

Supplementary Materials

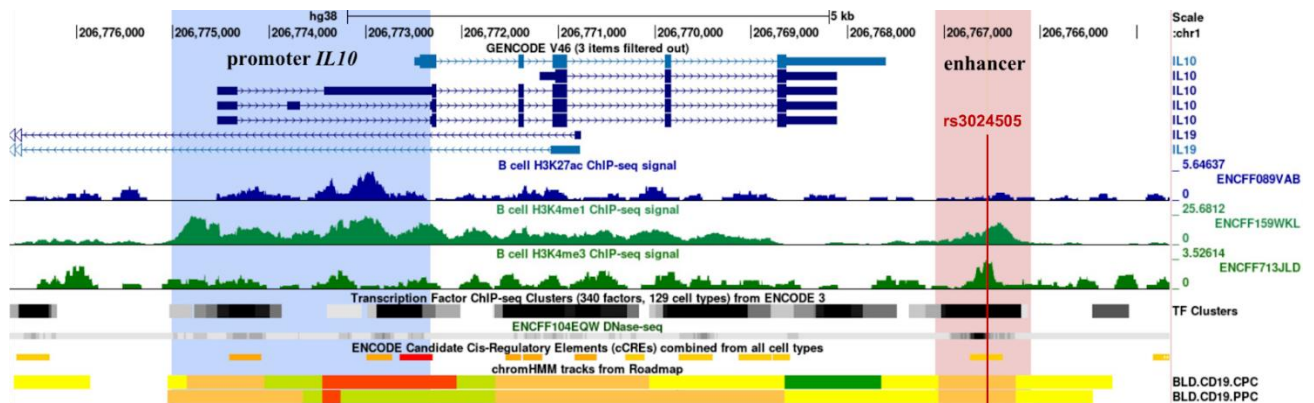


Figure S1. Schematic representation of the regulatory elements of *IL10* gene and SNP rs3024505 based on the UCSC Genome Browser visualization (GRCh38/hg38, reverse). The light blue area highlights the putative *IL10* promoter region, the light red – putative enhancer, and the vertical red line shows the location of the rs3024505. Histograms indicate the location of histone modifications in B cells typical of regulatory elements (H3K4 mono/tri-methylation, H3K27 acetylation; Roadmap epigenomic data). Chromatin state segmentation in different subsets of B cells represents ChromHMM model (Roadmap): red and orange denotes a state with a promoter-like signature, yellow denote states with an enhancer-like signature, green indicates a signature for a transcribed region. Rectangles mark regulatory elements positions according to ENCODE, DNase I hypersensitivity clusters (DNase I) in B cells (Roadmap), and transcription factor ChIP-seq (TF clusters; ENCODE).

Table S1. rs3024505 is associated with autoimmune pathologies.

Pathologies associated with the minor rs3024505(T) allele	Populations (odds ratio, OR), minor allele frequencies in cases and healthy controls	References
Systemic lupus erythematosus	<p>European American (1.30): 0.18 – case 0.15 – control</p> <p>United States (1.14): 0.17 – case 0.15 – control</p> <p>Sweden (1.21): 0.18 – case 0.15 – control</p>	[s1,2]
Crohn's disease	<p>New Zealand population (1.37): 0.21 – case 0.16 – control</p> <p>Danish population (1.34): 0.23 – case 0.18 – control</p> <p>Serbian population (1.82): 0.22 – case 0.14 – control</p>	[s3-5]
Ulcerative colitis	<p>Australian population (1.22): 0.18 – case 0.15 – control</p> <p>Danish population (1.37): 0.23 – case 0.18 – control</p>	[s4,6]
Sjögren's syndrome	<p>Italian population (1.52): 0.17 – case 0.12 – control</p>	[s7]

Table S2. rs3024505 minor allele frequencies for different populations (NCBI dbSNP).

Minor allele frequencies	Global	American	African	East Asian	European	South Asian
1000Genomes_30x	0.086	0.081	0.034	0.03	0.164	0.141
gnomAD	0.113	0.083	0.047	0.026	0.158	no data
ALFA	0.144	no data	0.045	0.027	0.155	0.122

Table S3. Oligonucleotides utilized in the study.

Oligonucleotide name	Sequence (5'→3')
Primers for amplification of IL10 promoter, enhancer and site-directed mutagenesis	
IL10_prom_BglII_F	TTTAGATCTGTCAGATCCTAACCTCAACCCT
IL10_prom_PagI_R	TAATCATGATAGGCAGGTTGCCTG
IL10_enh_BamHI_F	TGTGGATCCCGGCTAATTTTTTGCATTTT
IL10_enh_SalI_R	TAAGTCGACAGGTAGGTAAGAGACAAATGG
Enh_control_BamHI_F	AGGATCCGGATTACAGGTGTATTTACCAT
Enh_control_SalI_R	TATGTCGACGTTGATGTAATTCCTTTAAATCTAT
rs3024505(T)_F	TAAACACTAGTCTCCCTCACG
rs3024505(T)_R	CGTGAGGGAGACTAGTGTTTA
mutSTAT3-rs3024505(T)_F	TAAACACTAGGCTGCCTCACG
mutSTAT3-rs3024505(T)_R	CGTGAGGCAGCCTAGTGTTTA
mutSTAT3-rs3024505(C)_F	TAAACACTAGGCCGCCTCACG
mutSTAT3-rs3024505(C)_R	CGTGAGGCGGCCTAGTGTTTA

Primers for amplification of DNA probes for pull-down assay	
pull-down-rs3024505_F	AGGGGCACGGTGGCTGGGGA
pull-down-rs3024505_R	ACTGACCACAGCCTGTCCGC
pull-down-control_F	AACTCCTGGCCTCAAGTGATC
pull-down-control_R	TAGTGCCAGAAGCCCTGTTAG
siRNAs for STAT3 knockdown and primers for qPCR in real-time	
siRNA1-STAT3_sense	AACAUCUGCCUAGAUCGGCUAdTdT
siRNA1-STAT3_antisense	UAGCCGAUCUAGGCAGAUGUUDTdT
siRNA2-STAT3_sense	GGUACAUCAUGGGCUUUAUdTdT
siRNA2-STAT3_antisense	AUAAAGCCCAUGAUGUACCDTdT
scrambled_RNA_sense	GACCGCAUUCUACGAGACUAUdTdT
scrambled_RNA_antisense	AUAGUCUCGUAGAAUGCGGUCdTdT
rtPCR_STAT3_F	CTTTGAGACCGAGGTGTATCACC
rtPCR_STAT3_R	GGTCAGCATGTTGTACCACAGG

Supplementary references

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