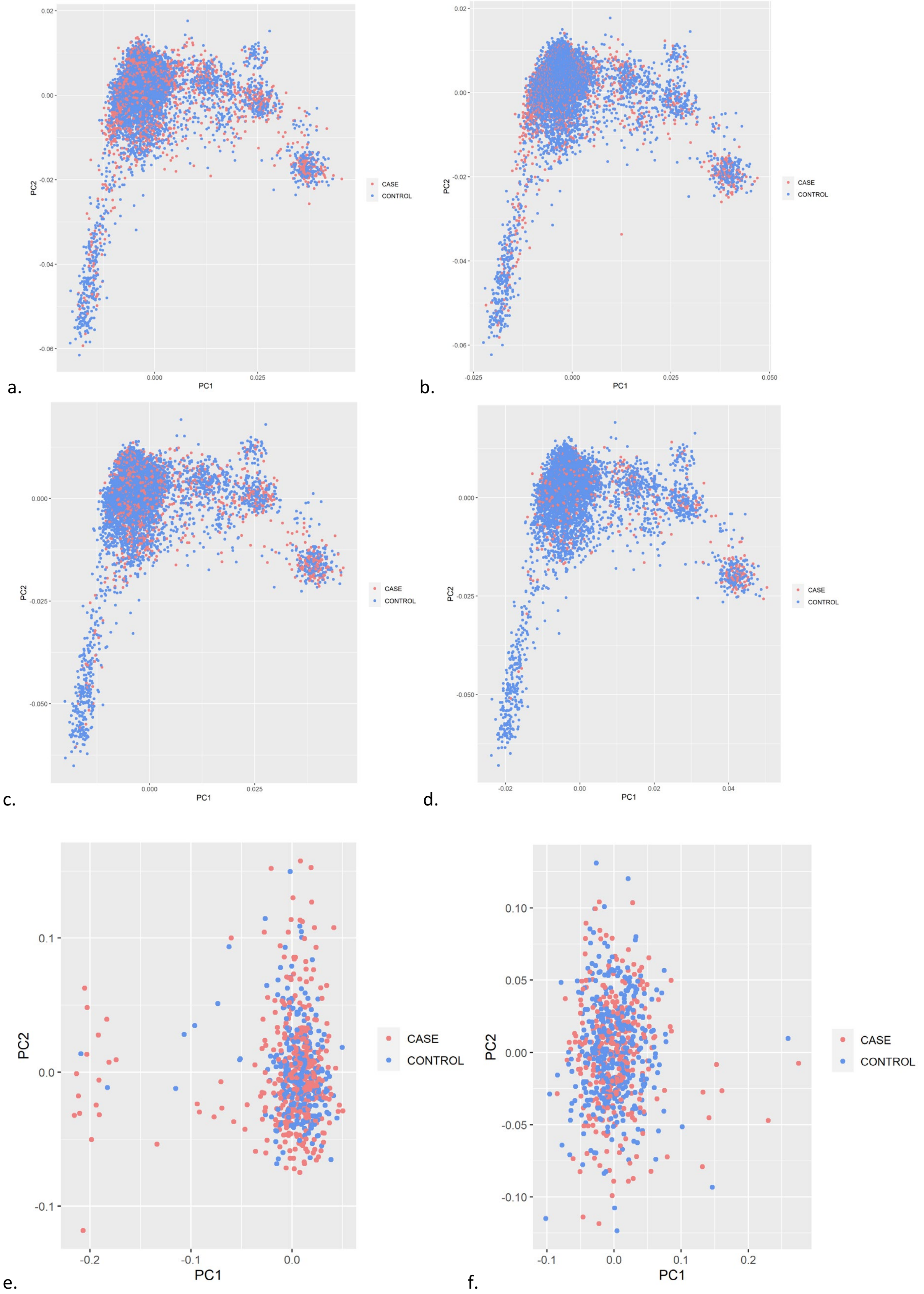
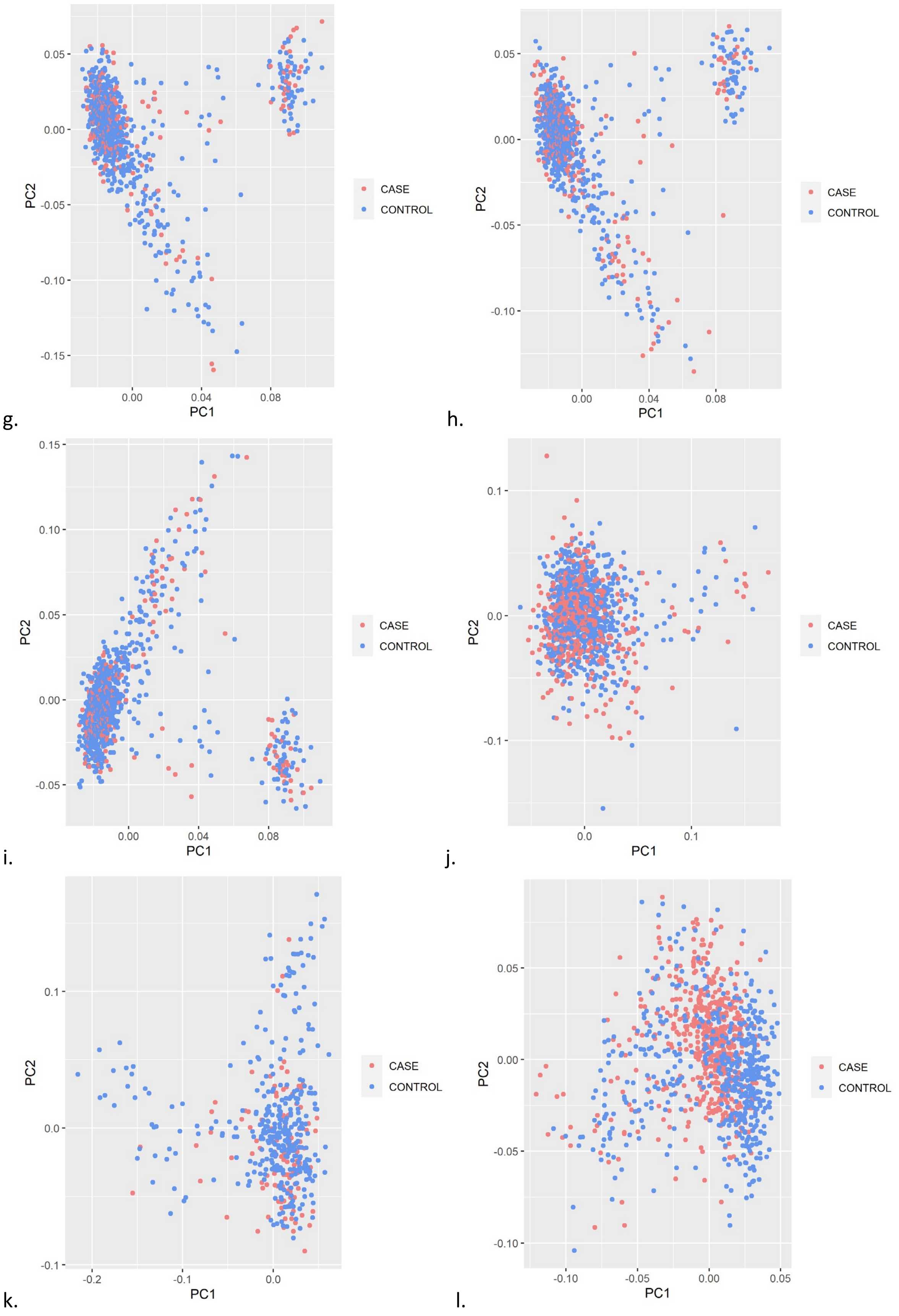
1. SUPPLEMENTARY FIGURES

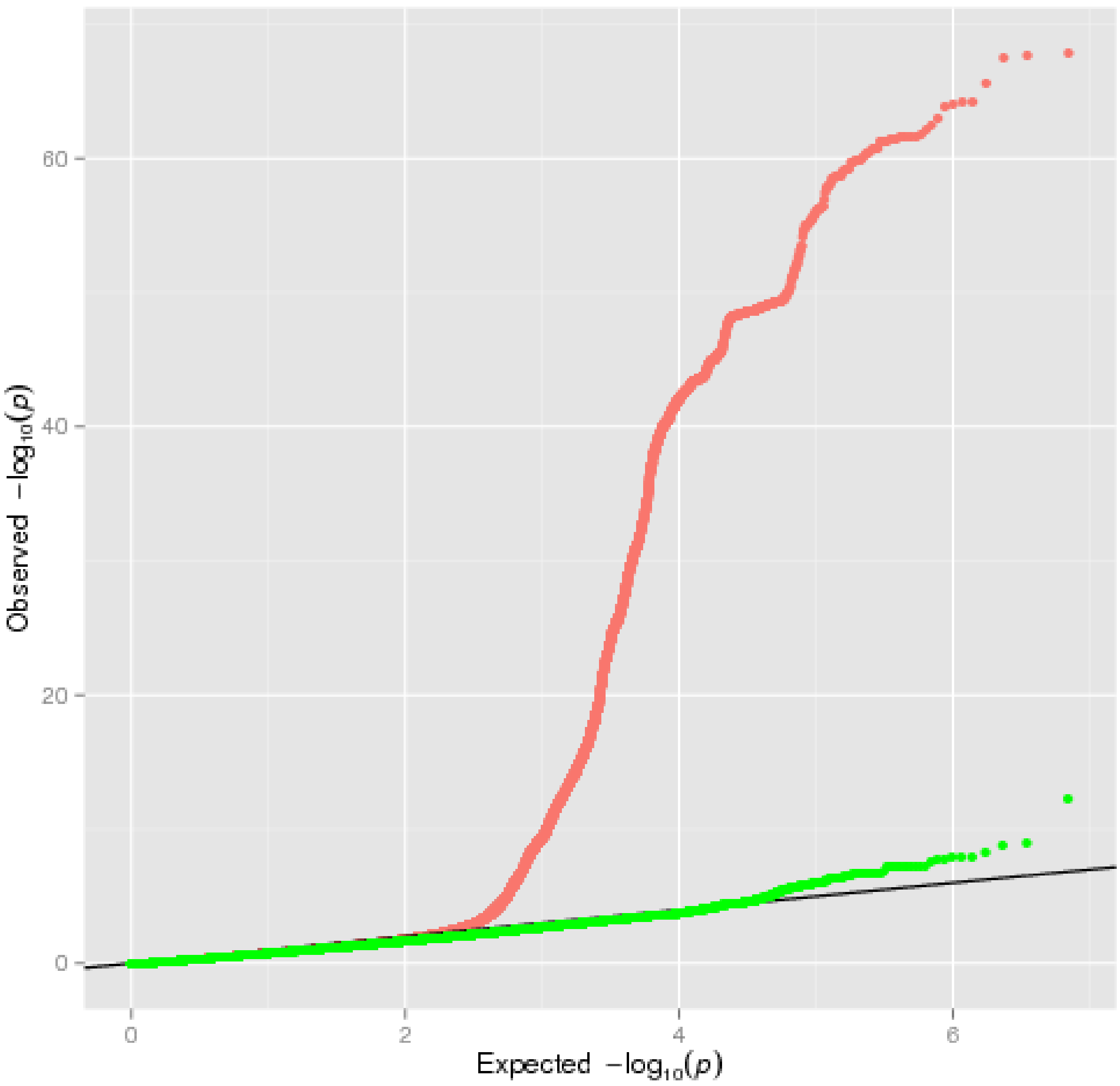


a. b. c. d. e. f.

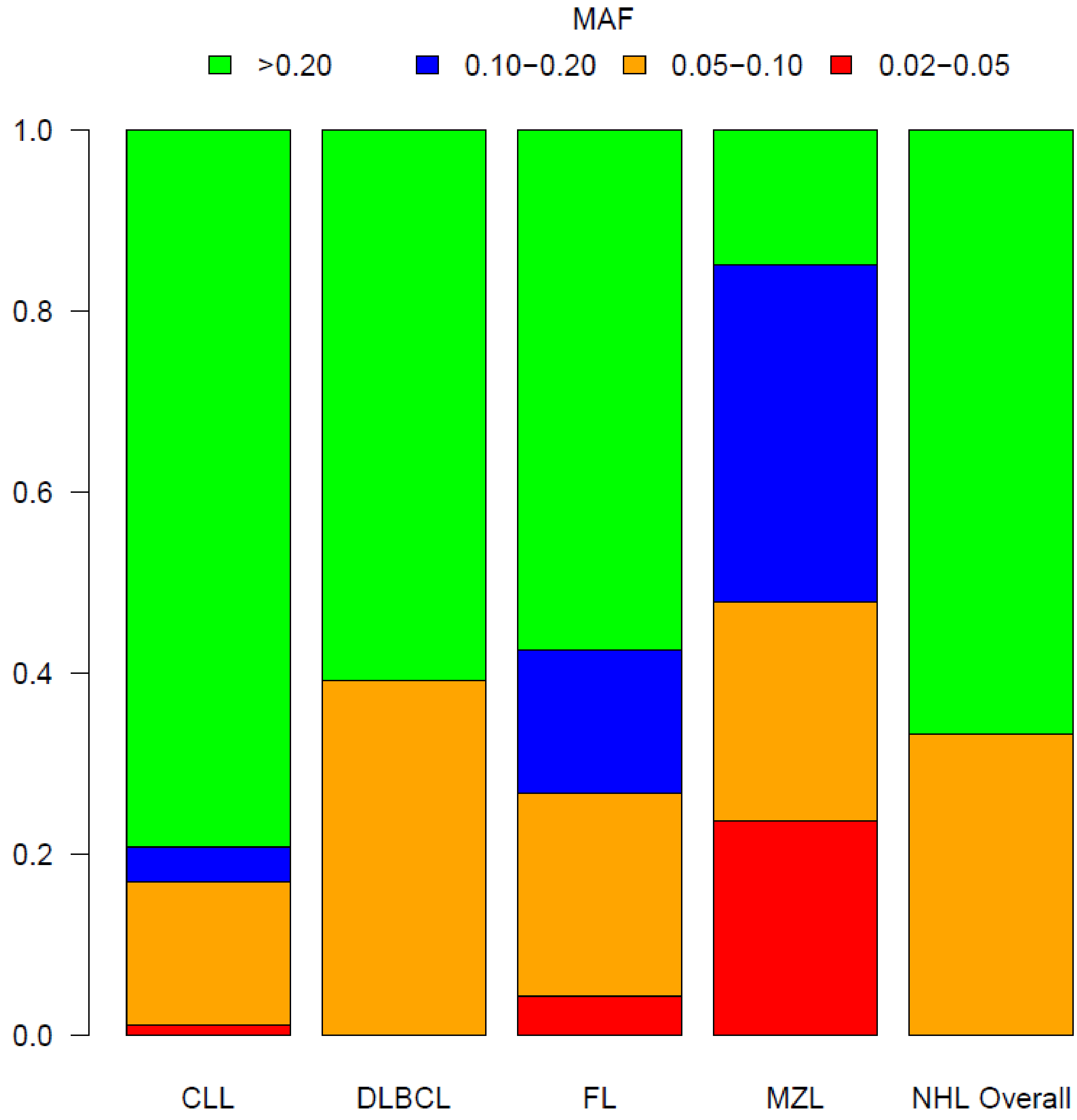
Supplementary Figure 1a-f. Plots of first two principal components (PC1 vs PC2) for each GWAS: a. NHL NCI GWAS (CLL), b. NHL NCI GWAS (DLBCL), c. NHL NCI GWAS (FL), d. NHL NCI GWAS (MZL), e. GEC, and f. USHER.



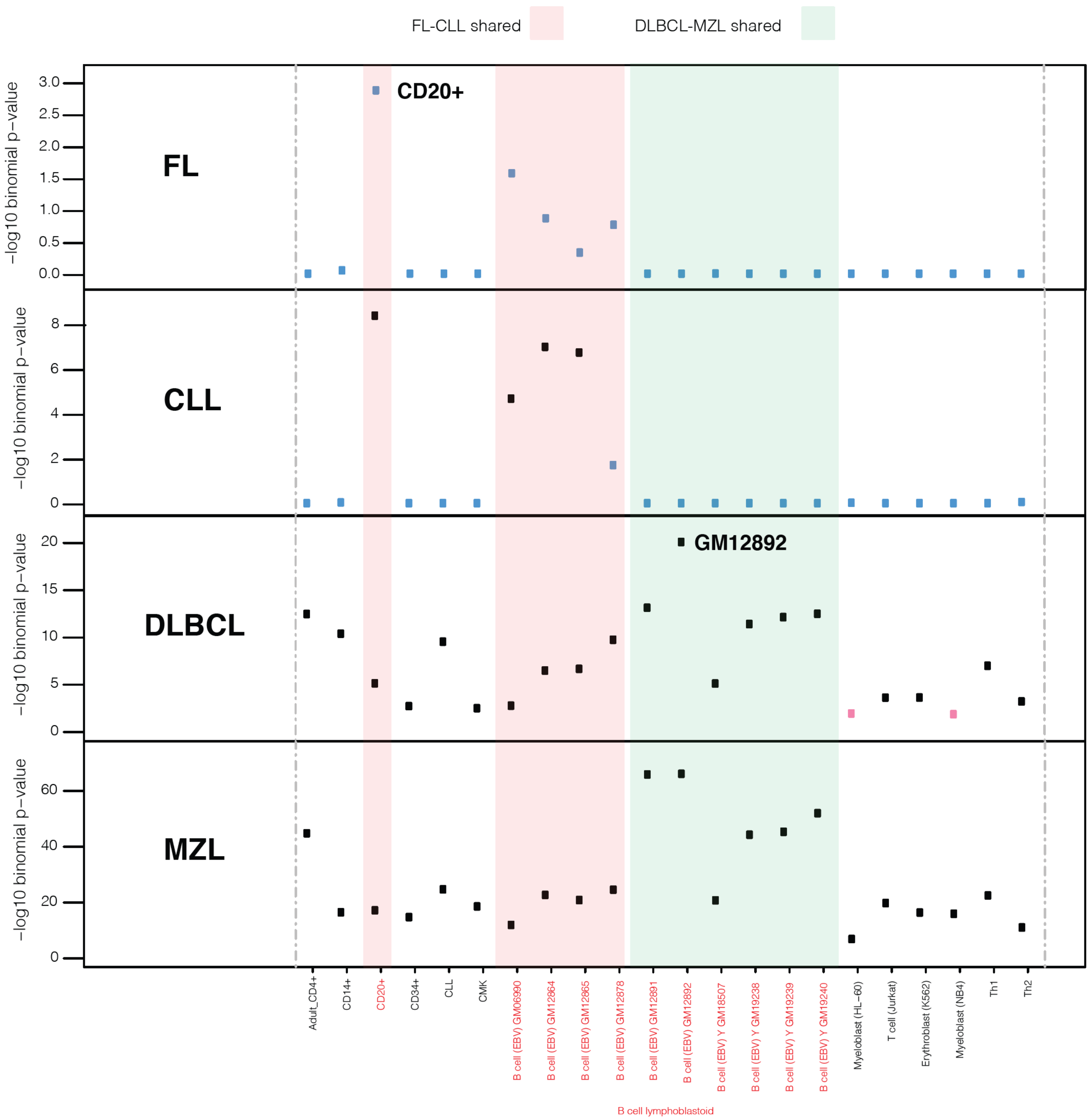
Supplementary Figure 1g-m. Plots of first two principal components (PC1 vs PC2) for each GWAS: g. UCSF2 (CLL), h. UCSF2 (DLBCL), i. UCSF2 (FL), j. SCALE, k. UCSF1/NHS, l. MAYO, and GELA/EPIC.



Supplementary Figure 2. Quantile-quantile (Q-Q) plot of the ASSET association p-values before (red; lambda=1.35) and after removing any SNPs within 500 kb of a previously established locus (green; lambda=0.79).



Supplementary Figure 3. Heritability portioned by minor allele frequency (MAF)



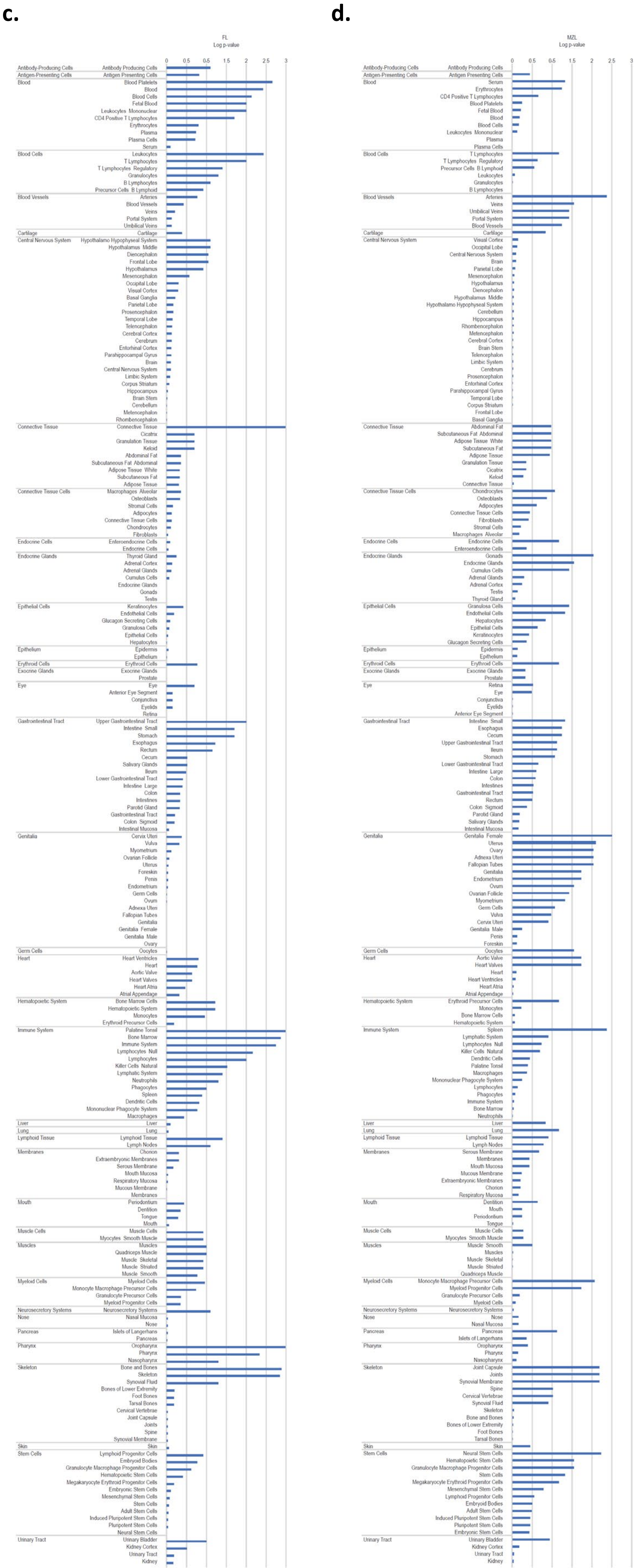
Supplementary Figure 4. FORGE2 analysis of DNase I enrichment in hematopoietic cells for specific NHL subtypes

a.


CLL
Log p-value
0
1
2
3
4
5
6
Antibody-Producing Cells
Antibody Producing Cells
Antigen-Presenting Cells
Antigen Presenting Cells
Blood
Blood
Blood Cells
Blood Platelets
CD4 Positive T Lymphocytes
Erythrocytes
Fetal Blood
Leukocytes Mononuclear
Plasma
Plasma Cells
Serum
Blood Cells
B Lymphocytes
Granulocytes
Leukocytes
Precursor Cells B Lymphoid
T Lymphocytes
T Lymphocytes Regulatory
Blood Vessels
Arteries
Blood Vessels
Portal System
Umbilical Veins
Veins
Cartilage
Cartilage
Central Nervous System
Basal Ganglia
Brain
Brain Stem
Central Nervous System
Cerebellum
Cerebral Cortex
Cerebrum
Corpus Striatum
Diencephalon
Entorhinal Cortex
Frontal Lobe
Hippocampus
Hypothalamo Hypophyseal System
Hypothalamus
Hypothalamus Middle
Limbic System
Mesencephalon
Metencephalon
Occipital Lobe
Parahippocampal Gyrus
Parietal Lobe
Prosencephalon
Rhombencephalon
Telencephalon
Temporal Lobe
Visual Cortex
Connective Tissue
Abdominal Fat
Adipose Tissue
Adipose Tissue White
Cicatrix
Connective Tissue
Granulation Tissue
Keloid
Subcutaneous Fat
Subcutaneous Fat Abdominal
Connective Tissue Cells
Adipocytes
Chondrocytes
Connective Tissue Cells
Fibroblasts
Macrophages Alveolar
Osteoblasts
Stromal Cells
Endocrine Cells
Endocrine Cells
Enteroendocrine Cells
Endocrine Glands
Adrenal Cortex
Adrenal Glands
Cumulus Cells
Endocrine Glands
Gonads
Testis
Thyroid Gland
Epithelial Cells
Endothelial Cells
Epithelial Cells
Glucagon Secreting Cells
Granulosa Cells
Hepatocytes
Keratinocytes
Epithelium
Epidermis
Epithelium
Erythroid Cells
Erythroid Cells
Exocrine Glands
Exocrine Glands
Prostate
Eye
Anterior Eye Segment
Conjunctiva
Eye
Eyelids
Retina
Gastrointestinal Tract
Cecum
Colon
Colon Sigmoid
Esophagus
Gastrointestinal Tract
Ileum
Intestinal Mucosa
Intestine Large
Intestine Small
Intestines
Lower Gastrointestinal Tract
Parotid Gland
Rectum
Salivary Glands
Stomach
Upper Gastrointestinal Tract
Genitalia
Adnexa Uteri
Cervix Uteri
Endometrium
Fallopian Tubes
Foreskin
Genitalia
Genitalia Female
Genitalia Male
Germ Cells
Myometrium
Ovarian Follicle
Ovary
Ovum
Penis
Uterus
Vulva
Germ Cells
Oocytes
Heart
Aortic Valve
Atrial Appendage
Heart
Heart Atria
Heart Valves
Heart Ventricles
Hematopoietic System
Bone Marrow Cells
Erythroid Precursor Cells
Hematopoietic System
Monocytes
Immune System
Bone Marrow
Dendritic Cells
Immune System
Killer Cells Natural
Lymphatic System
Lymphocytes
Lymphocytes Null
Macrophages
Mononuclear Phagocyte System
Neutrophils
Palatine Tonsil
Phagocytes
Spleen
Liver
Liver
Lung
Lung
Lymphoid Tissue
Lymph Nodes
Lymphoid Tissue
Membranes
Chorion
Extraembryonic Membranes
Membranes
Mouth Mucosa
Mucous Membrane
Respiratory Mucosa
Serous Membrane
Mouth
Dentition
Mouth
Periodontium
Tongue
Muscle Cells
Muscle Cells
Myocytes Smooth Muscle
Muscles
Muscle Skeletal
Muscle Smooth
Muscle Striated
Muscles
Quadriceps Muscle
Myeloid Cells
Granulocyte Precursor Cells
Monocyte Macrophage Precursor Cells
Myeloid Cells
Myeloid Progenitor Cells
Neurosecretory Systems
Neurosecretory Systems
Nose
Nasal Mucosa
Nose
Pancreas
Islets of Langerhans
Pancreas
Pharynx
Nasopharynx
Oropharynx
Pharynx
Skeleton
Bone and Bones
Bones of Lower Extremity
Cervical Vertebrae
Foot Bones
Joint Capsule
Joints
Skeleton
Spine
Synovial Fluid
Synovial Membrane
Tarsal Bones
Skin
Skin
Stem Cells
Adult Stem Cells
Embryoid Bodies
Embryonic Stem Cells
Granulocyte Macrophage Progenitor Cells
Hematopoietic Stem Cells
Induced Pluripotent Stem Cells
Lymphoid Progenitor Cells
Megakaryocyte Erythroid Progenitor Cells
Mesenchymal Stem Cells
Neural Stem Cells
Pluripotent Stem Cells
Stem Cells
Urinary Tract
Kidney
Kidney Cortex
Urinary Bladder
Urinary Tract

b.


DLBCL
Log p-value
0
0.5
1
1.5
2
2.5
3
Antibody-Producing Cells
Antibody Producing Cells
Antigen-Presenting Cells
Antigen Presenting Cells
Blood
Leukocytes Mononuclear
CD4 Positive T Lymphocytes
Blood
Blood Cells
Fetal Blood
Erythrocytes
Plasma Cells
Plasma
Blood Platelets
Serum
Blood Cells
T Lymphocytes
T Lymphocytes Regulatory
Leukocytes
B Lymphocytes
Precursor Cells B Lymphoid
Granulocytes
Blood Vessels
Portal System
Umbilical Veins
Veins
Blood Vessels
Arteries
Cartilage
Cartilage
Central Nervous System
Cerebellum
Rhombencephalon
Metencephalon
Brain Stem
Mesencephalon
Frontal Lobe
Corpus Striatum
Diencephalon
Basal Ganglia
Hypothalamus
Hypothalamo Hypophyseal System
Hypothalamus Middle
Occipital Lobe
Visual Cortex
Parietal Lobe
Central Nervous System
Brain
Temporal Lobe
Prosencephalon
Cerebrum
Telencephalon
Entorhinal Cortex
Parahippocampal Gyrus
Cerebral Cortex
Limbic System
Hippocampus
Connective Tissue
Connective Tissue
Cicatrix
Granulation Tissue
Keloid
Adipose Tissue
Subcutaneous Fat
Adipose Tissue White
Abdominal Fat
Subcutaneous Fat Abdominal
Connective Tissue Cells
Macrophages Alveolar
Connective Tissue Cells
Chondrocytes
Stromal Cells
Fibroblasts
Osteoblasts
Adipocytes
Endocrine Cells
Enteroendocrine Cells
Endocrine Cells
Endocrine Glands
Thyroid Gland
Adrenal Cortex
Adrenal Glands
Testis
Cumulus Cells
Endocrine Glands
Gonads
Epithelial Cells
Endothelial Cells
Keratinocytes
Epithelial Cells
Hepatocytes
Glucagon Secreting Cells
Granulosa Cells
Epithelium
Epidermis
Epithelium
Erythroid Cells
Erythroid Cells
Exocrine Glands
Exocrine Glands
Prostate
Eye
Anterior Eye Segment
Conjunctiva
Eyelids
Eye
Retina
Gastrointestinal Tract
Parotid Gland
Salivary Glands
Esophagus
Colon Sigmoid
Ileum
Upper Gastrointestinal Tract
Cecum
Intestinal Mucosa
Intestine Small
Stomach
Gastrointestinal Tract
Rectum
Colon
Intestine Large
Lower Gastrointestinal Tract
Intestines
Genitalia
Vulva
Genitalia Male
Cervix Uteri
Germ Cells
Penis
Foreskin
Ovum
Myometrium
Ovarian Follicle
Fallopian Tubes
Uterus
Endometrium
Genitalia
Genitalia Female
Ovary
Adnexa Uteri
Germ Cells
Oocytes
Heart
Heart Valves
Aortic Valve
Heart Ventricles
Heart
Atrial Appendage
Heart Atria
Hematopoietic System
Monocytes
Hematopoietic System
Bone Marrow Cells
Erythroid Precursor Cells
Immune System
Lymphocytes Null
Lymphocytes
Macrophages
Killer Cells Natural
Spleen
Mononuclear Phagocyte System
Lymphatic System
Dendritic Cells
Phagocytes
Immune System
Palatine Tonsil
Bone Marrow
Neutrophils
Liver
Liver
Lung
Lung
Lymphoid Tissue
Lymphoid Tissue
Lymph Nodes
Membranes
Mouth Mucosa
Chorion
Extraembryonic Membranes
Serous Membrane
Mucous Membrane
Membranes
Respiratory Mucosa
Mouth
Mouth
Periodontium
Dentition
Tongue
Muscle Cells
Muscle Cells
Myocytes Smooth Muscle
Muscles
Muscle Smooth
Muscles
Muscle Striated
Muscle Skeletal
Quadriceps Muscle
Myeloid Cells
Granulocyte Precursor Cells
Myeloid Progenitor Cells
Monocyte Macrophage Precursor Cells
Myeloid Cells
Neurosecretory Systems
Neurosecretory Systems
Nose
Nasal Mucosa
Nose
Pancreas
Islets of Langerhans
Pancreas
Pharynx
Pharynx
Oropharynx
Nasopharynx
Skeleton
Synovial Fluid
Joint Capsule
Joints
Synovial Membrane
Skeleton
Bone and Bones
Foot Bones
Tarsal Bones
Bones of Lower Extremity
Spine
Cervical Vertebrae
Skin
Skin
Stem Cells
Granulocyte Macrophage Progenitor Cells
Hematopoietic Stem Cells
Lymphoid Progenitor Cells
Stem Cells
Megakaryocyte Erythroid Progenitor Cells
Induced Pluripotent Stem Cells
Pluripotent Stem Cells
Adult Stem Cells
Neural Stem Cells
Mesenchymal Stem Cells
Embryonic Stem Cells
Embryoid Bodies
Urinary Tract
Urinary Bladder
Kidney Cortex
Kidney
Urinary Tract



Supplementary Figure 5. DEPICT analysis of gene expression across multiple cell types and tissues for genetic loci with $P < 1 \times 10^{-5}$ for a) CLL, b) DLBCL, c) FL, and d) MZL. Red indicates FDR <0.05.

Supplementary Table 1. Description of individual studies included in the NHL GWAS ASSET analysis and meta-analysis

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
NCI NHL GWAS (includes 22 studies)							
Alpha-Tocopherol, Beta-Carotene Cancer Prevention Study	ATBC	CLL-50 DLBCL-43 FL-17 MZL-1	240	Nested case-control, Finland	Identified through linkage to the Finnish Cancer Registry	Cohort participants without a diagnosis of cancer	**[PMID: 8205268]** The alpha-tocopherol, beta-carotene lung cancer prevention study: design, methods, participant characteristics, and compliance. The ATBC Cancer Prevention Study Group. *Ann Epidemiol* 1994 Jan;4(1):1-10.
American Cancer Society Cancer Prevention Study-II Nutrition Cohort	CPS-II	CLL-251 DLBCL-188 FL-141 MZL-52	220	Nested case-control, USA	Self-report through biannual questionnaires (starting in 1997). Verified by medical records or linkage to state cancer registry	Cohort participants alive at time of case diagnosis without cancer	**[PMID:11900235]** Calle EE. et al. The American Cancer Society Cancer Prevention Study II Nutrition Cohort: rationale, study design, and baseline characteristics. *Cancer* 2002;94:2490-501.
European Prospective Investigation into Cancer, Chronic Diseases, Nutrition and Lifestyles	EPIC	CLL-72 DLBCL-46 FL-46 MZL-8	265	Nested case-control, multiple European countries	Cases identified through population cancer registries in seven of the participating countries (Denmark, Italy, The Netherlands, Norway, Spain, Sweden and the UK) and through a combination of methods including health insurance records, cancer and pathology registries, and by active follow-up through study subjects and their next-of-kin in three countries (France, Germany and Greece)	Cohort participants matched by age, sex and study center who were alive and cancer-free at the time of diagnosis of the corresponding case	**[PMID:9126529]**Riboli E. et al. The EPIC Project: rationale and study design. European Prospective Investigation into Cancer and Nutrition. *Int J Epidemiol. Int J of Epidemiol* 1997;26(1):S6-14. **[PMID:12639222]** Riboli E. et al. European Prospective Investigation into Cancer and Nutrition (EPIC): study populations and data collection. *Public Health Nutr* 2002;5(6B):1113-24.
Health Professionals Follow-up Study	HPFS	CLL-19 DLBCL-12 FL-5 MZL-5	85	Nested case-control, USA	Self-report through bi-annual questionnaires. Verified by medical records and pathology report	Cohort participants alive at time of case diagnosis without cancer, matched on date of birth, ethnicity, date and time of day of blood collection, and fasting status	**[PMID: 1678444]** Rimm E. et al. Prospective study of alcohol consumption and risk of coronary disease in men. *Lancet* 1991;338:464-8.
The Melbourne Collaborative Cohort Study	MCCS	CLL-57 DLBCL-71 FL-58 MZL-8	75	Nested case-control, Australia	Incident cases ascertained through national cancer registries	Controls were unaffected cohort participants	**[PMID: 12484128]** Giles GG. et al. The Melbourne Collaborative Cohort Study. *IARC Sci Publ* 2002;156:69-70.

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
							[PMID: 28641380] Milne RL. et al. Cohort Profile: The Melbourne Collaborative Cohort Study (Health 2020)
Nurses' Health Study	NHS	CLL-18 DLBCL-28 FL-24 MZL-12	88	Nested case-control, USA	Self-report through bi-annual questionnaires. Verified by medical records and pathology report	Cohort participants alive at time of case diagnosis without cancer, matched on date of birth, ethnicity, date and time of day of blood collection, and fasting status	**[PMID: 15864280]** Colditz GA. et al. The Nurses' Health Study: lifestyle and health among women. *Nat Rev Cancer* 2005;5:388-96. **[PMID: 7658481]** Hankinson SE. et al. Alcohol, height and adiposity in relation to estrogen and prolactin levels in postmenopausal women. *J Natl Cancer Inst* 1995;87:1297-302.
New York University Women's Health Study	NYU-WHS	CLL-10 DLBCL-8 FL-11 MZL-6	53	Nested case-control, USA	Self-report through questionnaires every 2-4 years, confirmed by medical and pathology records; and linkages to tumor registries of NY, NJ and Florida and NDI	Cohort participants selected by incidence density sampling (alive and free of cancer at time of case diagnosis)	**[PMID: 7707406]** Toniolo P. et al. A prospective study of endogenous estrogens and breast cancer in postmenopausal women. *J Natl Cancer Inst* 1995; 87:190-7. **[PMID: 20373009]** Gu Y. et al. Circulating cytokines and risk of B-cell non-Hodgkin lymphoma: a prospective study. Cancer Causes Control 2010; 21(8):1323-33.
Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial	PLCO	CLL-278 DLBCL-153 FL-115 MZL-26	3076	Nested case-control, USA	Self-report through annual questionnaires. Verified by medical records and pathology report	Cohort participants alive at time of case diagnosis without cancer diagnosis	**[PMID: 20494998]** Troy JD, et al. Associations between anthropometry, cigarette smoking, alcohol consumption, and non-Hodgkin lymphoma in the Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial. *Am J Epidemiol* 2010;171:1270-81. **[PMID: 16054167]** Hayes RB et al. Methods for etiologic and early marker investigations in the PLCO trial. Mutat Res 2005;592:147-54.
Women's Health Initiative	WHI	CLL-226 DLBCL-240 FL-161 MZL-84	228	Nested case-control, USA	Self-report through semi-annual clinic visits or annual contact. Verified through medical records	Cohort participants without a diagnosis of cancer	**[PMID: 14575938]** Anderson GL, et al. Implementation of the Women's Health Initiative study design. *Ann Epidemiol* 2003 Oct;13(9 Suppl):S5-17.

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
British Columbia Non-Hodgkin Lymphoma Study	BC	CLL-26 DLBCL-92 FL-98 MZL-40	109	Population-based case-control study, Canada	First primary NHL diagnosis from Vancouver and Victoria metropolitan areas identified through the BC Cancer Registry (excluding HIV-infected and post-transplant cases)	Controls from the same areas, matched on area, age, and sex ascertained from the British Columbia Health Insurance files	**[PMID:17722095]** Spinelli JJ. et al. Organochlorines and risk of non-Hodgkin lymphoma. *Int J Cancer* 2007; 121(12):2767-75.
Epidemiology & Genetics Unit Lymphoma Case-Control study	ELCCS	CLL-0 DLBCL-229 FL-182 MZL-0	245	Population-based case-control study, UK	Cases were patients aged between 18-69 residing in predefined geographic areas and newly diagnosed with NHL between 1998 and 2003. Diagnoses were pathologically confirmed and coded to the WHO Classification for Oncology	For each case, one age- and sex- matched control was randomly selected from population based general practice registers	**[PMID: 15456990]** Willett EV. et al. Tobacco and alcohol consumption and the risk of non-Hodgkin lymphoma. *Cancer Causes Control* 2004;15:771-80. **[PMID: 19736055]** Worrillow L. et al. Polymorphisms in the nucleotide excision repair gene ERCC2/XPD and risk of non-Hodgkin lymphoma. Cancer Epidemiol 2009;33(3-4):257-60. **[PMID 20832384]** Crouch S. et al. Illness patterns prior to diagnosis of lymphoma: analysis of UK medical records. Cancer Epidemiol 2001;35(2):145-50.
Multicenter Italian study on gene-environment interactions in lymphoma etiology: translational aspects	Italian GxE	CLL-5 DLBCL-16 FL-16 MZL-6	45	Population-based case-control study, Italy	First primary NHL diagnosis identified in the Hematology Departments of the participating centers	Controls are randomly selected among residents in the study areas or among patients admitted for selected diagnosis in the referring hospital of the same areas of the respective cases, frequency matched to cases by gender, age, and residence	
National Cancer Institute-Surveillance, Epidemiology, and End Results Interdisciplinary Case-Control Study of Non-Hodgkin's Lymphoma	NCI-SEER	CLL-86 DLBCL-251 FL-217 MZL-62	270	Population-based case-control study, USA	First primary NHL diagnosis identified through 4 SEER registries (excluding HIV-infected cases)	Controls from the same areas, matched on area, age, and race ascertained though random digit dialing (<64 years of age) and CMMS files (≥65 years of age)	**[PMID: 15342441]** Chatterjee N. et al. Risk of non-Hodgkin's lymphoma and family history of lymphatic, hematology, and other cancers. *CEBP* 2004;13:1415-21. **[PMID: 17018637]** Wang SS. et al. Common genetic variants in proinflammatory and other

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
							immunoregulatory genes and risk for non-Hodgkin lymphoma. Cancer Res 2006;66(19):9771-80.
NSW non-Hodgkin lymphoma study	NSW	CLL-13 DLBCL-115 FL-146 MZL-34	154	Population-based case-control study, Australia	Incident NHL diagnosis identified through New South Wales (NSW) or Australian Capital Territory (ACT) cancer registry (excluding HIV-infected cases and transplant recipients)	Controls randomly selected from electoral rolls, matched on age, sex and State of residence at diagnosis	**[PMID: 15095310]** Hughes AM, et al. Pigmentary characteristics, sun sensitivity and non-Hodgkin lymphoma. *IJC* 2004;110:429-34.
Scandinavian Lymphoma Etiology Study	SCALE	CLL-395 DLBCL-405 FL-0 MZL-64	291	Population-based case-control study, Scandinavia	Patients with incident primary NHL diagnosed through rapid case-ascertainment network in Sweden and Denmark	Frequency matched (age in 10 year intervals, sex and country) population controls prospectively identified every 6 months in nationwide population registers (incidence density sampling).	**[PMID: 15687363]** Smedby KE. et al. Ultraviolet radiation exposure and risk of malignant lymphomas. *J Natl Cancer Inst* 2005;97(3)199-209.
Molecular Epidemiology of non-Hodgkin lymphoma	UCSF	CLL-22 DLBCL-38 FL-7 MZL-91	10	Population-based case-control study, USA	RCA/SEER Incident NHL diagnosis for patients diagnosed in hospitals in 6 San Francisco Bay Area Counties and who were residents of the Bay Area at the time of diagnosis	Controls ascertained through RDD were frequency matched to cases on age in 5-year groups, sex and county of residence; Random sampling of CMS lists for person residing in the same 6 Bay Area counties were used to supplement recruitment of controls aged 65+	[**PMID: 1863612**] Skibola CF. et al. Polymorphisms in the estrogen receptor 1 and vitamin C and matrix metalloproteinase gene families are associated with susceptibility to lymphoma. PLoS One 2008; 30;3(7):e2815.
Population-based case-control study in Connecticut women	Yale	CLL-39 DLBCL-126 FL-98 MZL-28	146	Population-based case-control study, USA	First primary NHL diagnosis identified through the Rapid Case Shared Resources from all the hospitals in Connecticut	Population-based controls through random digit dialing for cases <65 years and Medicare files for ≥65 years	**[PMID: 19822571]** Zhang Y et al. Genetic variations in xenobiotic metabolic pathway genes, personal hair dye use and risk of non-Hodgkin lymphoma. *Am J Epidemiol* 2009;170(10):1222-30.

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
Environmental and genetic risks factors study in adult lymphoma	ENGELA	CLL-44 DLBCL-56 FL-30 MZL-5	63	Hospital-based case-control study, France	Recent diagnosis of a NHL as per the WHO classification (ICD-O-3) / Cases with AIDS or on immunosuppressant drugs were not eligible. Path reports for 100%, slides review for selected NHL	Hospitalized in the same hospitals as the cases, for any reason except cancer, an accident or a disease directly related to the subject's occupation, smoking, or alcohol consumption. HIV negative.	**[PMID: 18781390]** Monnereau A. et al. Cigarette smoking, alcohol drinking, and risk of lymphoid neoplasms: results of a French case-control study. *Cancer Causes Control* 2008;19(10):1147-60.
Epilymph case-control study in six European countries	EpiLymph	CLL-158 DLBCL-198 FL-123 MZL-59	211	Multicenter case-control study, hospital-based and population-based, Europe	First primary lymphoma diagnosis (according to the 2001 WHO classification of lymphoma)	Controls from Germany and Italy were randomly selected by sampling from the general population, matched to cases on gender, 5-year age-group, and residence area. The rest of the centers used matched hospital controls, with eligibility criteria limited to diagnoses other than cancer, infectious diseases and immunodeficient diseases	**[PMID:16557575]** Besson H. et al. Tobacco smoking, alcohol drinking and non-Hodgkin's lymphoma: A European multicenter case-control study (Epilymph). *Int J Cancer* 2006;119:901-8.
Iowa-Mayo SPORE Molecular Epidemiology Resource	Iowa-Mayo SPORE	CLL-242 DLBCL-146 FL-228 MZL-112	0	Clinic-based case registry, USA	Consecutive patients with newly diagnosed, histologically-confirmed non-Hodgkin lymphoma (excluding HIV-infected cases) who were residents of US	N/A	**[PMID: 20713849]** Drake MT. et al. Vitamin D insufficiency and prognosis in non-Hodgkin's lymphoma. *J Clin Oncol* 2010;28:4191-8.
Mayo Clinic Case-Control Study of NHL and CLL	Mayo Case-Control	CLL-132 DLBCL-25 FL-245 MZL-75	343	Clinic-based case-control study, USA	Consecutive patients with newly diagnosed, histologically-confirmed non-Hodgkin lymphoma (excluding HIV-infected cases) who were residents of Minnesota, Iowa or Wisconsin	Controls were selected from patients seen in the general medicine clinics at Mayo with a pre-scheduled general medical examination, frequency on age, sex, and geographic region	**[PMID: 2168612]** Cerhan JR. et al. Design and validity of a clinic-based case-control study on the molecular epidemiology of lymphoma. *Int J Mol Epidemiol Genet* 2011;2(2):95-113.
Memorial-Sloan Kettering Lymphoproliferative disorders Study	MSKCC	CLL-36 DLBCL-175	4	Hospital-based case-study and NYCP controls, USA	Hospital clinic based ascertainment in a tertiary referral center	NYCP controls from same geographic area	**[PMID: 23349640]** Vijai J. et al. Susceptibility loci associated with specific and shared

Study Name	**Study Abbreviation**	**No. Cases**	**No. Controls**	**Design, location**	**Source of cases**	**Source of controls**	**Study Reference**
		FL-174 MZL-47					subtypes of lymphoid malignancies. *PLoS Genet* 2013;9(1):e1003220.
Genetic Epidemiology of CLL (GEC) Consortium GWAS	GEC	CLL-387	294	Family Study, USA	Eligible case probands with verified history of CLL in families were identified by investigators at Duke University, Mayo Clinic, the University of Texas M. D. Anderson Cancer Center, the National Cancer Institute (NCI), the University of Minnesota/Minneapolis Veterans Administration Medical Center, the University of California-San Diego, and the University of Utah	N/A	**[PMID: 21131588]** Slager SL, et al. Genome-wide association study identifies a novel susceptibility locus at 6p21.3 among familial CLL. *Blood* 2011;117:1911-16.
Molecular Epidemiology of non-Hodgkin lymphoma GWAS	UCSF2	CLL-213 DLBCL-254 FL-210	CLL-747 DLBCL-748 FL-746	Population-based case-control study, USA	RCA/SEER Incident NHL diagnosis for patients diagnosed in hospitals in 6 San Francisco Bay Area Counties and who were residents of the Bay Area at the time of diagnosis	Controls ascertained through RDD were frequency matched to cases on age in 5-year groups, sex and county of residence; Random sampling of CMS lists for person residing in the same 6 Bay Area counties were used to supplement recruitment of controls aged 65+	[**PMID: 19620980**] Conde L. et al. Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. *Nat Genet* 2010;42(8):661-4. **[PMID: 22697504]** Mikhak B. et al. Intake of vitamins d and a and calcium and risk of non-Hodgkin lymphoma: San Francisco Bay Area population-based case-control study. Nutr Cancer 2012;64(5):674-84.
Utah-Sheffield Hematology Epidemiology Research	USHER	CLL-321	405	Mixed: clinic- and population-based cases and controls, USA	Prevalent cases from Huntsman Cancer Hospital's Hematology Clinics and Prevalent cases identified in the Utah Cancer Registry, verified by medical records and pathology report	Controls from the same area frequency matched by sex and birth cohort using the Utah Population Database	
Mayo Clinic Case-Control Study of NHL and CLL and Iowa-Mayo SPORE Molecular Epidemiology Resource GWAS	MAYO	DLBCL-393	172	Clinic-based case-control study and clinic-based registry, USA	Consecutive patients with newly diagnosed, histologically-confirmed non-Hodgkin lymphoma (excluding HIV-infected cases) who were residents	Controls were selected from patients seen in the general medicine clinics at Mayo with a pre-scheduled general medical examination,	**[PMCID:PMC3110384]** Cerhan JR. et al. Design and validity of a clinic-based case-control study on the molecular epidemiology of lymphoma. Int J Mol Epidemiol Genet 2011;2(2):95-113.

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
					of Minnesota, Iowa or Wisconsin	frequency on age, sex, and geographic region	
Groupe d'Etude des Lymphomes de l'Adulte (GELA) /EPIC GWAS	GELA/EPIC	DLBCL-549	525	Cases from randomized clinical trial with population-based controls from EPIC	Patients recruited in the study that consented to DNA analysis	Participants from EPIC that were selected as controls for GWAS of breast and prostate cancer.	**[PMID: 22118442]** Récher C et al. Groupe d'Etude des Lymphomes de l'Adulte. Intensified chemotherapy with ACVBP plus rituximab versus standard CHOP plus rituximab for the treatment of diffuse large B-cell lymphoma (LNH03-2B): an open-label randomised phase 3 trial. Lancet. 2011 Nov 26;378(9806):1858-67. **[PMID: 23578722]** Delarue R, et al. A. Dose-dense rituximab-CHOP compared with standard rituximab-CHOP in elderly patients with diffuse large B-cell lymphoma (the LNH03-6B study): a randomised phase 3 trial. Lancet Oncol. 2013 May;14(6):525-33. **[PMID: 21482186]** Peyrade F, et al. Attenuated immunochemotherapy regimen (R-miniCHOP) in elderly patients older than 80 years with diffuse large B-cell lymphoma: a multicentre, single-arm, phase 2 trial. Lancet Oncol. 2011 May;12(5):460-8. **[PMID: 21546499]** Fitoussi O, et al. C. Survival impact of rituximab combined with ACVBP and upfront consolidation autotransplantation in high-risk diffuse large B-cell lymphoma for GELA. Haematologica. 2011 Aug;96(8):1136-43. **[PMID: 23235801]** Ketterer N,

Study Name	Study Abbreviation	No. Cases	No. Controls	Design, location	Source of cases	Source of controls	Study Reference
							et al. Phase III study of ACVBP versus ACVBP plus rituximab for patients with localized low-risk diffuse large B-cell lymphoma (LNH03-1B). Ann Oncol. 2013 Apr;24(4):1032-7. [PMID: 21743057] Schumacher et al. Genome-wide association study identifies new prostate cancer susceptibility loci. Hum Mol Genet. 2011 Oct 1;20(19):3867-75.
Scandinavian Lymphoma Etiology GWAS	SCALE	FL-376	791	Population-based case-control study, Scandinavia	Patients with incident primary NHL diagnosed through rapid case-ascertainment network in Sweden and Denmark	Frequency matched (age in 10-year intervals, sex and country) population controls prospectively identified every 6 months in nationwide population registers (incidence density sampling).	**[PMID: 15687363]** Smedby KE. et al. Ultraviolet radiation exposure and risk of malignant lymphomas. *J Natl Cancer Inst*. 2005;97(3)199-209.
Molecular Epidemiology of non-Hodgkin lymphoma GWAS	UCSF1/NHS	FL-119	349	Case series with population controls	RCA/SEER Incident NHL diagnosis for patients diagnosed in hospitals in 6 San Francisco Bay Area Counties and who were residents of the Bay Area at the time of diagnosis	Participants from the Nurses' Health Study that were selected as controls for a GWAS of endometrial cancer.	[PMID: 1863614] Skibola CF. et al. Polymorphisms in the estrogen receptor 1 and vitamin C and matrix metalloproteinase gene families are associated with susceptibility to lymphoma. *Plos One* 2008; 30;3(7):e2816. **[PMID: 12915497]** Holly EA. et al. Population-based study of non-Hodgkin lymphoma, histology, and medical history among human immunodeficiency virus-negative participants in San Francisco. *Am J Epidemiol* 2003; 158:316–27. **[PMID: 24096698]** De Vivo I et al. Genome-wide association study of endometrial ca*ncer* in E2C2. *Hum Genet* 2014; 133:211-24.

Supplementary Table 2. Characteristics of the cases and controls included in the NHL ASSET analysis and meta-analysis

	No. of subjects					% Male		Mean age (SD)	
Study	**CLL**	**DLBCL**	**FL**	**MZL**	**Controls**	**All Cases**	**Controls**	**All Cases**	**Controls**
NCI NHL	2,179	2,661	2,142	825	6,221	48.5%	72.8%	62 (12.6)	66 (10.1)
USCF2	213	254	210	0	748	57.2%	57.6%	62 (12.5)	61 (13.0)
GEC	387	0	0	0	294	65.1%	63.3%	61 (11.1)	63 (11.2)
USHER	321	0	0	0	405	59.8%	56.0%	63 (10.3)	64 (10.7)
MAYO	0	393	0	0	172	52.7%	38.4%	62 (14.4)	51 (13.7)
GELA/EPIC	0	549	0	0	525	57.0%	45.0%	59 (16.7)	58 (7.2)
SCALE	0	0	376	0	791	49.5%	31.7%	57 (9.5)	51 (11.6)
UCSF1/NHS	0	0	119	0	349	51.3%	0.0%	59 (12.9)	63 (8.6)
Total	**3,100**	**3,857**	**2,847**	**825**	**9,505**				

Supplementary Table 3. Information on genotyping, quality control, and imputation for studies included in the NHL ASSET analysis and meta-analysis

Study		Sample QC			Genotyping and Imputation							
		Inclusion/exclusion criteria			Platform	Genotype calling algorithm	Inclusion criteria for Imputation			SNPs that met QC criteria	SNPs in meta-analysis	Lambda
	No. of cases/ controls in file	Minimum sample call rate for inclusion	Exclusions	No.cases/ controls after exclusions			MAF	SNP Call rate*	P for HWE			
NCI NHL	8370/6390[a]	>=93%	1) Abnormal heterozygosity; 2) gender discordance; 3) unexpected duplicates; 4) Non CEU	7807/6221	Illumina OmniExpress/ Omni2.5	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	611844	21,554,489	1.026 (CLL) 1.016 (DLBCL) 1.022 (FL) 1.013 (MZL)
GEC	391/296	>=95%	1) Non CEU ; 2) PCA outliers	387/294	Affymetrix 6.0	Birdseed	>= 0.01	>=0.95	>=1e-6	687578	8,499,108	1.027
USHER	331/420	>=95%	1) Abnormal heterozygosity; 2) Non CEU; 3) Incomplete phenotype	321/405	Illumina HumanHap 610K	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	512171	8,476,283	1.021
UCSF2	683/751	>=95%	1) Abnormal heterozygosity; 2) PCA outlier	677/748	Illumina HumanCNV370 -Duo	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	290523	15,085,856	1.032 (CLL) 1.011 (DLBCL) 1.023 (FL)
SCALE	379/791	>=95%	Unexpected duplicates	376/791	Illumina HumanHap 317K	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	298045	14,205,416	1.026
UCSF1/NHS	120/349	>=95%	Incomplete phenotype	119/349	Illumina OmniExpress	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	614320	12,776,022	1.010
Mayo	398/172	>=95%	Non CEU	393/172	Illumina HumanHap 660W	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	523949	11,880,085	1.021
GELA/EPIC	754/928	>=95%	1) Non CEU; 2) NHL NOS subtype; 3) Controls not geneticall matched to cases based on PCA	549/525	Illuminaa HumanHap 610K and 660W	BeadStudio (GenCall)	>= 0.01	>=0.95	>=1e-6	513264	14,149,132	1.100

Supplementary Table 4. Description of individual studies included in the replication of NHL ASSET results

Study Name	**Study Abbreviation**	**No. Cases**	**No. Controls**	**Design, location**	**Source of cases**	**Source of controls**	**Study Reference**
Mayo Clinic Case-Control Study of NHL	Mayo Case-Control	CLL-308 DLBCL-305 FL-341 MZL-150	763	Clinic-based case-control study, USA	Consecutive patients with newly diagnosed, histologically-confirmed non-Hodgkin lymphoma (excluding HIV-infected cases) who were residents of Minnesota, Iowa or Wisconsin	Controls were selected from patients seen in the general medicine clinics at Mayo with a pre-scheduled general medical examination, frequency on age, sex, and geographic region	**[PMID: 21686124]** Cerhan JR. et al. Design and validity of a clinic-based case-control study on the molecular epidemiology of lymphoma. *Int J Mol Epidemiol Genet* 2011;2(2):95-113.
MD Anderson lymphoma case-control study	MD Anderson	CLL-645 DLBCL-374 FL-543 MZL-76	914	Case-control, USA	MD Anderson Cancer Center	Kelsey Seybold Clinics	
Memorial-Sloan Kettering Lymphoproliferative disorders Study	MSKCC	CLL-308 DLBCL-580 FL-467 MZL-228	368	Hospital-based case-study and NYCP controls, USA	Hospital clinic based ascertainment in a tertiary referral center	NYCP controls from same geographic area	**[PMID: 23349640]** Vijai J. et al. Susceptibility loci associated with specific and shared subtypes of lymphoid malignancies. *PLoS Genet*. 2013;9(1):e1003220.
Multicase-control study in Spain	MCC-Spain	CLL-143	140	Case-Control Study, Spain	Identified through medical records and/or cytogenetics laboratories in the hospital participating in the study	Participants without personal history of lymphoprolyferative disorder from the general population and frequency matched to CLL by age, sex and area of residence	**[PMID: 25613680]** Population-based multicase-control study in common tumors in Spain (MCC-Spain): rationale and study design. *Gac Sanit*. 2015 Jul-Aug;29(4):308-15

Supplementary Table 5. Characteristics of the cases and controls included in the replication for the ASSET analysis

	No. of subjects					% Male		Mean age (SD)	
Study	**CLL**	**DLBCL**	**FL**	**MZL**	**Controls**	**All Cases**	**Controls**	**All Cases**	**Controls**
Mayo Case-Control	308	305	341	150	763	58.5%	57.1%	62 (13)	62 (12)
MD Anderson	645	374	543	76	914	58.0%	64.4%	58 (12)	62(10)
MSKCC	308	580	467	228	368	52.8%	50.8%	58 (14)	53 (12)
MCC-Spain	143	0	0	0	140	51.20%	48.80%	67 (11)	67 (10)
Total	**1,404**	**1,259**	**1,351**	**454**	**2,185**				

Supplementary Table 6. Risk of four NHL subtypes and NHL overall associated with established loci for different lymphoid malignancies[1,2,3]

Locus	Nearest gene	Published SNP	Position (hg19)	Subtype	Published OR	Reference	Effect / Other allele	CLL OR	CLL P	DLBCL OR	DLBCL P	FL OR	FL P	MZL OR	MZL P	NHL OR	NHL P
CLL Published Loci																	
1p36.11	*MDS2*	rs34676223	23,943,735	CLL	1.19	Law PJ et al.	C/A	1.13	0.0003	1.01	0.76	1.00	1.00	0.97	0.56	1.05	0.05
1q42.13	*RHOU*	rs41271473	228,880,296	CLL	1.19	Law PJ et al.	G/A	1.14	0.0005	1.01	0.70	1.02	0.70	1.06	0.35	1.06	0.02
2p22.2	*QPCT*	rs3770745	37,596,089	CLL	1.24	Berndt et al.	T/C	1.22	1.36E-07	1.12	0.001	1.12	0.005	1.20	0.008	1.15	**3.22E-08**
2q13	*ACOXL*	rs13401811	111,616,104	CLL	1.41	Berndt et al.	G/A	1.41	4.08E-17	1.04	0.31	1.01	0.77	1.26	0.0009	1.14	2.66E-06
2q13	*ACOXL*	rs17483466	111,797,458	CLL	1.39	Di Bernardo et al.	G/A	1.39	5.96E-18	1.06	0.14	1.05	0.20	1.06	0.39	1.16	**2.47E-08**
2q13	*BCL2L11*	rs9308731	111,908,262	CLL	1.19	Berndt et al.	A/G	1.19	4.71E-08	1.08	0.01	**1.19**	**2.08E-07**	1.01	0.83	1.13	**2.31E-09**
2q33.1	*CASP8*	rs3769825	202,111,380	CLL	1.19	Berndt et al.	T/C	1.18	2.08E-07	1.05	0.14	1.03	0.32	1.17	0.005	1.09	0.0001
2q37.1	*SP140*	rs13397985	231,091,223	CLL	1.41	Di Bernardo et al.	G/T	1.47	6.17E-23	0.97	0.51	1.05	0.25	1.12	0.11	1.13	2.51E-06
2q37.3	*FARP2*	rs757978	242,371,101	CLL	1.39	Crowther-Swanepoel et al.	T/C	1.29	3.15E-07	0.91	0.05	1.04	0.45	0.92	0.33	1.06	0.08
3p24.1	*EOMES*	rs9880772	27,777,779	CLL	1.19	Berndt et al.	T/C	1.17	7.77E-07	**1.16**	**8.02E-07**	**1.15**	**3.30E-05**	1.14	0.01	1.15	**3.49E-11**
3q26.2	*MYNN*	rs10936599	169,492,101	CLL	1.27	Speedy et al.	C/T	1.16	5.01E-05	1.04	0.26	1.06	0.16	1.04	0.58	1.09	0.0006
3q28	*LPP*	rs9815073	188,115,682	CLL	1.18	Berndt et al.	C/A	1.20	5.35E-07	1.01	0.72	1.00	0.94	1.11	0.10	1.06	0.02
4q24	*BANK1*	rs71597109	102,741,002	CLL	1.17	Law PJ et al.	C/T	1.16	2.04E-05	1.03	0.32	0.94	0.10	1.08	0.22	1.05	0.05
4q25	*LEF1*	rs898518	109,016,824	CLL	1.20	Berndt et al.	A/C	1.17	4.57E-07	1.06	0.07	1.03	0.39	1.11	0.07	1.09	5.09E-05
4q35.1	*LOC728175*	rs57214277	185,254,772	CLL	1.13	Law PJ et al.	T/C	1.16	9.41E-06	0.96	0.21	0.91	0.009	0.99	0.82	1.01	0.63
5p15.33	*TERT*	rs10069690	1,279,790	CLL	1.20	Speedy et al.	T/C	1.21	5.56E-07	1.08	0.04	1.00	1.00	1.08	0.21	1.09	0.001
6p21.31	*BAK1*	rs210142	33,546,837	CLL	1.40	Slager et al.	C/T	1.20	1.59E-07	1.03	0.31	1.00	0.98	1.12	0.07	1.08	0.0008
6p21.31	*C6orf106*	rs3800461	34,616,322	CLL	1.20	Law PJ et al.	C/G	1.19	0.0003	1.14	0.004	1.07	0.17	1.01	0.91	1.14	8.49E-05
6p21.32	*HLA-DQB1*	rs9273363	32,626,272	CLL	1.26	Berndt et al.	A/C	1.26	3.66E-11	1.03	0.49	1.04	0.31	1.05	0.44	1.10	9.65E-05
6p25.2	*SERPINB6*	rs73718779	2,969,278	CLL	1.26	Berndt et al.	A/G	1.27	6.22E-07	1.05	0.26	1.04	0.43	1.04	0.62	1.10	0.004
6p25.3	*IRF4*	rs872071	411,064	CLL	1.54	Di Bernardo et al.	G/A	1.35	1.32E-21	1.07	0.03	1.00	0.95	1.00	0.95	1.13	**2.98E-09**
6q25.2	*IPCEF1, OPRM1*	rs2236256	154,478,440	CLL	1.23	Speedy et al.	C/A	1.05	0.12	0.96	0.21	0.99	0.81	0.92	0.13	1.00	0.98
7q31.33	*POT1*	rs17246404	124,462,661	CLL	1.22	Speedy et al.	C/T	1.11	0.002	0.99	0.66	1.02	0.53	1.01	0.83	1.04	0.07
8q22.3	*ODF1*	rs2511714	103,578,874	CLL	1.16	Speedy et al.	G/T	1.19	2.16E-07	1.01	0.83	1.01	0.79	0.88	0.02	1.05	0.02
8q24.21	*CASC19*	rs2456449	128,192,981	CLL	1.26	Crowther-Swanepoel et al.	G/A	1.25	1.98E-11	0.98	0.48	1.02	0.56	1.01	0.85	1.07	0.003
9p21.3	*CDKN2B-AS1*	rs1679013	22,206,987	CLL	1.19	Berndt et al.	C/T	1.20	1.84E-08	1.01	0.81	1.02	0.59	1.04	0.50	1.07	0.003
10q23.31	*ACTA2,FAS*	rs4406737	90,759,724	CLL	1.27	Berndt et al.	G/A	1.27	9.06E-14	1.05	0.13	1.12	0.0009	0.99	0.92	1.12	9.09E-08
11p15.5	*C11orf21*	rs7944004	2,311,152	CLL	1.20	Berndt et al.	T/G	1.18	8.61E-08	1.04	0.22	1.04	0.23	1.02	0.78	1.08	0.0005
11q23.2	*TMPRSS5*	rs61904987	113,517,203	CLL	1.24	Law PJ et al.	T/C	1.20	0.0002	1.04	0.41	1.02	0.71	1.18	0.07	1.08	0.02
11q24.1	*GRAMD1B*	rs735665	123,361,397	CLL	1.45	Di Bernardo et al.	A/G	1.65	1.10E-39	1.09	0.02	1.03	0.43	1.23	0.003	1.23	**1.54E-15**

Locus	Nearest gene	Published SNP	Position (hg19)	Subtype	Published OR	Reference	Effect / Other allele	CLL OR	CLL P	DLBCL OR	DLBCL P	FL OR	FL P	MZL OR	MZL P	NHL OR	NHL P
12q24.13	*OAS3*	rs10735079	113,380,008	CLL	1.18	Sava et al.	G/A	1.11	0.0009	1.03	0.30	0.98	0.48	1.03	0.58	1.04	0.05
15q15.1	*BMF*	rs8024033	40,403,657	CLL	1.22	Berndt et al.	C/G	1.21	1.76E-09	1.05	0.12	0.98	0.60	1.03	0.64	1.07	0.0009
15q21.3	*MNS1*	rs11636802	56,775,597	CLL	1.41	Berndt et al.	G/A	1.41	6.47E-13	1.12	0.02	1.11	0.04	1.07	0.45	1.20	**3.35E-08**
15q23	*PCAT29*	rs7176508	70,018,990	CLL	1.37	Di Bernardo et al.	A/G	1.31	8.36E-18	0.96	0.20	0.92	0.008	0.97	0.58	1.04	0.08
16q24.1	*IRF8*	rs391525	85,944,439	CLL	1.82	Slager et al.	A/G	1.32	2.09E-16	1.04	0.20	1.04	0.28	0.96	0.52	1.13	1.39E-07
16q24.1	*IRF8*	rs305061	85,975,659	CLL	1.22	Crowther-Swanepoel et al.	T/C	1.16	1.18E-05	1.01	0.63	0.99	0.81	1.05	0.41	1.05	0.02
18q21.1	*CXXC1*	rs1036935	47,843,534	CLL	1.15	Law PJ et al.	A/G	1.15	0.0002	0.99	0.70	0.99	0.77	0.90	0.11	1.03	0.25
18q21.32	*PMAIP1*	rs4368253	57,622,287	CLL	1.19	Berndt et al.	C/T	1.18	7.90E-07	1.01	0.75	1.02	0.64	1.09	0.16	1.07	0.006
18q21.33	*BCL2*	rs4987855	60,793,549	CLL	1.47	Berndt et al.	G/A	1.45	6.74E-11	1.15	0.007	**1.35**	**3.63E-07**	0.98	0.79	1.27	**2.30E-10**
18q21.33	*BCL2*	rs4987852	60,793,921	CLL	1.41	Berndt et al.	G/A	1.43	1.61E-09	1.15	0.02	1.25	0.0007	1.04	0.69	1.25	6.45E-08
19p13.3	*ZBTB7A*	rs7254272	4,069,119	CLL	1.17	Law PJ et al.	A/G	1.13	0.003	1.01	0.86	0.95	0.27	0.97	0.64	1.03	0.36
19q13.32	*PRKD2*	rs11083846	47,207,654	CLL	1.35	Di Bernardo et al.	A/G	1.10	0.01	0.96	0.28	1.02	0.65	0.99	0.83	1.02	0.40
22q13.33	*TYMP, ODF3B*	rs140522	50,971,266	CLL	1.15	Law PJ et al.	T/C	1.16	1.18E-05	1.08	0.02	1.06	0.09	1.05	0.44	1.09	6.14E-05
DLBCL Published Loci																	
2p23.3	*NCOA1*	rs79480871	24,694,472	DLBCL	1.34	Cerhan et al	T/C	1.17	0.02	1.40	8.25E-08	1.20	0.009	1.14	0.26	1.24	7.16E-07
6p21.33	*HLA-B*	rs2523607	31,322,790	DLBCL	1.32	Cerhan et al	A/T	**1.18**	**0.0006**	1.34	3.35E-09	1.03	0.49	**1.69**	**3.17E-08**	1.19	1.21E-06
6p25.3	*EXOC2*	rs116446171	484,453	DLBCL	2.20	Cerhan et al	G/C	1.23	0.08	2.36	4.33E-19	1.42	0.004	1.82	0.002	1.60	**1.90E-11**
8q24.21	*PVT1*	rs13255292	129,076,573	DLBCL	1.22	Cerhan et al	T/C	1.00	0.96	1.22	4.19E-10	**1.19**	**6.51E-07**	1.07	0.27	1.13	**3.67E-08**
8q24.21	*MIR1208*	rs4733601	129,269,466	DLBCL	1.18	Cerhan et al	A/G	1.06	0.06	1.19	6.03E-09	1.12	0.0009	1.12	0.04	1.12	**3.87E-08**
FL Published Loci																	
3q28	*LPP*	rs6444305	188,299,902	FL	1.21	Skibola et al	G/A	0.91	0.02	1.04	0.31	1.19	2.94E-06	1.02	0.70	1.04	0.11
6p21.32	*HLA region*	rs114137077 (rs17203612)	32,446,853	FL	1.84	Skibola et al	T/A	1.02	0.53	1.05	0.14	1.80	1.09E-66	0.89	0.05	1.20	**2.89E-16**
6p21.33	*HLA region*	rs116413016 (rs3130437)	31,220,895	FL	1.33	Skibola et al	C/A	1.04	0.18	**1.14**	**1.77E-05**	1.32	4.26E-16	1.06	0.31	1.14	**1.40E-09**
8q24.21	*PVT1*	rs13254990	129,076,451	FL	1.18	Skibola et al	T/C	1.00	0.94	**1.22**	**4.53E-10**	1.20	2.65E-07	1.07	0.28	1.14	**2.15E-08**
11q23.3	*CXCR5*	rs4938573	118,741,842	FL	1.34	Skibola et al	C/T	0.95	0.23	1.07	0.06	1.32	4.73E-12	1.00	0.96	1.10	0.0004
11q24.3	*ETS1*	rs4937362	128,492,739	FL	1.19	Skibola et al	T/C	1.10	0.003	1.01	0.68	1.20	2.06E-08	0.96	0.47	1.08	0.0001
18q21.33	*BCL2*	rs17749561	60,783,211	FL	1.34	Skibola et al	G/A	**1.44**	**9.04E-11**	1.16	0.006	1.36	1.31E-07	1.02	0.80	1.28	**7.64E-11**
MZL Published Loci																	
6p21.32	*BTNL2*	rs116502008 (rs9461741)	32,370,587	MZL	2.66	Vijai et al	C/G	1.07	0.55	**1.42**	**0.0002**	**1.77**	**6.62E-08**	2.40	9.11E-08	1.40	8.08E-07
6p21.33	*HLA-B*	rs116778584 (rs2922994)	31,335,901	MZL	1.64	Vijai et al	G/A	**1.22**	**4.51E-05**	**1.29**	**8.12E-07**	1.04	0.42	1.74	2.89E-08	1.19	2.04E-06
Waldenström Macroglobulinemia Published Loci																	
6p25.3	*EXOC2*	rs116446171	484,453	WM	21.14	McMaster M	G/C	1.23	0.08	**2.36**	**4.33E-19**	1.42	0.004	1.82	0.002	1.60	**1.90E-11**

Locus	Nearest gene	Published SNP	Position (hg19)	Subtype	Published OR	Reference	Effect / Other allele	CLL OR	CLL P	DLBCL OR	DLBCL P	FL OR	FL P	MZL OR	MZL P	NHL OR	NHL P
14q32.13	GLRX5	rs117410836	96,051,974	WM	4.9	McMaster M	C/T	1.16	0.15	1.14	0.17	1.21	0.07	1.31	0.14	1.13	0.08
Multiple Myeloma Published Loci																	
2p23.3	*DTNB*	rs7577599	25,613,146	MM	1.24	Broderick P, Mitchell JS	T/C	0.98	0.60	1.04	0.27	0.94	0.13	1.09	0.22	1.01	0.80
2q31.1	SP3	rs4325816	174,808,899	MM	1.12	Went M	T/C	1.06	0.15	1.07	0.07	1.12	0.003	1.10	0.14	1.07	0.005
3p22.1	*ULK4*	rs1052501	41,925,398	MM	1.32	Broderick P	G/A	1.05	0.22	1.03	0.40	1.00	0.94	0.98	0.83	1.04	0.19
3q26.2	*MYNN*	rs10936599	169,492,101	MM	1.26	Chubb D	G/A	**1.16**	**5.01E-05**	1.04	0.26	1.06	0.16	1.04	0.58	1.09	0.0006
5q15	*ELL2*	rs56219066	95,242,931	MM	1.25	Swaminathan B	T/C	1.05	0.20	1.00	0.89	1.05	0.17	0.97	0.62	1.03	0.28
5q23.2	CEP120	rs6595443	122,743,325	MM	1.11	Went M	T/A	1.06	0.06	1.02	0.59	1.09	0.01	0.97	0.57	1.04	0.07
6p21	*ATG5*	rs9372120	106,667,535	MM	1.18	Mitchell JS	G/T	0.98	0.67	1.02	0.64	1.07	0.11	1.13	0.08	1.03	0.33
6p21.33	*PSORS1C1*	rs2285803	31,107,258	MM	1.19	Chubb D	A/G	0.98	0.51	**0.88**	**0.0002**	**0.82**	**4.70E-08**	0.96	0.50	0.90	1.52E-05
6p22.3	*JARID2*	rs34229995	15,244,018	MM	1.37	Mitchell JS	G/C	1.30	0.01	1.21	0.06	1.11	0.34	1.23	0.29	1.16	0.03
7p15.3	*DNAH11*	rs4487645	21,938,240	MM	1.38	Broderick P	C/A	1.03	0.40	1.00	0.93	1.00	0.91	1.04	0.54	1.01	0.59
7q22.3	CCDC71L	rs17507636	106,291,118	MM	1.12	Went M	C/T	1.00	0.90	0.99	0.75	1.02	0.53	1.00	0.96	1.01	0.82
7q31.33	POT1-AS1	rs58618031	124,583,896	MM	1.12	Went M	T/C	1.11	0.002	1.01	0.77	1.03	0.50	1.05	0.44	1.05	0.03
7q36.1	*SMARCD3*	rs7781265	150,950,940	MM	1.19	Mitchell JS	T/C	0.98	0.74	1.00	0.98	0.94	0.22	0.89	0.17	0.98	0.51
8q24.21	*CCAT1*	rs1948915	128,222,421	MM	1.13	Mitchell JS	C/T	**1.15**	**3.50E-05**	1.02	0.60	1.02	0.52	1.02	0.79	1.05	0.03
9p21.3	*CDKN2A*	rs2811710	21,991,923	MM	1.15	Mitchell JS	G/A	**1.18**	**7.27E-07**	1.02	0.58	1.06	0.11	1.18	0.003	1.09	0.0002
10p12.1	*WAC*	rs2790457	28,856,819	MM	1.12	Mitchell JS	G/A	1.00	0.91	1.05	0.15	1.01	0.71	0.92	0.19	1.02	0.41
11q13.3	*CCND1*	rs9344 (rs603965)	69,462,910	MM t(11;4)	1.82	Weinhold N	G/A	0.98	0.46	0.94	0.04	1.01	0.73	1.00	0.93	0.98	0.25
16p11.2	LOC730183	rs13338946	30,700,858	MM	1.15	Went M	C/T	0.98	0.64	0.99	0.85	0.99	0.72	0.92	0.20	0.98	0.35
16q23.1	*RFWD3*	rs7193541	74,664,743	MM	1.13	Mitchell JS	T/C	**1.11**	**0.0006**	1.02	0.43	0.98	0.58	1.03	0.59	1.05	0.03
17p11.2	*TNFRSF13B*	rs4273077	16,849,139	MM	1.26	Chubb D	G/A	0.89	0.02	0.99	0.79	0.96	0.46	1.14	0.13	0.96	0.25
19p13.11	KLF2	rs11086029	16,438,661	MM	1.14	Went M	T/A	1.04	0.26	0.97	0.43	0.92	0.03	1.01	0.93	0.98	0.42
20q13.13	*PREX1*	rs6066835	47,355,009	MM	1.26	Mitchell JS	C/T	0.97	0.57	0.90	0.04	1.04	0.53	1.08	0.40	0.98	0.59
22q13	*TOM1*	rs138740	35,699,582	MM	1.18	Swaminathan B, Mitchell JS	C/T	0.95	0.15	1.02	0.51	0.99	0.80	0.96	0.53	0.99	0.52
22q13.1	*CBX7*	rs877529	39,542,292	MM	1.23	Chubb D	A/G	0.96	0.15	0.99	0.66	0.99	0.81	0.96	0.51	0.98	0.26
Acute Lymphoblastic Leukemia Published Loci																	
2q22.3	TEX41	rs17481869	146,124,454	ALL (ETV6-RUNX1)	2.14	Vijayakrishnan J	A/C	1.06	0.37	0.98	0.71	1.04	0.55	1.34	0.006	1.03	0.47
3q28	*TP63*	rs17505102	189,401,776	ALL (ETV6-RUNX1)	1.59	Ellinghaus E	G/C	0.95	0.28	0.92	0.06	1.08	0.14	1.00	0.98	0.98	0.57
7p12.2	*IKZF1*	rs11978267	50,466,304	ALL	1.69	Trevino LR	G/A	1.10	0.008	1.03	0.32	1.01	0.78	1.05	0.40	1.05	0.05
7p15.3	SP4	rs2390536	21,485,397	ALL	1.18	Wiemels et al	A/G	1.00	0.99	1.03	0.36	1.04	0.24	0.99	0.84	1.02	0.35

Locus	Nearest gene	Published SNP	Position (hg19)	Subtype	Published OR	Reference	Effect / Other allele	CLL OR	CLL P	DLBCL OR	DLBCL P	FL OR	FL P	MZL OR	MZL P	NHL OR	NHL P
8q24.21	LINC00977	rs28665337	130,194,104	ALL	1.34	Vijayakrishnan J	A/C	1.00	0.98	0.97	0.52	0.95	0.27	1.06	0.51	0.98	0.50
9p21.3	*CDKN2A*	rs3731249	21,970,916	ALL	2.23	Xu H (2015)	T/C	1.03	0.73	1.02	0.83	0.93	0.46	0.97	0.86	0.97	0.57
9p21.3	*CDKN2A*	rs3731217	21,984,661	ALL	1.41	Sherborne AL	G/T	**0.79**	**5.76E-07**	0.91	0.03	0.92	0.07	0.84	0.02	0.88	1.92E-05
10p12.2	*PIP4K2A*	rs10828317 (rs2230469)	22,839,628	ALL	1.23	Xu H (2013), Migliorini G	T/C	1.00	0.99	1.01	0.73	1.06	0.09	0.96	0.43	1.02	0.47
10p14	*GATA3*	rs3824662	8,104,208	ALL	1.31	Migliorini G, Perez-Andreu V (2013)	T/G	0.92	0.05	0.98	0.58	0.96	0.31	1.05	0.52	0.95	0.09
10q21.2	*ARID5B*	rs10821936	63,723,577	ALL	1.91	Trevino LR, Xu H	C/T	0.91	0.008	1.01	0.85	1.02	0.63	0.95	0.33	0.98	0.42
10q26.13	*LHPP*	rs35837782	126,293,309	ALL	1.21	Vijayakrishnan J	G/A	1.00	0.96	1.09	0.009	1.07	0.04	1.05	0.37	1.05	0.03
11q12.1	*OR5AL1*	rs1945213	56,175,671	ALL (ETV6-RUNX1)	1.28	Ellinghaus E	G/C	0.97	0.43	1.01	0.83	0.95	0.16	0.97	0.64	0.98	0.37
12q23.1	*ELK3*	rs4762284	96,612,762	ALL	1.19	Vijayakrishnan J	T/A	0.99	0.72	0.99	0.71	1.02	0.67	1.01	0.92	1.00	0.87
14q11.2	*CEBPE*	rs2239633	23,589,057	ALL	1.34	Papaemmanuil E, Migliorini G	G/A	0.99	0.86	0.99	0.80	0.98	0.62	1.00	0.96	0.99	0.59
17q12	GSDMB/ IKZF3	rs2290400	38,066,240	ALL	1.17	Wiemels et al	T/C	0.99	0.64	0.99	0.76	0.93	0.02	1.05	0.40	0.97	0.16
Hodgkin Lymphoma Published Loci																	
2p16.1	*LINC01185*	rs1432295	61,066,666	HL	1.22	Enciso-Mora V	G/A	1.06	0.09	1.04	0.21	0.96	0.21	1.13	0.03	1.03	0.21
3p24.1	*EOMES*	rs3806624	27,764,623	HL	1.26	Frampton M	G/A	1.16	**2.34E-06**	**1.16**	**7.28E-07**	**1.15**	**2.46E-05**	1.14	0.02	1.15	**5.59E-11**
3q28	LPP	rs4459895	187,954,414	HL	1.30	Sud A	A/C	0.98	0.69	1.05	0.20	**1.26**	**1.71E-07**	0.98	0.78	1.09	0.01
5q31.1	*IL13*	rs20541	131,995,964	HL	1.47	Urayama KY	A/G	1.03	0.45	0.99	0.72	1.01	0.73	0.98	0.81	1.01	0.79
6p21.31	IP6K3; UQCC2	rs649775	33,684,313	HL	1.29	Sud A	A/G	1.09	0.13	1.10	0.09	0.95	0.42	1.10	0.35	1.04	0.32
6p21.32	*HLA-DRA*	rs6903608	32,428,285	HL	1.70	Cozen W, Enciso-Mora V, Frampton M	G/A	0.92	0.01	0.93	0.02	**0.64**	**1.48E-34**	1.05	0.44	0.85	**2.08E-13**
6p21.32	*HLA-DPB1*	rs2281389	33,059,796	HL	1.64	Moutsianas L	C/T	1.06	0.13	0.94	0.12	0.86	0.0009	0.84	0.02	0.94	0.05
6p21.33	*MICB*	rs2248462	31,446,796	HL	1.64	Urayama KY	G/A	1.01	0.86	1.06	0.12	**0.85**	**2.54E-05**	1.13	0.07	0.97	0.22
6q22.33	PTPRK	rs9482849	128,288,536	HL	1.20	Sud A	C/T	1.09	0.06	1.01	0.85	0.97	0.56	0.93	0.37	1.02	0.56
6q23.3	*HBS1L*	rs7745098	135,415,004	HL	1.21	Frampton M	G/A	1.02	0.60	1.05	0.14	1.02	0.47	1.00	0.95	1.02	0.39
6q23.3	AHI1	rs6928977	135,626,348	HL	1.17	Sud A	G/T	1.03	0.36	1.05	0.13	1.03	0.36	1.05	0.34	1.03	0.18
6q23.3	OLIG3	rs1002658	137,981,584	HL	1.19	Sud A	T/C	0.98	0.68	1.03	0.50	1.03	0.47	0.87	0.06	1.01	0.72
8q24.21	*MIR1208*	rs2019960	129,192,271	HL	1.33	Enciso-Mora V	G/A	0.97	0.48	1.06	0.09	1.01	0.85	0.97	0.63	1.01	0.82
10p14	*GATA3-AS1*	rs501764	8,093,034	HL	1.39	Enciso-Mora V, Frampton M	C/A	1.04	0.31	1.06	0.12	1.10	0.02	1.07	0.35	1.09	0.002
10p14	GATA3	rs3781093	8,101,927	HL	1.28	Sud A	T/C	1.09	0.06	1.00	0.95	1.07	0.15	1.02	0.83	1.05	0.09
11q23.1	POU2AF1	rs7111520	111,249,611	HL	1.19	Sud A	A/G	0.89	0.0009	1.04	0.27	0.98	0.62	0.88	0.03	0.97	0.13
13q34	UPF3A	rs112998813	115,059,729	NSHL	1.39	Sud A	C/T	1.00	0.97	1.03	0.58	0.97	0.60	1.00	0.99	0.99	0.86

Locus	Nearest gene	Published SNP	Position (hg19)	Subtype	Published OR	Reference	Effect / Other allele	CLL OR	CLL P	DLBCL OR	DLBCL P	FL OR	FL P	MZL OR	MZL P	NHL OR	NHL P
16p11.2	CORO1A	rs6565176	30,174,926	HL	1.16	Sud A	T/C	1.03	0.33	1.03	0.38	1.02	0.64	0.99	0.86	1.02	0.39
16p13.13	CLEC16A	rs34972832	11,198,938	NSHL	1.24	Sud A	A/G	0.89	0.002	1.08	0.04	1.09	0.03	1.05	0.48	1.02	0.39
19p13.3	*TCF3*	rs1860661	1,650,134	HL	1.23	Cozen W	A/G	0.96	0.27	1.06	0.06	1.10	0.008	1.05	0.40	1.03	0.14
20q13.12	NCOA5	rs2425752	44,702,120	HL	1.15	Sud A	T/C	1.00	0.92	1.09	0.01	1.05	0.17	1.06	0.35	1.04	0.08
Published Loci for NHL, LM or Subsets of LM																	
3q22.2	*NCK1*	rs11715604 (rs67060434)	136,589,549	CLL,HL	-	Law PJ et al.	T/A	1.02	0.69	1.01	0.82	1.02	0.74	0.89	0.15	1.01	0.84
3q27.3	*BCL6 - LPP-AS2*	rs6773854	187,649,419	BCELL	1.44	Tan DE	C/T	1.05	0.24	1.07	0.08	1.11	0.009	1.01	0.85	1.06	0.01
6p21.32	*TRNAI25*	rs4530903	32,581,889	NHL	1.37	Vijai J	T/C	0.78	7.39E-07	1.21	3.41E-05	1.93	3.88E-42	1.03	0.77	1.19	**3.14E-08**
11q12.1	*OR10Q2P*	rs12289961	58,060,192	LM	1.29	Vijai J	T/C	1.02	0.62	0.99	0.82	1.02	0.66	1.02	0.75	1.01	0.73

[1] Based on GWAS meta-analysis results for CLL (3,100 cases, 7668 controls), DLBCL (3,857 cases, 7,666 controls), FL (2,847 cases, 8,109 controls), and MZL (825 cases, 6,221 controls).

Red bold indicates remained significant after adjustment for multiple testing for that particular subtype

Black bold for NHL risk indicates $P < 5x10^{-8}$

Supplementary Table 7. Loci discovered to be associated with one or more NHL subtypes in the ASSET analysis ($P< 5 \times 10^{-8}$)

Locus	Nearest gene	SNP	Position	Contributing subtypes (direction of association)	Contributing subtypes with P<0.01* (direction of association)	OR†	P
Novel loci							
10q23.1	*SH2D4B*	rs9421684	82462346	DLBCL(+), FL(+), MZL(+)	DLBCL(+), FL(+), MZL(+)	1.21	2.40E-08
Previously subtype-specific loci							
2q13	*ACOXL*	rs72832868	111607676	CLL(+), MZL(+)	CLL(+), MZL(+)	1.36	1.49E-14
2q37.1	*SP140*	rs7557418	231098071	CLL(+), DLBCL(-)	CLL(+)	1.47	2.76E-20
2q37.3	*FARP2, SEPT2*	rs3755397	242294913	CLL(+), DLBCL(-), MZL(-)	CLL(+)	1.36	4.64E-09
3p24.1	*EOMES*	rs4680838	27783476	CLL(+), DLBCL(+), FL(+), MZL(+)	CLL(+), FL(+), DLBCL(+)	1.16	2.69E-09
3q13.33	*CD86*	rs2681416	121817613	DLBCL(+), FL(+), MZL(-)	DLBCL(+), FL(+)	1.20	1.26E-09
6p21.32	*HLA-DQA1*	rs28383311	32587011	FL(+), CLL(-), MZL(-)	FL(+), CLL(-)	1.91	1.66E-68
6p21.33	*TNXB*	rs12524664	32029431	FL(+), CLL(-), MZL(-)	FL(+)	1.75	5.87E-18
6p25.3	*IRF4*	rs872071	411064	CLL(+), FL(-), MZL(-)	CLL(+)	1.35	2.40E-19
8q24.21	*CASC19*	rs2445610	128197088	CLL(+), DLBCL(-)	CLL(+)	1.25	1.92E-10
8q24.21	*PVT1*	rs13254990	129076451	DLBCL(+), FL(+)	DLBCL(+), FL(+)	1.21	5.10E-11
10q23.31	*FAS*	rs4406737	90759724	CLL(+), MZL(-)	CLL(+)	1.27	4.79E-11
11q23.3	*CXCR5*	rs4936441	118725660	FL(+), CLL(-)	FL(+)	1.33	7.69E-11
11q24.1	*GRAMD1B*	rs34057425	123341589	CLL(+), FL(-)	CLL(+)	1.49	7.04E-22
15q23	*PCAT29*	rs11072113	70018281	CLL(+), FL(-)	CLL(+)	1.32	2.26E-17
16q24.1	*IRF8*	rs11649318	85946481	CLL(+), MZL(-)	CLL(+)	1.32	1.97E-14
18q21.33	*BCL2*	rs17676949	60785638	CLL(+), FL(+)	CLL(+), FL(+)	1.41	4.63E-12

*Includes only those contributing subtypes with an association P<0.01 for that SNP

†Odds ratio for the positive association

Supplementary Table 8. Association results for four SNPs taken forward for replication after ASSET analysis

						Discovery			Replication			Joint Analysis		
Chr	**Nearest gene(s)**	**SNP**	**Position**	**Risk/ Other allele**	**Subtype**	**No. Cases/ No. controls**	**OR**	**P**	**No. Cases/ No. controls**	**OR**	**P**	**No. Cases/ No. controls**	**OR**	**P**
10q23.1	*SH2D4B*	rs9421684	82462346	A/G	DLBCL	3,857/7,666	1.17	2.00E-05	1,211/2,014	1.01	0.85	5,068/9,680	1.13	0.0001
					FL	2,846/8,106	1.22	1.35E-06	1,314/2,014	0.93	0.28	4,160/10,120	1.13	0.0004
					MZL	825/6,221	1.31	8.91E-05	445/2,014	1.06	0.58	1,270/8,235	1.22	0.0004
					Combined	7,528/8,803	1.21	2.40E-08	2,970/2,014	0.98	0.77	10,498/10,817	1.14	6.08E-06
1p31.1	*DNAJB4*	rs34517439	78450517	A/C	CLL	3,096/7,663	1.30	1.56E-06	1,394/2,082	1.13	0.12	4,490/9,745	1.24	1.39E-06
					DLBCL	3,855/7,662	1.20	0.0009	1,245/1,942	0.80	0.02	5,100/9,604	1.08	0.09
					FL	2,843/8,103	1.28	3.18E-05	1,333/1,942	0.98	0.80	4,176/10,045	1.17	0.001
					Combined	9,794/9,490	1.26	7.32E-07	3,972/2,082	0.99	0.83	13,766/11,572	1.15	0.0001
1q44	*CNST*	rs12127426	246809307	T/C	DLBCL	3,853/7,664	1.30	1.95E-06	1,214/2,029	1.05	0.62	5,067/9,693	1.24	1.12E-05
					FL	2,845/8,105	1.26	0.0002	1,322/2,029	1.03	0.75	4,167/10,134	1.19	0.001
					MZL	825/6,221	1.37	0.002	442/2,029	1.01	0.94	1,267/8,250	1.24	0.01
					Combined	7,523/8,800	1.29	8.84E-07	2,978/2,029	1.04	0.63	10,501/10,829	1.21	1.38E-05
10q23.33	*HHEX*	rs11187157	94502244	C/T	CLL	3,097/7,664	1.16	4.00E-06	1,376/2,142	1.27	4.36E-06	4,473/9,806	**1.19**	**2.05E-10**
					FL	2,845/8,105	1.15	5.36E-05	1,336/2,002	1.06	0.30	4,181/10,107	1.12	7.84E-05
					MZL	825/6,221	1.15	0.01	431/2,002	1.06	0.47	1,256/8,223	1.12	0.01
					Combined	6,767/8,800	1.16	9.70E-07	3,143/2,142	1.15	0.0009	9,910/10,942	**1.15**	**3.27E-09**

Supplementary Table 9. Loci associated with risk of B-cell NHL ($P < 5 \times 10^{-8}$) based on a meta-analysis of four NHL subtypes (CLL, DLBCL, FL, and MZL)

Locus	Nearest gene	SNP	Position	No cases / no controls	Risk allele	Other allele	RAF	OR (95% CI)	P
Previously reported loci									
2p22.2	*QPCT*	rs3770745	37596089	10,621/9,496	T	C	0.22	1.15 (1.10-1.21)	3.22E-08
2q13	*BCL2L11*	rs6708784	111927379	10,625/9,499	G	A	0.48	1.16 (1.11-1.21)	4.30E-12
3p24.1	*EOMES*	rs4680838	27783476	10,624/9,498	G	A	0.47	1.15 (1.10-1.20)	3.07E-11
3q13.33	*CD86*	rs9831894	121800487	10,627/9,503	A	C	0.60	1.14 (1.09-1.19)	1.43E-09
6p21.32	*HLA-DQB1*	rs3134987	32642050	10,621/9,496	T	A	0.74	1.25 (1.19-1.31)	4.89E-19
6p21.33	*MSH5, MSH5-SAPCD1*	rs3130487	31723389	10,628/9,499	T	C	0.85	1.21 (1.13-1.28)	1.49E-09
6p22.1	*HLA-G*	rs9258811	29832526	10,625/9,499	T	C	0.74	1.17 (1.12-1.23)	1.06E-10
6p25.3	*EXOC2*	rs116446171	484453	10,625/9,499	G	C	0.02	1.60 (1.39-1.83)	1.90E-11
8q24.21	*PVT1*	rs34642439	129070955	10,627/9,501	G	A	0.40	1.13 (1.08-1.18)	9.20E-09
11q24.1	*GRAMD1B*	rs35923643	123355391	10,622/9,497	G	A	0.19	1.23 (1.17-1.30)	9.55E-16
15q21.3	*MNS1*	rs16976932	56781255	10,622/9,498	A	G	0.11	1.21 (1.14-1.29)	5.79E-09
16q24.1	*IRF8*	rs375288	85927871	10,621/9,498	G	A	0.67	1.15 (1.10-1.21)	5.63E-10
18q21.33	*BCL2*	rs17676949	60785638	10,625/9,498	G	A	0.91	1.28 (1.19-1.38)	7.11E-11
Failed to Replicate (see Supplementary Table 8)									
1p31.1	*DNAJB4*	rs34517439	78450517	10,622/9,496	A	C	0.11	1.23 (1.14-1.32)	1.76E-08
10q23.1	*SH2D4B*	rs9421684	82462346	10,628/9,503	A	G	0.19	1.19 (1.13-1.25)	2.39E-11

Supplementary Table 10. Loci associated with risk of lymphoid malignancy ($P < 5x10^{-8}$) based on meta-analysis of NHL, MM, and HL

Locus	Nearest gene	SNP	Position	Study	Effect allele	Other allele	OR	CI	P
Previously reported loci									
2p22.2	*QPCT*	rs3770745	37596089	NHL	T	C	1.15	(1.10-1.21)	3.22E-08
				MM	T	C	1.07	(0.93-1.22)	0.3437
				Combined	**T**	**C**	**1.14**	**(1.09-1.20)**	**3.62E-08**
2q13	*BCL2L11*	rs3789068	111909247	NHL	G	A	1.16	(1.11-1.21)	6.62E-12
				MM	G	A	1.01	(0.90-1.12)	0.9231
				HL	G	A	1.10	(1.01-1.19)	0.025903
				Combined	**G**	**A**	**1.13**	**(1.09-1.17)**	**1.22E-11**
2q37.1	*SP140*	rs6436922	231098040	NHL	G	A	1.14	(1.08-1.20)	6.72E-07
				MM	G	A	1.24	(1.08-1.42)	0.002498
				Combined	**G**	**A**	**1.15**	**(1.10-1.21)**	**1.11E-08**
3p24.1	*EOMES*	rs3806624	27764623	NHL	G	A	1.15	(1.10-1.20)	5.59E-11
				MM	G	A	1.02	(0.92-1.14)	0.6972
				HL	G	A	1.17	(1.08-1.27)	0.000229
				Combined	**G**	**A**	**1.14**	**(1.10-1.18)**	**4.64E-13**
3q13.33	*CD86*	rs9831894	121800487	NHL	C	A	0.88	(0.84-0.91)	1.43E-09
				MM	C	A	0.96	(0.86-1.08)	0.5209
				HL	C	A	0.92	(0.85-1.00)	0.048624
				Combined	**C**	**A**	**0.89**	**(0.86-0.93)**	**7.48E-10**
6p25.3	*EXOC2*	rs76106586	483593	NHL	G	A	1.59	(1.39-1.82)	2.76E-11
				MM	G	A	1.02	(0.67-1.56)	0.9228
				Combined	**G**	**A**	**1.53**	**(1.34-1.74)**	**1.94E-10**
6p22.1	*HLA-H, HLA-G*	rs9258807	29832481	NHL	C	T	0.85	(0.81-0.89)	1.29E-10
				MM	C	T	0.93	(0.68-1.28)	0.6751
				Combined	**C**	**T**	**0.85**	**(0.81-0.89)**	**1.39E-10**
6p21.32	*HLA-DQB1*	rs4538746	32632113	NHL	T	C	1.23	(1.18-1.29)	7.96E-18
				MM	T	C	1.06	(0.87-1.29)	0.5928
				Combined	**T**	**C**	**1.22**	**(1.17-1.28)**	**2.13E-17**
8q24.21	*MIR1208, PVT1*	rs2142199	129266826	NHL	C	T	0.89	(0.85-0.93)	3.53E-08
				MM	C	T	0.89	(0.80-0.99)	0.03751
				Combined	**C**	**T**	**0.89**	**(0.86-0.93)**	**3.85E-09**
11q24.1	*GRAMD1B*	rs35923643	123355391	NHL	G	A	1.23	(1.17-1.30)	9.55E-16
				MM	G	A	0.93	(0.81-1.06)	0.2851
				Combined	**G**	**A**	**1.19**	**(1.14-1.25)**	**7.62E-13**
15q21.3	*MNS1*	rs72742686	56783550	NHL	A	G	1.21	(1.14-1.30)	9.31E-09
				MM	A	G	1.16	(0.97-1.39)	0.1092
				Combined	**A**	**G**	**1.21**	**(1.13-1.28)**	**2.79E-09**
16q24.1	*IRF8*	rs375288	85927871	NHL	A	G	0.87	(0.83-0.91)	5.63E-10
				MM	A	G	1.02	(0.91-1.15)	0.7413
				Combined	**A**	**G**	**0.89**	**(0.85-0.92)**	**1.42E-08**
18q21.33	*BCL2*	rs17676949	60785638	NHL	A	G	0.78	(0.72-0.84)	7.11E-11
				MM	A	G	0.77	(0.64-0.93)	0.007263
				Combined	**A**	**G**	**0.78**	**(0.73-0.83)**	**1.85E-12**

Locus	Nearest gene	SNP	Position	Study	Effect allele	Other allele	OR	CI	P
Failed to Replicate (see Supplementary Table 8)									
1p31.1	*GIPC2*	rs17391694	78623626	NHL	T	C	1.18	(1.09-1.27)	1.26E-05
				MM	T	C	1.06	(0.90-1.26)	0.4705
				HL	T	C	1.31	(1.14-1.50)	9.59E-05
				Combined	**T**	**C**	**1.19**	**(1.12-1.26)**	**2.49E-08**
10q23.1	*SH2D4B*	rs12217242	82455988	NHL	A	G	0.64	(0.56-0.74)	1.03E-10
				MM	A	G	1.04	(0.69-1.56)	0.8567
				Combined	**A**	**G**	**0.67**	**(0.59-0.77)**	**1.14E-09**

Supplementary Table 11. Genetic correlations (SE) among four NHL subtypes

	NHL Subtype			
	CLL	**DLBCL**	**FL**	**MZL**
CLL		0.54 (0.26)	0.20 (0.16)	0.70 (0.33)
DLBCL	0.54 (0.26)		0.43 (0.32)	0.86 (0.64)
FL	0.20 (0.16)	0.43 (0.32)		0.44 (0.31)
MZL	0.70 (0.33)	0.86 (0.64)	0.44 (0.31)	

Supplementary Table 12. DEPICT gene-set enrichment results with false discovery rate (FDR<0.2) for NHL subtypes

Original gene set ID	Original gene set description	Nominal P value	FDR
DLBCL			
GO:0043383	negative T cell selection	1.54E-06	<0.05
GO:0045060	negative thymic T cell selection	1.63E-06	<0.05
MZL			
GO:0033365	protein localization to organelle	6.33E-06	<0.20
CLL			
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	1.86E-05	<0.20
MP:0000334	decreased granulocyte number	3.41E-05	<0.20
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	3.52E-05	<0.20
MP:0005154	increased B cell proliferation	4.03E-05	<0.20
GO:0032393	MHC class I receptor activity	5.49E-05	<0.20
GO:0006917	induction of apoptosis	6.38E-05	<0.20
GO:0012502	induction of programmed cell death	8.15E-05	<0.20
MP:0000322	increased granulocyte number	8.23E-05	<0.20
MP:0002022	increased lymphoma incidence	8.62E-05	<0.20
ENSG00000112658	SRF PPI subnetwork	9.80E-05	<0.20
MP:0002144	abnormal B cell differentiation	1.01E-04	<0.20
ENSG00000120889	TNFRSF10B PPI subnetwork	1.16E-04	<0.20
MP:0008215	decreased immature B cell number	1.18E-04	<0.20
ENSG00000163902	RPN1 PPI subnetwork	1.42E-04	<0.20
KEGG_AUTOIMMUNE_THYROID_DISEASE	KEGG_AUTOIMMUNE_THYROID_DISEASE	1.42E-04	<0.20
MP:0000691	enlarged spleen	1.63E-04	<0.20
ENSG00000056558	TRAF1 PPI subnetwork	1.82E-04	<0.20
GO:0009897	external side of plasma membrane	1.99E-04	<0.20
KEGG_ALLOGRAFT_REJECTION	KEGG_ALLOGRAFT_REJECTION	2.06E-04	<0.20
MP:0008111	abnormal granulocyte differentiation	2.16E-04	<0.20
MP:0002461	increased immunoglobulin level	2.19E-04	<0.20
GO:0042113	B cell activation	2.32E-04	<0.20
MP:0008127	decreased dendritic cell number	2.45E-04	<0.20
MP:0008210	increased mature B cell number	2.47E-04	<0.20
GO:0005164	tumor necrosis factor receptor binding	2.71E-04	<0.20
MP:0001802	arrested B cell differentiation	2.76E-04	<0.20
MP:0008664	decreased interleukin-12 secretion	2.98E-04	<0.20
MP:0005070	impaired NK cell cytolysis	3.16E-04	<0.20
MP:0002494	increased IgM level	3.18E-04	<0.20
ENSG00000010278	CD9 PPI subnetwork	3.55E-04	<0.20
KEGG_GRAFT_VERSUS_HOST_DISEASE	KEGG_GRAFT_VERSUS_HOST_DISEASE	3.81E-04	<0.20
MP:0005153	abnormal B cell proliferation	3.82E-04	<0.20
GO:0002237	response to molecule of bacterial origin	4.07E-04	<0.20
MP:0008500	increased IgG2a level	4.30E-04	<0.20
MP:0008173	increased follicular B cell number	4.37E-04	<0.20
MP:0005348	increased T cell proliferation	4.77E-04	<0.20
GO:0007249	I-kappaB kinase/NF-kappaB cascade	4.86E-04	<0.20
GO:0046649	lymphocyte activation	4.89E-04	<0.20
MP:0008186	increased pro-B cell number	4.97E-04	<0.20
GO:0042100	B cell proliferation	5.01E-04	<0.20
MP:0004762	increased anti-double stranded DNA antibody level	5.08E-04	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
MP:0001805	decreased IgG level	5.27E-04	<0.20
GO:0032813	tumor necrosis factor receptor superfamily binding	5.30E-04	<0.20
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON:LYMPHOID_CELL	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON:LYMPHOID_CELL	5.37E-04	<0.20
MP:0002619	abnormal lymphocyte morphology	5.39E-04	<0.20
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	5.47E-04	<0.20
GO:0001817	regulation of cytokine production	5.52E-04	<0.20
MP:0000240	extramedullary hematopoiesis	5.54E-04	<0.20
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	5.64E-04	<0.20
ENSG00000147168	IL2RG PPI subnetwork	5.68E-04	<0.20
GO:0001816	cytokine production	5.71E-04	<0.20
ENSG00000168040	FADD PPI subnetwork	5.94E-04	<0.20
GO:0001558	regulation of cell growth	5.94E-04	<0.20
MP:0002492	decreased IgE level	5.99E-04	<0.20
KEGG_ASTHMA	KEGG_ASTHMA	6.03E-04	<0.20
KEGG_JAK_STAT_SIGNALING_PATHWAY	KEGG_JAK_STAT_SIGNALING_PATHWAY	6.21E-04	<0.20
MP:0002362	abnormal spleen marginal zone morphology	6.22E-04	<0.20
MP:0008474	absent spleen germinal center	6.28E-04	<0.20
GO:0045321	leukocyte activation	6.55E-04	<0.20
MP:0000702	enlarged lymph nodes	6.55E-04	<0.20
MP:0008495	decreased IgG1 level	6.69E-04	<0.20
MP:0005014	increased B cell number	6.73E-04	<0.20
MP:0002743	glomerulonephritis	6.86E-04	<0.20
MP:0000693	spleen hyperplasia	6.93E-04	<0.20
MP:0003725	increased autoantibody level	6.95E-04	<0.20
MP:0000708	thymus hyperplasia	7.32E-04	<0.20
MP:0002831	absent Peyer's patches	7.44E-04	<0.20
GO:0005548	phospholipid transporter activity	7.47E-04	<0.20
MP:0003799	impaired macrophage chemotaxis	7.48E-04	<0.20
MP:0000685	abnormal immune system morphology	7.61E-04	<0.20
GO:0032496	response to lipopolysaccharide	7.85E-04	<0.20
GO:0005126	cytokine receptor binding	8.24E-04	<0.20
GO:0002683	negative regulation of immune system process	8.31E-04	<0.20
MP:0008498	decreased IgG3 level	8.43E-04	<0.20
MP:0000218	increased leukocyte cell number	8.46E-04	<0.20
GO:0031347	regulation of defense response	8.64E-04	<0.20
MP:0002455	abnormal dendritic cell antigen presentation	8.71E-04	<0.20
KEGG_TYPE_I_DIABETES_MELLITUS	KEGG_TYPE_I_DIABETES_MELLITUS	8.76E-04	<0.20
MP:0001800	abnormal humoral immune response	9.02E-04	<0.20
GO:0043122	regulation of I-kappaB kinase/NF-kappaB cascade	9.18E-04	<0.20
MP:0001790	abnormal immune system physiology	9.43E-04	<0.20
GO:0030308	negative regulation of cell growth	9.56E-04	<0.20
MP:0004794	increased anti-nuclear antigen antibody level	9.61E-04	<0.20
MP:0002376	abnormal dendritic cell physiology	9.64E-04	<0.20
GO:0050776	regulation of immune response	9.75E-04	<0.20
GO:0071887	leukocyte apoptotic process	9.88E-04	<0.20
MP:0008497	decreased IgG2b level	9.98E-04	<0.20
REACTOME_G1_PHASE	REACTOME_G1_PHASE	1.01E-03	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
REACTOME_CYCLIN_D_ASSOCIATED_EVENTS_IN_G1	REACTOME_CYCLIN_D_ASSOCIATED_EVENTS_IN_G1	1.01E-03	<0.20
GO:0071219	cellular response to molecule of bacterial origin	1.01E-03	<0.20
MP:0008522	abnormal lymph node germinal center morphology	1.02E-03	<0.20
MP:0002499	chronic inflammation	1.02E-03	<0.20
ENSG00000103197	TSC2 PPI subnetwork	1.02E-03	<0.20
MP:0002493	increased IgG level	1.03E-03	<0.20
ENSG00000135446	CDK4 PPI subnetwork	1.03E-03	<0.20
GO:0030183	B cell differentiation	1.04E-03	<0.20
MP:0005013	increased lymphocyte cell number	1.07E-03	<0.20
ENSG00000121858	TNFSF10 PPI subnetwork	1.11E-03	<0.20
MP:0002459	abnormal B cell physiology	1.11E-03	<0.20
MP:0000689	abnormal spleen morphology	1.12E-03	<0.20
ENSG00000165025	SYK PPI subnetwork	1.13E-03	<0.20
MP:0008045	decreased NK cell number	1.14E-03	<0.20
MP:0005094	abnormal T cell proliferation	1.14E-03	<0.20
ENSG00000054267	ARID4B PPI subnetwork	1.16E-03	<0.20
ENSG00000126456	IRF3 PPI subnetwork	1.17E-03	<0.20
MP:0008209	decreased pre-B cell number	1.18E-03	<0.20
MP:0009339	decreased splenocyte number	1.18E-03	<0.20
GO:0042611	MHC protein complex	1.19E-03	<0.20
MP:0001844	autoimmune response	1.20E-03	<0.20
MP:0002497	increased IgE level	1.22E-03	<0.20
MP:0008189	increased transitional stage B cell number	1.23E-03	<0.20
ENSG00000134470	IL15RA PPI subnetwork	1.24E-03	<0.20
GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	1.24E-03	<0.20
MP:0001806	decreased IgM level	1.24E-03	<0.20
REACTOME_DEATH_RECEPTOR__SIGNALLING	REACTOME_DEATH_RECEPTOR__SIGNALLING	1.25E-03	<0.20
REACTOME_EXTRINSIC_PATHWAY_FOR_APOPTOSIS	REACTOME_EXTRINSIC_PATHWAY_FOR_APOPTOSIS	1.25E-03	<0.20
MP:0002463	abnormal neutrophil physiology	1.25E-03	<0.20
GO:0071222	cellular response to lipopolysaccharide	1.26E-03	<0.20
MP:0004978	decreased B-1 B cell number	1.26E-03	<0.20
MP:0005093	decreased B cell proliferation	1.26E-03	<0.20
MP:0008476	increased spleen red pulp amount	1.32E-03	<0.20
MP:0004392	abnormal CD8-positive T cell physiology	1.35E-03	<0.20
MP:0002458	abnormal B cell number	1.37E-03	<0.20
ENSG00000162889	MAPKAPK2 PPI subnetwork	1.39E-03	<0.20
GO:0002285	lymphocyte activation involved in immune response	1.41E-03	<0.20
ENSG00000091181	IL5RA PPI subnetwork	1.41E-03	<0.20
GO:0030098	lymphocyte differentiation	1.42E-03	<0.20
MP:0008578	decreased circulating interferon-gamma level	1.46E-03	<0.20
MP:0008481	increased spleen germinal center number	1.49E-03	<0.20
ENSG00000159110	IFNAR2 PPI subnetwork	1.50E-03	<0.20
ENSG00000206505	HLA-A PPI subnetwork	1.50E-03	<0.20
ENSG00000077238	IL4R PPI subnetwork	1.51E-03	<0.20
GO:0051250	negative regulation of lymphocyte activation	1.51E-03	<0.20
MP:0008102	lymph node hyperplasia	1.51E-03	<0.20
GO:0071216	cellular response to biotic stimulus	1.54E-03	<0.20
MP:0005017	decreased B cell number	1.54E-03	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
MP:0002418	increased susceptibility to viral infection	1.54E-03	<0.20
MP:0008657	increased interleukin-1 beta secretion	1.61E-03	<0.20
MP:0002401	abnormal lymphopoiesis	1.61E-03	<0.20
MP:0003945	abnormal lymphocyte physiology	1.62E-03	<0.20
ENSG00000113494	PRLR PPI subnetwork	1.63E-03	<0.20
ENSG00000123268	ATF1 PPI subnetwork	1.65E-03	<0.20
MP:0000709	enlarged thymus	1.67E-03	<0.20
REACTOME_INTERFERON_GAMMA_SIGNALING	REACTOME_INTERFERON_GAMMA_SIGNALING	1.68E-03	<0.20
GO:0006213	pyrimidine nucleoside metabolic process	1.69E-03	<0.20
MP:0005015	increased T cell number	1.69E-03	<0.20
GO:0002521	leukocyte differentiation	1.71E-03	<0.20
GO:0032943	mononuclear cell proliferation	1.72E-03	<0.20
KEGG_APOPTOSIS	KEGG_APOPTOSIS	1.74E-03	<0.20
KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	1.77E-03	<0.20
MP:0008049	increased memory T cell number	1.82E-03	<0.20
GO:0045926	negative regulation of growth	1.83E-03	<0.20
GO:0051092	positive regulation of NF-kappaB transcription factor activity	1.84E-03	<0.20
ENSG00000124334	IL9R PPI subnetwork	1.84E-03	<0.20
MP:0004816	abnormal class switch recombination	1.92E-03	<0.20
ENSG00000165732	DDX21 PPI subnetwork	1.93E-03	<0.20
MP:0000694	spleen hypoplasia	1.95E-03	<0.20
GO:0001783	B cell apoptotic process	1.96E-03	<0.20
MP:0003132	increased pre-B cell number	1.99E-03	<0.20
ENSG00000112062	MAPK14 PPI subnetwork	2.01E-03	<0.20
GO:0045088	regulation of innate immune response	2.03E-03	<0.20
MP:0008211	decreased mature B cell number	2.03E-03	<0.20
GO:0070227	lymphocyte apoptotic process	2.06E-03	<0.20
MP:0008214	increased immature B cell number	2.06E-03	<0.20
ENSG00000124762	CDKN1A PPI subnetwork	2.08E-03	<0.20
GO:0046651	lymphocyte proliferation	2.09E-03	<0.20
MP:0000688	lymphoid hyperplasia	2.11E-03	<0.20
ENSG00000119535	CSF3R PPI subnetwork	2.12E-03	<0.20
ENSG00000145386	CCNA2 PPI subnetwork	2.12E-03	<0.20
ENSG00000027697	IFNGR1 PPI subnetwork	2.15E-03	<0.20
GO:0034097	response to cytokine stimulus	2.18E-03	<0.20
MP:0001655	multifocal hepatic necrosis	2.18E-03	<0.20
ENSG00000012124	CD22 PPI subnetwork	2.28E-03	<0.20
MP:0002412	increased susceptibility to bacterial infection	2.28E-03	<0.20
ENSG00000086061	DNAJA1 PPI subnetwork	2.28E-03	<0.20
MP:0002460	decreased immunoglobulin level	2.29E-03	<0.20
ENSG00000159128	IFNGR2 PPI subnetwork	2.29E-03	<0.20
ENSG00000005844	ITGAL PPI subnetwork	2.31E-03	<0.20
GO:0050868	negative regulation of T cell activation	2.32E-03	<0.20
ENSG00000081985	IL12RB2 PPI subnetwork	2.33E-03	<0.20
ENSG00000142677	IL22RA1 PPI subnetwork	2.33E-03	<0.20
KEGG_LEISHMANIA_INFECTION	KEGG_LEISHMANIA_INFECTION	2.34E-03	<0.20
ENSG00000168685	IL7R PPI subnetwork	2.34E-03	<0.20
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	2.37E-03	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
GO:0042612	MHC class I protein complex	2.38E-03	<0.20
GO:0002695	negative regulation of leukocyte activation	2.39E-03	<0.20
MP:0001601	abnormal myelopoiesis	2.40E-03	<0.20
GO:0045619	regulation of lymphocyte differentiation	2.44E-03	<0.20
REACTOME_TRAF6_MEDIATED_NF:KB_ACTIVATION	REACTOME_TRAF6_MEDIATED_NF:KB_ACTIVATION	2.44E-03	<0.20
ENSG00000116678	LEPR PPI subnetwork	2.46E-03	<0.20
MP:0008826	abnormal splenic cell ratio	2.49E-03	<0.20
MP:0008097	increased plasma cell number	2.54E-03	<0.20
ENSG00000122756	CNTFR PPI subnetwork	2.56E-03	<0.20
ENSG00000158869	FCER1G PPI subnetwork	2.57E-03	<0.20
MP:0008475	intermingled spleen red and white pulp	2.58E-03	<0.20
MP:0003156	abnormal leukocyte migration	2.59E-03	<0.20
ENSG00000115415	STAT1 PPI subnetwork	2.62E-03	<0.20
ENSG00000139687	RB1 PPI subnetwork	2.62E-03	<0.20
MP:0010766	abnormal NK cell physiology	2.63E-03	<0.20
ENSG00000143398	PIP5K1A PPI subnetwork	2.63E-03	<0.20
ENSG00000117400	MPL PPI subnetwork	2.64E-03	<0.20
MP:0008751	abnormal interleukin level	2.69E-03	<0.20
ENSG00000126767	ELK1 PPI subnetwork	2.70E-03	<0.20
ENSG00000185436	IL28RA PPI subnetwork	2.70E-03	<0.20
ENSG00000123496	IL13RA2 PPI subnetwork	2.71E-03	<0.20
ENSG00000164485	IL22RA2 PPI subnetwork	2.71E-03	<0.20
ENSG00000103522	IL21R PPI subnetwork	2.71E-03	<0.20
GO:0070661	leukocyte proliferation	2.72E-03	<0.20
REACTOME_NF:KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL	REACTOME_NF:KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL	2.73E-03	<0.20
GO:0008633	activation of pro-apoptotic gene products	2.77E-03	<0.20
KEGG_VIRAL_MYOCARDITIS	KEGG_VIRAL_MYOCARDITIS	2.77E-03	<0.20
ENSG00000159113	ENSG00000159113 PPI subnetwork	2.79E-03	<0.20
REACTOME_INTERLEUKIN:2_SIGNALING	REACTOME_INTERLEUKIN:2_SIGNALING	2.80E-03	<0.20
ENSG00000185291	IL3RA PPI subnetwork	2.82E-03	<0.20
ENSG00000137070	IL11RA PPI subnetwork	2.82E-03	<0.20
ENSG00000145623	OSMR PPI subnetwork	2.82E-03	<0.20
ENSG00000134352	IL6ST PPI subnetwork	2.83E-03	<0.20
MP:0004799	increased susceptibility to experimental autoimmune encephalomyelitis	2.85E-03	<0.20
MP:0008168	decreased B-1a cell number	2.86E-03	<0.20
ENSG00000131724	IL13RA1 PPI subnetwork	2.87E-03	<0.20
ENSG00000085117	CD82 PPI subnetwork	2.87E-03	<0.20
ENSG00000142166	IFNAR1 PPI subnetwork	2.88E-03	<0.20
ENSG00000010671	BTK PPI subnetwork	2.89E-03	<0.20
MP:0010769	abnormal survival	2.89E-03	<0.20
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	2.89E-03	<0.20
MP:0000729	abnormal myogenesis	2.92E-03	<0.20
ENSG00000214826	ENSG00000214826 PPI subnetwork	2.93E-03	<0.20
ENSG00000111788	ENSG00000111788 PPI subnetwork	2.93E-03	<0.20
ENSG00000016402	IL20RA PPI subnetwork	2.94E-03	<0.20
GO:0009607	response to biotic stimulus	2.94E-03	<0.20
GO:0071345	cellular response to cytokine stimulus	2.99E-03	<0.20

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MP:0005025	abnormal response to infection	3.00E-03	<0.20
ENSG00000100385	IL2RB PPI subnetwork	3.04E-03	<0.20
MP:0008499	increased IgG1 level	3.06E-03	<0.20
MP:0009395	increased nucleated erythrocyte cell number	3.06E-03	<0.20
REACTOME_RIG:IMDA5_MEDIATED_INDUCTION_OF_IFN:ALPHABETA_PATHWAYS	REACTOME_RIG:IMDA5_MEDIATED_INDUCTION_OF_IFN: ALPHABETA_PATHWAYS	3.07E-03	<0.20
GO:0060333	interferon-gamma-mediated signaling pathway	3.09E-03	<0.20
GO:0000307	cyclin-dependent protein kinase holoenzyme complex	3.12E-03	<0.20
ENSG00000101773	RBBP8 PPI subnetwork	3.12E-03	<0.20
ENSG00000206156	ENSG00000206156 PPI subnetwork	3.20E-03	<0.20
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3.26E-03	<0.20
MP:0002451	abnormal macrophage physiology	3.33E-03	<0.20
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	3.35E-03	<0.20
ENSG00000110324	IL10RA PPI subnetwork	3.36E-03	<0.20
ENSG00000105369	CD79A PPI subnetwork	3.38E-03	<0.20
ENSG00000104689	TNFRSF10A PPI subnetwork	3.39E-03	<0.20
ENSG00000204592	HLA-E PPI subnetwork	3.42E-03	<0.20
GO:0045621	positive regulation of lymphocyte differentiation	3.48E-03	<0.20
GO:0001818	negative regulation of cytokine production	3.48E-03	<0.20
GO:0048534	hemopoietic or lymphoid organ development	3.49E-03	<0.20
ENSG00000105810	CDK6 PPI subnetwork	3.49E-03	<0.20
MP:0008208	decreased pro-B cell number	3.52E-03	<0.20
MP:0008044	increased NK cell number	3.54E-03	<0.20
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	3.57E-03	<0.20
ENSG00000158796	DEDD PPI subnetwork	3.61E-03	<0.20
GO:0004861	cyclin-dependent protein kinase inhibitor activity	3.66E-03	<0.20
MP:0008181	increased marginal zone B cell number	3.66E-03	<0.20
ENSG00000129562	DAD1 PPI subnetwork	3.66E-03	<0.20
GO:0046631	alpha-beta T cell activation	3.68E-03	<0.20
ENSG00000162594	IL23R PPI subnetwork	3.73E-03	<0.20
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	3.78E-03	<0.20
ENSG00000110931	CAMKK2 PPI subnetwork	3.80E-03	<0.20
REACTOME_REGULATION_OF_IFNA_SIGNALING	REACTOME_REGULATION_OF_IFNA_SIGNALING	3.81E-03	<0.20
MP:0008617	increased circulating interleukin-12 level	3.83E-03	<0.20
MP:0008496	decreased IgG2a level	3.86E-03	<0.20
ENSG00000187266	EPOR PPI subnetwork	3.86E-03	<0.20
MP:0008567	decreased interferon-gamma secretion	3.86E-03	<0.20
MP:0003850	abnormal thymocyte activation	3.88E-03	<0.20
ENSG00000113594	LIFR PPI subnetwork	3.88E-03	<0.20
ENSG00000198517	MAFK PPI subnetwork	3.92E-03	<0.20
ENSG00000100368	CSF2RB PPI subnetwork	3.94E-03	<0.20
REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	3.94E-03	<0.20
MP:0008722	abnormal chemokine secretion	3.95E-03	<0.20
MP:0003009	abnormal cytokine secretion	3.96E-03	<0.20
GO:0032649	regulation of interferon-gamma production	4.03E-03	<0.20
GO:0019884	antigen processing and presentation of exogenous antigen	4.05E-03	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
MP:0002444	abnormal T cell physiology	4.07E-03	<0.20
MP:0002026	leukemia	4.12E-03	<0.20
MP:0005616	decreased susceptibility to type IV hypersensitivity reaction	4.13E-03	<0.20
MP:0002023	B cell derived lymphoma	4.19E-03	<0.20
REACTOME_INTERLEUKIN:3_5_AND_GM:CSF_SIGNALING	REACTOME_INTERLEUKIN:3_5_AND_GM:CSF_SIGNALING	4.21E-03	<0.20
GO:0045582	positive regulation of T cell differentiation	4.21E-03	<0.20
GO:0019221	cytokine-mediated signaling pathway	4.22E-03	<0.20
ENSG00000147065	MSN PPI subnetwork	4.24E-03	<0.20
MP:0000717	abnormal lymphocyte cell number	4.25E-03	<0.20
MP:0008182	decreased marginal zone B cell number	4.28E-03	<0.20
ENSG00000175505	CLCF1 PPI subnetwork	4.28E-03	<0.20
GO:0004065	arylsulfatase activity	4.29E-03	<0.20
MP:0001585	hemolytic anemia	4.30E-03	<0.20
ENSG00000134460	IL2RA PPI subnetwork	4.33E-03	<0.20
GO:0050871	positive regulation of B cell activation	4.35E-03	<0.20
MP:0005461	abnormal dendritic cell morphology	4.37E-03	<0.20
KEGG_SMALL_CELL_LUNG_CANCER	KEGG_SMALL_CELL_LUNG_CANCER	4.37E-03	<0.20
GO:0051707	response to other organism	4.41E-03	<0.20
ENSG00000206509	HLA-F PPI subnetwork	4.53E-03	<0.20
GO:0034341	response to interferon-gamma	4.54E-03	<0.20
ENSG00000111679	PTPN6 PPI subnetwork	4.57E-03	<0.20
ENSG00000073009	IKBKG PPI subnetwork	4.58E-03	<0.20
GO:0005048	signal sequence binding	4.58E-03	<0.20
GO:0050853	B cell receptor signaling pathway	4.59E-03	<0.20
ENSG00000080839	RBL1 PPI subnetwork	4.59E-03	<0.20
GO:0016538	cyclin-dependent protein kinase regulator activity	4.62E-03	<0.20
GO:2000106	regulation of leukocyte apoptotic process	4.69E-03	<0.20
ENSG00000101017	CD40 PPI subnetwork	4.70E-03	<0.20
ENSG00000160712	IL6R PPI subnetwork	4.70E-03	<0.20
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	4.71E-03	<0.20
ENSG00000159216	RUNX1 PPI subnetwork	4.80E-03	<0.20
GO:0071346	cellular response to interferon-gamma	4.84E-03	<0.20
ENSG00000113302	IL12B PPI subnetwork	4.87E-03	<0.20
MP:0006082	CNS inflammation	4.87E-03	<0.20
ENSG00000206452	HLA-C PPI subnetwork	4.87E-03	<0.20
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	4.96E-03	<0.20
ENSG00000150455	TIRAP PPI subnetwork	4.97E-03	<0.20
MP:0008217	abnormal B cell activation	5.04E-03	<0.20
GO:0016798	hydrolase activity, acting on glycosyl bonds	5.04E-03	<0.20
KEGG_PRIMARY_IMMUNODEFICIENCY	KEGG_PRIMARY_IMMUNODEFICIENCY	5.04E-03	<0.20
MP:0002495	increased IgA level	5.10E-03	<0.20
MP:0005078	abnormal cytotoxic T cell physiology	5.11E-03	<0.20
ENSG00000176406	RIMS2 PPI subnetwork	5.25E-03	<0.20
ENSG00000123080	CDKN2C PPI subnetwork	5.27E-03	<0.20
ENSG00000111276	CDKN1B PPI subnetwork	5.30E-03	<0.20
GO:0030888	regulation of B cell proliferation	5.32E-03	<0.20
GO:0009617	response to bacterium	5.33E-03	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
MP:0002957	intestinal adenocarcinoma	5.37E-03	<0.20
MP:0002356	abnormal spleen red pulp morphology	5.40E-03	<0.20
GO:0032609	interferon-gamma production	5.42E-03	<0.20
GO:0002292	T cell differentiation involved in immune response	5.49E-03	<0.20
GO:0010740	positive regulation of intracellular protein kinase cascade	5.54E-03	<0.20
ENSG00000122966	CIT PPI subnetwork	5.57E-03	<0.20
GO:0045580	regulation of T cell differentiation	5.65E-03	<0.20
GO:0005529	GO:0005529	5.66E-03	<0.20
KEGG_HEMATOPOIETIC_CELL_LINEAGE	KEGG_HEMATOPOIETIC_CELL_LINEAGE	5.73E-03	<0.20
REACTOME_MITOTIC_G1:G1S_PHASES	REACTOME_MITOTIC_G1:G1S_PHASES	5.74E-03	<0.20
MP:0002442	abnormal leukocyte physiology	5.75E-03	<0.20
GO:0044247	cellular polysaccharide catabolic process	5.76E-03	<0.20
GO:0009251	glucan catabolic process	5.76E-03	<0.20
GO:0050864	regulation of B cell activation	5.78E-03	<0.20
GO:0042092	type 2 immune response	5.83E-03	<0.20
GO:0005980	glycogen catabolic process	5.84E-03	<0.20
MP:0004939	abnormal B cell morphology	5.85E-03	<0.20
ENSG00000131323	TRAF3 PPI subnetwork	5.91E-03	<0.20
ENSG00000178363	CALML3 PPI subnetwork	5.91E-03	<0.20
ENSG00000175197	DDIT3 PPI subnetwork	5.92E-03	<0.20
MP:0000219	increased neutrophil cell number	5.98E-03	<0.20
ENSG00000170248	PDCD6IP PPI subnetwork	5.99E-03	<0.20
GO:0002718	regulation of cytokine production involved in immune response	6.03E-03	<0.20
ENSG00000198223	CSF2RA PPI subnetwork	6.06E-03	<0.20
MP:0008071	absent B cells	6.10E-03	<0.20
GO:0030097	hemopoiesis	6.12E-03	<0.20
MP:0009790	decreased susceptibility to viral infection induced morbidity/mortality	6.16E-03	<0.20
ENSG00000137403	HLA-F PPI subnetwork	6.19E-03	<0.20
GO:0004601	peroxidase activity	6.25E-03	<0.20
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	6.25E-03	<0.20
GO:0042110	T cell activation	6.32E-03	<0.20
ENSG00000182481	KPNA2 PPI subnetwork	6.38E-03	<0.20
ENSG00000215769	ENSG00000215769 PPI subnetwork	6.38E-03	<0.20
MP:0004952	increased spleen weight	6.54E-03	<0.20
MP:0008603	decreased circulating interleukin-4 level	6.54E-03	<0.20
ENSG00000115935	WIPF1 PPI subnetwork	6.58E-03	<0.20
GO:0051249	regulation of lymphocyte activation	6.64E-03	<0.20
ENSG00000175104	TRAF6 PPI subnetwork	6.65E-03	<0.20
GO:0051318	G1 phase	6.66E-03	<0.20
MP:0002490	abnormal immunoglobulin level	6.67E-03	<0.20
GO:0046632	alpha-beta T cell differentiation	6.67E-03	<0.20
GO:0002694	regulation of leukocyte activation	6.68E-03	<0.20
MP:0005011	increased eosinophil cell number	6.69E-03	<0.20
GO:0002440	production of molecular mediator of immune response	6.72E-03	<0.20
KEGG_ONE_CARBON_POOL_BY_FOLATE	KEGG_ONE_CARBON_POOL_BY_FOLATE	6.75E-03	<0.20
ENSG00000137275	RIPK1 PPI subnetwork	6.81E-03	<0.20
MP:0003172	abnormal lysosome physiology	6.85E-03	<0.20

Original gene set ID	Original gene set description	Nominal P value	FDR
ENSG00000136810	TXN PPI subnetwork	6.89E-03	<0.20
MP:0001858	intestinal inflammation	6.90E-03	<0.20
GO:0002819	regulation of adaptive immune response	6.92E-03	<0.20
MP:0010373	myeloid hyperplasia	6.96E-03	<0.20
GO:0002286	T cell activation involved in immune response	6.98E-03	<0.20
MP:0002357	abnormal spleen white pulp morphology	7.00E-03	<0.20
ENSG00000115738	ID2 PPI subnetwork	7.05E-03	<0.20
GO:0010907	positive regulation of glucose metabolic process	7.18E-03	<0.20
GO:0030101	natural killer cell activation	7.29E-03	<0.20
ENSG00000166710	B2M PPI subnetwork	7.30E-03	<0.20
ENSG00000128272	ATF4 PPI subnetwork	7.36E-03	<0.20
ENSG00000099985	OSM PPI subnetwork	7.46E-03	<0.20
MP:0000367	abnormal coat/ hair morphology	7.46E-03	<0.20
ENSG00000141522	ARHGDIA PPI subnetwork	7.47E-03	<0.20
REACTOME_NF:KB_ACTIVATION_THROUGH_FADDRIP:1_PATHWAY_MEDIATED_BY_CASPASE:8_AND_:10	REACTOME_NF:KB_ACTIVATION_THROUGH_FADDRIP:1_PATHWAY_MEDIATED_BY_CASPASE:8_AND_:10	7.50E-03	<0.20
GO:0002478	antigen processing and presentation of exogenous peptide antigen	7.51E-03	<0.20
GO:0000080	G1 phase of mitotic cell cycle	7.51E-03	<0.20
ENSG00000064012	CASP8 PPI subnetwork	7.55E-03	<0.20
MP:0008561	decreased tumor necrosis factor secretion	7.73E-03	<0.20
ENSG00000026103	FAS PPI subnetwork	7.74E-03	<0.20
ENSG00000177455	CD19 PPI subnetwork	7.74E-03	<0.20
MP:0001807	decreased IgA level	7.76E-03	<0.20
GO:0050866	negative regulation of cell activation	7.78E-03	<0.20
GO:0030217	T cell differentiation	7.80E-03	<0.20
GO:0060759	regulation of response to cytokine stimulus	7.82E-03	<0.20
MP:0008719	impaired neutrophil recruitment	7.88E-03	<0.20
ENSG00000013573	DDX11 PPI subnetwork	7.90E-03	<0.20
GO:2000242	negative regulation of reproductive process	7.95E-03	<0.20
MP:0008074	increased CD4-positive T cell number	8.04E-03	<0.20
GO:0004012	phospholipid-translocating ATPase activity	8.13E-03	<0.20
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	8.16E-03	<0.20
GO:0006916	anti-apoptosis	8.16E-03	<0.20
GO:0002764	immune response-regulating signaling pathway	8.20E-03	<0.20
ENSG00000115232	ITGA4 PPI subnetwork	8.27E-03	<0.20
KEGG_NON_SMALL_CELL_LUNG_CANCER	KEGG_NON_SMALL_CELL_LUNG_CANCER	8.32E-03	<0.20
ENSG00000117242	ENSG00000117242 PPI subnetwork	8.52E-03	<0.20
MP:0002816	colitis	8.55E-03	<0.20
ENSG00000171855	IFNB1 PPI subnetwork	8.83E-03	<0.20
GO:0001959	regulation of cytokine-mediated signaling pathway	8.83E-03	<0.20
ENSG00000127191	TRAF2 PPI subnetwork	8.90E-03	<0.20
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	8.98E-03	<0.20
ENSG00000206279	DAXX PPI subnetwork	9.06E-03	<0.20
ENSG00000204209	DAXX PPI subnetwork	9.06E-03	<0.20
ENSG00000206206	DAXX PPI subnetwork	9.06E-03	<0.20
ENSG00000112964	GHR PPI subnetwork	9.08E-03	<0.20
ENSG00000172179	PRL PPI subnetwork	9.08E-03	<0.20
ENSG00000171791	BCL2 PPI subnetwork	9.17E-03	<0.20

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ENSG00000109471	IL2 PPI subnetwork	9.22E-03	<0.20
ENSG00000107643	MAPK8 PPI subnetwork	9.42E-03	<0.20
MP:0002446	abnormal macrophage morphology	9.50E-03	<0.20
ENSG00000061273	HDAC7 PPI subnetwork	9.61E-03	<0.20
GO:0072527	pyrimidine-containing compound metabolic process	9.64E-03	<0.20
MP:0008174	decreased follicular B cell number	9.74E-03	<0.20
MP:0004974	decreased regulatory T cell number	9.80E-03	<0.20
MP:0008190	decreased transitional stage B cell number	1.00E-02	<0.20
REACTOME_GPVI:MEDIATED_ACTIVATION_CASCADE	REACTOME_GPVI:MEDIATED_ACTIVATION_CASCADE	0.01	<0.20
ENSG00000012048	BRCA1 PPI subnetwork	0.01	<0.20
ENSG00000168884	TNIP2 PPI subnetwork	0.01	<0.20
ENSG00000145907	G3BP1 PPI subnetwork	0.01	<0.20
ENSG00000102226	USP11 PPI subnetwork	0.01	<0.20
GO:0002700	regulation of production of molecular mediator of immune response	0.01	<0.20
ENSG00000096996	IL12RB1 PPI subnetwork	0.01	<0.20
ENSG00000136111	TBC1D4 PPI subnetwork	0.01	<0.20
GO:0001819	positive regulation of cytokine production	0.01	<0.20
MP:0002123	abnormal hematopoiesis	0.01	<0.20
GO:0002252	immune effector process	0.01	<0.20
ENSG00000168811	IL12A PPI subnetwork	0.01	<0.20
GO:0016049	cell growth	0.01	<0.20
GO:0045620	negative regulation of lymphocyte differentiation	0.01	<0.20
MP:0008050	decreased memory T cell number	0.01	<0.20
MP:0002419	abnormal innate immunity	0.01	<0.20
ENSG00000155380	SLC16A1 PPI subnetwork	0.01	<0.20
GO:0008624	induction of apoptosis by extracellular signals	0.01	<0.20
GO:0002757	immune response-activating signal transduction	0.01	<0.20
GO:0004576	oligosaccharyl transferase activity	0.01	<0.20
ENSG00000109906	ZBTB16 PPI subnetwork	0.01	<0.20
REACTOME_INTERFERON_SIGNALING	REACTOME_INTERFERON_SIGNALING	0.01	<0.20
GO:0000932	cytoplasmic mRNA processing body	0.01	<0.20
ENSG00000170312	CDK1 PPI subnetwork	0.01	<0.20
REACTOME_REGULATION_OF_IFNG_SIGNALING	REACTOME_REGULATION_OF_IFNG_SIGNALING	0.01	<0.20
REACTOME_GAB1_SIGNALOSOME	REACTOME_GAB1_SIGNALOSOME	0.01	<0.20
GO:0002684	positive regulation of immune system process	0.01	<0.20
ENSG00000110092	CCND1 PPI subnetwork	0.01	<0.20
GO:0031341	regulation of cell killing	0.01	<0.20
ENSG00000143514	TP53BP2 PPI subnetwork	0.01	<0.20

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