**SUPPORTING INFORMATION**

**Supplement to:**

**A comprehensive evaluation of the role of genetic variation in follicular lymphoma survival**

Fredrik Baecklund et. al. 2014

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**Supplementary Table 1** Top SNPs associated with lymphoma-specific death ($p_{random} < 5.0 \times 10^{-5}$) in the meta-analysis of FL patients in SCALE and UCSF (N=586). The six top SNPs on chromosome 17 and the two top SNPs on chromosome 1 are in LD (in SCALE $r^2 \geq 0.96$ and $r^2 = 0.7$, respectively). The minor allele (A1) was investigated for association. A2=major allele, MAF= minor allele frequency, NA= not applicable

| | | | | | | SCALE | | UCSF | | Meta-analysis | | Heterogeneity | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CHR | SNP | Position | A1 | A2 | MAF | HR (95% CI) | $p_{SCALE}$ | HR (95% CI) | $p_{UCSF}$ | HR (95% CI) | $p_{RANDOM}$ | $p_{HET}$ | $I^2$ | Gene | Left gene | Right gene |
| 17 | rs10491178 | 64661568 | A | G | 0.06 | 3.10 (1.97; 4.89) | 1.13E-06 | 3.50 (1.28; 9.53) | 1.36E-02 | 3.17 (2.09; 4.79) | 5.24E-08 | 0.83 | 0 | ABCA10 | ABCA6 | LOC100133319 |
| 17 | rs6502005 | 64615106 | C | A | 0.06 | 3.06 (1.94; 4.84) | 1.49E-06 | 3.79 (1.33; 10.9) | 1.20E-02 | 3.17 (2.09; 4.82) | 6.48E-08 | 0.71 | 0 | ABCA6 | ABCA9 | ABCA10 |
| 17 | rs8067965 | 64629023 | G | A | 0.06 | 3.06 (1.94; 4.84) | 1.49E-06 | 3.55 (1.25; 10.0) | 1.61E-02 | 3.14 (2.07; 4.76) | 8.12E-08 | 0.80 | 0 | ABCA6 | ABCA9 | ABCA10 |
| 17 | rs7212506 | 64613313 | G | A | 0.06 | 3.06 (1.94; 4.84) | 1.49E-06 | 3.54 (1.25; 10.0) | 1.62E-02 | 3.14 (2.07; 4.76) | 8.15E-08 | 0.80 | 0 | ABCA6 | ABCA9 | ABCA10 |
| 1 | rs3131729 | 57971355 | A | G | 0.13 | 2.58 (1.77; 3.76) | 9.24E-07 | 2.00 (0.92; 4.31) | 7.58E-02 | 2.45 (1.75; 3.44) | 2.22E-07 | 0.56 | 0 | DAB1 | C8B | LOC729423 |
| 17 | rs1468514 | 64608807 | A | G | 0.06 | 3.09 (1.91; 5.00) | 4.16E-06 | 3.55 (1.25; 10.0) | 1.61E-02 | 3.17 (2.05; 4.90) | 2.24E-07 | 0.82 | 0 | ABCA6 | ABCA9 | ABCA10 |
| 17 | rs2886048 | 64600537 | A | G | 0.06 | 3.09 (1.91; 5.00) | 4.16E-06 | 3.55 (1.25; 10.0) | 1.61E-02 | 3.17 (2.05; 4.90) | 2.24E-07 | 0.82 | 0 | ABCA6 | ABCA9 | ABCA10 |
| 4 | rs11932201 | 14304530 | C | A | 0.17 | 2.10 (1.48; 2.97) | 2.93E-05 | 2.50 (1.13; 5.55) | 2.29E-02 | 2.16 (1.57; 2.97) | 2.24E-06 | 0.69 | 0 | NA | LOC152742 | LOC441009 |
| 1 | rs1323822 | 57999180 | A | G | 0.11 | 2.38 (1.60; 3.56) | 2.21E-05 | 1.84 (0.84; 4.04) | 1.24E-01 | 2.26 (1.58; 3.23) | 7.76E-06 | 0.57 | 0 | DAB1 | C8B | LOC729423 |
| 19 | rs2250066 | 56220931 | A | G | 0.15 | 2.07 (1.45; 2.97) | 7.31E-05 | 2.35 (1.01; 5.44) | 4.40E-02 | 2.11 (1.52; 2.94) | 9.38E-06 | 0.79 | 0 | KLK11 | KLK10 | KLK12 |
| 20 | rs846222 | 58658321 | A | G | 0.20 | 2.08 (1.44; 2.99) | 8.21E-05 | 1.94 (0.91; 4.12) | 8.14E-02 | 2.05 (1.48; 2.85) | 1.74E-05 | 0.87 | 0 | NA | MTCO2L | CDH4 |
| 18 | rs2061158 | 63168592 | A | G | 0.19 | 2.00 (1.43; 2.82) | 6.27E-05 | 1.69 (0.84; 3.40) | 1.38E-01 | 1.94 (1.43; 2.63) | 2.22E-05 | 0.67 | 0 | NA | CDH19 | DSEL |
| 17 | rs8074294 | 61902137 | G | A | 0.39 | 1.82 (1.33; 2.48) | 1.54E-04 | 1.85 (0.95; 3.59) | 6.61E-02 | 1.83 (1.38; 2.42) | 2.67E-05 | 0.97 | 0 | PRKCA | APOH | CACNG5 |
| 6 | rs10484325 | 7502047 | G | A | 0.17 | 2.14 (1.50; 3.05) | 2.80E-05 | 1.45 (0.59; 3.55) | 4.15E-01 | 2.03 (1.46; 2.82) | 2.77E-05 | 0.43 | 0 | DSP | LOC100131914 | C6orf151 |
| 9 | rs11788432 | 94828444 | G | A | 0.29 | 1.82 (1.30; 2.56) | 5.50E-04 | 2.82 (1.27; 6.26) | 1.00E-02 | 1.95 (1.42; 2.66) | 2.93E-05 | 0.32 | 0 | FGD3 | LOC642959 | SUSD3 |
| 7 | rs2060723 | 131551689 | A | G | 0.38 | 1.81 (1.33; 2.46) | 1.55E-04 | 1.71 (0.93; 3.16) | 8.13E-02 | 1.79 (1.36; 2.35) | 3.25E-05 | 0.88 | 0 | PLXNA4 | LOC100129705 | FLJ40288 |
| 7 | rs12668564 | 95278209 | G | A | 0.21 | 1.82 (1.30; 2.56) | 5.36E-04 | 2.22 (1.14; 4.32) | 1.77E-02 | 1.90 (1.40; 2.57) | 3.31E-05 | 0.61 | 0 | DYNC1I1 | PDK4 | SLC25A13 |
| 4 | rs1868416 | 59316610 | G | A | 0.41 | 1.82 (1.34; 2.49) | 1.53E-04 | 1.66 (0.92; 2.99) | 8.72E-02 | 1.79 (1.36; 2.35) | 3.49E-05 | 0.78 | 0 | NA | SRIL | LPHN3 |
| 13 | rs9551348 | 26475083 | G | A | 0.20 | 1.82 (1.28; 2.57) | 7.72E-04 | 2.25 (1.15; 4.43) | 1.75E-02 | 1.90 (1.39; 2.59) | 4.78E-05 | 0.58 | 0 | NA | GPR12 | LOC100129306 |

**Supplementary Table 2.** Relative risk[A] of lymphoma-specific and all-cause death in SCALE (N=373), and lymphoma progression in SCALE Sweden (N=231) for the top SNPs in the pooled analysis of SCALE and UCSF. The minor allele was investigated for association. The minor allele (A1) was investigated for association. A2=major allele, MAF= minor allele frequency, NA= not applicable

| | | | | | | SCALE | | | | SCALE Sweden | | |
| | | | | | | Lymphoma-specific death | | All-cause death | | Lymphoma progression | | |
| CHR | SNP | Position | A1 | A2 | MAF | HR (95% CI) | p | HR (95% CI) | p | HR (95% CI) | p | Gene |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 17 | rs10491178 | 64661568 | A | G | 0.06 | 3.10 (1.97; 4.89) | 1.13E-06 | 2.00 (1.35; 2.97) | 5.68E-04 | 1.02 (0.63; 1.65) | 9.40E-1 | ABCA10 |
| 1 | rs3131729 | 57971355 | A | G | 0.13 | 2.58 (1.77; 3.76) | 9.24E-07 | 1.86 (1.37; 2.53) | 6.46E-05 | 1.68 (1.20; 2.35) | 2.00E-3 | DAB1 |
| 4 | rs11932201 | 14304530 | C | A | 0.17 | 2.10 (1.48; 2.97) | 2.93E-05 | 1.56 (1.17; 2.08) | 2.30E-03 | 1.31 (0.97; 1.75) | 7.00E-2 | NA |
| 19 | rs2250066 | 56220931 | A | G | 0.15 | 2.07 (1.45; 2.97) | 7.31E-05 | 1.50 (1.10; 2.04) | 1.05E-02 | 1.13 (0.82; 1.56) | 4.70E-1 | KLK11 |

[A] Estimated with Hazard ratio, HR, and 95% confidence interval, CI. Adjusted for age at diagnosis, sex and three principal components.

**Supplementary Table 3.** Relative risk[A] of lymphoma-specific death and lymphoma progression for SNPs previously associated with follicular lymphoma risk[B]. The minor allele (A1) was investigated for association. A2=major allele, MAF= minor allele frequency

| CHR | Gene | SNP | Position | A1 | A2 | MAF | Lymphoma-specific death | | Progression[C] | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | HR (95% CI)[A] | p | HR (95% CI)[A] | p |
| 2 | BCL2L11 | rs3789068 | 111625718 | A | G | 0.45 | 1.22 (0.91; 1.63) | 0.19 | 0.96 (0.78; 1.19) | 0.74 |
| 6 | HLA II- region | rs2647012 | 32772436 | A | G | 0.32 | 0.70 (0.47; 1.02) | 0.06 | 0.92 (0.69; 1.22) | 0.56 |
| 6 | HLA II- region | rs10484561 | 32773398 | C | A | 0.18 | 0.91 (0.62; 1.33) | 0.62 | 0.77 (0.58; 1.02) | 0.07 |
| 10 | FAS | rs4934436 | 90773300 | G | A | 0.48 | 0.84 (0.62; 1.14) | 0.27 | 0.98 (0.78; 1.25) | 0.89 |
| 13 | TNFSF13B (BAFF) | rs2582869 | 107710146 | A | G | 0.40 | 1.32 (0.97; 1.79) | 0.07 | 1.08 (0.86; 1.36) | 0.51 |

[A] Estimated with Hazard ratio, HR, and 95% confidence interval, CI. Adjusted for age at diagnosis, sex and three principal components.

[B] rs6457327 has previously been associated with both FL risk and prognosis. The results are shown in Table 4.

[c] Swedish cases only (N=231) for time to progression

**Supplementary Figure 1**. Manhattan plot of the -log10(p-values) for the association with lymphoma-specific death in SCALE (A) and UCSF (B), by chromosome and within chromosome location. The top ten SNPs in the meta-analysis are highlighted (light green). The red line indicates the cut off level for genome-wide significance -log10(5.0 x10$^{-8}$)
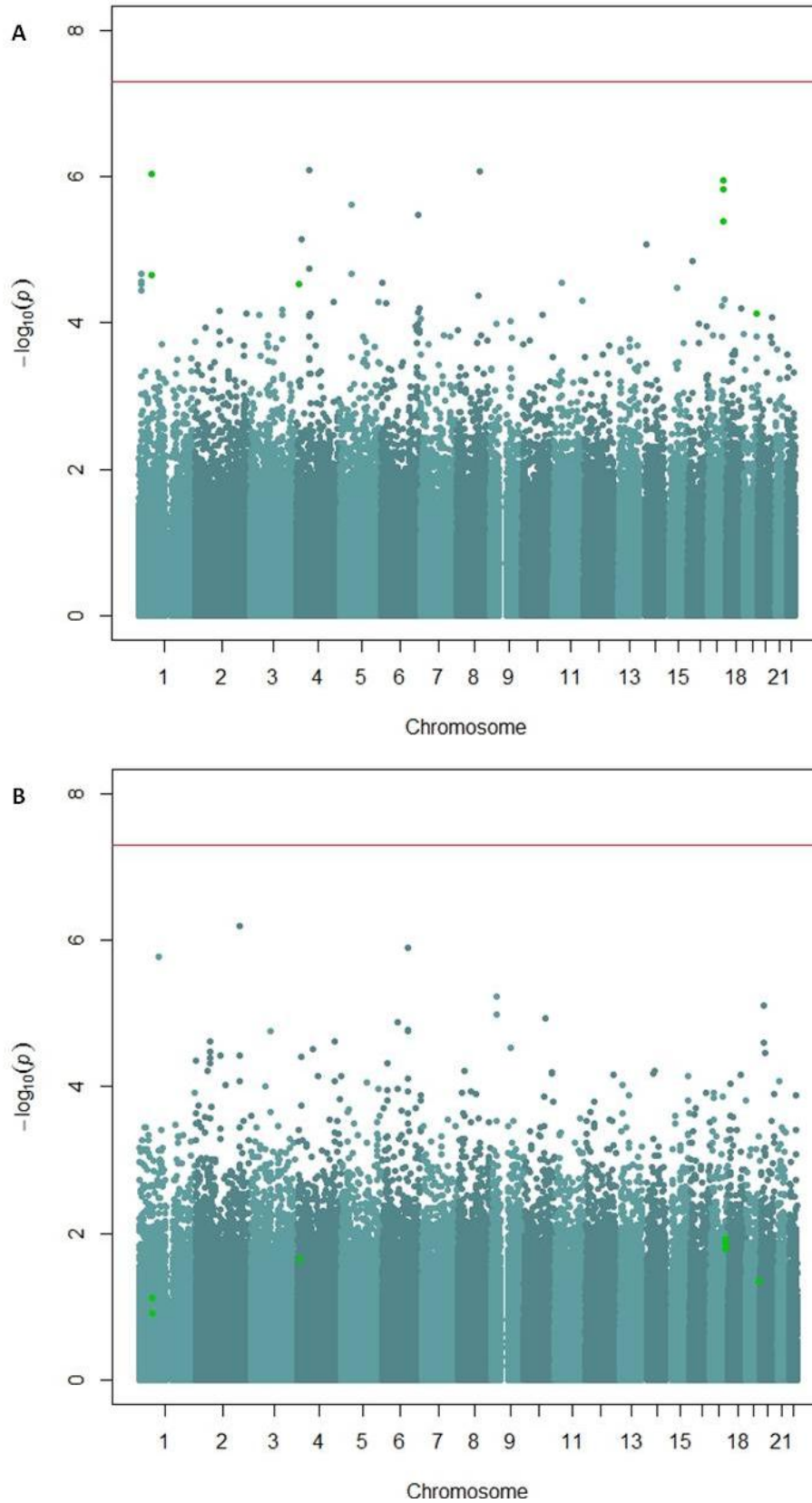
**Supplementary Figure 2**. QQ plot of the observed versus the expected -log(p-values) for the association with lymphoma-specific death in SCALE (A) and UCSF (B)
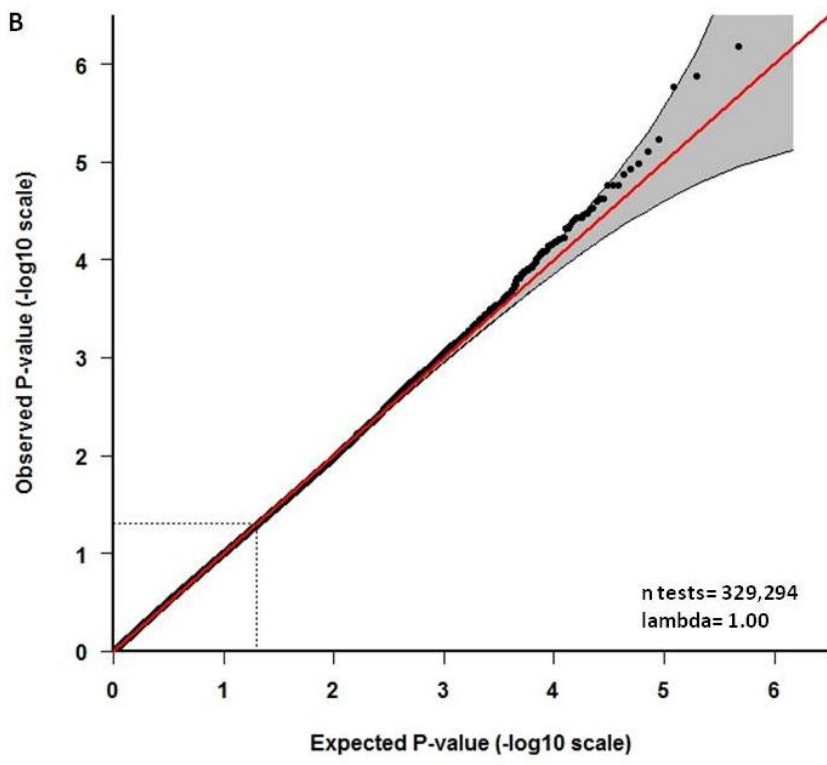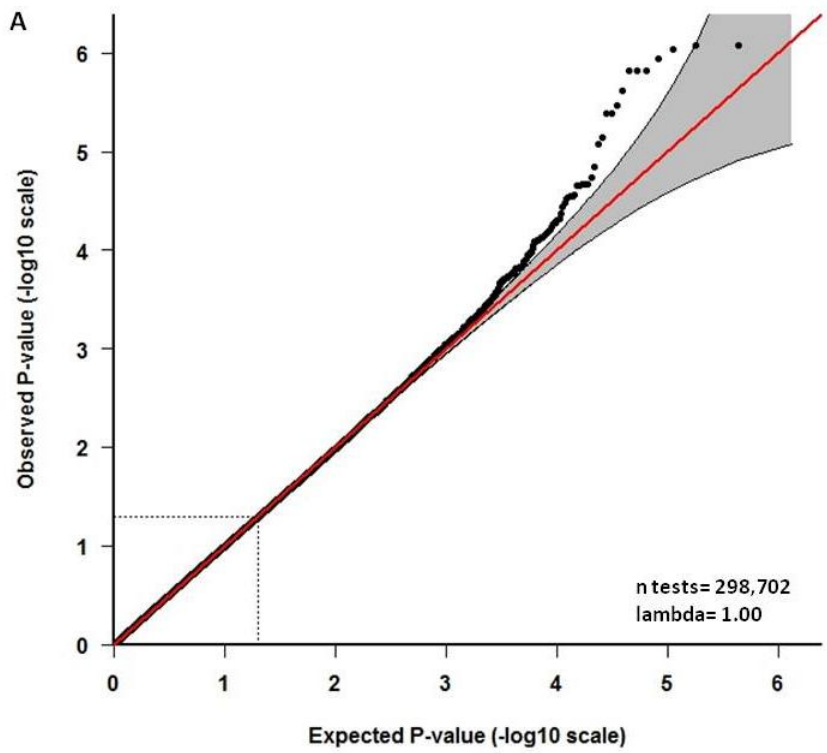
**Supplementary Figure 3.** Manhattan plot of the -log10(p-values) for the association with lymphoma-specific death in the meta-analysis of SCALE and UCSF. The top ten SNPs ($p_{random} \leq 10^{-6}$) are highlighted (light green). The red line indicates the cut off level for genome-wide significance -log10(5.0 x$10^{-8}$)
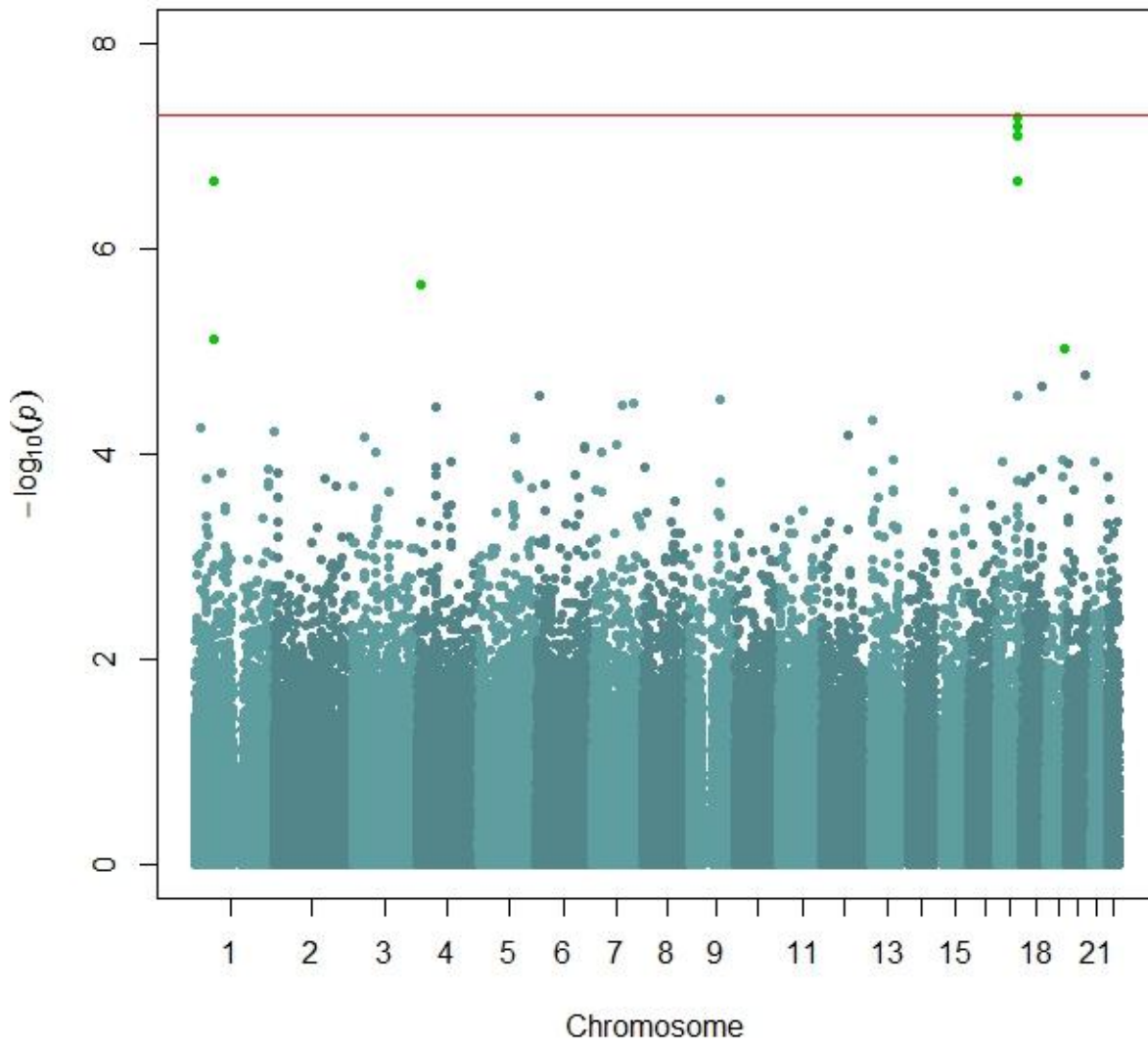
**Supplementary Figure 4**. QQ plot of the observed versus the expected -log(p-values) for the association with lymphoma-specific death in the meta-analysis of SCALE and UCSF
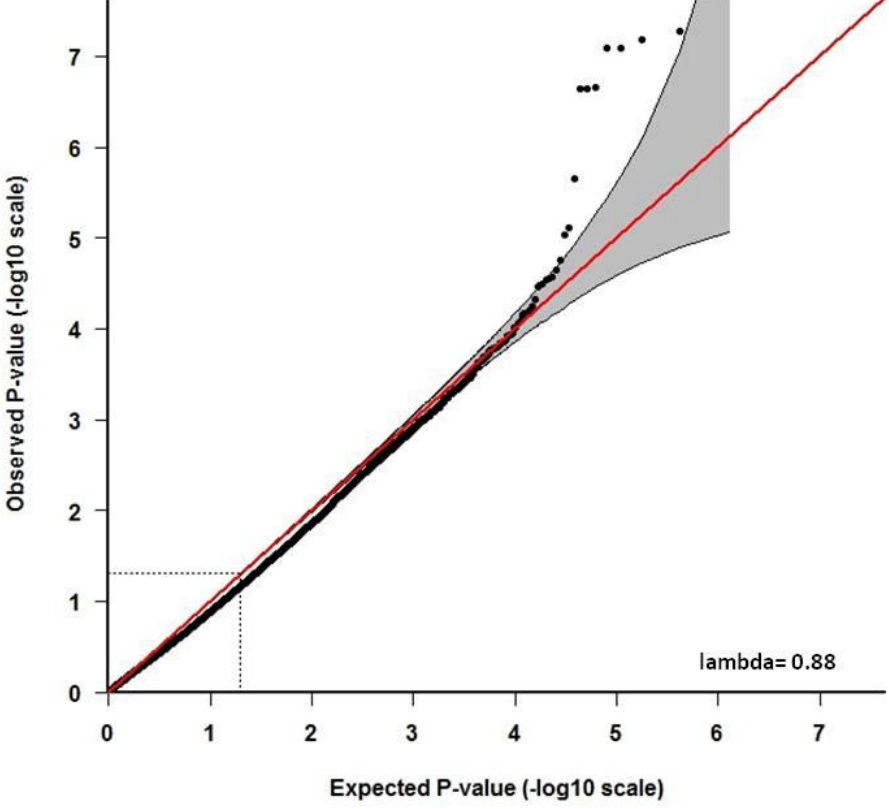
**Supplementary Figure 5**. Regional association plot of the top locus in the combined analysis on 17q, displaying the p-values of association in SCALE, extent of LD with rs10491178 as reference (using data from 1000 Genomes EUR), relation of SNPs and genes, and estimated recombination rates at each position
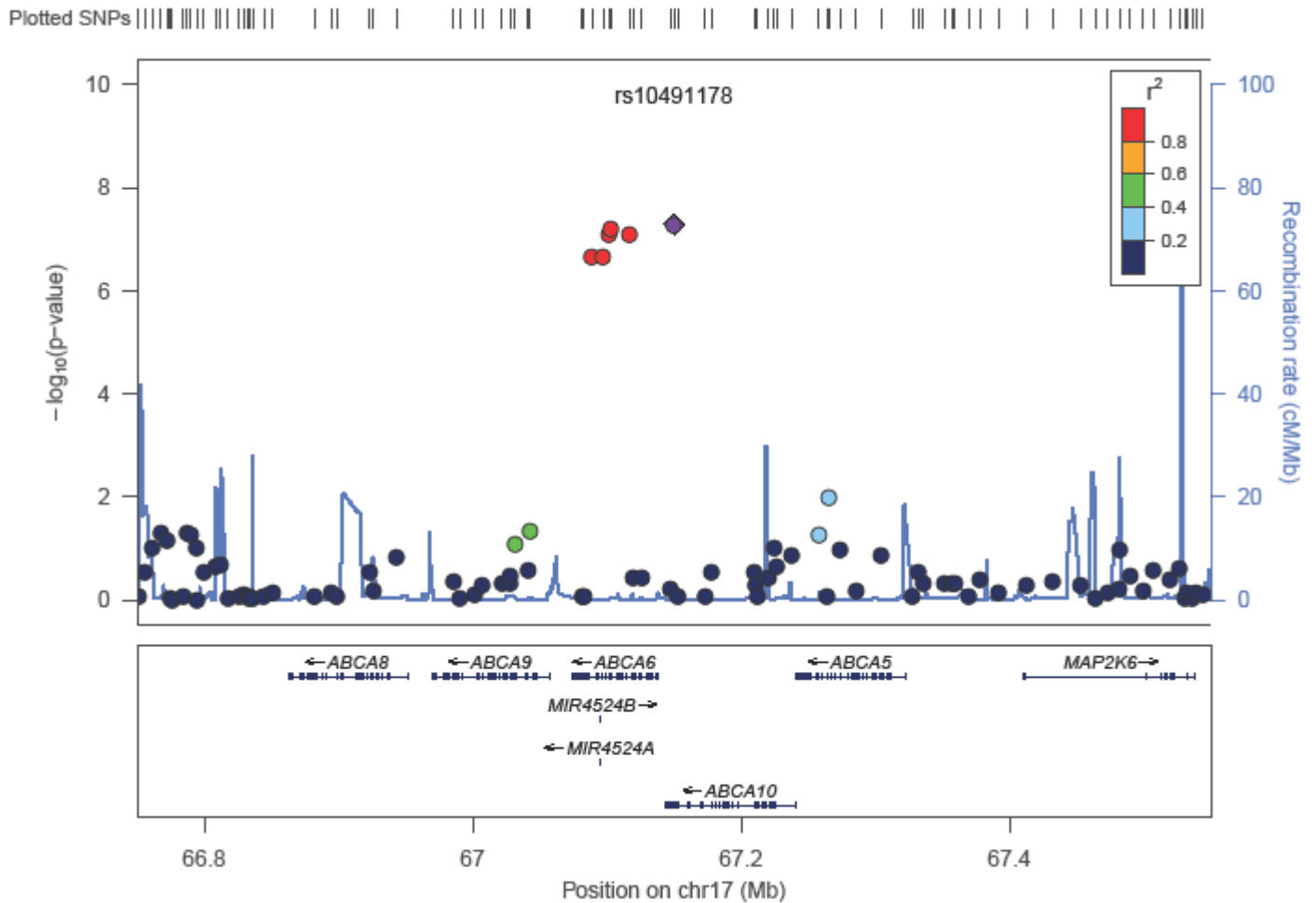
**Supplementary Figure 6**. Estimations of the power to detect associations between selected candidate SNPs and lymphoma-specific death and lymphoma progression, respectively, for different effect sizes and minor allele frequencies (MAF)