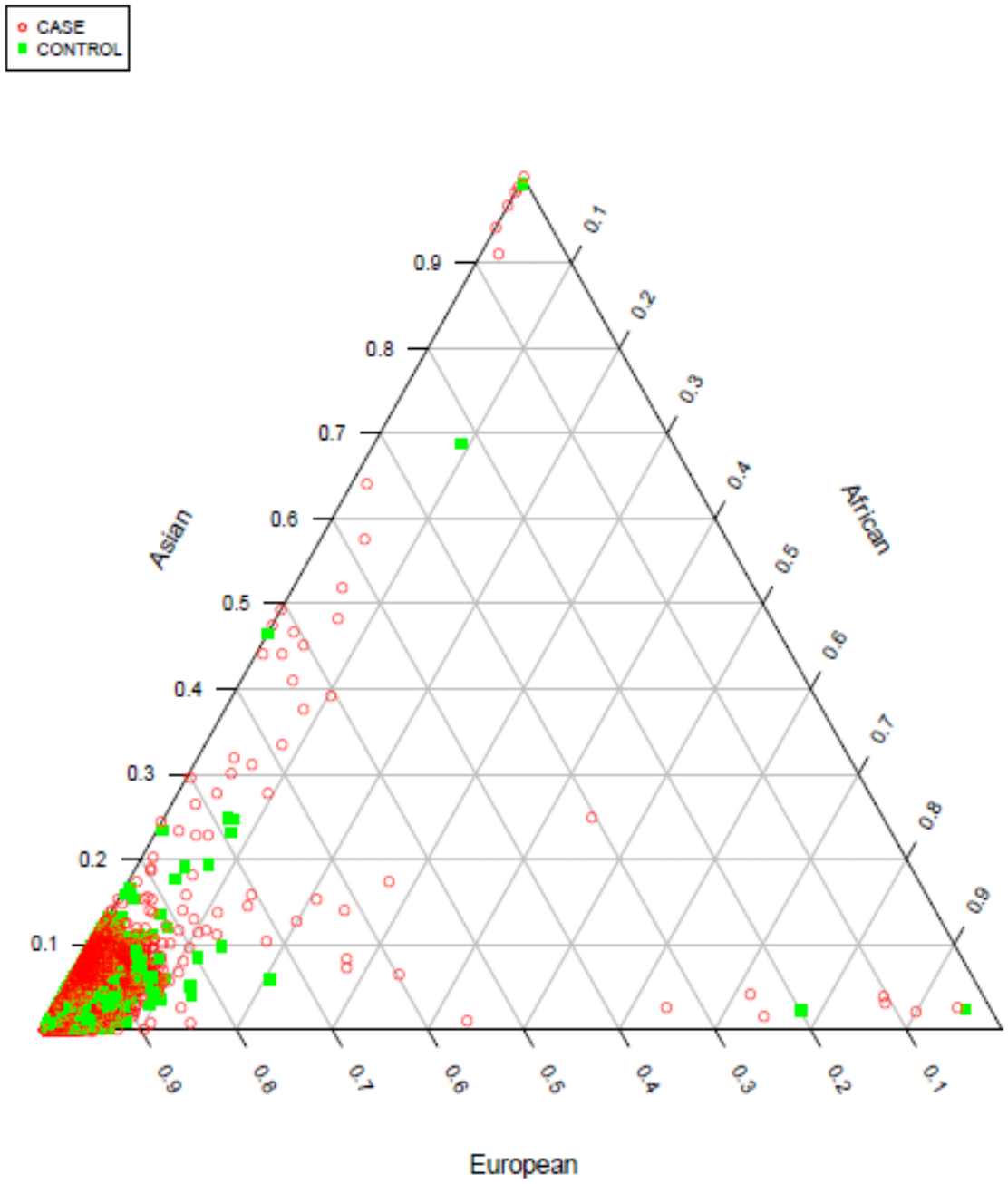
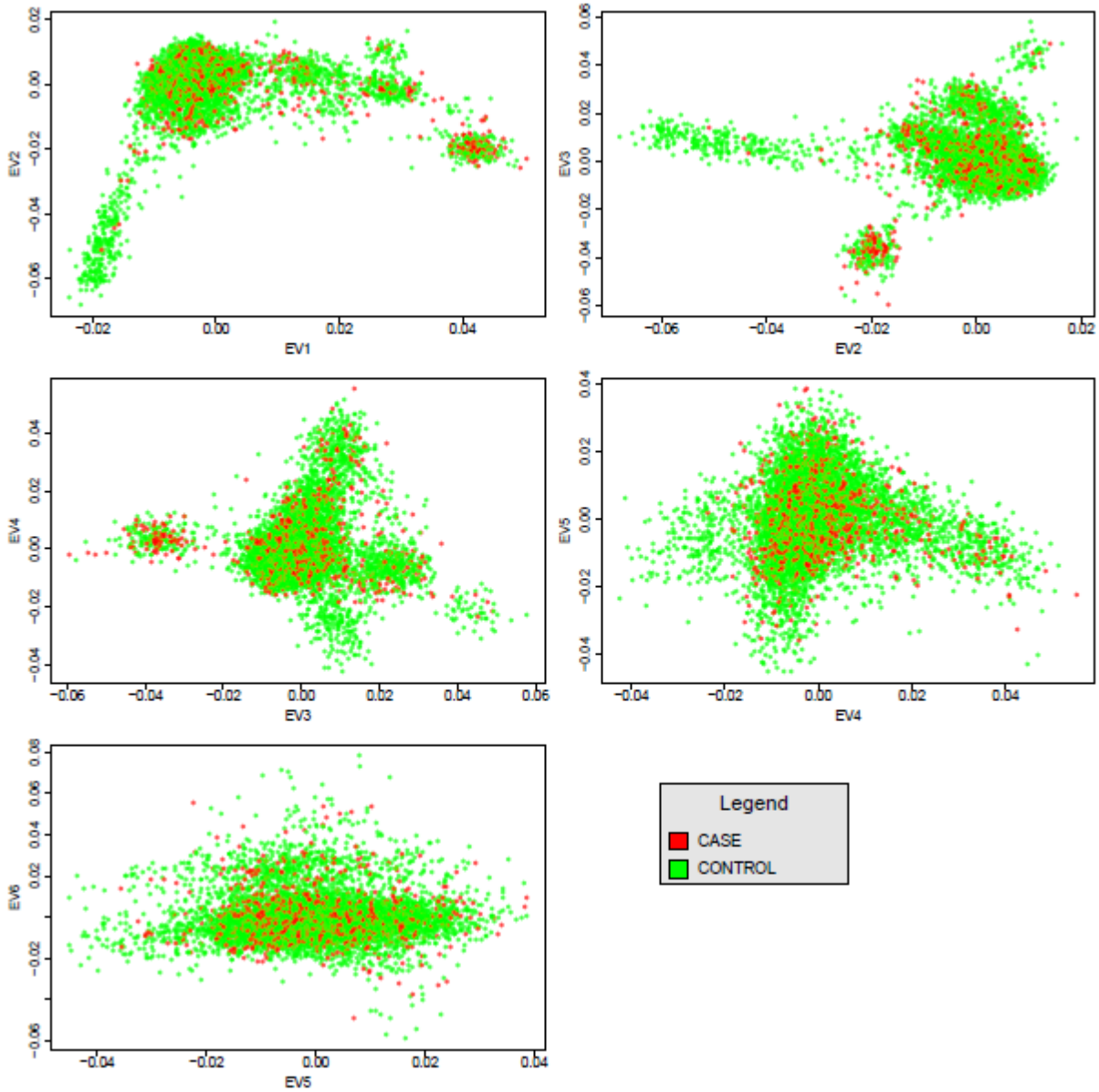
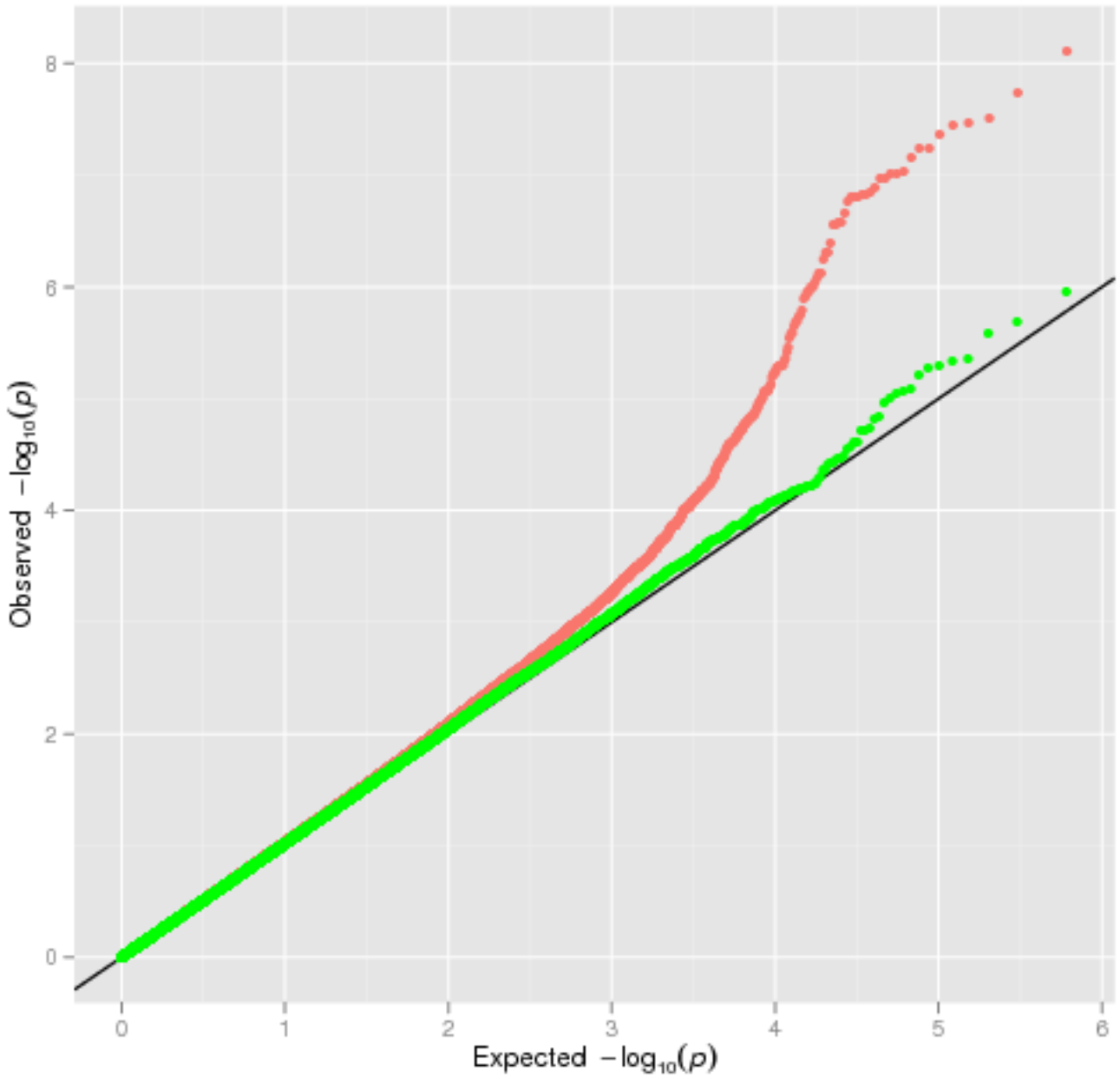
## SUPPLEMENTARY FIGURES



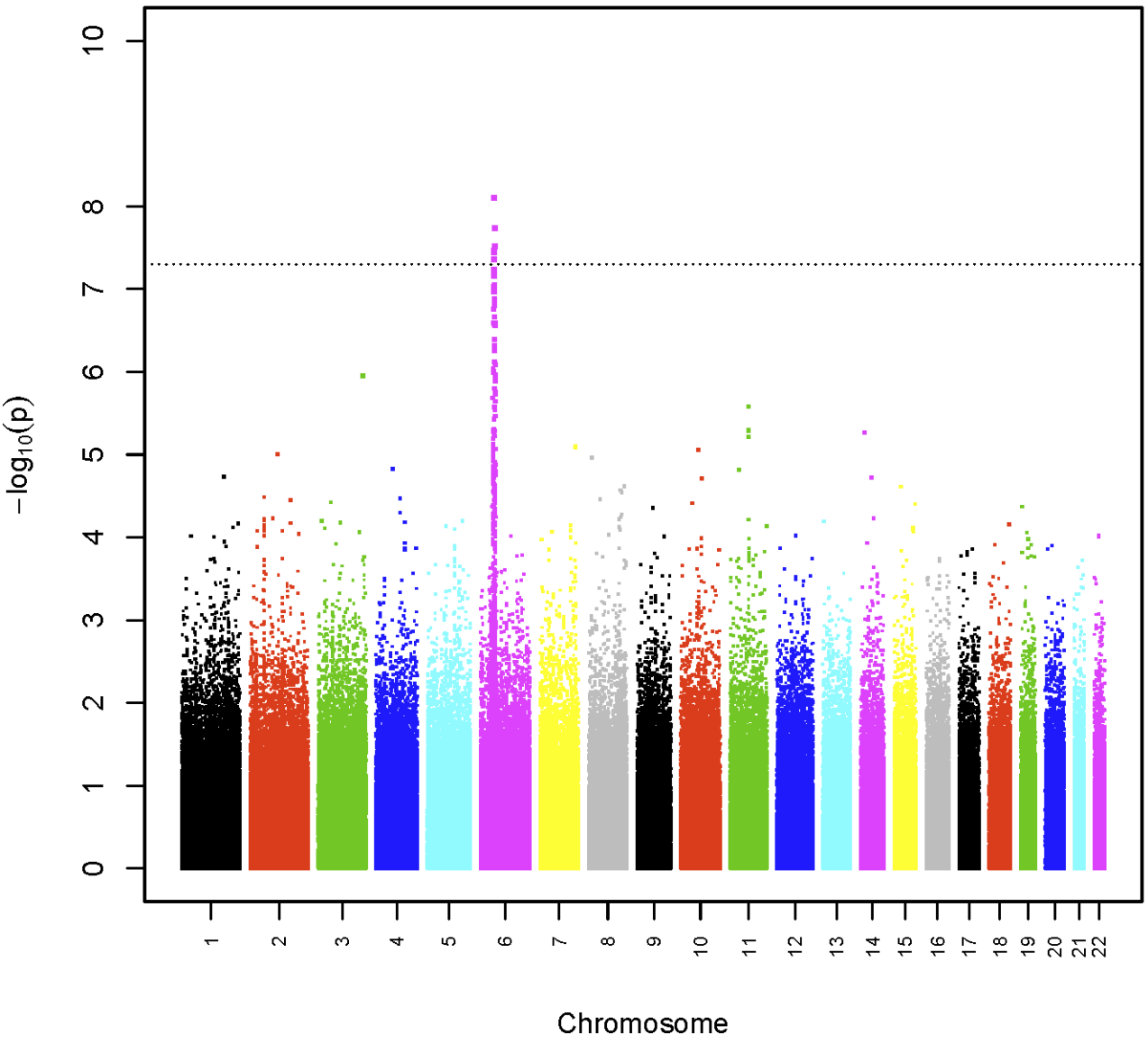

**Supplementary Figure 1. Plot of estimated admixture for individuals in MZL GWAS (stage 1). For details, see the Methods. Individuals with <80% European ancestry were excluded.**



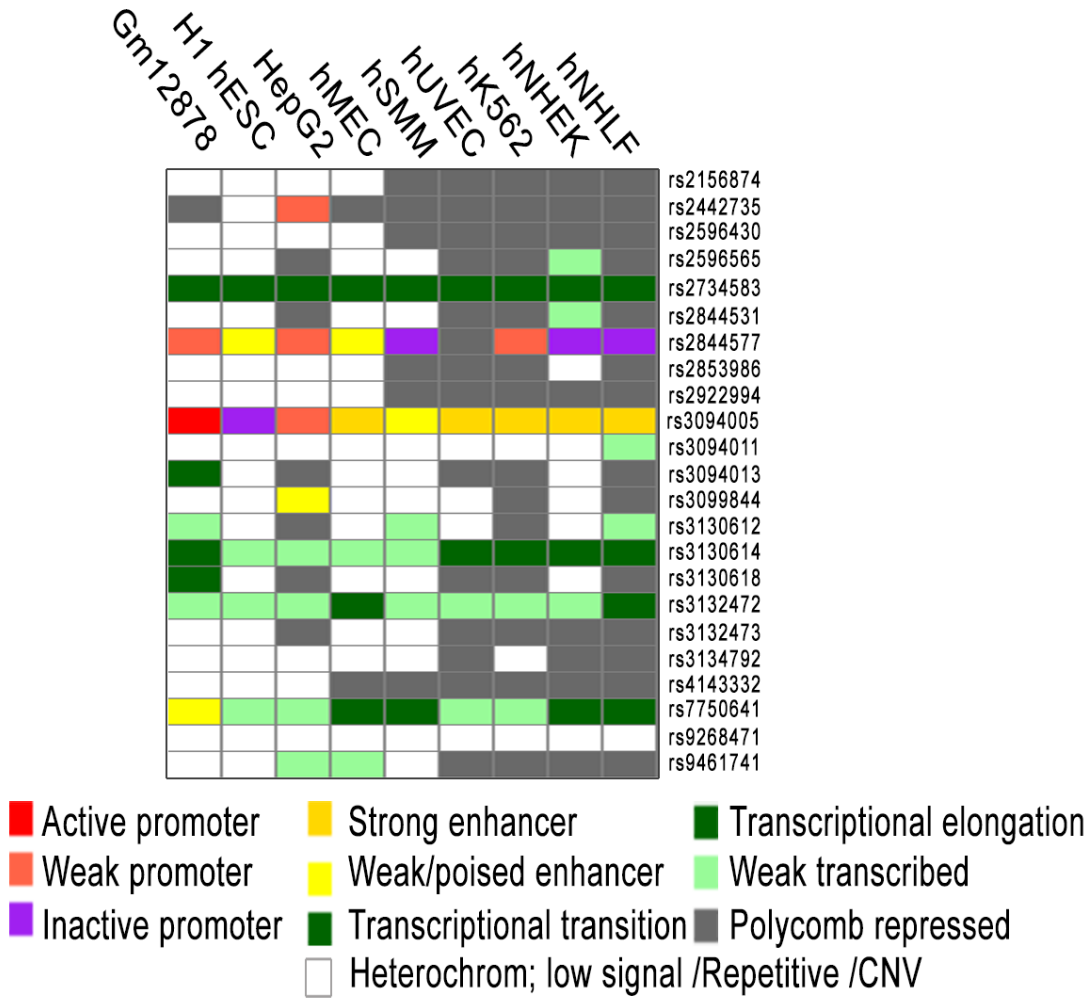

**Supplementary Figure 2. Plot of top eigenvectors from MZL GWAS (stage 1) data based on principal components analysis. For details, see Methods.**




**Supplementary Figure 3. Quantile-quantile (Q-Q) plot of the association results for MZL from stage 1 (NHL-GWAS) (red) and after removing SNPs located in the HLA region (green)**




**Supplementary Figure 4. Manhattan plot of the MZL GWAS (Stage 1) showing chromosomes on X axis and the $-\log_{10}$ of *P*-values on Y axis**




**Supplementary Figure 5. Chromatin states affected by MZL GWAS SNPs and their correlated SNPs ($r^2$=1) from 1000 Genomes data**

## SUPPLEMENTARY TABLES

Supplementary Table 1. Description and design of studies included in stage 1 and stage 2 comprising 1397 cases and 7782 controls

| Study Name | Study Abbreviation | No. MZL Cases[a] | No. Controls[a] | Design, location | Source of cases | Source of controls | Study Reference |
|---|---|---|---|---|---|---|---|
| **Stage 1 - NHL-GWAS** | | | | | | | |
| **Cohort Studies** | | | | | | | |
| Alpha-Tocopherol, Beta-Carotene Lung Cancer Prevention Study | ATBC | 1 | 240[b] | 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 | 56 | 220[b] | 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. Cancer 2002;94:2490-501. |
| European Prospective Investigation into Cancer, Chronic Diseases, Nutrition and Lifestyles | EPIC | 13 | 773 | 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. Public Health Nutr 2002;5(6B):1113-24. |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Health Professionals Follow-up Study | HPFS | 5 | 86 | 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. Lancet 1991;338:464-8. |
| The Melbourne Collaborative Cohort Study | MCCS | 9 | 246 | 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. IARC Sci Publ 2002;156:69-70. |
| Nurses' Health Study | NHS | 12 | 90 | 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. 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. J Natl Cancer Inst 1995;87:1297-302. |
| New York University Women's Health Study | NYU-WHS | 6 | 56 | 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. 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. Cancer Causes Control 2010; 21(8):1323-33. |
| Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial | PLCO | 28 | 3076[b] | 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. 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. Mutat Res 2005;592:147-54. |

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|---|---|---|---|---|---|---|---|
| Women's Health Initiative | WHI | 91 | 395 | 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. |
| **Population-based case-control studies** | | | | | | | |
| British Columbia Non-Hodgkin Lymphoma Study | BCCA | 41 | 390 | 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. Int J Cancer 2007; 121(12):2767-75. |
| Epidemiology & Genetics Unit Lymphoma Case-Control study | ELCCS | 0 | 461 | 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. Cancer Causes Control 2004;15:771-80.<br>**[PMID: 19736055]** Worrillow L. et al. Polymorphisms in the nucleotide excision repair gene ERCC2/XPD and risk of non-Hodgkin lymphoma. Cancer Epidemiol. Cancer Epidemiol 2009;33(3-4):257-60.<br>**[PMID 20832384]** Crouch S. et al. Illness patterns prior to diagnosis of lymphoma: analysis of UK medical records. Cancer Epidemiol. Cancer Epidemiol 2001;35(2):145-50. |
| Multicenter Italian study on gene-environment interactions in lymphoma etiology: translational aspects | Italian GxE | 8 | 54 | Population-based case-control study, Italy | First primary NHL diagnosis identified in the Hematology Departments of the participating centres | Cohort participants alive at time of case diagnosis without cancer | |
| National Cancer Institute-Surveillance, Epidemiology, and End Results Interdisciplinary Case-Control Study of Non-Hodgkin's Lymphoma | NCI-SEER | 65 | 689 | 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. CEBP 2004;13:1415-21.<br>**[PMID: 17018637]** Wang SS. et al. Common genetic variants in proinflammatory and other immunoregulatory genes and risk for non-Hodgkin lymphoma. Cancer Res. Cancer Res 2006;66(19):9771-80. |

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|---|---|---|---|---|---|---|---|
| NSW non-Hodgkin lymphoma study | NSW | 39 | 397 | Population-based case-control study, Australia and New Zealand | Incident NHL diagnosis identified through NSW or 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. IJC 2004;110:429-34. |
| Scandinavian Lymphoma Etiology Study | SCALE | 64 | 301 | 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. J Natl Cancer Inst 2005;97(3)199-209. |
| Molecular Epidemiology of non-Hodgkin lymphoma | UCSF2 | 94 | 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: 20639881**] Skibola CF. et al. Genetic variants at 6p21.33 are associated with susceptibility to follicular lymphoma. Nat Genet. Nat Genet 2009;41(8):873-5. [**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. Nutr Cancer 2012;64(5):674-84. |
| Population-based case-control study in Connecticut women | Yale | 28 | 504 | 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. Am J Epidemiol 2009;170(10):1222-30. |
| **Clinic or hospital-based or mixed case-control studies** | | | | | | | |
| Environmental and genetic risks factors study in adult lymphoma | ENGELA | 8 | 278 | 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. Cancer Causes Control 2008;19(10):1147-60. |

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|---|---|---|---|---|---|---|---|
| Epilymph case-control study in six European countries | EpiLymph | 71 | 1172 | 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. Int J Cancer 2006;119:901-8. |
| Iowa-Mayo SPORE Molecular Epidemiology Resource | Iowa-Mayo SPORE | 113 | 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 | **[PMCID:PMC2953973]** Drake MT. et al. Vitamin D insufficiency and prognosis in non-Hodgkin's lymphoma. J Clin Oncol. J Clin Oncol 2010;28:4191-8. |
| Mayo Clinic Case-Control Study of NHL and CLL | Mayo Case-Control | 78 | 911 | 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 | **[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. Int J Mol Epidemiol Genet 2011;2(2):95-113. |
| Memorial-Sloan Kettering Lymphoproliferative disorders Study | MSKCC | 67 | 9 | Hospital-based case-study and NYCP controls, USA | Hospital clinic based ascertainment in a tertiary referral center | NYCP controls from same geographic area | **[PMID: 12691155]** Yossepowitch O. et al. BRCA1 and BRCA2 germline mutations in lymphoma patients. Leuk Lymphoma. Leuk Lymphoma 2003;44(1):127-31. |
| **Stage 2 - Replication studies** | | | | | | | |
| Iowa-Mayo SPORE Molecular Epidemiology Resource | Iowa-Mayo SPORE | 60 | 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 | **[PMCID:PMC2953973]** Drake MT. et al. Vitamin D insufficiency and prognosis in non-Hodgkin's lymphoma. J Clin Oncol. J Clin Oncol 2010;28:4191-8. |
| Mayo Clinic Case-Control Study of NHL | Mayo Case-Control | 55 | 386 | Clinic-based case-control study, USA | Consecutive patients with newly diagnosed, histologically-confirmed non-Hodgkin lymphoma (excluding HIV-infected cases) who were residents of | Controls were selected from patients seen in the general medicine clinics at Mayo with a pre-scheduled general medical examination, frequency on | **[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. Int J Mol Epidemiol Genet |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | | | | Minnesota, Iowa or Wisconsin | age, sex, and geographic region | 2011;2(2):95-113. |
| MD Anderson lymphoma case-control study | MD Anderson | 74 | 76 | Case-control, USA | MD Anderson Cancer Center | Kelsey Seybold Clinics | |
| Memorial-Sloan Kettering Lymphoproliferative disorders Study | MSKCC | 223 | 378 | 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]** Susceptibility loci associated with specific and shared subtypes of lymphoid malignancies. PLoS Genet. 2013;9(1):e1003220. |
| NCI Replication Study | NCI Rep | 88 | 120 | Mixed study of population and hospital-based cases and controls | MZL cases from the stage 1 studies that did not have sufficient DNA for scanning or failed in scanning due to low completion. | Subset of controls from the stage 1 studies that were not scanned or failed scanning due to low completion. | |

[a]Number of cases and controls with DNA available.
[b]Controls scanned previously on the Illumina Omni2.5.

Supplementary Table 2. Stage 1 subjects genotyped, quality control exclusions, and subjects included in the analysis

| | Genotyped Subjects | | Exclusions | | | | | | | | | | Final subjects included in the analysis | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | High missing rate | | Gender discordance | | Unexpected duplicates | | Non CEU | | Previously scanned | | | | |
| **Study** | **Cases** | **Controls** | **Cases** | **Controls** | **Cases** | **Controls** | **Cases** | **Controls** | **Cases** | **Controls** | **Cases** | **Controls** | **Cases** | **Controls** | **Total** |
| **Cohort studies** | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| ATBC | 1 | - | - | - | - | - | - | - | - | - | - | 240 | 1 | 240 | 241 |
| CPS-II | 56 | - | 4 | - | - | - | - | - | - | - | - | 220 | 52 | 220 | 272 |
| EPIC | 10 | 275 | 2 | 9 | - | 1 | - | - | - | - | - | - | 8 | 265 | 273 |
| HPFS | 5 | 86 | - | 0 | - | - | - | - | - | 1 | - | - | 5 | 85 | 90 |
| MCCS | 9 | 76 | 1 | 1 | - | - | - | - | - | | - | - | 8 | 75 | 83 |
| NHS | 12 | 90 | - | 2 | - | - | - | - | - | - | - | - | 12 | 88 | 100 |
| NYU-WHS | 6 | 56 | - | 3 | - | - | - | - | - | - | - | - | 6 | 53 | 59 |
| PLCO | 28 | - | - | - | - | - | 2 | - | - | - | - | 3076 | 26 | 3076 | 3102 |
| WHI | 91 | 250 | 5 | 19 | - | - | 1 | - | 1 | 3 | - | - | 84 | 228 | 312 |
| **Subtotal** | 218 | 833 | 12 | 34 | - | 1 | 3 | - | 1 | 4 | - | 3536 | 202 | 4330 | 4532 |
| **Population-based case-control studies** | | | - | - | - | - | - | - | - | - | - | - | - | - | - |
| BCCA | 41 | 110 | 1 | 1 | - | - | - | - | - | - | - | - | 40 | 109 | 149 |
| ELCCS | - | 251 | - | 5 | - | 1 | - | - | - | - | - | - | - | 245 | 245 |
| Italian GxE | 9 | 54 | 3 | 8 | - | 1 | - | - | - | - | - | - | 6 | 45 | 51 |
| NCI-SEER | 65 | 298 | 2 | 23 | - | 2 | - | - | 1 | 3 | - | - | 62 | 270 | 332 |
| NSW | 34 | 157 | - | 2 | - | 1 | - | - | - | - | - | - | 34 | 154 | 188 |
| SCALE | 64 | 299 | - | 6 | - | - | - | - | - | 2 | - | - | 64 | 291 | 355 |
| UCSF2 | 94 | 10 | 1 | 0 | - | - | - | - | 2 | - | - | - | 91 | 10 | 101 |
| YALE | 28 | 149 | - | 3 | - | - | - | - | - | - | - | - | 28 | 146 | 174 |
| **Subtotal** | 335 | 1328 | 7 | 48 | - | 5 | - | - | 3 | 5 | - | - | 325 | 1270 | 1595 |
| **Clinic or hospital-based or mixed case-control studies** | | | - | - | - | - | - | - | - | - | - | - | - | - | - |
| ENGELA | 8 | 77 | 3 | 14 | - | - | - | - | - | - | - | - | 5 | 63 | 68 |
| EpiLymph | 71 | 250 | 12 | 35 | - | - | - | 1 | - | 3 | - | - | 59 | 211 | 270 |
| Iowa-Mayo SPORE | 113 | - | 1 | 0 | - | - | - | - | - | - | - | - | 112 | - | 112 |
| Mayo Case-Control | 78 | 357 | 2 | 12 | - | - | - | 1 | 1 | 1 | - | - | 75 | 343 | 418 |
| MSKCC | 67 | 9 | 18 | 5 | - | - | - | - | 2 | - | - | - | 47 | 4 | 51 |
| **Subtotal** | 337 | 693 | 36 | 66 | - | - | - | 2 | 3 | 4 | - | - | 298 | 621 | 919 |
| **Grand total** | **890** | **2854** | **55** | **148** | **-** | **6** | **3** | **2** | **7** | **13** | **-** | **3536** | **825** | **6221** | **7046** |

Supplementary Table 3. Characteristics and summary of the cases and controls included in the final analysis for MZL GWAS and replication

| | No. of subjects | | % Male | | Mean age (SD) | |
|---|---|---|---|---|---|---|
| **Study** | **Cases** | **Controls** | **Cases** | **Controls** | **Cases** | **Controls** |
| **STAGE 1 GWAS** | | | | | | |
| ATBC | 1 | 240 | 100.0% | 100.0% | 61.00 (0.00) | 68.35 (7.67) |
| BCCA | 40 | 109 | 47.5% | 56.0% | 65.05 (10.75) | 60.70 (12.66) |
| CPS-II | 52 | 220 | 50.0% | 49.5% | 72.96 (7.33) | 68.41 (6.28) |
| EPIC | 8 | 265 | 37.5% | 45.3% | 59.00 (7.38) | 62.65 (8.42) |
| ENGELA | 5 | 63 | 100.0% | 65.1% | 58.40 (7.39) | 55.25 (11.34) |
| EpiLymph | 59 | 211 | 35.6% | 54.0% | 59.93 (14.24) | 59.31 (12.96) |
| HPFS | 5 | 85 | 100.0% | 100.0% | 64.20 (8.16) | 70.56 (8.43) |
| Iowa-Mayo SPORE | 112 | 0 | 47.3% | NA | 63.51(10.35) | NA |
| Italian GxE | 6 | 45 | 66.7% | 62.2% | 55.83 (14.68) | 55.38 (11.68) |
| MAYO Case-control | 75 | 343 | 41.3% | 61.2% | 62.88 (11.47) | 60.90 (13.35) |
| MCCS | 8 | 75 | 50.0% | 52.0% | 68.88 (8.25) | 70.96 (7.85) |
| MSKCC | 47 | 4 | 36.2% | 0.0% | 59.17 (11.78) | 41.25 (9.36) |
| NCI-SEER | 62 | 270 | 51.6% | 54.1% | 60.21 (13.11) | 56.57 (11.94) |
| NHS | 12 | 88 | 0.0% | 0.0% | 71.92 (3.35) | 64.01 (6.91) |
| NSW | 34 | 154 | 44.1% | 60.4% | 59.56 (11.71) | 57.19 (11.13) |
| NYU-WHS | 6 | 53 | 0.0% | 0.0% | 74.33(7.99) | 76.17 (9.20) |
| PLCO | 26 | 3076 | 53.8% | 95.7% | 71.31 (7.21) | 69.54 (6.19) |
| SCALE | 64 | 291 | 57.8% | 57.7% | 60.33(9.95) | 60.01(12.12) |
| UCSF2 | 91 | 10 | 51.6% | 60.0% | 60.33 (14.73) | 43.40 (14.83) |
| ELCCS | 0 | 245 | NA | 50.6% | NA | 53.19 (8.19) |
| WHI | 84 | 228 | 0.0% | 0.0% | 72.90(7.16) | 77.66(6.58) |
| YALE | 28 | 146 | 0.0% | 0.0% | 63.57 (11.47) | 61.68 (13.47) |
| Total | 825 | 6221 | 40.5% | 72.8% | 63.94(12.18) | 66.04(10.44) |
| **REPLICATION** | | | | | | |
| MD Anderson | 74 | 76 | 39.19% | 39.47% | 59.32 (10.08) | 59.26 (9.87) |
| MSKCC | 223 | 378 | 43.95% | 17.99% | 61.09 (13.55) | 57.80 (11.69) |
| MAYO | 115 | 383 | 47.83% | 57.96% | 60.41 (13.54) | 62.13 (12.33) |
| NCI Replication | 44 | 69 | 56.82% | 39.13% | 65.75 (10.75) | 60.80 (14.79) |
| Total | 456 | 906 | 45.39% | 38.30% | 61.08 (12.86) | 59.98 (12.23) |
| **Grand Total** | 1281 | 7127 | 42.23% | 68.39% | 62.92 (12.50) | 65.27 (10.87) |

## Supplementary Table 4. Association with MZL for all SNPs taken forward for replication

| SNP | Chr | Position[a] | Risk allele[b] | Other allele | RAF[c] | Genotyped/ Imputed[d] | Stage | No. of cases | No. of controls | OR | (95% CI) | *P* | $P_{heterogeneity}$ | $I^2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs9461741 | 6 | 32370587 | C | G | 0.018 | i (0.999) | Stage 1 | 824 | 6220 | 2.40 | (1.74-3.31) | 9.11E-08 | | |
| | | | | | 0.030 | g | Stage 2 | 453 | 877 | 3.06 | (2.10-4.46) | 5.24E-09 | | |
| | | | | | | | **Combined** | **1277** | **7097** | **2.66** | **(2.08-3.39)** | **3.95E-15** | **0.216** | **34.69** |
| rs2922994 | 6 | 31335901 | G | A | 0.113 | i (1.00) | Stage 1 | 825 | 6221 | 1.74 | (1.43-2.12) | 2.89E-08 | | |
| | | | | | 0.094 | g | Stage 2 | 405 | 832 | 1.43 | (1.08-1.90) | 0.01 | | |
| | | | | | | | **Combined** | **1230** | **7053** | **1.64** | **(1.39-1.92)** | **2.43E-09** | **0.507** | **0** |
| rs7750641 | 6 | 31129310 | T | C | 0.113 | g | Stage 1 | 825 | 6221 | 1.68 | (1.38-2.04) | 2.57E-07 | | |
| | | | | | 0.095 | g | Stage 2 | 451 | 900 | 1.38 | (1.05-1.80) | 0.02 | | |
| | | | | | | | **Combined** | **1276** | **7121** | **1.57** | **(1.34-1.84)** | **3.34E-08** | **0.186** | **40.52** |
| rs9268671 | 6 | 32414290 | G | A | 0.685 | i (0.992) | Stage 1 | 825 | 6220 | 1.39 | (1.23-1.56) | 5.53E-08 | | |
| | | | | | 0.312 | g | Stage 2 | 445 | 894 | 0.96 | (0.81-1.15) | 0.66 | | |
| | | | | | | | **Combined** | **1270** | **7114** | **1.27** | **(1.15-1.41)** | **1.91E-06** | **0.001** | **85.15** |
| rs76788097 | 14 | 61729493 | G | A | 0.062 | i (0.986) | Stage 1 | 824 | 6221 | 1.63 | (1.32-2.01) | 6.64E-06 | | |
| | | | | | 0.064 | g | Stage 2 | 447 | 897 | 1.33 | (0.97-1.83) | 0.08 | | |
| | | | | | | | **Combined** | **1271** | **7118** | **1.53** | **(1.28-1.82)** | **2.31E-06** | **0.244** | **29.10** |
| rs76588427 | 2 | 21135687 | A | G | 0.017 | i (0.989) | Stage 1 | 825 | 6220 | 2.38 | (1.65-3.44) | 4.02E-06 | | |
| | | | | | 0.022 | g | Stage 2 | 448 | 901 | 1.53 | (0.92-2.55) | 0.10 | | |
| | | | | | | | **Combined** | **1273** | **7121** | **2.05** | **(1.52-2.76)** | **2.70E-06** | **0.209** | **36.06** |
| rs1202393 | 7 | 148915298 | A | G | 0.139 | i (0.998) | Stage 1 | 825 | 6220 | 1.41 | (1.21-1.64) | 7.05E-06 | | |
| | | | | | 0.157 | g | Stage 2 | 450 | 896 | 1.08 | (0.86-1.36) | 0.51 | | |
| | | | | | | | **Combined** | **1275** | **7116** | **1.30** | **(1.15-1.48)** | **3.60E-05** | **0.002** | **84.22** |
| rs55825400 | 8 | 76068956 | A | G | 0.025 | i (0.891) | Stage 1 | 824 | 6220 | 2.41 | (1.67-3.48) | 2.43E-06 | | |
| | | | | | 0.026 | g | Stage 2 | 449 | 904 | 1.21 | (0.72-2.04) | 0.47 | | |
| | | | | | | | **Combined** | **1273** | **7124** | **1.92** | **(1.42-2.59)** | **1.94E-05** | **0.043** | **68.33** |
| rs6768604 | 3 | 185704345 | A | G | 0.279 | g | Stage 1 | 825 | 6221 | 1.35 | (1.20-1.54) | 8.59E-07 | | |
| | | | | | 0.270 | g | Stage 2 | 452 | 895 | 0.93 | (0.77-1.12) | 0.45 | | |
| | | | | | | | **Combined** | **1277** | **7116** | **1.21** | **(1.10-1.35)** | **0.0002** | **0.004** | **82.03** |
| rs59059443 | 5 | 29727289 | T | C | 0.037 | i (0.813) | Stage 1 | 824 | 6220 | 2.13 | (1.55-2.93) | 2.72E-06 | | |
| | | | | | 0.055 | g | Stage 2 | 451 | 895 | 0.89 | (0.60-1.31) | 0.54 | | |
| | | | | | | | **Combined** | **1275** | **7115** | **1.50** | **(1.17-1.91)** | **0.001** | **0.001** | **84.64** |

[a]Position according to human reference NCBI37/hg19; [b]Allele associated with an increased risk of MZL; [c]Risk allele frequency in controls; [d]g=genotyped, i=imputed (info) p-values and odds-ratios were generated by using logistic regression. Heterogeneity in the effect estimates was assessed using Cochran's Q statistic and estimating the $I^2$ statistic.

**Supplementary Table 5. Risk associated with MZL for SNPs in the HLA region previously reported to be associated with other lymphoma subtypes**

| SNP | Position | Effect allele | Other allele | Genotyped /Imputed | EAF | No. of cases | No. of controls | OR | 95% CI | *P* | NHL subtype association | PubMed ID | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs6457327 | 31074030 | C | A | g | 0.617 | 825 | 6221 | 1.05 | (0.94-1.18) | 0.37 | FL | 19620980 | Skibola CF *et al.* |
| rs2248462 | 31446796 | A | G | g | 0.209 | 825 | 6221 | 0.88 | (0.77-1.01) | 0.07 | HD | 22286212 | Urayama KY *et al.* |
| rs3132453 | 31604044 | G | T | g | 0.933 | 825 | 6221 | 0.98 | (0.78-1.23) | 0.86 | B-cell lymphoma | 23047821 | Nieters A *et al.* |
| rs204999 | 32109979 | G | A | g | 0.261 | 825 | 6221 | 0.97 | (0.84-1.10) | 0.67 | NS-HD | 22086417 | Cozen W *et al.* |
| rs926070 | 32257566 | A | G | g | 0.681 | 825 | 6221 | 0.90 | (0.80-1.01) | 0.08 | CLL | 24292274 | Speedy HE *et al.* |
| rs9268528 | 32383108 | G | A | g | 0.379 | 825 | 6221 | 0.88 | (0.79-0.98) | 0.02 | NS-HD | 22086417 | Cozen W *et al.* |
| rs9268542 | 32384721 | G | A | g | 0.383 | 825 | 6221 | 0.87 | (0.78-0.97) | 0.02 | NS-HD | 22086417 | Cozen W *et al.* |
| rs6903608 | 32428285 | T | C | g | 0.680 | 825 | 6221 | 0.96 | (0.85-1.07) | 0.44 | HD | 21037568 | Enciso-Mora V *et al.* |
| rs9268853 | 32429643 | C | T | g | 0.306 | 825 | 6221 | 0.92 | (0.82-1.04) | 0.17 | Lymphoma | 23349640 | Vijai J *et al.* |
| rs2395185 | 32433167 | T | G | g | 0.306 | 825 | 6221 | 0.92 | (0.82-1.04) | 0.17 | HD | 22286212 | Urayama KY *et al.* |
| rs2858870 | 32572251 | C | T | i (0.937) | 0.108 | 824 | 6220 | 0.84 | (0.71-1.01) | 0.06 | NS-HD | 22086417 | Cozen W *et al.* |
| rs674313 | 32578082 | T | C | i (0.997) | 0.260 | 825 | 6220 | 1.14 | (1.01-1.30) | 0.04 | CLL | 21131588 | Slager SL *et al.* |
| rs4530903 | 32581889 | T | C | g | 0.114 | 825 | 6221 | 1.03 | (0.87-1.21) | 0.77 | Lymphoma | 23349640 | Vijai J *et al.* |
| rs9272535 | 32606756 | A | G | i (0.952) | 0.263 | 824 | 6220 | 1.18 | (1.04-1.33) | 0.01 | CLL | 21131588 | Slager SL *et al.* |
| rs9273363 | 32626272 | A | C | g | 0.270 | 825 | 6221 | 1.05 | (0.93-1.19) | 0.44 | CLL | 23770605 | Berndt SI *et al.* |
| rs2647012 | 32664458 | C | T | i (1.0) | 0.601 | 825 | 6221 | 0.89 | (0.79-0.99) | 0.04 | FL | 21533074 | Smedby KE *et al.* |
| rs10484561 | 32665420 | G | T | i (1.0) | 0.121 | 825 | 6221 | 0.99 | (0.84-1.17) | 0.92 | FL | 20639881 | Conde L *et al.* |
| rs2647045 | 32668100 | A | G | i (0.996) | 0.236 | 825 | 6221 | 0.94 | (0.83-1.06) | 0.30 | Lymphoma | 23349640 | Vijai J *et al.* |
| rs2621416 | 32741868 | C | T | g | 0.276 | 825 | 6221 | 0.93 | (0.83-1.05) | 0.27 | Lymphoma | 23349640 | Vijai J *et al.* |
| rs241447 | 32796751 | C | T | g | 0.269 | 825 | 6221 | 0.94 | (0.83-1.06) | 0.28 | FL | 22911331 | Cerhan J *et al.* |

Abbreviations: HD: Hodgkin's lymphoma; CLL: Chronic Lymphocytic leukemia; NS-HD: Nodular sclerosing Hodgkin's lymphoma; FL: Follicular Lymphoma; EAF: Effect Allele Frequency; OR: Odds-ratio; P: p-value

## Supplementary Table 6. Associations with MZL for the HLA allele and amino acid position imputed from the GWAS data

| Marker | Risk allele | Other allele | MAF | INFO | OR | 95% CI | *P* |
|---|---|---|---|---|---|---|---|
| *HLA-B*0801* | Pr | Ab | 0.115 | 1.02 | 1.67 | (1.38-2.01) | 7.79E-08 |
| *HLA-B* Asp at position 9 | Pr | Ab | 0.115 | 1.02 | 1.67 | (1.38-2.01) | 7.94E-08 |
| *HLA-B*08* | Pr | Ab | 0.115 | 1.02 | 1.67 | (1.38-2.01) | 7.94E-08 |
| *HLA-DRB1*0102* | Pr | Ab | 0.017 | 1.06 | 2.24 | (1.64-3.07) | 5.08E-07 |
| *HLA-DRβ1* Ala at position 85 | Ala | Val | 0.035 | 1.00 | 1.84 | (1.44-2.34) | 7.80E-07 |

Alleles: Pr=present, Ab=absent, Ala=Alanine, Val=Valine, MAF=Minor Allele Frequency, INFO= marker imputation quality information, OR=odds-ratio and P=p-value
Logistic regression analysis using the log-additive model and age of onset, gender and significant eigenvalues used as covariates.

## Supplementary Table 7. Results for the two novel loci stratified by MZL subtype (MALT vs. non-MALT)

| | | | | MALT | | | | Non-MALT | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SNP | Risk allele[a] | Other allele | RAF[b] | No. of cases/ No. of controls | OR | 95% CI | *P* | No. of cases/ No. of controls | OR | 95% CI | *P* | $P_{heterogeneity}$ |
| rs2922994 | G | A | 0.11 | 358/6221 | 1.92 | (1.50-2.47) | 2.43E-07 | 467/6221 | 1.58 | (1.23-2.03) | 0.0004 | 0.6 |
| rs9461741 | C | G | 0.02 | 358/6220 | 2.95 | (1.89-4.62) | 2.19E-06 | 466/6220 | 2.44 | (1.57-3.79) | 7.27E-05 | 0.05 |

[a]Allele associated with an increased risk of MZL; [b]Risk allele frequency in controls. p-values and odds-ratios were generated by using logistic regression . Heterogeneity in the effect estimates was assessed using Cochran's Q statistic and estimating the $I^2$ statistic.

## Supplementary Table 8. Association results for *H.pylori*-associated SNPs with MZL and MALT

| Group | SNP | Chr | Position | Other Allele | Effect Allele | f-Case | f-Ctrl | OR | (95% CI) | *P* |
|---|---|---|---|---|---|---|---|---|---|---|
| MZL | rs4833103 | 4 | 38815502 | A | C | 0.526 | 0.465 | 1.15 | (1.03-1.28) | 0.01 |
| MZL | rs11568818 | 11 | 102401661 | T | C | 0.479 | 0.449 | 1.14 | (1.03-1.27) | 0.01 |
| MZL | rs2066844 | 16 | 50745926 | C | T | 0.033 | 0.045 | 0.74 | (0.58-0.96) | 0.02 |
| MALT | rs4833103 | 4 | 38815502 | A | C | 0.5098 | 0.4654 | 1.04 | (0.89-1.22) | 0.59 |
| MALT | rs11568818 | 11 | 102401661 | T | C | 0.4679 | 0.4495 | 1.09 | (0.94-1.28) | 0.26 |
| MALT | rs2066844 | 16 | 50745926 | C | T | 0.0405 | 0.0454 | 0.90 | (0.62-1.30) | 0.58 |

Chr: chromosome; Position: hg19 coordinate start, f-Case: allele frequency in cases, f-Ctrl: allele frequency in controls, OR=odds-ratio and P=p-value
Logistic regression analysis using the log-additive model and age of onset, gender and significant eigenvalues used as covariates.

## Supplementary Table 9. eQTL associations for the MZL SNPs from a childhood asthma study (data from Dixon et al.)*

| MZL SNP | Gene transcript | Effect allele | Other allele | Beta for MZL SNP[a] | *P* for MZL SNP[a] | *P* for MZL SNP conditioned on peak SNP[b] | Peak SNP for transcript[c] | Beta for Peak SNP[d] | *P* for Peak SNP[d] | *P* for peak SNP conditioned on MZL SNP[e] |
|---|---|---|---|---|---|---|---|---|---|---|
| rs2922994 | *HLA-C* | A | G | -2.564 | 7.06E-11 | 9.06E-06 | rs140242258 | 0.836 | 7.36E-25 | 1.31E-22 |
| rs7750641 | *HLA-C* | C | T | -0.544 | 1.02E-12 | 3.98E-08 | rs140242258 | 0.836 | 7.36E-25 | 1.53E-22 |
| rs2922994 | *HLA-B* | A | G | -1.225 | 1.59E-05 | 0.013 | rs140242258 | 0.461 | 3.51E-15 | 5.31E-13 |
| rs7750641 | 1557242_at | C | T | -0.443 | 3.12E-06 | 3.42E-05 | rs80296299 | 0.988 | 5.23E-12 | 1.97E-10 |

[*]See Methods for details
[a]Beta and p-value for the association between the MZL SNP and gene transcript.
[b]p-value for the association between the MZL SNP and gene transcript after adjustment for the peak SNP
[c]Peak SNP is the most significant SNP associated with the gene transcript
[d]Beta and p-value for the association between the peak SNP and the gene transcript
[e]P-value for the association between the peak SNP and the gene transcript after adjustment for the MZL SNP

**Supplementary Table 10. eQTL associations with the correlated SNP for the HLA SNP rs2922994. Only those with FDR p-value≤0.05 are shown.**

| SNP | CHR:POS | $r^2$ | Probe | *P* | FDR |
|---|---|---|---|---|---|
| rs2524069 | 6:31244789 | 0.86 | RNF5:NM_006913.RNF5 | 3.16E-06 | 0.006 |
| rs2844613 | 6:31243846 | 0.86 | RNF5:NM_006913.RNF5 | 2.55E-06 | 0.006 |
| rs2524067 | 6:31245821 | 0.86 | RNF5:NM_006913.RNF5 | 3.16E-06 | 0.006 |
| rs3099844 | 6:31448976 | 0.92 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs2596565 | 6:31353329 | 1 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs3132510 | 6:31172151 | 1 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs3131643 | 6:31442782 | 0.84 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs3134792 | 6:31312326 | 1 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs2524078 | 6:31242649 | 0.81 | RNF5:NM_006913.RNF5 | 1.95E-05 | 0.024 |
| rs3094005 | 6:31465047 | 0.92 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs2734583 | 6:31505480 | 0.92 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs3131618 | 6:31434621 | 0.92 | RNF5:NM_006913.RNF5 | 5.55E-05 | 0.024 |
| rs9266669 | 6:31348077 | 0.87 | RNF5:NM_006913.RNF5 | 3.94E-05 | 0.024 |
| rs2844577 | 6:31334422 | 1 | LY6G6E:NR_003673.LY6G6E | 7.22E-05 | 0.029 |
| rs1634726 | 6:30985828 | 0.81 | LY6G6E:NR_003673.LY6G6E | 9.99E-05 | 0.037 |
| rs2524069 | 6:31244789 | 0.86 | HLA-E:NM_005516.HLA-E | 1.83E-04 | 0.045 |
| rs2524069 | 6:31244789 | 0.86 | FLOT1:NM_005803.FLOT1 | 3.62E-04 | 0.045 |
| rs2844613 | 6:31243846 | 0.86 | HLA-E:NM_005516.HLA-E | 2.41E-04 | 0.045 |
| rs2844613 | 6:31243846 | 0.86 | FLOT1:NM_005803.FLOT1 | 2.41E-04 | 0.045 |
| rs4143332 | 6:31348365 | 1 | FLOT1:NM_005803.FLOT1 | 3.17E-04 | 0.045 |
| rs4143332 | 6:31348365 | 1 | RNF5:NM_006913.RNF5 | 2.76E-04 | 0.045 |
| rs3099844 | 6:31448976 | 0.92 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs2524067 | 6:31245821 | 0.86 | HLA-E:NM_005516.HLA-E | 1.83E-04 | 0.045 |
| rs2524067 | 6:31245821 | 0.86 | FLOT1:NM_005803.FLOT1 | 3.62E-04 | 0.045 |
| rs3132473 | 6:31408329 | 0.9 | LY6G6E:NR_003673.LY6G6E | 1.71E-04 | 0.045 |
| rs2596565 | 6:31353329 | 1 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs3132510 | 6:31172151 | 1 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs3131643 | 6:31442782 | 0.84 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs3130923 | 6:31462135 | 0.84 | FLOT1:NM_005803.FLOT1 | 2.47E-04 | 0.045 |
| rs3132472 | 6:31386131 | 0.92 | FLOT1:NM_005803.FLOT1 | 3.17E-04 | 0.045 |
| rs3132472 | 6:31386131 | 0.92 | RNF5:NM_006913.RNF5 | 2.76E-04 | 0.045 |
| rs2844559 | 6:31340075 | 1 | RNF5:NM_006913.RNF5 | 2.15E-04 | 0.045 |
| rs3134792 | 6:31312326 | 1 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs2524078 | 6:31242649 | 0.81 | FLOT1:NM_005803.FLOT1 | 3.55E-04 | 0.045 |
| rs2922994 | 6:31335901 | NA | FLOT1:NM_005803.FLOT1 | 3.17E-04 | 0.045 |
| rs2922994 | 6:31335901 | NA | RNF5:NM_006913.RNF5 | 2.76E-04 | 0.045 |
| rs3130614 | 6:31476458 | 0.92 | FLOT1:NM_005803.FLOT1 | 3.17E-04 | 0.045 |
| rs3130614 | 6:31476458 | 0.92 | RNF5:NM_006913.RNF5 | 2.76E-04 | 0.045 |
| rs3094005 | 6:31465047 | 0.92 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs2734583 | 6:31505480 | 0.92 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs3131618 | 6:31434621 | 0.92 | FLOT1:NM_005803.FLOT1 | 3.72E-04 | 0.045 |
| rs9266669 | 6:31348077 | 0.87 | FLOT1:NM_005803.FLOT1 | 2.65E-04 | 0.045 |
| rs2596430 | 6:31335431 | 1 | FLOT1:NM_005803.FLOT1 | 3.17E-04 | 0.045 |
| rs2596430 | 6:31335431 | 1 | RNF5:NM_006913.RNF5 | 2.76E-04 | 0.045 |
| rs2156874 | 6:31335976 | 1 | FLOT1:NM_005803.FLOT1 | 3.17E-04 | 0.045 |
| rs2156874 | 6:31335976 | 1 | RNF5:NM_006913.RNF5 | 2.76E-04 | 0.045 |
| rs3130612 | 6:31482097 | 0.92 | RNF5:NM_006913.RNF5 | 3.86E-04 | 0.046 |

| | | | | | |
|---|---|---|---|---|---|
| rs2524078 | 6:31242649 | 0.81 | DPCR1:NM_080870.DPCR1 | 4.11E-04 | 0.048 |

**Supplementary Table 11. Functional motif annotations from HaploReg analysis of newly-discovered MZL risk loci and their correlated ($r^2$ > 0.80) SNPs**

| chr | pos (hg19) | LD ($r^2$) | variant | Ref | Alt | EUR freq | SiPhy cons | Promoter histone marks | Enhancer histone marks | DNAse | Proteins bound | Motifs changed | GENCODE genes | dbSNP func annot | SNP in LD |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 31326074 | 0.87 | rs2853999 | A | T | 0.09 | | HepG2 | GM12878, NHLF | CD34+_Mobilized | POL2 | STAT | 1.1kb 5' of HLA-B | | rs2156874 |
| 6 | 31326703 | 0.91 | rs2523593 | T | C | 0.09 | | | NHLF, GM12878 | Hepatocytes | | E2A,Myc,Pax-4 | 1.7kb 5' of HLA-B | | rs2156874 |
| 6 | 31327890 | 0.95 | rs2523584 | A | G | 0.09 | | | | | | 6 altered motifs | 2.9kb 5' of HLA-B | | rs2156874 |
| 6 | 31328988 | 0.95 | rs2523573 | C | G | 0.09 | | | | | | 4 altered motifs | 4kb 5' of HLA-B | | rs2156874 |
| 6 | 31329374 | 0.95 | rs2596545 | A | C | 0.09 | | | | | | 5 altered motifs | 4.4kb 5' of HLA-B | | rs2156874 |
| 6 | 31329642 | 0.95 | rs2596547 | C | T | 0.09 | | | | | | AP-1,Foxa,Foxj1 | 4.7kb 5' of HLA-B | | rs2156874 |
| 6 | 31329691 | 0.95 | rs2523571 | T | A | 0.09 | | | | | | 5 altered motifs | 4.7kb 5' of HLA-B | | rs2156874 |
| 6 | 31332920 | 1 | rs2523546 | G | A | 0.09 | | | | | | Pax-5,Pax-8,SRF | 5kb 5' of U6 | | rs2156874 |
| 6 | 31334422 | 1 | rs2844577 | T | C | 0.09 | | 6 cell types | H1, HMEC | AoSMC | | Pou6f1 | 3.5kb 5' of U6 | | rs2156874 |
| 6 | 31335431 | 1 | rs2596430 | T | C | 0.09 | | | | | | HDAC2,HNF4 | 2.5kb 5' of U6 | | rs2156874 |
| 6 | 31335901 | 1 | rs2922994 | A | G | 0.09 | | | | | | 4 altered motifs | 2kb 5' of U6 | | rs2156874 |
| 6 | 31335976 | 1 | rs2156874 | G | C | 0.09 | | | | | | CEBPB,Cdc5,Mef2 | 1.9kb 5' of U6 | | rs2156874 |
| 6 | 31338844 | 0.86 | rs2853986 | T | C | 0.09 | | | | | | | 826bp 3' of U6 | | rs2156874 |
| 6 | 31339996 | 0.94 | rs2523524 | G | A | 0.09 | | | | | | ELF1,GR,p300 | 2kb 3' of U6 | | rs2156874 |
| 6 | 31340075 | 0.94 | rs2844559 | C | T | 0.09 | | | | | | | 2kb 3' of AL671883.1 | | rs2156874 |
| 6 | 31344390 | 0.83 | rs2905719 | A | G | 0.09 | | | | Osteobl | | COMP1 | 2.2kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31346653 | 0.85 | rs2442735 | A | G | 0.09 | | HepG2 | | 5 cell types | | HIF1,Pax-5,Zfp161 | 4.5kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31346849 | 0.85 | rs11433356 | CG | C | 0.09 | | | HepG2 | | | GR,Hmx,SREBP | 4.7kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31348365 | 0.85 | rs4143332 | G | A | 0.09 | | | | | | TLX1::NFIC | 6.2kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31348519 | 0.85 | rs4143333 | A | G | 0.09 | | | | | | Nkx2 | 6.3kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31353171 | 0.8 | rs2844531 | A | G | 0.09 | | | | | | STAT | 11kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31353329 | 0.8 | rs2596565 | G | A | 0.09 | | | | pHTE | | SP1 | 11kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31353435 | 0.8 | rs2844530 | C | G | 0.09 | | | | pHTE | | CCNT2,EWSR1-FLI1,UF1H3BETA | 11kb 5' of AL671883.1 | | rs2156874 |
| 6 | 31348822 | 0.86 | rs201523396 | AAT | A | 0.08 | | | | | | 10 altered motifs | 6.6kb 5' of AL671883.1 | | rs2442735 |
| 6 | 31348830 | 0.84 | rs200032555 | TA | T | 0.08 | | | | | | 31 altered motifs | 6.6kb 5' of AL671883.1 | | rs2442735 |
| 6 | 31462135 | 0.87 | rs3130923 | G | A | 0.08 | | 9 cell types | | 25 cell types | 5 bound proteins | 7 altered motifs | 522bp 5' of MICB | | rs2442735 |
| 6 | 31465047 | 0.87 | rs3094005 | G | T | 0.08 | | GM12878, HepG2, H1 | 6 cell types | HMEC | | 5 altered motifs | MICB | | rs2442735 |
| 6 | 31469774 | 0.87 | rs3095233 | A | G | 0.08 | | | GM12878 | | | Bbx,Sox | MICB | intronic | rs2442735 |
| 6 | 31473746 | 0.9 | rs3130616 | G | A | 0.08 | | | | | | 21 altered motifs | MICB | intronic | rs2442735 |
| 6 | 31473957 | 0.83 | rs3134900 | C | G | 0.09 | | | | | | ATF3,NRSF | MICB | missense | rs2442735 |
| 6 | 31476458 | 0.88 | rs3130614 | T | A | 0.08 | | | | | | Ets,Mef2 | MICB | intronic | rs2442735 |
| 6 | 31482097 | 0.9 | rs3130612 | T | G | 0.08 | | | | | | 6 altered motifs | 3.2kb 3' of MICB | | rs2442735 |
| 6 | 31483481 | 0.92 | rs9267445 | G | C | 0.08 | | | | | | HNF4,Rad21 | 4.6kb 3' of MICB | | rs2442735 |
| 6 | 31505480 | 1 | rs2734583 | A | G | 0.08 | | | | Fibrobl,WERI-Rb-1 | | | ATP6V1G2-DDX39B | intronic | rs2442735 |
| 6 | 31514247 | 1 | rs9267488 | A | G | 0.08 | | 4 cell types | 5 cell types | | KAP1 | 4 altered motifs | ATP6V1G2 | intronic | rs2442735 |
| 6 | 31546850 | 0.93 | rs1800628 | G | A | 0.08 | | | NHEK, GM12878, HMEC | GM12864 | POL24H8,POL2 | 6 altered motifs | 736bp 3' of TNF | | rs2442735 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 31558702 | 0.9 | rs3130063 | C | T | 0.08 | | | | | | Rad21,SMC3 | NCR3 | intronic | rs2442735 |
| 6 | 31566168 | 0.93 | rs3130631 | C | G | 0.08 | | HepG2 | GM12878 | HepG2 | 5 bound proteins | HIF1,HNF4 | 5.4kb 5' of NCR3 | | rs2442735 |
| 18 | 53721590 | 0.92 | rs1970748 | A | G | 0.51 | | | | | | 4 altered motifs | AC006305.1 | | rs2852986 |
| 18 | 53733950 | 0.99 | rs2109685 | G | A | 0.51 | | | | NHDF-Ad | | | AC006305.1 | | rs2852986 |
| 18 | 53734603 | 0.99 | rs2535726 | A | G | 0.51 | | | HSMM | 19 cell types | CTCF,P300 | GR,STAT | AC006305.1 | | rs2852986 |
| 18 | 53735471 | 0.99 | rs2535727 | G | A | 0.51 | | | 4 cell types | 4 cell types | | 5 altered motifs | AC006305.1 | | rs2852986 |
| 18 | 53735635 | 0.99 | rs2535728 | G | T | 0.51 | | | 4 cell types | 14 cell types | | NF-I,Nanog,Pou2f2 | AC006305.1 | | rs2852986 |
| 18 | 53736180 | 0.9 | rs2535729 | G | A | 0.49 | | | 4 cell types | 5 cell types | | 9 altered motifs | AC006305.1 | | rs2852986 |
| 18 | 53740116 | 1 | rs2852986 | G | A | 0.51 | | | | | | Sox | AC006305.1 | | rs2852986 |
| 18 | 53740183 | 0.99 | rs1073719 | T | C | 0.51 | | | | | | p300 | AC006305.1 | | rs2852986 |
| 6 | 31436738 | 0.92 | rs76650611 | A | T | 0.08 | | | GM12878 | | | | HCP5 | | rs3099844 |
| 6 | 31448564 | 1 | rs3099843 | G | T | 0.09 | | | | | | 4 altered motifs | 3.3kb 3' of HCP5 | | rs3099845 |
| 6 | 31448976 | 1 | rs3099844 | C | A | 0.09 | | | HepG2 | | | 6 altered motifs | 3.7kb 3' of HCP5 | | rs3099846 |
| 6 | 31449552 | 0.86 | rs3130908 | T | C | 0.08 | | | HepG2 | | | 11 altered motifs | 4.3kb 3' of HCP5 | | rs3099847 |
| 6 | 31449710 | 0.82 | rs3130909 | T | C | 0.09 | | | HepG2 | | | 6 altered motifs | 4.4kb 3' of HCP5 | | rs3099848 |
| 6 | 31450637 | 1 | rs3131642 | G | A | 0.09 | | | | | | | 5.4kb 3' of HCP5 | | rs3099849 |
| 6 | 31451370 | 1 | rs3132470 | A | G | 0.09 | | | | HIPEpiC,SKMC | CEBPB | CEBPA,CEBPB | 6.1kb 3' of HCP5 | | rs3099850 |
| 6 | 31451836 | 1 | rs3094011 | T | C | 0.09 | | | | | | Pou3f3 | 6.6kb 3' of HCP5 | | rs3099851 |
| 6 | 31451848 | 1 | rs3094010 | C | T | 0.09 | | | | | | Ets | 6.6kb 3' of HCP5 | | rs3099852 |
| 6 | 31377978 | 1 | rs2523495 | C | T | 0.09 | | | | | | Pax-5,SETDB1 | MICA | intronic | rs3132472 |
| 6 | 31386131 | 1 | rs3132472 | G | A | 0.09 | | | | HFF | | 4 altered motifs | HCP5 | | rs3132472 |
| 6 | 31408329 | 1 | rs3132473 | T | A | 0.09 | | | | | | CAC-binding-protein,Foxj2 | HCP5 | | rs3132473 |
| 6 | 31410521 | 0.98 | rs3093958 | A | G | 0.08 | | HepG2 | | 40 cell types | 4 bound proteins | | XXbac-BPG181B23.4 | | rs3132473 |
| 6 | 31414051 | 0.98 | rs141516569 | CTTTTT | C | 0.08 | | | | | | 14 altered motifs | XXbac-BPG181B23.4 | | rs3132473 |
| 6 | 31414241 | 0.98 | rs9267092 | G | T | 0.09 | | | | | | Mef2 | XXbac-BPG181B23.4 | | rs3132473 |
| 6 | 31427395 | 0.85 | rs9267123 | G | C | 0.1 | | | | | | | HCP5 | | rs3132473 |
| 6 | 31428920 | 0.93 | rs3130477 | T | C | 0.09 | | | | FibroP,NHDF-Ad,WI-38 | | 4 altered motifs | HCP5 | | rs3132473 |
| 6 | 31430010 | 0.93 | rs3132089 | G | A | 0.09 | | | GM12878, NHEK, NHLF | | | 11 altered motifs | HCP5 | | rs3132473 |
| 6 | 31430065 | 0.93 | rs3099839 | C | T | 0.09 | | H1 | 5 cell types | | | Pou2f2,Smad3 | HCP5 | | rs3132473 |
| 6 | 31430694 | 0.93 | rs3094605 | G | C | 0.09 | | H1, HepG2 | 4 cell types | | 5 bound proteins | 4 altered motifs | HCP5 | | rs3132473 |
| 6 | 31430752 | 0.93 | rs3132090 | G | A | 0.09 | | H1, HepG2 | 4 cell types | NHEK,Caco-2 | 11 bound proteins | 8 altered motifs | HCP5 | | rs3132473 |
| 6 | 31431813 | 0.93 | rs3130907 | A | G | 0.09 | | GM12878, NHEK | HepG2 | | POL2 | RXRA | HCP5 | 3'-UTR | rs3132473 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 31433693 | 0.93 | rs3128986 | T | C | 0.09 | GM12878 | | POL2 | 9 altered motifs | HCP5 | rs3132473 |
| 6 | 31434331 | 0.93 | rs3131619 | A | T | 0.09 | | | POL2 | Pax-5 | HCP5 | rs3132473 |
| 6 | 31434366 | 0.93 | rs3094013 | G | A | 0.09 | | | POL2 | AIRE | HCP5 | rs3132473 |
| 6 | 31434520 | 0.86 | rs3094012 | G | C | 0.09 | | Osteobl | POL2,POL24H8 | 4 altered motifs | HCP5 | rs3132473 |
| 6 | 31434621 | 0.92 | rs3131618 | A | G | 0.08 | | | POL2 | CDP | HCP5 | rs3132473 |
| 6 | 31300197 | 0.8 | rs79158921 | G | A | 0.09 | | | | Nkx2 | 21kb 3' of HLA-B | rs3134792 |
| 6 | 31306420 | 0.83 | rs1625792 | G | A | 0.09 | | | | Mef2 | 15kb 3' of HLA-B | rs3134792 |
| 6 | 31306639 | 0.8 | rs1634753 | C | T | 0.1 | | | | BDP1,Dobox4 | 15kb 3' of HLA-B | rs3134792 |
| 6 | 31308476 | 0.86 | rs2854019 | T | A | 0.09 | | | KAP1 | AP-1,Sox | 13kb 3' of HLA-B | rs3134792 |
| 6 | 31308562 | 0.82 | rs2854018 | C | T | 0.09 | | | | 5 altered motifs | 13kb 3' of HLA-B | rs3134792 |
| 6 | 31308717 | 0.86 | rs402175 | G | A | 0.09 | | | | Gfi1,Pax-4 | 13kb 3' of HLA-B | rs3134792 |
| 6 | 31308988 | 0.85 | rs1634776 | C | T | 0.09 | | | | BDP1,SETDB1 | 13kb 3' of HLA-B | rs3134792 |
| 6 | 31309785 | 0.88 | rs3132474 | G | A | 0.1 | | | | Sox | 12kb 3' of HLA-B | rs3134792 |
| 6 | 31310372 | 0.84 | rs9265811 | C | T | 0.1 | | | | DMRT5,Irf | 11kb 3' of HLA-B | rs3134792 |
| 6 | 31311318 | 0.84 | rs9265827 | A | G | 0.11 | | | | 4 altered motifs | 10kb 3' of HLA-B | rs3134792 |
| 6 | 31311449 | 0.92 | rs9265831 | T | A | 0.09 | | | | Pou2f2,Pou3f3,Smad | 10kb 3' of HLA-B | rs3134792 |
| 6 | 31311912 | 0.8 | rs2394976 | G | T | 0.11 | | | | 5 altered motifs | 9.7kb 3' of HLA-B | rs3134792 |
| 6 | 31311950 | 1 | rs2256747 | T | C | 0.09 | | | | GR,Hoxa7,Rad21 | 9.7kb 3' of HLA-B | rs3134792 |
| 6 | 31312020 | 1 | rs2256750 | G | A | 0.09 | | | | 7 altered motifs | 9.6kb 3' of HLA-B | rs3134792 |
| 6 | 31312259 | 1 | rs2844589 | G | A | 0.09 | | | | | 9.4kb 3' of HLA-B | rs3134792 |
| 6 | 31312326 | 1 | rs3134792 | T | G | 0.09 | | | | HEN1,PEBP | 9.3kb 3' of HLA-B | rs3134792 |
| 6 | 31312492 | 1 | rs2854010 | A | G | 0.09 | | | | SRF | 9.2kb 3' of HLA-B | rs3134792 |
| 6 | 31312607 | 1 | rs9265857 | G | C | 0.09 | | | | 5 altered motifs | 9kb 3' of HLA-B | rs3134792 |
| 6 | 31312656 | 0.98 | rs2394978 | C | T | 0.09 | | | | AP-1,HNF4,ZEB1 | 9kb 3' of HLA-B | rs3134792 |
| 6 | 31312729 | 0.98 | rs2394979 | G | A | 0.09 | | | | E2F,Irx,SRF | 8.9kb 3' of HLA-B | rs3134792 |
| 6 | 31312941 | 0.98 | rs2394980 | C | T | 0.09 | | 6 cell types | CTCF | Gfi1,Gfi1b,TATA | 8.7kb 3' of HLA-B | rs3134792 |
| 6 | 31313029 | 0.86 | rs2394981 | G | T | 0.09 | | 6 cell types | CTCF | 4 altered motifs | 8.6kb 3' of HLA-B | rs3134792 |
| 6 | 31313221 | 0.94 | rs9265886 | A | C | 0.09 | | HPAEC | | CTCF | 8.4kb 3' of HLA-B | rs3134792 |
| 6 | 31313367 | 0.94 | rs7450305 | T | C | 0.09 | | AoAF,HPAF | | GLI,Hoxa7,Pax-1 | 8.3kb 3' of HLA-B | rs3134792 |
| 6 | 31313677 | 1 | rs9265908 | C | T | 0.09 | | | | HDAC2,Pax-5 | 8kb 3' of HLA-B | rs3134792 |
| 6 | 31313722 | 0.97 | rs9265910 | C | T | 0.09 | | | | 4 altered motifs | 7.9kb 3' of HLA-B | rs3134792 |
| 6 | 31314274 | 1 | rs7749555 | A | G | 0.09 | | | | CEBPB | 7.4kb 3' of HLA-B | rs3134792 |
| 6 | 31314652 | 1 | rs2507998 | A | G | 0.09 | | | | 7 altered motifs | 7kb 3' of HLA-B | rs3134792 |
| 6 | 31314938 | 0.97 | rs9265937 | C | T | 0.09 | | | | Brachyury,Irf,SREBP | 6.7kb 3' of HLA-B | rs3134792 |
| 6 | 31315005 | 0.95 | rs9265938 | C | T | 0.09 | | | | | 6.6kb 3' of HLA-B | rs3134792 |
| 6 | 31315027 | 0.95 | rs9265939 | A | G | 0.09 | | | | HNF1,YY1 | 6.6kb 3' of HLA-B | rs3134792 |
| 6 | 31315058 | 0.95 | rs9265942 | C | G | 0.09 | | | | Sox,TEF | 6.6kb 3' of HLA-B | rs3134792 |
| 6 | 31315138 | 0.95 | rs9265946 | G | A | 0.09 | | | | NRSF | 6.5kb 3' of HLA-B | rs3134792 |
| 6 | 31315193 | 0.95 | rs9265948 | C | T | 0.09 | | | | 4 altered motifs | 6.5kb 3' of HLA-B | rs3134792 |
| 6 | 31315229 | 0.92 | rs9265949 | C | T | 0.09 | | | | Foxp1,Pou2f2 | 6.4kb 3' of HLA-B | rs3134792 |
| 6 | 31315339 | 0.97 | rs9265954 | C | T | 0.09 | | | | Pdx1 | 6.3kb 3' of HLA-B | rs3134792 |
| 6 | 31315618 | 0.94 | rs9265964 | A | G | 0.09 | | | | 5 altered motifs | 6kb 3' of HLA-B | rs3134792 |
| 6 | 31315629 | 0.94 | rs9265965 | T | C | 0.09 | | H7-hESC | | 4 altered motifs | 6kb 3' of HLA-B | rs3134792 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 31315649 | 0.9 | rs9265967 | G | T | 0.08 | | | H7-hESC | | 4 altered motifs | 6kb 3' of HLA-B | | rs3134792 |
| 6 | 31315663 | 0.94 | rs9265968 | A | T | 0.09 | | | H7-hESC | | GCNF,Pax-5,RXRA | 6kb 3' of HLA-B | | rs3134792 |
| 6 | 31315792 | 0.97 | rs9265971 | T | C | 0.09 | | | | | CDP | 5.9kb 3' of HLA-B | | rs3134792 |
| 6 | 31315805 | 0.97 | rs9265972 | G | C | 0.09 | | | | | CDP | 5.8kb 3' of HLA-B | | rs3134792 |
| 6 | 31315861 | 0.97 | rs9265973 | G | A | 0.09 | | | | | HNF4 | 5.8kb 3' of HLA-B | | rs3134792 |
| 6 | 31315879 | 0.97 | rs9265974 | T | G | 0.09 | | | | | Pax-8,STAT | 5.8kb 3' of HLA-B | | rs3134792 |
| 6 | 31315933 | 0.97 | rs9265976 | A | G | 0.09 | | | | | 8 altered motifs | 5.7kb 3' of HLA-B | | rs3134792 |
| 6 | 31316044 | 0.97 | rs9265979 | C | T | 0.09 | | | | | 5 altered motifs | 5.6kb 3' of HLA-B | | rs3134792 |
| 6 | 31316080 | 0.92 | rs9265982 | C | T | 0.09 | | | | | BAF155,Osf2,PEBP | 5.6kb 3' of HLA-B | | rs3134792 |
| 6 | 31316234 | 0.97 | rs9265985 | A | C | 0.09 | | | PanIsletD | FOXA1 | 7 altered motifs | 5.4kb 3' of HLA-B | | rs3134792 |
| 6 | 31316448 | 0.97 | rs9265990 | T | A | 0.09 | | | | | Irf,STAT | 5.2kb 3' of HLA-B | | rs3134792 |
| 6 | 31316520 | 0.97 | rs9265993 | G | A | 0.09 | | | | | AIRE,Foxp3 | 5.1kb 3' of HLA-B | | rs3134792 |
| 6 | 31316526 | 0.94 | rs9265994 | T | C | 0.09 | | | | | AIRE,TCF12 | 5.1kb 3' of HLA-B | | rs3134792 |
| 6 | 31316613 | 0.97 | rs9265998 | G | A | 0.09 | | | GM19240,CD20+,GM12865 | | 4 altered motifs | 5kb 3' of HLA-B | | rs3134792 |
| 6 | 31316695 | 0.94 | rs9266001 | C | A | 0.09 | | | GM19240,Adult_CD4_Th0,GM12865 | | Hmbox1,Pax-6 | 5kb 3' of HLA-B | | rs3134792 |
| 6 | 31316911 | 0.94 | rs2923008 | G | T | 0.09 | | | | | 4 altered motifs | 4.7kb 3' of HLA-B | | rs3134792 |
| 6 | 31317063 | 0.97 | rs3016017 | A | G | 0.09 | | | | | EBF | 4.6kb 3' of HLA-B | | rs3134792 |
| 6 | 31317065 | 0.97 | rs2923007 | T | C | 0.09 | | | | | CEBPB,Nanog,STAT | 4.6kb 3' of HLA-B | | rs3134792 |
| 6 | 31318308 | 0.95 | rs2596510 | G | T | 0.09 | | | WERI-Rb-1 | POL24H8 | Pax-2 | 3.3kb 3' of HLA-B | | rs3134792 |
| 6 | 31318432 | 0.95 | rs2596508 | T | C | 0.09 | | GM12878 | GM19240,Melano,GM12865 | POL2,POL24H8 | Pax-5,Smad3,Smad | 3.2kb 3' of HLA-B | | rs3134792 |
| 6 | 31321267 | 0.84 | rs2596500 | A | C | 0.09 | GM12878 | | CD20+ | POL24H8,POL2 | Cdx,PLZF,RFX5 | 381bp 3' of HLA-B | | rs3134792 |
| 6 | 31037872 | 0.8 | rs200744629 | TTTTC | T | 0.08 | | | | | 7 altered motifs | 10kb 3' of HCG22 | | rs7750641 |
| 6 | 31044463 | 0.81 | rs3094671 | T | C | 0.09 | | | Osteobl,SKMC | | CEBPB,Hoxa5,Hoxa7 | 6.3kb 5' of U6 | | rs7750641 |
| 6 | 31051675 | 0.81 | rs3095311 | A | G | 0.09 | | 4 cell types | 57 cell types | 4 bound proteins | NF-I,Nanog | 788bp 3' of U6 | | rs7750641 |
| 6 | 31058340 | 0.8 | rs3130544 | C | A | 0.08 | | | | | CHOP::CEBPalpha,ERalpha-a,RORalpha1 | 7.5kb 3' of U6 | | rs7750641 |
| 6 | 31079644 | 0.86 | rs2233980 | G | A | 0.08 | | HSMM | | | Roaz | C6orf15 | synonymous | rs7750641 |
| 6 | 31081434 | 0.9 | rs3094222 | A | G | 0.09 | | 4 cell types | | | Maf | 1.1kb 5' of PSORS1C1 | | rs7750641 |
| 6 | 31085356 | 0.9 | rs3130985 | C | T | 0.09 | NHEK | 4 cell types | Th1,PanIsletD,PanIslets | GATA3 | 6 altered motifs | CDSN | intronic | rs7750641 |
| 6 | 31094703 | 0.9 | rs3130557 | C | T | 0.09 | | 4 cell types | 6 cell types | | ERalpha-a,Gfi1,PU.1 | PSORS1C1 | intronic | rs7750641 |
| 6 | 31098734 | 0.9 | rs3132541 | A | C | 0.09 | | | | | | PSORS1C1 | intronic | rs7750641 |
| 6 | 31100974 | 0.9 | rs3130562 | T | C | 0.09 | | | | | 13 altered motifs | PSORS1C1 | intronic | rs7750641 |
| 6 | 31102618 | 0.85 | rs3130566 | C | G | 0.1 | | | | | Mef2 | PSORS1C1 | intronic | rs7750641 |
| 6 | 31102790 | 0.85 | rs3132566 | G | T | 0.1 | | | | | 5 altered motifs | PSORS1C1 | intronic | rs7750641 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 31103195 | 0.85 | rs3094669 | C | G | 0.1 | | | | | | 4 altered motifs | PSORS1C1 | intronic | rs7750641 |
| 6 | 31105147 | 0.85 | rs3131010 | C | T | 0.1 | | | GM12878, HepG2 | | | BDP1,GR,Pax-8 | PSORS1C1 | intronic | rs7750641 |
| 6 | 31129310 | 1 | rs7750641 | C | T | 0.09 | | | GM12878 | HMEC,Osteobl | POL2 | PTF1-beta,Rad21,ZBTB7A | TCF19 | missense | rs7750641 |
| 6 | 31175946 | 0.8 | rs1619179 | A | C | 0.09 | | | HepG2 | | | 4 altered motifs | 4.2kb 3' of HCG27 | | rs7750641 |
| 6 | 32353864 | 1 | rs9268471 | G | A | | | | | | | 13 altered motifs | 4.4kb 5' of HCG23 | | rs9268471 |
| 6 | 32339784 | 0.81 | rs9501618 | A | C | 0.01 | | | Huvec | | | CEBPB,PLZF,p300 | 99bp 5' of C6orf10 | | rs9461741 |
| 6 | 32342119 | 0.91 | rs73729220 | A | G | 0.01 | | | | | FOSL2, FOXA1 | | 2.4kb 5' of C6orf10 | | rs9461741 |
| 6 | 32370587 | 1 | rs9461741 | G | C | 0.01 | | | | | | 7 altered motifs | BTNL2 | intronic | rs9461741 |

**Supplementary Table 12. Functional motif annotations from RegulomeDB analysis of newly-discovered MZL risk loci and their correlated ($r^2$ > 0.80) SNPs**

| #chr | coordinate | rsid | score | Transcription Factor Binding site, Factors used for ChIP-seq |
|---|---|---|---|---|
| chr6 | 31430751 | rs3132090 | 2a | SMARCC1, RFX5, GTF2F1, IRF3, TFAP2C, TFAP2A, NFKB1, CEBPB, BRCA1, USF2, SP1 |
| chr6 | 31462134 | rs3130923 | 2b | SPI1, HEY1, TFAP2C, NANOG, E2F1 |
| chr6 | 31430693 | rs3094605 | 2b | SMARCC1, RFX5, TFAP2C, TFAP2A, NFKB1 |
| chr6 | 31051674 | rs3095311 | 2b | JUND, TRIM28, CEBPB, GTF3C2 |
| chr6 | 31085355 | rs3130985 | 2b | GATA3 |
| chr6 | 31129309 | rs7750641 | 2b | POLR2A |
| chr6 | 31566167 | rs3130631 | 3a | HNF4A, HNF4G, USF1, RXRA, SP1 |
| chr6 | 31433692 | rs3128986 | 3a | POLR2A |
| chr6 | 31318431 | rs2596508 | 3a | POLR2A |
| chr6 | 31546849 | rs1800628 | 4 | POLR2A |
| chr6 | 31451369 | rs3132470 | 4 | CEBPB |
| chr6 | 31410520 | rs3093958 | 4 | YY1, RAD21, CTCF, SMC3 |
| chr6 | 31312940 | rs2394980 | 4 | CTCF |
| chr6 | 31313028 | rs2394981 | 4 | CTCF |
| chr6 | 31318307 | rs2596510 | 4 | POLR2A |
| chr6 | 31326073 | rs2853999 | 5 | POLR2A |
| chr6 | 31346652 | rs2442735 | 5 | |
| chr6 | 31465046 | rs3094005 | 5 | |
| chr6 | 31505479 | rs2734583 | 5 | |
| chr6 | 31514246 | rs9267488 | 5 | ZNF263, TRIM28 |
| chr6 | 31558701 | rs3130063 | 5 | |
| chr6 | 31386130 | rs3132472 | 5 | |
| chr6 | 31428919 | rs3130477 | 5 | |
| chr6 | 31431812 | rs3130907 | 5 | POLR2A |
| chr6 | 31434330 | rs3131619 | 5 | |
| chr6 | 31434365 | rs3094013 | 5 | POLR2A |
| chr6 | 31434519 | rs3094012 | 5 | POLR2A |
| chr6 | 31434620 | rs3131618 | 5 | POLR2A |
| chr6 | 31308475 | rs2854019 | 5 | TRIM28 |
| chr6 | 31313366 | rs7450305 | 5 | |
| chr6 | 31315628 | rs9265965 | 5 | |
| chr6 | 31315648 | rs9265967 | 5 | |
| chr6 | 31315662 | rs9265968 | 5 | |
| chr6 | 31316233 | rs9265985 | 5 | FOXA1 |
| chr6 | 31316612 | rs9265998 | 5 | |
| chr6 | 31316694 | rs9266001 | 5 | |
| chr6 | 31321266 | rs2596500 | 5 | POLR2A |
| chr6 | 31044462 | rs3094671 | 5 | |
| chr6 | 31094702 | rs3130557 | 5 | |
| chr6 | 32342118 | rs73729220 | 5 | FOSL2, FOXA1 |