.87	0.01	9.86	2.77	2.49	2.51	3.02	0.00	18.50
Lymphocytes	72.44	16.22	70.08	74.80	18.90	91.20	72.55	17.06	70.81	74.29	16.40	93.30
Myeloid Dendritic Cells	2.32	1.70	2.07	2.56	0.08	9.35	2.39	1.81	2.21	2.58	0.08	9.50
Monocytes	23.45	15.24	21.23	25.66	5.54	73.40	23.33	15.89	21.70	24.95	4.24	75.90
Naive CD4+ T Cells	11.05	7.71	9.93	12.17	1.23	39.50	10.32	7.38	9.56	11.07	0.34	45.40
Naive CD8+ T Cells	6.09	3.87	5.52	6.65	0.64	21.50	5.82	3.66	5.44	6.19	0.40	20.90

Note. SD = standard deviation, CL = confidence limit

stim=IL-21

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	9.54	5.46	8.75	10.34	0.43	29.10	9.67	6.08	9.05	10.29	0.56	45.80
Non-T Lymphocytes	16.74	6.76	15.76	17.73	2.26	33.50	16.50	7.59	15.72	17.27	2.05	51.50
Plasmoid Dendritic Cells	0.54	0.45	0.48	0.61	0.01	2.57	0.64	0.59	0.58	0.71	0.02	4.52
Plasmablasts	0.18	0.12	0.16	0.20	0.00	0.66	0.19	0.15	0.17	0.20	0.00	1.48
Transitional B Cells	0.19	0.15	0.17	0.21	0.00	0.70	0.16	0.14	0.15	0.18	0.00	0.97

Note. SD = standard deviation, CL = confidence limit

stim=IL-6

	Cases **n = 187**						**Controls** **n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	6.11	3.06	5.67	6.56	0.45	17.80	5.76	3.21	5.44	6.09	0.32	20.30
CD16+ NK Cells	1.23	1.63	1.00	1.47	0.00	9.96	1.20	1.38	1.06	1.34	0.00	7.95
CD16+ Monocytes	1.95	3.71	1.41	2.48	0.00	45.40	1.98	3.78	1.59	2.36	0.02	41.00
CD16- NK Cells	3.15	2.54	2.78	3.52	0.08	15.30	2.85	2.40	2.61	3.10	0.03	17.60
CD16- Monocytes	22.68	15.34	20.45	24.91	1.06	72.20	22.39	15.18	20.84	23.93	1.21	74.00
CD19+ Lymphocytes	8.20	3.62	7.68	8.73	1.54	23.50	8.23	3.88	7.83	8.62	2.26	26.00
CD4+ T Cells	29.87	10.16	28.40	31.35	4.99	63.20	30.00	10.36	28.95	31.05	6.98	58.60
CD4-CD8- T Cells	4.74	5.00	4.01	5.47	0.06	26.40	5.11	5.29	4.57	5.65	0.10	30.00
CD8+ T Cells	16.09	6.91	15.09	17.10	3.33	41.90	15.98	6.49	15.32	16.64	1.94	37.40
Dendritic Cells	3.72	3.24	3.25	4.19	0.07	21.50	4.31	4.38	3.87	4.76	0.19	33.10
HLADR+ NK Cells	1.13	1.29	0.94	1.32	0.00	9.64	1.07	1.27	0.94	1.20	0.00	8.83
HLADR+CD38+ CD4+ T Cells	3.24	5.36	2.46	4.02	0.08	32.20	2.84	4.31	2.40	3.28	0.03	30.20
HLADR+CD38+ CD8+ T Cells	1.58	2.39	1.23	1.92	0.06	15.30	1.48	2.21	1.25	1.70	0.08	18.60
IgD+CD27+ B Cells	2.52	2.12	2.21	2.83	0.07	11.60	2.33	2.23	2.11	2.56	0.03	18.40
IgD+CD27- B Cells	2.69	1.97	2.40	2.97	0.08	11.20	2.48	1.91	2.29	2.68	0.01	10.60
IgD-CD27+ B Cells	0.38	0.37	0.33	0.44	0.01	2.34	0.38	0.36	0.34	0.41	0.02	2.60
IgD-CD27- B Cells	0.52	0.55	0.44	0.60	0.02	3.07	0.57	0.59	0.51	0.63	0.00	3.84
NK Cells	4.52	3.31	4.04	5.00	0.09	16.40	4.21	3.09	3.89	4.52	0.04	20.20
NKT Cells	5.56	6.30	4.64	6.47	0.00	38.80	4.90	5.53	4.34	5.47	0.00	41.50
T Cells	51.93	13.82	49.92	53.94	10.30	76.50	52.40	14.38	50.94	53.86	12.60	78.10
Regulatory T Cells	1.86	2.34	1.52	2.20	0.01	18.70	1.58	1.92	1.38	1.77	0.01	14.90
Basophils	1.15	1.33	0.95	1.34	0.10	11.40	1.13	1.41	0.99	1.28	0.03	13.10
Central Memory CD4+ T Cells	4.40	2.41	4.05	4.75	0.58	13.00	4.49	2.47	4.24	4.74	0.21	15.40
Central Memory CD8+ T Cells	1.62	1.30	1.43	1.81	0.06	9.33	1.58	1.08	1.47	1.69	0.06	6.72
Effector CD4+ T Cells	7.95	5.55	7.14	8.76	0.15	26.90	8.11	5.93	7.51	8.72	0.00	31.20
Effector CD8+ T Cells	5.62	4.25	5.00	6.24	0.14	27.80	5.68	4.15	5.25	6.10	0.00	22.60
Effector Memory CD4+ T Cells	5.71	4.51	5.06	6.37	0.04	17.80	6.40	5.21	5.87	6.93	0.00	24.00
Effector Memory CD8+ T Cells	2.38	2.23	2.05	2.70	0.01	10.20	2.60	2.45	2.35	2.85	0.00	16.90
Lymphocytes	71.15	16.52	68.75	73.56	18.60	92.10	71.34	16.99	69.61	73.06	24.40	93.50
Myeloid Dendritic Cells	2.09	1.63	1.86	2.33	0.06	9.79	2.18	1.72	2.00	2.35	0.14	8.33
Monocytes	24.67	15.67	22.39	26.95	5.69	74.80	24.42	15.88	22.81	26.04	4.21	74.50
Naive CD4+ T Cells	11.82	7.79	10.68	12.95	1.17	41.20	11.02	7.51	10.25	11.78	0.31	46.50
Naive CD8+ T Cells	6.48	3.89	5.91	7.04	0.52	21.90	6.12	3.73	5.74	6.50	0.47	22.40

Note. SD = standard deviation, CL = confidence limit

stim=IL-6

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	8.78	5.14	8.03	9.52	0.15	27.70	9.01	5.78	8.42	9.60	0.63	37.60
Non-T Lymphocytes	15.94	6.54	14.99	16.89	1.88	34.20	15.84	7.20	15.11	16.57	3.20	46.70
Plasmoid Dendritic Cells	0.50	0.45	0.44	0.57	0.01	2.60	0.61	0.59	0.55	0.67	0.00	3.87
Plasmablasts	0.21	0.16	0.19	0.23	0.00	1.13	0.20	0.15	0.19	0.22	0.00	1.18
Transitional B Cells	0.21	0.19	0.18	0.23	0.00	1.52	0.17	0.14	0.16	0.19	0.00	0.82

Note. SD = standard deviation, CL = confidence limit

stim=IL-7

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	6.08	2.95	5.65	6.51	0.53	17.40	5.76	3.28	5.42	6.09	0.37	20.50
CD16+ NK Cells	1.21	1.61	0.98	1.44	0.00	10.30	1.19	1.38	1.05	1.33	0.00	7.83
CD16+ Monocytes	1.92	3.72	1.38	2.46	0.00	40.40	1.86	3.30	1.53	2.20	0.02	34.00
CD16- NK Cells	3.20	2.47	2.84	3.55	0.05	13.10	2.91	2.39	2.67	3.15	0.02	16.70
CD16- Monocytes	22.04	15.28	19.83	24.25	1.34	77.40	22.03	15.67	20.44	23.63	1.08	75.30
CD19+ Lymphocytes	8.19	3.59	7.67	8.71	1.08	23.40	8.32	3.98	7.91	8.72	2.04	28.50
CD4+ T Cells	30.01	10.47	28.50	31.53	6.23	63.90	29.99	10.72	28.90	31.09	6.93	59.90
CD4-CD8- T Cells	4.98	5.23	4.22	5.73	0.08	28.30	5.35	5.50	4.79	5.91	0.06	30.70
CD8+ T Cells	15.98	6.83	14.99	16.97	2.06	43.60	15.93	6.60	15.26	16.60	1.52	38.00
Dendritic Cells	3.94	3.42	3.44	4.43	0.05	19.60	4.66	4.91	4.16	5.16	0.25	40.40
HLADR+ NK Cells	1.11	1.27	0.93	1.30	0.01	7.92	1.06	1.29	0.93	1.19	0.00	9.45
HLADR+CD38+ CD4+ T Cells	3.24	5.48	2.45	4.03	0.14	32.00	2.73	4.11	2.31	3.14	0.05	27.90
HLADR+CD38+ CD8+ T Cells	1.55	2.32	1.21	1.88	0.06	14.30	1.44	2.29	1.21	1.67	0.03	19.20
IgD+CD27+ B Cells	2.46	2.09	2.16	2.76	0.09	11.90	2.35	2.40	2.11	2.60	0.05	19.40
IgD+CD27- B Cells	2.70	1.89	2.43	2.97	0.09	9.63	2.46	1.84	2.27	2.65	0.01	9.31
IgD-CD27+ B Cells	0.38	0.35	0.33	0.43	0.02	2.29	0.37	0.35	0.34	0.41	0.01	2.37
IgD-CD27- B Cells	0.54	0.58	0.46	0.63	0.01	3.57	0.58	0.58	0.52	0.63	0.00	3.84
NK Cells	4.55	3.23	4.08	5.02	0.05	14.60	4.26	3.07	3.95	4.58	0.03	18.80
NKT Cells	5.22	6.03	4.34	6.09	0.00	41.60	4.78	5.49	4.22	5.34	0.00	42.30
T Cells	52.22	13.94	50.20	54.23	10.30	77.00	52.61	14.91	51.09	54.13	11.10	80.30
Regulatory T Cells	1.80	2.15	1.48	2.11	0.01	14.60	1.59	1.87	1.40	1.78	0.00	13.20
Basophils	1.14	1.34	0.95	1.33	0.07	10.80	1.10	1.39	0.96	1.24	0.00	13.80
Central Memory CD4+ T Cells	4.47	2.50	4.11	4.84	0.52	13.50	4.55	2.58	4.29	4.81	0.16	18.20
Central Memory CD8+ T Cells	1.61	1.27	1.42	1.79	0.06	8.07	1.62	1.16	1.50	1.73	0.00	8.07
Effector CD4+ T Cells	8.08	5.71	7.26	8.91	0.18	27.40	8.09	5.93	7.49	8.69	0.01	29.90
Effector CD8+ T Cells	5.61	4.21	5.01	6.22	0.06	28.30	5.66	4.23	5.23	6.09	0.00	23.50
Effector Memory CD4+ T Cells	5.99	4.60	5.32	6.65	0.03	20.20	6.53	5.22	5.99	7.06	0.00	22.10
Effector Memory CD8+ T Cells	2.45	2.22	2.13	2.77	0.01	9.48	2.65	2.44	2.40	2.89	0.00	17.80
Lymphocytes	71.87	16.70	69.45	74.28	12.90	93.20	71.96	17.66	70.16	73.76	21.70	94.00
Myeloid Dendritic Cells	2.16	1.62	1.92	2.39	0.04	9.31	2.29	1.85	2.10	2.47	0.13	8.75
Monocytes	24.00	15.72	21.72	26.27	4.80	77.60	23.95	16.39	22.28	25.62	4.37	75.90
Naive CD4+ T Cells	11.48	7.85	10.34	12.61	1.17	41.50	10.84	7.53	10.07	11.60	0.39	44.50
Naive CD8+ T Cells	6.31	3.87	5.75	6.87	0.50	21.70	6.02	3.81	5.63	6.41	0.41	22.10

Note. SD = standard deviation, CL = confidence limit

stim=IL-7

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	9.03	5.25	8.27	9.79	0.11	26.60	9.42	6.24	8.78	10.05	0.54	44.90
Non-T Lymphocytes	16.22	6.70	15.25	17.19	1.32	33.80	16.25	7.61	15.47	17.02	3.19	50.90
Plasmoid Dendritic Cells	0.52	0.44	0.46	0.58	0.01	2.29	0.65	0.64	0.58	0.72	0.03	4.62
Plasmablasts	0.19	0.14	0.17	0.21	0.00	0.83	0.20	0.16	0.18	0.21	0.00	1.70
Transitional B Cells	0.19	0.16	0.17	0.21	0.00	0.74	0.17	0.15	0.15	0.18	0.00	1.00

Note. SD = standard deviation, CL = confidence limit

stim=LPS

	Cases n = 187						**Controls n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	6.12	3.00	5.68	6.57	0.40	17.70	5.90	3.31	5.56	6.24	0.25	22.20
CD16+ NK Cells	1.30	1.72	1.05	1.55	0.00	10.40	1.27	1.52	1.12	1.43	0.00	7.85
CD16+ Monocytes	1.60	3.12	1.14	2.06	0.00	32.70	1.43	2.07	1.21	1.64	0.00	15.90
CD16- NK Cells	3.48	2.71	3.08	3.88	0.08	15.00	3.25	2.73	2.98	3.53	0.02	21.10
CD16- Monocytes	20.38	15.13	18.15	22.61	3.27	76.60	19.83	15.15	18.28	21.39	1.58	75.00
CD19+ Lymphocytes	8.25	3.60	7.72	8.78	1.14	21.00	8.42	4.15	7.99	8.85	1.99	29.40
CD4+ T Cells	30.70	10.74	29.11	32.28	4.09	65.90	30.79	11.04	29.66	31.92	1.67	59.10
CD4-CD8- T Cells	5.22	5.55	4.40	6.04	0.07	29.70	5.72	5.93	5.11	6.33	0.06	35.40
CD8+ T Cells	16.69	7.00	15.66	17.72	1.99	44.40	16.44	6.65	15.76	17.12	1.02	38.90
Dendritic Cells	3.99	3.31	3.50	4.48	0.14	21.80	4.97	6.10	4.34	5.59	0.16	76.10
HLADR+ NK Cells	1.17	1.46	0.95	1.38	0.02	9.91	1.12	1.42	0.97	1.26	0.00	11.20
HLADR+CD38+ CD4+ T Cells	2.94	5.34	2.15	3.73	0.14	29.60	2.61	4.16	2.19	3.04	0.01	27.30
HLADR+CD38+ CD8+ T Cells	1.46	2.30	1.12	1.79	0.06	16.00	1.39	2.26	1.16	1.62	0.01	18.00
IgD+CD27+ B Cells	2.42	2.19	2.10	2.75	0.07	11.40	2.33	2.47	2.08	2.59	0.03	21.60
IgD+CD27- B Cells	2.72	1.95	2.43	3.00	0.13	10.50	2.55	1.88	2.36	2.75	0.00	10.50
IgD-CD27+ B Cells	0.40	0.38	0.34	0.45	0.03	2.61	0.39	0.38	0.35	0.42	0.01	2.62
IgD-CD27- B Cells	0.59	0.63	0.50	0.69	0.01	3.41	0.63	0.67	0.56	0.70	0.00	4.39
NK Cells	4.94	3.52	4.42	5.46	0.14	15.70	4.66	3.47	4.31	5.02	0.03	26.30
NKT Cells	5.31	6.59	4.34	6.29	0.00	42.40	4.96	6.13	4.33	5.59	0.00	45.10
T Cells	53.89	14.21	51.79	55.98	6.51	78.40	54.33	14.88	52.81	55.86	10.30	81.10
Regulatory T Cells	1.73	2.27	1.40	2.07	0.01	18.40	1.63	2.06	1.42	1.84	0.00	15.40
Basophils	1.12	1.38	0.92	1.32	0.08	11.30	1.10	1.39	0.96	1.24	0.05	15.20
Central Memory CD4+ T Cells	4.67	2.84	4.25	5.09	0.30	14.40	4.81	2.93	4.50	5.11	0.13	16.40
Central Memory CD8+ T Cells	1.69	1.39	1.49	1.90	0.06	8.90	1.70	1.27	1.57	1.83	0.04	8.52
Effector CD4+ T Cells	8.26	5.83	7.40	9.12	0.36	27.60	8.41	6.16	7.77	9.04	0.00	33.60
Effector CD8+ T Cells	5.95	4.44	5.30	6.61	0.06	28.80	5.88	4.27	5.44	6.32	0.00	24.40
Effector Memory CD4+ T Cells	6.34	4.90	5.62	7.07	0.08	21.70	6.81	5.36	6.26	7.36	0.00	23.00
Effector Memory CD8+ T Cells	2.66	2.35	2.31	3.01	0.01	10.50	2.82	2.58	2.55	3.08	0.00	20.70
Lymphocytes	74.05	17.01	71.54	76.56	9.55	94.80	74.72	17.13	72.97	76.48	17.60	97.70
Myeloid Dendritic Cells	2.16	1.61	1.92	2.40	0.11	9.32	2.28	1.68	2.11	2.45	0.11	9.61
Monocytes	21.99	16.11	19.61	24.37	3.35	84.20	21.30	15.85	19.68	22.93	1.66	75.80
Naive CD4+ T Cells	11.43	7.91	10.26	12.60	1.39	38.20	10.79	7.52	10.02	11.56	0.12	41.30
Naive CD8+ T Cells	6.39	4.03	5.80	6.98	0.64	21.80	6.04	3.82	5.65	6.43	0.06	21.70

Note. SD = standard deviation, CL = confidence limit

stim=LPS

	Cases n = 187						**Controls n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	9.48	5.31	8.70	10.27	0.31	28.70	10.18	7.60	9.40	10.96	0.68	76.20
Non-T Lymphocytes	16.67	6.68	15.68	17.65	1.48	34.00	17.16	8.81	16.26	18.06	2.66	80.90
Plasmoid Dendritic Cells	0.54	0.46	0.47	0.61	0.00	3.10	0.71	0.84	0.62	0.80	0.02	8.56
Plasmablasts	0.19	0.12	0.17	0.21	0.00	0.61	0.19	0.15	0.18	0.21	0.00	1.27
Transitional B Cells	0.18	0.15	0.16	0.21	0.00	0.92	0.16	0.14	0.15	0.18	0.00	1.18

Note. SD = standard deviation, CL = confidence limit

stim=PMA

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	6.23	3.04	5.78	6.67	0.24	17.40	5.94	3.25	5.60	6.27	0.26	20.00
CD16+ NK Cells	1.31	1.84	1.04	1.58	0.00	12.00	1.30	1.69	1.12	1.47	0.00	9.72
CD16+ Monocytes	1.40	2.13	1.08	1.71	0.00	17.30	1.38	2.23	1.15	1.60	0.00	22.60
CD16- NK Cells	4.14	3.35	3.65	4.64	0.06	16.70	3.77	3.03	3.46	4.08	0.03	18.60
CD16- Monocytes	18.71	13.44	16.73	20.70	3.73	69.20	18.27	13.72	16.86	19.68	1.39	65.50
CD19+ Lymphocytes	7.94	3.51	7.42	8.46	1.36	22.70	7.99	4.12	7.56	8.41	1.51	28.60
CD4+ T Cells	31.51	10.67	29.94	33.09	6.75	58.90	31.56	10.91	30.44	32.68	2.20	61.10
CD4-CD8- T Cells	5.33	5.85	4.46	6.19	0.09	33.30	5.93	6.26	5.29	6.58	0.13	38.50
CD8+ T Cells	17.03	7.05	15.99	18.07	3.37	47.50	16.99	6.64	16.31	17.67	1.04	40.80
Dendritic Cells	3.66	2.89	3.23	4.08	0.19	18.10	4.23	4.63	3.76	4.71	0.23	59.20
HLADR+ NK Cells	1.22	1.55	0.99	1.45	0.02	10.50	1.17	1.48	1.01	1.32	0.00	10.50
HLADR+CD38+ CD4+ T Cells	2.90	5.44	2.10	3.70	0.03	33.10	2.64	4.39	2.19	3.09	0.00	27.40
HLADR+CD38+ CD8+ T Cells	1.41	2.28	1.07	1.74	0.05	14.20	1.37	2.31	1.14	1.61	0.00	18.00
IgD+CD27+ B Cells	2.40	2.09	2.09	2.71	0.04	10.20	2.29	2.34	2.05	2.53	0.02	19.10
IgD+CD27- B Cells	2.85	2.04	2.55	3.15	0.13	10.30	2.63	1.90	2.43	2.82	0.00	9.95
IgD-CD27+ B Cells	0.38	0.36	0.33	0.43	0.00	2.62	0.38	0.38	0.34	0.42	0.00	2.47
IgD-CD27- B Cells	0.59	0.61	0.50	0.68	0.02	3.54	0.64	0.72	0.57	0.72	0.00	5.19
NK Cells	5.62	4.20	5.00	6.24	0.13	18.30	5.21	3.78	4.82	5.59	0.04	21.20
NKT Cells	5.45	6.69	4.46	6.44	0.00	42.40	5.07	6.08	4.44	5.70	0.00	46.10
T Cells	55.10	13.49	53.11	57.09	11.00	78.00	55.85	14.25	54.38	57.31	9.92	81.10
Regulatory T Cells	1.81	2.25	1.48	2.14	0.01	17.20	1.55	1.91	1.35	1.74	0.00	15.10
Basophils	1.19	1.42	0.98	1.40	0.07	12.10	1.18	1.49	1.02	1.33	0.04	15.20
Central Memory CD4+ T Cells	4.89	2.95	4.45	5.32	0.52	14.40	4.91	3.05	4.60	5.22	0.21	21.60
Central Memory CD8+ T Cells	1.71	1.26	1.52	1.89	0.04	7.21	1.72	1.20	1.59	1.84	0.02	7.98
Effector CD4+ T Cells	8.18	5.54	7.36	8.99	0.38	24.30	8.40	5.94	7.79	9.02	0.00	31.50
Effector CD8+ T Cells	6.04	4.48	5.38	6.70	0.06	31.10	6.07	4.24	5.63	6.50	0.00	24.40
Effector Memory CD4+ T Cells	6.37	4.80	5.67	7.08	0.10	22.70	6.88	5.24	6.34	7.42	0.00	23.80
Effector Memory CD8+ T Cells	2.69	2.32	2.35	3.03	0.00	11.40	2.94	2.58	2.67	3.20	0.00	14.60
Lymphocytes	75.70	15.27	73.45	77.95	18.30	93.60	76.12	15.74	74.50	77.74	18.40	96.50
Myeloid Dendritic Cells	2.05	1.52	1.83	2.27	0.13	9.43	2.06	1.53	1.90	2.22	0.13	9.36
Monocytes	20.14	14.23	18.04	22.24	3.98	72.10	19.70	14.49	18.21	21.19	1.40	73.90
Naive CD4+ T Cells	12.08	8.31	10.86	13.31	0.78	41.90	11.37	7.70	10.58	12.16	0.15	44.50
Naive CD8+ T Cells	6.59	3.91	6.01	7.17	0.71	23.10	6.27	3.74	5.89	6.66	0.03	21.20

Note. SD = standard deviation, CL = confidence limit

stim=PMA

	Cases **n = 187**						**Controls** **n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	9.99	6.04	9.10	10.88	0.42	37.00	10.11	6.79	9.41	10.81	0.47	63.90
Non-T Lymphocytes	17.14	7.12	16.09	18.19	1.85	47.30	16.99	8.19	16.15	17.83	2.43	69.20
Plasmoid Dendritic Cells	0.49	0.47	0.42	0.56	0.01	3.30	0.59	0.69	0.52	0.66	0.01	7.79
Plasmablasts	0.18	0.12	0.16	0.20	0.00	0.75	0.18	0.17	0.17	0.20	0.00	1.59
Transitional B Cells	0.19	0.15	0.17	0.22	0.00	0.76	0.18	0.16	0.16	0.20	0.00	0.99

Note. SD = standard deviation, CL = confidence limit

stim=Unstim

	Cases **n = 187**						**Controls** **n = 374**					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
B Cells	5.83	3.06	5.39	6.27	0.36	19.40	5.58	3.10	5.26	5.89	0.26	19.50
CD16+ NK Cells	1.28	1.74	1.03	1.54	0.00	13.30	1.19	1.39	1.05	1.33	0.00	8.88
CD16+ Monocytes	1.93	2.95	1.50	2.36	0.02	33.00	1.97	4.22	1.54	2.40	0.02	45.00
CD16- NK Cells	2.93	2.39	2.59	3.28	0.00	16.10	2.78	2.25	2.56	3.01	0.04	17.30
CD16- Monocytes	22.71	15.04	20.54	24.88	3.75	81.50	22.40	15.63	20.82	23.99	2.26	77.30
CD19+ Lymphocytes	7.85	3.57	7.34	8.37	1.01	25.00	8.02	3.95	7.61	8.42	1.83	28.80
CD4+ T Cells	30.76	10.01	29.31	32.20	6.42	60.70	30.70	10.41	29.64	31.76	3.47	57.90
CD4-CD8- T Cells	4.17	4.29	3.55	4.79	0.06	25.50	4.61	4.63	4.14	5.09	0.06	23.70
CD8+ T Cells	16.54	6.83	15.56	17.53	3.51	44.20	16.28	6.54	15.62	16.95	0.85	36.20
Dendritic Cells	3.44	3.45	2.94	3.93	0.01	22.00	4.20	5.20	3.67	4.73	0.09	42.60
HLADR+ NK Cells	1.05	0.93	0.91	1.18	0.00	5.40	1.03	1.04	0.92	1.13	0.01	7.38
HLADR+CD38+ CD4+ T Cells	3.65	5.69	2.83	4.47	0.06	37.90	3.10	4.22	2.67	3.53	0.03	30.30
HLADR+CD38+ CD8+ T Cells	1.74	2.42	1.39	2.09	0.03	16.30	1.62	2.24	1.40	1.85	0.08	17.60
IgD+CD27+ B Cells	2.40	1.98	2.11	2.68	0.09	10.50	2.25	1.99	2.05	2.45	0.04	13.30
IgD+CD27- B Cells	2.61	2.00	2.32	2.90	0.10	12.50	2.44	1.87	2.25	2.63	0.00	9.59
IgD-CD27+ B Cells	0.37	0.37	0.32	0.42	0.01	2.73	0.38	0.36	0.34	0.41	0.01	2.52
IgD-CD27- B Cells	0.46	0.52	0.39	0.54	0.00	3.28	0.51	0.53	0.46	0.57	0.00	3.33
NK Cells	4.35	3.31	3.87	4.83	0.01	18.50	4.12	2.98	3.82	4.42	0.05	19.90
NKT Cells	5.68	6.69	4.71	6.65	0.00	40.80	4.78	5.82	4.19	5.38	0.00	44.00
T Cells	52.65	12.91	50.79	54.52	12.10	76.50	52.90	14.00	51.48	54.33	7.53	79.20
Regulatory T Cells	1.85	2.44	1.50	2.21	0.01	20.90	1.65	2.01	1.44	1.85	0.00	15.10
Basophils	1.18	1.56	0.95	1.40	0.07	12.80	1.09	1.30	0.96	1.22	0.06	13.00
Central Memory CD4+ T Cells	4.71	2.55	4.34	5.07	0.29	13.50	4.85	2.80	4.56	5.13	0.20	18.10
Central Memory CD8+ T Cells	1.68	1.32	1.49	1.87	0.05	10.10	1.67	1.17	1.55	1.79	0.03	6.82
Effector CD4+ T Cells	7.26	5.04	6.54	7.99	0.22	23.20	7.45	5.33	6.91	7.99	0.00	28.90
Effector CD8+ T Cells	5.36	4.15	4.76	5.96	0.05	27.60	5.37	3.90	4.97	5.76	0.00	20.50
Effector Memory CD4+ T Cells	5.11	4.11	4.52	5.70	0.05	16.70	5.64	4.63	5.17	6.11	0.00	23.00
Effector Memory CD8+ T Cells	2.16	2.09	1.86	2.46	0.01	9.79	2.37	2.32	2.14	2.61	0.00	17.80
Lymphocytes	71.34	15.95	69.04	73.65	14.20	94.80	71.56	17.23	69.81	73.31	10.80	93.40
Myeloid Dendritic Cells	1.96	1.63	1.72	2.19	0.01	8.62	2.10	1.80	1.92	2.29	0.04	10.60
Monocytes	24.68	15.24	22.48	26.88	3.83	81.80	24.44	16.24	22.79	26.09	4.55	77.80
Naive CD4+ T Cells	13.67	8.21	12.49	14.86	1.41	37.10	12.76	7.67	11.98	13.53	0.21	40.50
Naive CD8+ T Cells	7.34	4.08	6.76	7.93	0.88	22.20	6.88	3.96	6.47	7.28	0.42	23.40

Note. SD = standard deviation, CL = confidence limit

stim=Unstim

	Cases n = 187						Controls n = 374					
Cell	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***	***Mean***	***SD***	***Lower CL***	***Upper CL***	***Minimum***	***Maximum***
Non-B Lymphocytes	8.28	5.37	7.50	9.05	0.02	25.80	8.77	6.47	8.11	9.43	0.26	46.00
Non-T Lymphocytes	15.25	6.76	14.27	16.22	1.22	38.00	15.51	7.89	14.70	16.31	2.04	53.20
Plasmoid Dendritic Cells	0.41	0.40	0.36	0.47	0.00	2.46	0.55	0.67	0.48	0.61	0.01	5.58
Plasmablasts	0.21	0.14	0.19	0.23	0.00	0.79	0.20	0.16	0.19	0.22	0.00	1.09
Transitional B Cells	0.21	0.18	0.18	0.23	0.00	1.07	0.17	0.14	0.16	0.18	0.00	0.81

Note. SD = standard deviation, CL = confidence limit