**SUPPLEMENTARY MATERIAL**

**A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relation to chronic lymphocytic leukemia**

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[Figure S1.](#FigS1) Individual genome-wide association studies of IgM anti-PC in the discovery phase

[Figure S2.](#FigS2) Marks of regulation in the LD block of 11q24.1 from UCSC Genome Browser

[Figure S3.](#FigS3) Functional prediction of rs35923643 in leukemia- or immune- cells

[Figure S4.](#FigS4) Evidence for affecting binding from RegulomeDB

[Figure S5.](#FigS5) IgM anti-PC values before and after the first CLL diagnosis

[Figure S6.](#FigS6) Global allele frequency of SNP rs735665

[Figure S7.](#FigS7) Functional partners with RUNX3 predicted from STRING database

[Figure S8.](#FigS8) Potential functional pathways RUNX3 involved from STRING database

[Table S1.](#TableS1) Genome-wide significant SNPs in the discovery GWAS meta-analysis of IgM anti-PC

[Table S2.](#TableS2) Replication results for the eight genome-wide significant SNPs in PRACSIS

[Table S3.](#TableS3) Meta-analysis for the successfully replicated SNPs (sorted by association P-value)

[Table S4.](#TableS4) Levels of IgM anti-PC among genotypes of rs735665 and rs35923643

[Table S5.](#TableS5) Polygenic risk score analyses between immunoglobulins and CLL risk

[Table S6.](#TableS6) Signal for each transcription factor and matched sequence from FIMO

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| **Figure S1. Individual genome-wide association studies of IgM anti-PC in the discovery phase** |
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| **Figure S2. Marks of regulation in the LD block of 11q24.1 from UCSC Genome Browser** |
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| **Figure S3. Functional prediction of rs35923643 in leukemia- or immune- cells** |
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| **Figure S4. Evidence for affecting binding from RegulomeDB** |
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| **Figure S5. IgM anti-PC values before and after the first CLL diagnosis** |
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| **Figure S6. Global allele frequency of SNP rs735665 in the 1000 Genomes Project Phase 3 from Ensembl (GRCh37/hg19)** |
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| **Figure S7. Functional partners with RUNX3 predicted from STRING database (version 10)** |
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| **Figure S8. Potential functional pathways RUNX3 involved from STRING database** |
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| **Table S1. Genome-wide significant SNPs in the discovery GWAS meta-analysis of IgM anti-PC** | | | | | | | | | | | | |
| **SNP** | | **CHR** | **POS** | **A1** | **A2** | **FREQ\_ A1** | **INFO** | **Beta** | **SE** | **I2(%)** | **Phet** | **P-value** |
| **rs35871881** | | **11** | **123356451** | **G** | **A** |  |  | **0.174** | **0.031** | **61.2** | **0.08** | **1.95e-08** |
|  | *TwinGene* |  |  | G | A | 0.250 | 0.986 | 0.158 | 0.049 |  |  | 0.001 |
|  | *PIVUS* |  |  | G | A | 0.241 | 0.970 | 0.263 | 0.053 |  |  | 7.72e-07 |
|  | *MDC* |  |  | G | A | 0.215 | 0.969 | 0.086 | 0.059 |  |  | 0.145 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **rs12798553** | | **11** | **123353693** | **A** | **G** |  |  | **0.174** | **0.031** | **61.0** | **0.08** | **1.98e-08** |
|  | *TwinGene* |  |  | A | G | 0.248 | 0.980 | 0.160 | 0.049 |  |  | 0.001 |
|  | *PIVUS* |  |  | A | G | 0.240 | 0.969 | 0.263 | 0.053 |  |  | 8.58e-07 |
|  | *MDC* |  |  | A | G | 0.215 | 0.967 | 0.085 | 0.059 |  |  | 0.151 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **rs35923643** | | **11** | **123355391** | **G** | **A** |  |  | **0.177** | **0.032** | **53.9** | **0.11** | **2.51e-08** |
|  | *TwinGene* |  |  | G | A | 0.230 | 0.999 | 0.153 | 0.050 |  |  | 0.002 |
|  | *PIVUS* |  |  | G | A | 0.225 | 0.980 | 0.263 | 0.054 |  |  | 1.18e-06 |
|  | *MDC* |  |  | G | A | 0.188 | 0.987 | 0.101 | 0.061 |  |  | 0.097 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **rs141373354** | | **1** | **68736970** | **A** | **G** |  |  | **0.578** | **0.104** | **0.0** | **0.71** | **2.60e-08** |
|  | *TwinGene* |  |  | A | G | 0.980 | 0.910 | 0.625 | 0.159 |  |  | 9.22e-05 |
|  | *PIVUS* |  |  | A | G | 0.986 | 0.901 | 0.658 | 0.203 |  |  | 0.001 |
|  | *MDC* |  |  | A | G | 0.980 | 0.913 | 0.457 | 0.181 |  |  | 0.011 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **rs116361873** | | **1** | **68728886** | **G** | **A** |  |  | **0.576** | **0.104** | **0.0** | **0.68** | **2.99e-08** |
|  | *TwinGene* |  |  | G | A | 0.981 | 0.918 | 0.626 | 0.159 |  |  | 8.83e-05 |
|  | *PIVUS* |  |  | G | A | 0.986 | 0.910 | 0.660 | 0.202 |  |  | 0.001 |
|  | *MDC* |  |  | G | A | 0.981 | 0.935 | 0.446 | 0.181 |  |  | 0.014 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **rs735665** | | **11** | **123361397** | **A** | **G** |  |  | **0.174** | **0.031** | **54.3** | **0.11** | **3.12e-08** |
|  | *TwinGene* |  |  | A | G | 0.232 | NA | 0.145 | 0.050 |  |  | 0.004 |
| *PIVUS* |  |  | A | G | 0.229 | NA | 0.261 | 0.053 |  |  | 1.05e-06 |
| *MDC* |  |  | A | G | 0.188 | NA | 0.103 | 0.060 |  |  | 0.089 |
|  | | |  | | | | | | | | | |
| **rs36020612** | | **11** | **123344435** | **T** | **C** |  |  | **0.182** | **0.033** | **61.1** | **0.08** | **3.73e-08** |
|  | *TwinGene* |  |  | T | C | 0.222 | 0.963 | 0.161 | 0.052 |  |  | 0.002 |
|  | *PIVUS* |  |  | T | C | 0.218 | 0.909 | 0.279 | 0.057 |  |  | 9.47e-07 |
|  | *MDC* |  |  | T | C | 0.186 | 0.900 | 0.090 | 0.064 |  |  | 0.156 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **rs36051450** | | **11** | **123344959** | **C** | **T** |  |  | **0.179** | **0.033** | **60.6** | **0.08** | **4.26e-08** |
|  | *TwinGene* |  |  | C | T | 0.224 | 0.962 | 0.158 | 0.052 |  |  | 0.002 |
|  | *PIVUS* |  |  | C | T | 0.221 | 0.932 | 0.274 | 0.056 |  |  | 1.00e-06 |
|  | *MDC* |  |  | C | T | 0.187 | 0.924 | 0.089 | 0.063 |  |  | 0.154 |
| CHR: chromosome number; POS: position of the SNP in human genome (GRCh37/hg19); A1: effect allele; A2: non-effect allele; FREQ\_A1: frequency of effect allele; INFO: imputation quality info; Beta: effect size per standard deviation of rank order normalized IgM anti-PC per allele; SE: standard error; I²: the percentage of variation across studies that is due to heterogeneity rather than chance; Phet: P-value for heterogeneity; NA: not available, because SNP was directly genotyped; PIVUS: Prospective Investigation of the Vasculature in Uppsala Seniors; MDC: Malmö Diet and Cancer study. | | | | | | | | | | | | |

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| **Table S2. Replication results for the eight genome-wide significant SNPs in PRACSIS** | | | | | | | | | |
| **SNP** | **CHR** | **POS** | **A1** | **A2** | **FREQ\_ A1** | **INFO** | **Beta** | **SE** | **P-value** |
| rs35871881 | 11 | 123356451 | G | A | 0.230 | 0.953 | 0.184 | 0.067 | 0.0064 |
| rs12798553 | 11 | 123353693 | A | G | 0.229 | 0.946 | 0.185 | 0.068 | 0.0064 |
| rs35923643 | 11 | 123355391 | G | A | 0.205 | 0.975 | 0.247 | 0.069 | 0.0004 |
| rs141373354 | 1 | 68736970 | A | G | 0.982 | 0.883 | 0.305 | 0.219 | 0.1644 |
| rs116361873 | 1 | 68728886 | G | A | 0.982 | 0.904 | 0.306 | 0.219 | 0.1640 |
| rs735665 | 11 | 123361397 | A | G | 0.206 | 0.993 | 0.244 | 0.068 | 0.0004 |
| rs36020612 | 11 | 123344435 | T | C | 0.199 | 0.933 | 0.250 | 0.072 | 0.0005 |
| rs36051450 | 11 | 123344959 | C | T | 0.201 | 0.947 | 0.250 | 0.071 | 0.0004 |
| CHR: chromosome number; POS: position of the SNP in human genome (GRCh37/hg19); A1: effect allele; A2: non-effect allele; FREQ\_A1: frequency of effect allele; INFO: imputation quality info; Beta: effect size per standard deviation of rank order normalized IgM anti-PC per allele; SE: standard error. | | | | | | | | | |

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| **Table S3. Meta-analysis for the successfully replicated SNPs (sorted by association P-value)** | | | | | | |
| SNP (Position) | Study | Info | Beta | SE | P-value | Phet |
| rs35923643 G/A | Meta |  | 0.189 | 0.029 | 4.34×10-11 | 0.159 |
| (Chr11: 123355391) | *TwinGene* | 0.999 | 0.153 | 0.050 | 0.002 |  |
|  | *PIVUS* | 0.980 | 0.263 | 0.054 | 1.18×10-6 |  |
|  | *MDC* | 0.987 | 0.101 | 0.061 | 0.097 |  |
|  | *PRACSIS* | 0.975 | 0.247 | 0.069 | 0.0004 |  |
|  |  |  |  |  |  |  |
| rs735665 A/G | Meta |  | 0.186 | 0.028 | 5.03×10-11 | 0.150 |
| (Chr11: 123361397) | *TwinGene* | NA | 0.145 | 0.050 | 0.004 |  |
|  | *PIVUS* | NA | 0.261 | 0.053 | 1.05×10-6 |  |
|  | *MDC* | NA | 0.103 | 0.060 | 0.089 |  |
|  | *PRACSIS* | 0.993 | 0.244 | 0.068 | 0.0004 |  |
|  |  |  |  |  |  |  |
| rs36020612 T/C | Meta |  | 0.193 | 0.030 | 1.06×10-10 | 0.118 |
| (Chr11: 123344435) | *TwinGene* | 0.963 | 0.161 | 0.052 | 0.002 |  |
|  | *PIVUS* | 0.909 | 0.279 | 0.057 | 9.47×10-7 |  |
|  | *MDC* | 0.900 | 0.090 | 0.064 | 0.156 |  |
|  | *PRACSIS* | 0.933 | 0.250 | 0.072 | 0.0005 |  |
|  |  |  |  |  |  |  |
| rs36051450 C/T | Meta |  | 0.191 | 0.030 | 1.09×10-10 | 0.116 |
| (Chr11: 123344959) | *TwinGene* | 0.962 | 0.158 | 0.052 | 0.002 |  |
|  | *PIVUS* | 0.932 | 0.274 | 0.056 | 1.00×10-6 |  |
|  | *MDC* | 0.924 | 0.089 | 0.063 | 0.154 |  |
|  | *PRACSIS* | 0.947 | 0.250 | 0.071 | 0.0004 |  |
|  |  |  |  |  |  |  |
| rs12798553 A/G | Meta |  | 0.176 | 0.028 | 3.17×10-10 | 0.158 |
| (Chr11: 123353693) | *TwinGene* | 0.980 | 0.160 | 0.049 | 0.001 |  |
|  | *PIVUS* | 0.969 | 0.263 | 0.053 | 8.58×10-7 |  |
|  | *MDC* | 0.967 | 0.085 | 0.059 | 0.151 |  |
|  | *PRACSIS* | 0.946 | 0.185 | 0.068 | 0.0064 |  |
|  |  |  |  |  |  |  |
| rs35871881 G/A | Meta |  | 0.176 | 0.028 | 3.25×10-10 | 0.160 |
| (Chr11: 123356451) | *TwinGene* | 0.986 | 0.158 | 0.049 | 0.001 |  |
|  | *PIVUS* | 0.970 | 0.263 | 0.053 | 7.72×10-7 |  |
|  | *MDC* | 0.969 | 0.086 | 0.059 | 0.145 |  |
|  | *PRACSIS* | 0.953 | 0.184 | 0.067 | 0.0064 |  |
| SNP is presented with effect allele/alternative allele (chromosome number and position in human genome GRCh37/ hg19). Info: imputation quality; NA: not available, because SNP is directly genotyped; Beta: effect size per standard deviation of rank order normalized IgM anti-PC per allele; SE: standard error; Phet: P-value for heterogeneity; The two SNPs (rs141373354 and rs116361873) on chromosome 1 are not successfully replicated in PRACSIS, association P-values are 0.1644 and 0.1640, respectively. | | | | | | |

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| **Table S4. Levels of IgM anti-PC among genotypes of rs735665 and rs35923643** | | | | | | | | |
|  |  |  |  | **Discovery phase** | | |  | **Replication** |
|  |  |  |  | ***TwinGene*** | ***PIVUS*** | ***MDC*** |  | ***PRACSIS*** |
| **Genotypes of rs735665** |  | **NGG** |  | 697 | 568 | 556 |  | 407 |
|  | **NGA** |  | 411 | 322 | 254 |  | 212 |
|  | **NAA** |  | 67 | 55 | 33 |  | 27 |
|  |  |  |  |  |  |  |  |  |
| **Raw values of**  **IgM anti-PC** |  | **GG** |  | 40.3 (23.2-67.2) | 39.5 (24.8-68.1) | 46.0 (28.6-75.1) |  | 31.9 (19.7-56.3) |
|  | **GA** |  | 48.7 (23.8-83.2) | 45.8 (28.9-75.6) | 51.1 (32.8-75.5) |  | 39.7 (24.1-71.0) |
|  | **AA** |  | 40.6 (21.1-78.6) | 52.0 (34.6-110.9) | 58.6 (34.4-78.1) |  | 47.1 (28.9-59.7) |
|  |  |  |  |  |  |  |  |  |
| **Normalized values of**  **IgM anti-PC in GWAS** |  | **GG** |  | -0.07±0.99 | -0.11±0.98 | -0.05±0.99 |  | -0.11±1.01 |
|  | **GA** |  | 0.14±1.03 | 0.13±0.99 | 0.05±1.00 |  | 0.18±0.98 |
|  | **AA** |  | 0.01±1.08 | 0.43±1.09 | 0.22±0.86 |  | 0.23±0.69 |
|  |  |  |  |  |  |  |  |  |
| **Genotypes of rs35923643** |  | **NAA** |  | 705 | 564 | 583 |  | 409 |
|  | **NAG** |  | 403 | 312 | 266 |  | 210 |
|  | **NGG** |  | 67 | 53 | 33 |  | 27 |
|  |  |  |  |  |  |  |  |  |
| **Raw values of**  **IgM anti-PC** |  | **AA** |  | 40.0 (23.1-66.8) | 39.4 (24.8-68.1) | 47.2 (28.9-75.5) |  | 31.9 (19.6-56.2) |
|  | **AG** |  | 50.7 (24.0-83.9) | 46.8 (29.1-76.3) | 51.7 (32.8-77.4) |  | 39.7 (24.1-71.0) |
|  | **GG** |  | 40.6 (21.1-78.6) | 49.8 (34.6-107.9) | 58.6 (34.4-78.1) |  | 47.1 (28.9-59.7) |
|  |  |  |  |  |  |  |  |  |
| **Normalized values of**  **IgM anti-PC in GWAS** |  | **AA** |  | -0.08±0.99 | -0.11±0.98 | -0.04±1.00 |  | -0.11±1.01 |
|  | **AG** |  | 0.16±1.03 | 0.14±0.99 | 0.05±1.01 |  | 0.18±0.98 |
|  | **GG** |  | 0.01±1.08 | 0.41±1.10 | 0.22±0.86 |  | 0.23±0.69 |
| PIVUS: Prospective Investigation of the Vasculature in Uppsala Seniors; MDC: Malmö Diet and Cancer study; PRACSIS: Prognosis and Risk in Acute Coronary Syndromes in Sweden. | | | | | | | | |

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| **Table S5. Polygenic risk score analyses between immunoglobulins and CLL risk** | | | | | | |
| **Base — Target** | **PT** | **NSNPs** | **OR** | **SE** | **r2** | **P-value** |
| **IgA — CLL** | 5.0e-15 | 2 | 1.06 | 0.17 | 0.00% | 0.75 |
| 5.0e-10 | 10 | 0.89 | 0.11 | 0.01% | 0.29 |
| 5.0e-09 | 22 | 0.87 | 0.09 | 0.02% | 0.12 |
| **5.0e-08\*** | **31** | **0.88** | **0.08** | **0.02%** | **0.11** |
| 5.0e-07 | 41 | 0.93 | 0.07 | 0.00% | 0.31 |
| 1.0e-06 | 45 | 0.91 | 0.07 | 0.02% | 0.20 |
|  |  |  |  |  |  |  |
| **IgG — CLL** | 5.0e-15 | 5 | 0.69 | 0.10 | 0.12% | 0.007 |
| 5.0e-10 | 10 | 0.68 | 0.10 | 0.14% | 0.0003 |
| 5.0e-09 | 12 | 0.67 | 0.10 | 0.15% | 0.0001 |
| 5.0e-08 | 17 | 0.73 | 0.09 | 0.12% | 0.0004 |
| **5.0e-07\*** | **20** | **0.68** | **0.09** | **0.18%** | **3.9e-06** |
| 1.0e-06 | 22 | 0.67 | 0.09 | 0.20% | 1.2e-05 |
|  |  |  |  |  |  |  |
| **IgM — CLL** | 5.0e-15 | 5 | 0.84 | 0.16 | 0.01% | 0.27 |
| 5.0e-10 | 18 | 0.70 | 0.09 | 0.14% | 0.0001 |
| 5.0e-09 | 33 | 0.72 | 0.07 | 0.19% | 5.3e-06 |
| **5.0e-08\*** | **43** | **0.69** | **0.07** | **0.28%** | **4.2e-08** |
| 5.0e-07 | 59 | 0.79 | 0.06 | 0.14% | 0.0001 |
| 1.0e-06 | 66 | 0.75 | 0.06 | 0.23% | 8.4e-07 |
|  |  |  |  |  |  |  |
| **IgM anti-PC — CLL** | **5.0e-08\*** | **1** | **17.55** | **0.36** | **0.59%** | **1.2e-15** |
| **5.0e-07\*** | **1** | **17.55** | **0.36** | **0.59%** | **1.2e-15** |
| **1.0e-06\*** | **1** | **17.55** | **0.36** | **0.59%** | **1.2e-15** |
| 5.0e-06 | 6 | 1.87 | 0.11 | 0.31% | 7.3e-09 |
| 5.0e-05 | 39 | 1.11 | 0.04 | 0.05% | 0.02 |
| 5.0e-04 | 386 | 1.00 | 0.02 | 0.00% | 0.87 |
| 0.005 | 3237 | 1.00 | 0.01 | 0.00% | 0.90 |
| 0.05 | 22405 | 1.02 | 0.003 | 0.24% | 3.1e-07 |
| 0.5 | 137132 | 1.01 | 0.002 | 0.10% | 0.001 |
| Standardized polygenic risk score (PRS) of the base phenotype was used to predict the target phenotype. PT: P-value threshold of the association between single nucleotide polymorphisms (SNPs) and the base phenotype, \* means the best PT that defined as the threshold corresponding to the largest explained variance; NSNPs: number of independent SNPs included in the best PT quantile; OR: odds ratio per standard deviation; SE: standard error; r2: Nagelkerke r2, the proportion of target variation explained by PRS of SNPs in the best PT quantile. | | | | | | |

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| **Table S6. Signal for each transcription factor and matched sequence from FIMO** | | | | | | | | |
| **TF** | **Signal** | **Motif** | **Strand** | **Start** | **End** | **P-value** | **Q-value** | **Matched Sequence** |
| [ATF2](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355100&t=123355620&g=wgEncodeRegTfbsClusteredV3&i=ATF2&l=123355269&r=123355752&db=hg19) | 487 | M1 | - | 389 | 399 | 0.00986 | 1 | CTGAGGTTTTG |
| [BCL11A](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355290&t=123355423&g=wgEncodeRegTfbsClusteredV3&i=BCL11A&l=123355269&r=123355752&db=hg19) | 426 | × |  |  |  |  |  |  |
| [BCL3](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355193&t=123355549&g=wgEncodeRegTfbsClusteredV3&i=BCL3&l=123355269&r=123355752&db=hg19) | 202 | × |  |  |  |  |  |  |
| [CEBPB](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355079&t=123355595&g=wgEncodeRegTfbsClusteredV3&i=CEBPB&l=123355269&r=123355752&db=hg19) | 264 | × |  |  |  |  |  |  |
| [FOXM1](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355286&t=123355460&g=wgEncodeRegTfbsClusteredV3&i=FOXM1&l=123355269&r=123355752&db=hg19) | 549 | × |  |  |  |  |  |  |
| [IRF4](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355177&t=123355507&g=wgEncodeRegTfbsClusteredV3&i=IRF4&l=123355269&r=123355752&db=hg19) | 160 | M2 | + | 381 | 395 | 0.00665 | 1 | CCAACCCCCAAAACC |
| M3 | + | 384 | 398 | 0.00369 | 1 | ACCCCCAAAACCTCA |
| [MEF2A](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355227&t=123355517&g=wgEncodeRegTfbsClusteredV3&i=MEF2A&l=123355269&r=123355752&db=hg19) | 144 | × |  |  |  |  |  |  |
| [MTA3](https://genome-euro.ucsc.edu/cgi-bin/hgEncodeVocab?ra=encode%2Fcv.ra&target=%22MTA3%22) | 496 | × |  |  |  |  |  |  |
| [NFATC1](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355053&t=123355649&g=wgEncodeRegTfbsClusteredV3&i=NFATC1&l=123355269&r=123355752&db=hg19) | 331 | × |  |  |  |  |  |  |
| [NFIC](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355190&t=123355547&g=wgEncodeRegTfbsClusteredV3&i=NFIC&l=123355269&r=123355752&db=hg19) | 732 | M4 | - | 386 | 391 | 0.00862 | 0.528 | TTGGGG |
| [PAX5](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355238&t=123355502&g=wgEncodeRegTfbsClusteredV3&i=PAX5&l=123355269&r=123355752&db=hg19) | 388 | M5 | - | 378 | 397 | 0.00555 | 0.499 | GAGGTTTTGGGGGTTGGAGG |
| [PML](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355017&t=123355701&g=wgEncodeRegTfbsClusteredV3&i=PML&l=123355269&r=123355752&db=hg19) | 319 | × |  |  |  |  |  |  |
| [POU2F2](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355198&t=123355518&g=wgEncodeRegTfbsClusteredV3&i=POU2F2&l=123355269&r=123355752&db=hg19) | 327 | × |  |  |  |  |  |  |
| [RELA](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355200&t=123355570&g=wgEncodeRegTfbsClusteredV3&i=RELA&l=123355269&r=123355752&db=hg19) | 228 | × |  |  |  |  |  |  |
| [RUNX3](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355186&t=123355550&g=wgEncodeRegTfbsClusteredV3&i=RUNX3&l=123355269&r=123355752&db=hg19) | 1000 | M6 | - | 391 | 397 | 0.000944 | 0.216 | GAGGTTT |
|  |  | M7 | + | 391 | 400 | 0.00029 | 0.208 | AAACCTCAGA |
|  |  | M7 | + | 382 | 391 | 0.00409 | 0.602 | CAACCCCCAA |
|  |  | M8 | + | 384 | 399 | 0.000894 | 0.301 | ACCCCCAAAACCTCAG |
|  |  | M8 | + | 383 | 398 | 0.00279 | 0.335 | AACCCCCAAAACCTCA |
|  |  | M8 | + | 376 | 391 | 0.00289 | 0.335 | CCCCTCCAACCCCCAA |
|  |  | M9 | + | 382 | 399 | 4.5e-05 | 0.0607 | CAACCCCCAGAACCTCAG |
|  |  | M9 | + | 382 | 399 | 1.86e-05 | 0.0251 | CAACCCCCAAAACCTCAG |
|  |  | M9 | + | 391 | 408 | 0.00673 | 0.479 | AAACCTCAGAAATTGGCT |
|  |  | M10 | + | 391 | 400 | 0.000414 | 0.229 | AAACCTCAGA |
|  |  | M10 | + | 383 | 392 | 0.000972 | 0.341 | AACCCCCAAA |
|  |  | M10 | + | 382 | 391 | 0.00156 | 0.369 | CAACCCCCAA |
| [RXRA](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355241&t=123355417&g=wgEncodeRegTfbsClusteredV3&i=RXRA&l=123355269&r=123355752&db=hg19) | 131 | M11 | - | 382 | 396 | 0.0012 | 0.423 | AGGTTTTGGGGGTTG |
|  |  | M11 | - | 381 | 395 | 0.00358 | 0.834 | GGTTTTGGGGGTTGG |
|  |  | M12 | - | 389 | 405 | 0.00907 | 0.699 | CAATTTCTGAGGTTTTG |
| [SP1](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355206&t=123355526&g=wgEncodeRegTfbsClusteredV3&i=SP1&l=123355269&r=123355752&db=hg19) | 156 | × |  |  |  |  |  |  |
| [SPI1](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355190&t=123355446&g=wgEncodeRegTfbsClusteredV3&i=SPI1&l=123355269&r=123355752&db=hg19) | 1000 | M13 | + | 314 | 328 | 8.52e-06 | 0.0117 | ATGAGGAACAGAGAG |
| M14 | + | 314 | 324 | 0.000166 | 0.226 | ATGAGGAACAG |
| [STAT5A](https://genome-euro.ucsc.edu/cgi-bin/hgEncodeVocab?ra=encode%2Fcv.ra&target=%22STAT5A%22) | 357 | M15 | - | 375 | 390 | 0.00373 | 0.367 | TGGGGGTTGGAGGGGG |
|  |  | M15 | - | 385 | 400 | 0.00495 | 0.367 | TCTGAGGTTTTGGGGG |
|  |  | M15 | - | 387 | 402 | 0.00503 | 0.367 | TTTCTGAGGTTTTGGG |
|  |  | M15 | - | 377 | 392 | 0.00982 | 0.431 | TTTGGGGGTTGGAGGG |
| [TBL1XR1](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355200&t=123355610&g=wgEncodeRegTfbsClusteredV3&i=TBL1XR1&l=123355269&r=123355752&db=hg19) | 220 | × |  |  |  |  |  |  |
| [TCF12](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355246&t=123355506&g=wgEncodeRegTfbsClusteredV3&i=TCF12&l=123355269&r=123355752&db=hg19) | 154 | × |  |  |  |  |  |  |
| [TCF3](https://genome-euro.ucsc.edu/cgi-bin/hgc?c=chr11&o=123355216&t=123355520&g=wgEncodeRegTfbsClusteredV3&i=TCF3&l=123355269&r=123355752&db=hg19) | 131 | × |  |  |  |  |  |  |

The position of rs35923643 (at the 391bp of submitted sequence) is labeled in red. M1: Haib\_ATF2\_H1-hESC\_ Motif1 \_fw\_ic0; M2: IRF4\_full\_TCAAGG20NCG\_AD\_NCGAAACCGAAACYN\_fw\_ic0; M3: Irf4\_fw\_ic0; M4: MA0161\_NFIC\_fw \_ic0; M5: MA0014\_Pax5\_fw\_ic0; M6: Haib\_RUNX3\_GM12878\_Motif1\_fw\_ic0; M7: RUNX3\_ DBD\_TACGGA30NGGC\_AI\_NAACCGCAAN\_fw\_ic0; M8: RUNX3\_DBD\_TACGGA30NGGC\_AI\_NA ACCGC AAACCRCAN\_fw\_ic0; M9: RUNX3\_DBD\_TACGGA30NGGC\_AI\_WAACCRCAAWAACCRCAN\_fw\_ ic0; M10: RUNX3\_full\_TCTCCC20NGA\_AE\_NAACCRCAAN\_fw\_ic0; M11: MA0074\_RXRA\_VDR\_fw\_ic0; M12: MA0115\_NR1H2\_RXRA\_fw\_ic0; M13: Haib\_SPI1\_GM12878\_Motif1\_fw\_ic0; M14: Haib\_SPI1\_K562\_Motif1\_ fw\_ic0; M15: Haib\_STAT5A \_GM12878\_Motif1\_fw\_ic0.