**Supplemental Figures and Tables**

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**Supplemental Figure 1.** **Differential allelic transcription factor binding activities in peripheral blood mononuclear cells (PBMCs)**

This figure depicts electrophoretic mobility shift assays (EMSA) analysis meant to characterise the binding properties of the risk allele vs. non-risk allele to nuclear protein extract (NE) from PBMCs and interacting protein of NE and antibody, respectively. EMSA were performed using 5`biotinylated probes corresponding to location including rs3024490 (A, B, C, D and E), rs1518110 (F, G) and rs1554286 (H). (A), (B), (C), (D) and (E) show no special binding for the rs3024490 T-allele or G-allele with interacting protein of NE and anti-TBX21, NE and anti-TBX15, NE and anti-MGA, NE and anti-TBX4 or NE and anti-TBX5, respectively. (F) and (G) show no special binding for the rs1518110 T-allele or G-allele with interacting protein of NE and anti-LMX1A or NE and anti-LMX1B, respectively. (H) shows no binding for the rs1554286 T-allele or C-allele with interacting protein of NE and anti-NFATC3.

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**Supplemental Figure 2. Epigenomic profiling identifies rs3024490 and** **linkage disequilibrium (LD) single nucleotide polymorphisms (SNPs) as candidate functional SNPs**

Associated variants rs3024490 and LD SNPs (hg19 chr1:206944233-206946634) are plotted with the ENCODE (top) and the Roadmap Epigenomics project (bottom) tracking for peripheral blood mononuclear cells. Rs3024490 and LD SNPs were annotated as “enhancer SNPs” based on a 25-state model predicted by histone-modified ChromHMM (top) and H3K27ac and H3K4Me1 enhancer-specific enrichments (bottom).

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| Supplemental Table 1. DNA sequence designed for primers of luciferase gene-reporter assay  |
| Construct risk haplotype (TTT) | CTTATAAGATCCTGCTGGCGCTCTATACTTTATTGGCTAGGAGAAGTAAAGAAAT(rs3024490)GTCTGATTCGAGGTGAAGATGCTCCCCATGCCTTGCAGCAGGGAAATTTAAATTGCCTCTGCTTAGAGCGTTTCCAGACCTGAAAGACCAGTGGTTTAGGGAAGCACTCTACATGAGGGAAACCTGCATTAGAAGGAGCTTCTTAATCCCTGGGATCTTTCCAAGCTAAACTGGATGTCTACAGTGGGGAGAAAGAAAAGCAGAGAACAGGACATGAGGGGGGCTCAAGGCCCCGAAGGGTTGACATAGGTGTCCCTTAAAGCCGAATGTAGCTCCGCAGAAAGAAGACCAGGACTGAGTCAAGCTTCTGCTTTCCCTTCAAAATCGGCCAGATTTTTTAAATAACTTGACTCTGAGGAGGAGGACCTGATTTAAGTGATGGTCCCATCACTGTTGAATCCTCTGTTTTTAAAACTCCCCTTTTGATTTTTTTGGGCCAGAGCCAATTTT(rs1518110)ATTTAAAAAAAAAAATCTCTAAATGAAAGGGCATCAAAAAGACCGCATTTCAGTTATTTCCCCAAACCTCAAGTTCATTCTCCTTTTGTTCTTCCTGCAGGTGAGAGCAGGGGCGGGGTGCTGGGGGAGTGTGCAGCATGATTAAGGGAAGGGAGACTCTGCTTCCTGATTGCAGGGAATTGGGTTTGTTTCCTTCGCTTTGAAAAGGAGAAGTGGGAAGATGTTAACTCAGCACATCCAGCAGCCAGAGGGTTTACAAAGGGCTCAGTCCCTTCGGGGAGGCTTCTGGTGAAGGAGGATCGCTAGAACCAAGCTGTCCTCTTAAGCTAGTTGCAGCAGCCCCTCCTCCCAGCCACCTCCGCCAATCTCTCACTCACCTTTGGCTCCTGCCCTTAGGTAAGTAGCAGATCAGTTT(rs1554286)TTTCCCTTGCAGCTGCCCCCAAAATACCATCTCCTACAGACCAGCAGGGACACTCACATCCACAGACACAGCAAAGACAC |
| Construct non-risk haplotype (GGC) | CTTATAAGATCCTGCTGGCGCTCTATACTTTATTGGCTAGGAGAAGTAAAGAAAG(rs3024490)GTCTGATTCGAGGTGAAGATGCTCCCCATGCCTTGCAGCAGGGAAATTTAAATTGCCTCTGCTTAGAGCGTTTCCAGACCTGAAAGACCAGTGGTTTAGGGAAGCACTCTACATGAGGGAAACCTGCATTAGAAGGAGCTTCTTAATCCCTGGGATCTTTCCAAGCTAAACTGGATGTCTACAGTGGGGAGAAAGAAAAGCAGAGAACAGGACATGAGGGGGGCTCAAGGCCCCGAAGGGTTGACATAGGTGTCCCTTAAAGCCGAATGTAGCTCCGCAGAAAGAAGACCAGGACTGAGTCAAGCTTCTGCTTTCCCTTCAAAATCGGCCAGATTTTTTAAATAACTTGACTCTGAGGAGGAGGACCTGATTTAAGTGATGGTCCCATCACTGTTGAATCCTCTGTTTTTAAAACTCCCCTTTTGATTTTTTTGGGCCAGAGCCAATTTG(rs1518110)ATTTAAAAAAAAAAATCTCTAAATGAAAGGGCATCAAAAAGACCGCATTTCAGTTATTTCCCCAAACCTCAAGTTCATTCTCCTTTTGTTCTTCCTGCAGGTGAGAGCAGGGGCGGGGTGCTGGGGGAGTGTGCAGCATGATTAAGGGAAGGGAGGCTCTGCTTCCTGATTGCAGGGAATTGGGTTTGTTTCCTTCGCTTTGAAAAGGAGAAGTGGGAAGATGTTAACTCAGCACATCCAGCAGCCAGAGGGTTTACAAAGGGCTCAGTCCCTTCGGGGAGGCTTCTGGTGAAGGAGGATCGCTAGAACCAAGCTGTCCTCTTAAGCTAGTTGCAGCAGCCCCTCCTCCCAGCCACCTCCGCCAATCTCTCACTCACCTTTGGCTCCTGCCCTTAGGTAAGTAGCAGATCAGTTC(rs1554286)TTTCCCTTGCAGCTGCCCCCAAAATACCATCTCCTACAGACCAGCAGGGACACTCACATCCACAGACACAGCAAAGACAC |
| Construct Homo sapiens T-box 1 (TBX1) | atgcacttcagcaccgtcaccagggacatggaagccttcacggccagcagcctgagcagcctgggggccgcggggggcttcccgggcgccgcgtcgcccggcgccgacccgtacggcccgcgcgagcccccgccgccgccgccgcgctacgacccgtgcgccgccgccgcccccggcgccccgggcccgccgccgccgccgcacgcctacccgtttgcgccggccgccggggccgccaccagcgccgccgccgagcccgagggccccggggccagctgcgcggccgcagccaaggcgccggtgaagaagaacgcgaaggtggccggtgtgagcgtgcagctagagatgaaggcgctgtgggacgagttcaaccagctgggcaccgagatgatcgtcaccaaggccggcaggcggatgtttcccaccttccaagtgaagctcttcggcatggatcccatggccgactatatgctgctcatggacttcgtgccggtggacgataagcgctaccggtacgccttccacagctcctcctggctggtggcggggaaggccgaccctgccacgccaggccgcgtgcactaccacccggactcgcctgccaagggcgcgcagtggatgaagcaaatcgtgtccttcgacaagctcaagctgaccaacaacctactggacgacaacggccacattattctgaattccatgcacagataccagccccgcttccacgtggtctatgtggacccacgcaaagatagcgagaaatatgccgaggagaacttcaaaacctttgtgttcgaggagacacgattcaccgcggtcactgcctaccagaaccatcggatcacgcagctcaagattgccagcaatcccttcgcgaaaggcttccgggactgtgaccctgaggactggccccggaaccaccggcccggcgcactgccgctcatgagcgccttcgcgcgctcgcggaaccccgtggcttccccgacgcagcccagcggcacggagaaagacgcggctgaggcccggcgagaattccagcgcgacgcgggcgggccagcagtgctcggggacccggcgcatcctccgcagctgctggcccgggtgctaagcccctcgctgcccggggccggcggcgccggcggcttagtcccgctgcccggcgcgcccggaggccggcccagtcccccgaaccccgagctgcgcctggaggcgcccggcgcatcggagccgctgcaccaccacccctacaaatatccggccgccgcctacgaccactatctcggggccaagagccggccggcgccctacccgctgcccggcctgcgtggccacggctaccacccgcacgcgcatccgcaccaccaccaccaccccgtgagtccagccgccgcggccgccgccgccgctgccgcagctgccgcggccgccaacatgtactcgtcggccggagccgcgccgcccggctcctacgactattgccccagataa |

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| Supplemental Table 2. The basic characteristics of all subjects |
| ID | sex | age (years) |
| C1 | Male | 44 |
| C2 | Female | 42 |
| C3 | Male | 45 |
| C4 | Female | 42 |
| C5 | Male | 47 |
| C6 | Male | 41 |
| C7 | Female | 38 |
| C8 | Male | 27 |
| C9 | Female | 40 |
| BD1 | Male | 44 |
| BD2 | Female | 29 |
| BD3 | Male | 30 |
| BD4 | Female | 33 |
| BD5 | Male | 45 |
| BD6 | Male | 30 |
| BD7 | Male | 42 |
| BD8 | Male | 27 |
| BD9 | Male | 38 |

C=healthy controls; BD= patients with Behcet's disease

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| Supplemental Table 3. Variants linked to rs3024490 in 1000 GENOMES: phase\_3: CHB |
| Variant | Location | Distance (bp) | r2 | D' | Consequence Type | Located in gene |
| rs1518111 | 1:206944645 | 666 | 1 | 1 |  intron variant | IL10 |
| rs1800872 | 1:206946407 | 1096 | 1 | 1 |  upstream gene variant | - |
| rs1800871 | 1:206946634 | 1323 | 1 | 1 |  upstream gene variant | - |
| rs1518110 | 1:206944861 | 450 | 0.975 | 1 |  intron variant | IL10 |
| rs1554286 | 1:206944233 | 1078 | 0.951 | 1 |  intron variant | IL10 |

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| Supplemental Table 4. Variants linked to rs3024490 in 1000 GENOMES: phase\_3: CHS |
| Variant | Location | Distance (bp) | r2 | D' | Consequence Type | Located in gene |
| rs1518110 | 1:206944861 | 450 | 1 | 1 |  intron variant | IL10 |
| rs1518111 | 1:206944645 | 666 | 1 | 1 |  intron variant | IL10 |
| rs1800872 | 1:206946407 | 1096 | 1 | 1 |  upstream gene variant | - |
| rs1800871 | 1:206946634 | 1323 | 1 | 1 |  upstream gene variant | - |
| rs1554286 | 1:206944233 | 1078 | 0.897 | 1 |  intron variant | IL10 |

Supplemental Table 5. A list of TFs from JASPAR predicted to bind similar DNA motifs containing alleles

|  |  |  |
| --- | --- | --- |
| SNPs | Alleles  |  Transcription factors |
| rs3024490 | G  | TBX1, TBX21, TBX15, MGA, TBX4, TBX5, FOXO3  |
| T risk | FOXO3 |
| rs1518110 | G | ZNF384 |
| T risk | LMX1A, LMX1B, ZNF384 |
| rs1554286 | C | No |
| T risk | NFATC3 |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **footprintDB template** | **Source** | **Organisms** | **STAMP e-value** | **Motif similarity** | **footprinDB PWM / Consensus** |
| [MA0690.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5852" \t "_blank): TBX21 | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 3.6e-06 | 7.59 / 10 | **AGTAAAGAAAGGTCTGATTCG**[**--------aAGGTGTGAA---**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5852) |
| [MA0803.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5836): TBX15 | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 7.4e-06 | 6.66 / 8 | **AGTAAAGAAAGGTCTGATTCG**[**---------AGGTGTGA----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5836) |
| [MA0805.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5840): TBX1 | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 7.5e-06 | 6.66 / 8 | **AGTAAAGAAAGGTCTGATTCG**[**---------AGGTGTGA----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5840) |
| [MA0801.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5530): MGA | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 1.1e-05 | 6.61 / 8 | **AGTAAAGAAAGGTCTGATTCG**[**---------AGGTGTGA----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5530) |
| [MA0806.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5856): TBX4 | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 1.4e-05 | 6.57 / 8 | **AGTAAAGAAAGGTCTGATTCG**[**---------AGGTGTgA----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5856) |
| [MA0807.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5858): TBX5 | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 1.9e-05 | 6.52 / 8 | **AGTAAAGAAAGGTCTGATTCG**[**---------AGGTGTkA----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5858) |

 Supplemental Table 6. A list of TFs predicted to bind only a similar DNA motif containing rs3024490-G

Supplemental Table 7. A list of TFs predicted to bind only a similar DNA motif containing rs1518110-T

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **footprintDB template** | **Source** | **Organisms** | **STAMP e-value** | **Motif similarity** | **footprinDB PWM / Consensus** |
| [MA0702.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5502" \t "_blank): LMX1A | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 1.3e-05 | 6.57 / 8 | **GAGCCAATTTTATTTAAAAAA**[**---------tTAATTAa----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5502) |
| [MA0703.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=5503): LMX1B | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 1.8e-05 | 6.52 / 8 | **GAGCCAATTTTATTTAAAAAA**[**---------tTaATTra----**](http://floresta.eead.csic.es/footprintdb/index.php?motif=5503) |

 Supplemental Table 8. A list of TFs predicted to bind only a similar DNA motif containing rs1554286-T

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **footprintDB template** | **Source** | **Organisms** | **STAMP e-value** | **Motif similarity** | **footprinDB PWM / Consensus** |
| [MA0625.1](http://floresta.eead.csic.es/footprintdb/index.php?motif=13378" \t "_blank): NFATC3 | [JASPAR 2018](http://jaspar.genereg.net/) | [Homo sapiens](http://es.wikipedia.org/wiki/Homo_sapiens) | 1.4e-06 | 7.74 / 10 | **GCAAGGGAAAAAACTGATCTG**[**--aryGGAAAaw---------**](http://floresta.eead.csic.es/footprintdb/index.php?motif=13378) |