SUPPLEMENTARY INFORMATION

Variants in the *DDX6-CXCR5* autoimmune disease risk locus influence the regulatory network in immune cells and salivary gland

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SUPPLEMENTAL NOTE

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SNP Name	Reference Allele	Alternative Allele	Non-Risk	Risk	Notes
rs57494551	C (major)	T (minor)	T	C	Reference is risk allele
rs10892294	G (major)	C (minor)	C	G	Reference is risk allele
rs4936443	C (minor)	T (major)	C	T	
rs4938572	C (minor)	T (major)	C	T	
rs7117261	T (minor)	C (major)	T	C	
rs4938573	C (minor)	T (major)	C	T	
rs12365699	G (major)	A (minor)	G	A	

Supplemental Table 2: Patient-Derived EBV B Cell Genotypes

Cell Line	Haplotype	Allele	Application Used
p1000068-2	Heterozygous		Luciferase & EMSA (pooled)
p1000069-5	Heterozygous		Luciferase & EMSA (pooled)
p1000334-2	Heterozygous		Luciferase & EMSA (pooled)
p1000181-5	Homozygous	Minor allele (1) Non-Risk	Luciferase & EMSA (pooled), 3C
p1000370-0	Homozygous	Minor allele (1) Non-Risk	3C
p1000373-7	Homozygous	Major allele (2) Risk	Luciferase & EMSA (pooled)
p1000333-5	Homozygous	Major allele (2) Risk	Luciferase & EMSA (pooled), 3C
p1000161-0	Homozygous	Major allele (2) Risk	3C

Supplemental Table 3: EMSA Probes

EMSA Probe Name		Sequence
rs57494551-altT-F	Non-Risk	TTCCTCCTGCCGACCCTGCTGCGCACCACATT**T**CTATATTCGCCTCCTCTCAGGCGCTCC
rs57494551-altT-R	Non-Risk	GGAGCGCCTGAGAGGAGGCGAATATAG**A**AATGTGGTGCGCAGCAGGGTCGGCAGGAGGAA
rs57494551-refC-F	Risk	TTCCTCCTGCCGACCCTGCTGCGCACCACATT**C**CTATATTCGCCTCCTCTCAGGCGCTCC
rs57494551-refC-R	Risk	GGAGCGCCTGAGAGGAGGCGAATATAG**G**AATGTGGTGCGCAGCAGGGTCGGCAGGAGGAA
rs10892294-altC-F	Non-Risk	GGTTTCCTGCCACTAGTCAATCTGCAGA**C**ACTTTTATTGATTCTTGAAAATACAACTGTG
rs10892294-altC-R	Non-Risk	CACAGTTGTATTTTCAAGAATCAATAAAAGT**G**TCTGCAGATTGACTAGTGGCAGGAAACC
rs10892294-refG-F	Risk	GGTTTCCTGCCACTAGTCAATCTGCAGA**G**ACTTTTATTGATTCTTGAAAATACAACTGTG
rs10892294-refG-R	Risk	CACAGTTGTATTTTCAAGAATCAATAAAAGT**C**TCTGCAGATTGACTAGTGGCAGGAAACC
rs4936443-refC-F	Non-Risk	AGGTTTAGTTTGCCTGGAGAGAAACAGGC**C**GGAGAGAGACTGCGGCCTCCCTAGGGTCTT
rs4936443-refC-R	Non-Risk	AAGACCCTAGGGAGGCCGCAGTCTCTCTCC**G**GCCTGTTTCTCTCCAGGCAAACTAAACCT
rs4936443-altT-F	Risk	AGGTTTAGTTTGCCTGGAGAGAAACAGGC**T**GGAGAGAGACTGCGGCCTCCCTAGGGTCTT
rs4936443-altT-R	Risk	AAGACCCTAGGGAGGCCGCAGTCTCTCTCC**A**GCCTGTTTCTCTCCAGGCAAACTAAACCT
rs4938572-refC-F	Non-Risk	CGGCAAATTCCTCCAGCTCAGTGGCTGCTGGG**C**AGCAGCACAGCCGGTTTCTCTCAAGGG
rs4938572-refC-R	Non-Risk	CCCTTGAGAGAAACCGGCTGTGCTGCT**G**CCCAGCAGCCACTGAGCTGGAGGAATTTGCCG
rs4938572-altT-F	Risk	CGGCAAATTCCTCCAGCTCAGTGGCTGCTGGG**T**AGCAGCACAGCCGGTTTCTCTCAAGGG
rs4938572-altT-R	Risk	CCCTTGAGAGAAACCGGCTGTGCTGCTACCCAGCAGCCACTGAGCTGGAGGAATTTGCCG
rs7117261-refT-F	Non-Risk	CCCTTCTTTCCTGTCCCTGGGCACTTCCC**T**GGCTGCTCTCTTTCCCCACTGCCCAGCCCA
rs7117261-refT-R	Non-Risk	TGGGCTGGGCAGTGGGGAAAGAGAGCAGCCAGGGAAGTGCCCAGGGACAGGAAAGAAGGG
rs7117261-altC-F	Risk	CCCTTCTTTCCTGTCCCTGGGCACTTCCC**C**GGCTGCTCTCTTTCCCCACTGCCCAGCCCA
rs7117261-altC-R	Risk	TGGGCTGGGCAGTGGGGAAAGAGAGCAGCC**G**GGGAAGTGCCCAGGGACAGGAAAGAAGGG
rs4938573-refC-F	Non-Risk	TCACTTGTGTAATTCATCAACAAACTTTA**C**TGAGCACCTAATAGGCACTGAGTGTTTTCG
rs4938573-refC-R	Non-Risk	CGAAAACACTCAGTGCCTATTAGGTGCTCA**G**TAAAGTTTGTTGATGAATTACACAAGTGA
rs4938573-altT-F	Risk	TCACTTGTGTAATTCATCAACAAACTTTA**T**TGAGCACCTAATAGGCACTGAGTGTTTTCG
rs4938573-altT-R	Risk	CGAAAACACTCAGTGCCTATTAGGTGCTCA**A**TAAAGTTTGTTGATGAATTACACAAGTGA
rs12365699-refG-F	Non-Risk	TCATTTGGAAACCTCTCTCGGAGGAGCTCC**G**TGATCAAGGTGCAGATGCGGCAGGTGGGC
rs12365699-refG-R	Non-Risk	GCCCACCTGCCGCATCTGCACCTTGATCA**C**GGAGCTCCTCCGAGAGAGGTTTCCAAATGA
rs12365699-altA-F	Risk	TCATTTGGAAACCTCTCTCGGAGGAGCTCC**A**TGATCAAGGTGCAGATGCGGCAGGTGGGC
rs12365699-altA-R	Risk	GCCCACCTGCCGCATCTGCACCTTGATCA**T**GGAGCTCCTCCGAGAGAGGTTTCCAAATGA

Supplemental Table 4: Luciferase Reporter Assay gBlocks

rs57494551-refC	ACCCTCTGGTACCTGTTATTGACCCGCAAGGCCTACTGCAATCAAGCAGCGGCCGGT TTGCTTCTAAACCGAGCCCTCCAATACAGCATGTCCCTGCCGCCCCCTATAGGGCCG CCTCGTACCCTATAACCTCCACCATCATCCCCCTAAGTCCTTGCCGCCCCCTTCGGCC TCATATTCCCTCATCTTCGATAAAGCTACTCCGAGTACTTAGCCTGTTCCTCCTGCCGA CCCTGCTGCGCACCACATT**C**CTATATTCGCCTCCTCTCAGGCGCTCCCACCCCACAC AGCTGCCGACCGCCTTCCTCCCCAGGCCCGGCCAGGCCTTAGGCCTCCGCCCGAGA GTCCCCCAGAGCCGGCCCGGGGGGCTCCCCACAGCCCCCAAAGCACCGCTGACCT CGACCCCACCACCTCACCCCAAGCCTCGCGACTCGGGCCCGTGTCCTACCAACGAG GCCACTCCCGCTCGGCACCCTCGGTCCTTTATAAGCTTTGTTGAC
rs57494551-altT	ACCCTCTGGTACCTGTTATTGACCCGCAAGGCCTACTGCAATCAAGCAGCGGCCGGT TTGCTTCTAAACCGAGCCCTCCAATACAGCATGTCCCTGCCGCCCCCTATAGGGCCG CCTCGTACCCTATAACCTCCACCATCATCCCCCTAAGTCCTTGCCGCCCCCTTCGGCC TCATATTCCCTCATCTTCGATAAAGCTACTCCGAGTACTTAGCCTGTTCCTCCTGCCGA CCCTGCTGCGCACCACATT**T**CTATATTCGCCTCCTCTCAGGCGCTCCCACCCCACACA GCTGCCGACCGCCTTCCTCCCCAGGCCCGGCCAGGCCTTAGGCCTCCGCCCGAGAG TCCCCCAGAGCCGGCCCGGGGGGCTCCCCACAGCCCCCAAAGCACCGCTGACCTC GACCCCACCACCTCACCCCAAGCCTCGCGACTCGGGCCCGTGTCCTACCAACGAGG CCACTCCCGCTCGGCACCCTCGGTCCTTTATAAGCTTTGTTGAC
rs10892294-refG	TTCTCCTTGGTACCGGGTATTTTCCAAGTTAGTTCAGGGGCAGTTGCCGAGGAATAAC ACTGATGGGGGTTCACACTATGGCGATCTTGTTGAACTGCCTGATGTTGGTTTGTGTA ATCTGCCCCCTTTGTGCCCAAGAACCTGTGACAAGATTCTGCTTCTGACAACCTTCTG TGCAGGGGTAGCGACAGGAGTCTGAACAATCATTAAGTGTCCAGCCCTGGTTTCCTG CCACTAGTCAATCTGCAGA**G**ACTTTTATTGATTCTTGAAAATACAACTGTGATTGTAGG TTTGGGCCCTGGGAATGTAATTTATAGCTAAAGAATGGGCAATGTCTTCTGTCCTGAG TGCCATGGTTGGATTGTGTAACATCTGTGGCTACCAGGACAAGGAAGGAACAAAGGA AGACAAAAGTATTTCAGTGCAGAGATCTTCTCAGTGACCCTCCTTGCTTTTCATCTGCC TGATGAATTTTAAAGACTACTTAAGCTTGTCATCAT
rs10892294-altC	TTCTCCTTGGTACCGGGTATTTTCCAAGTTAGTTCAGGGGCAGTTGCCGAGGAATAAC ACTGATGGGGGTTCACACTATGGCGATCTTGTTGAACTGCCTGATGTTGGTTTGTGTA ATCTGCCCCCTTTGTGCCCAAGAACCTGTGACAAGATTCTGCTTCTGACAACCTTCTG TGCAGGGGTAGCGACAGGAGTCTGAACAATCATTAAGTGTCCAGCCCTGGTTTCCTG CCACTAGTCAATCTGCAGA**C**ACTTTTATTGATTCTTGAAAATACAACTGTGATTGTAGG TTTGGGCCCTGGGAATGTAATTTATAGCTAAAGAATGGGCAATGTCTTCTGTCCTGAG TGCCATGGTTGGATTGTGTAACATCTGTGGCTACCAGGACAAGGAAGGAACAAAGGA AGACAAAAGTATTTCAGTGCAGAGATCTTCTCAGTGACCCTCCTTGCTTTTCATCTGCC TGATGAATTTTAAAGACTACTTAAGCTTGTCATCAT
rs4936443-refC	GCTGGAGGGTACCAAAGGCCTGGAGAGCTCCCAGCGCCCTCTGAGACATGGCTCCA GGTCACACAGCCCAAAGCCTTGGCCTGTTTTGTACGTGGACGGGGCAAAGAGAACAC CCTCGCCGCTTCTCTCTGCCTTTAGCAGGGCTGTAGGAAACCCCCACCAGAGACCTC CAGCTTGGAGAGGAAAGAGTGGAACAGCCCTCTGGAAGCAAGTTACCCACAGGTTTA GTTTGCCTGGAGAGAAACAGGC**C**GGAGAGAGACTGCGGCCTCCCTAGGGTCTTCTG ACGGCAAATTCCTCCAGCTCAGTGGCTGCTGGG**C**AGCAGCACAGCCGGTTTCTCTCA AGGGCACACCCCACACACCGCGTCACTGTGCACTAGCCTCAGATGACAGACAAGCCT TTCACAAGACTTTTGTGGCACTGTTCATTTCTGAGACCTTCTCTATGATGAGCTCAAAC TGCTTACCTCAGAGAAGAAACTGCGTGCACAAGCTTAGAAAGC Green=rs4938572

Supplementary Table 4 Continued

rs4936443-altT	GCTGGAGGGTACCAAAGGCCTGGAGAGCTCCCAGCGCCCTCTGAGACATGGCTCCA GGTCACACAGCCCAAAGCCTTGGCCTGTTTTGTACGTGGACGGGGCAAAGAGAACAC CCTCGCCGCTTCTCTCTGCCTTTAGCAGGGCTGTAGGAAACCCCCACCAGAGACCTC CAGCTTGGAGAGGAAAGAGTGGAACAGCCCTCTGGAAGCAAGTTACCCACAGGTTTA GTTTGCCTGGAGAGAAACAGGC**T**GGAGAGAGACTGCGGCCTCCCTAGGGTCTTCTGA CGGCAAATTCCTCCAGCTCAGTGGCTGCTGGG**C**AGCAGCACAGCCGGTTTCTCTCAA GGGCACACCCCACACACCGCGTCACTGTGCACTAGCCTCAGATGACAGACAAGCCTT TCACAAGACTTTTGTGGCACTGTTCATTTCTGAGACCTTCTCTATGATGAGCTCAAACT GCTTACCTCAGAGAAGAAACTGCGTGCACAAGCTTAGAAAGC Green=rs4938572
rs4938572-refC	GCCTTGGCGGTACCCTGTTTTGTACGTGGACGGGGCAAAGAGAACACCCTCGCCGCT TCTCTCTGCCTTTAGCAGGGCTGTAGGAAACCCCCACCAGAGACCTCCAGCTTGGAG AGGAAAGAGTGGAACAGCCCTCTGGAAGCAAGTTACCCACAGGTTTAGTTTGCCTGG AGAGAAACAGGC**C**GGAGAGAGACTGCGGCCTCCCTAGGGTCTTCTGACGGCAAATT CCTCCAGCTCAGTGGCTGCTGGG**C**AGCAGCACAGCCGGTTTCTCTCAAGGGCACAC CCCACACACCGCGTCACTGTGCACTAGCCTCAGATGACAGACAAGCCTTTCACAAGA CTTTTGTGGCACTGTTCATTTCTGAGACCTTCTCTATGATGAGCTCAAACTGCTTACCT CAGAGAAGAAACTGCGTGCACAGAAAGCTGCTGAGGCCAGCTTGGGGCCCCTTCTTT CCTGTCCCTGGGCACTTCCC**T**GGCTGCTCTAAGCTTCTTTCCCC Red=rs4936443 Blue=rs7117261
rs4938572-altT	GCCTTGGCGGTACCCTGTTTTGTACGTGGACGGGGCAAAGAGAACACCCTCGCCGCT TCTCTCTGCCTTTAGCAGGGCTGTAGGAAACCCCCACCAGAGACCTCCAGCTTGGAG AGGAAAGAGTGGAACAGCCCTCTGGAAGCAAGTTACCCACAGGTTTAGTTTGCCTGG AGAGAAACAGGC**C**GGAGAGAGACTGCGGCCTCCCTAGGGTCTTCTGACGGCAAATT CCTCCAGCTCAGTGGCTGCTGGG**T**AGCAGCACAGCCGGTTTCTCTCAAGGGCACACC CCACACACCGCGTCACTGTGCACTAGCCTCAGATGACAGACAAGCCTTTCACAAGAC TTTTGTGGCACTGTTCATTTCTGAGACCTTCTCTATGATGAGCTCAAACTGCTTACCTC AGAGAAGAAACTGCGTGCACAGAAAGCTGCTGAGGCCAGCTTGGGGCCCCTTCTTTC CTGTCCCTGGGCACTTCCC**T**GGCTGCTCTAAGCTTCTTTCCCC Red=rs4936443 Blue=rs7117261
rs7117261-refT	GCTCAGTGGTACCGGCTGCTGGG**C**AGCAGCACAGCCGGTTTCTCTCAAGGGCACAC CCCACACACCGCGTCACTGTGCACTAGCCTCAGATGACAGACAAGCCTTTCACAAGA CTTTTGTGGCACTGTTCATTTCTGAGACCTTCTCTATGATGAGCTCAAACTGCTTACCT CAGAGAAGAAACTGCGTGCACAGAAAGCTGCTGAGGCCAGCTTGGGGCCCCTTCTTT CCTGTCCCTGGGCACTTCCC**T**GGCTGCTCTCTTTCCCCACTGCCCAGCCCAAGGAGT CCCCTCTGCAGCTGACCCGGGTTCAGCCTCCAGAACAGCGAGTTCCACAGCCCTGAA GCCTGGCCATCGTCCCTTTTCTGGACACTGGACTGGTTCATAGGGCTCAGTGCCCTG CGGCTTTCTCCTCCCCACCACAGGCCTGGGAGGGGCAAGAAGCACCAGTTTGTTTTC TGGGTCAGCCTGCAGCAAAGAGCGACTGCAAGCTTCCTCACC Green=rs4938572
rs7117261-altC	GCTCAGTGGTACCGGCTGCTGGG**C**AGCAGCACAGCCGGTTTCTCTCAAGGGCACAC CCCACACACCGCGTCACTGTGCACTAGCCTCAGATGACAGACAAGCCTTTCACAAGA CTTTTGTGGCACTGTTCATTTCTGAGACCTTCTCTATGATGAGCTCAAACTGCTTACCT CAGAGAAGAAACTGCGTGCACAGAAAGCTGCTGAGGCCAGCTTGGGGCCCCTTCTTT CCTGTCCCTGGGCACTTCCC**C**GGCTGCTCTCTTTCCCCACTGCCCAGCCCAAGGAGT CCCCTCTGCAGCTGACCCGGGTTCAGCCTCCAGAACAGCGAGTTCCACAGCCCTGAA GCCTGGCCATCGTCCCTTTTCTGGACACTGGACTGGTTCATAGGGCTCAGTGCCCTG CGGCTTTCTCCTCCCCACCACAGGCCTGGGAGGGGCAAGAAGCACCAGTTTGTTTTC TGGGTCAGCCTGCAGCAAAGAGCGACTGCAAGCTTCCTCACC Green=rs4938572

Supplementary Table 4 Continued

rs4938573-refC	ACTACTGGTACCGATTTACATATCACACATGTGCTCATCCATCCATTCACCAAACCTCT GTTGACTGCTCGCGCTGCCCTGCGTTCCTGGCACTGTGCAGGGTTATAATCTAGTAG GAAAGACCTGACAAGGTCACAGATGTCAGTACTGAAAGGAAGAGTAGGGTAGATGGC CACCCCACCCCCACCCCAACCTCAAAAAAGAGACTAAAAAATTACTGTCACTTGTGTA ATTCATCAACAAACTTTA**C**TGAGCACCTAATAGGCACTGAGTGTTTTCGTGTATTGATC ACGCATTGATCCTCACAATAACCTTTGAGATGGGTTGTGCCATTTACACAGGGCGAAG AAGAGAGACTGGCCACTGTCACACAGCTACTGATATCCAAGCTGAGATCCAAAGCTC CTCTGCTTCTCCTGATGAGAATGAGCACCACAGGCAGGCCACAGAAAAACACCCAGG AGAGCCAAACTCAGACCCACCCCAGAAGCTTATTTCC
rs4938573-altT	ACTACTGGTACCGATTTACATATCACACATGTGCTCATCCATCCATTCACCAAACCTCT GTTGACTGCTCGCGCTGCCCTGCGTTCCTGGCACTGTGCAGGGTTATAATCTAGTAG GAAAGACCTGACAAGGTCACAGATGTCAGTACTGAAAGGAAGAGTAGGGTAGATGGC CACCCCACCCCCACCCCAACCTCAAAAAAGAGACTAAAAAATTACTGTCACTTGTGTA ATTCATCAACAAACTTTA**T**TGAGCACCTAATAGGCACTGAGTGTTTTCGTGTATTGATC ACGCATTGATCCTCACAATAACCTTTGAGATGGGTTGTGCCATTTACACAGGGCGAAG AAGAGAGACTGGCCACTGTCACACAGCTACTGATATCCAAGCTGAGATCCAAAGCTC CTCTGCTTCTCCTGATGAGAATGAGCACCACAGGCAGGCCACAGAAAAACACCCAGG AGAGCCAAACTCAGACCCACCCCAGAAGCTTATTTCC
rs12365699-refG	CACAAGAGGTACCGCCGTTGGCGGGATTTCCCATTGTCCCCCTTGGGTAGGTAAGGC CAGGTGGCTGCTCCATCTCTGCCACCTCCAGCGCCGGTCCCACTGTGTCAGCAGCC CTGTCCCCTACTGCTGTGTCATCAATTACTCTCAGGTGCCTGGCCCCCACCCAGTGG CCCCCACCTTGCAGCCCCGAAGGCTTCCTTCCTGGGGCAGCAGGGCCGAGTCATTT GGAAACCTCTCTCGGAGGAGCTCC**G**TGATCAAGGTGCAGATGCGGCAGGTGGGCCG GCCTCAATCATGTCTCCAATTGCGACGGTGAATGCGGTGAGGAGTTTCGTTGGCCCA TCACCTCTGCCTTGGGCCTGGCTCACTTTCACTGCTGAGTTAGTTCCACGGCCGCCTT TGATGATGCCGCTTCAGCATCTTTTTTCTTCGGCGTTTCCTGCTCCTTTGTTTTCAAGG TCACTCTGTCCTGCCTGCCCCACTCTGGGCCAAGCTTACCCAAG
rs12365699-altA	CACAAGAGGTACCGCCGTTGGCGGGATTTCCCATTGTCCCCCTTGGGTAGGTAAGGC CAGGTGGCTGCTCCATCTCTGCCACCTCCAGCGCCGGTCCCACTGTGTCAGCAGCC CTGTCCCCTACTGCTGTGTCATCAATTACTCTCAGGTGCCTGGCCCCCACCCAGTGG CCCCCACCTTGCAGCCCCGAAGGCTTCCTTCCTGGGGCAGCAGGGCCGAGTCATTT GGAAACCTCTCTCGGAGGAGCTCC**A**TGATCAAGGTGCAGATGCGGCAGGTGGGCCG GCCTCAATCATGTCTCCAATTGCGACGGTGAATGCGGTGAGGAGTTTCGTTGGCCCA TCACCTCTGCCTTGGGCCTGGCTCACTTTCACTGCTGAGTTAGTTCCACGGCCGCCTT TGATGATGCCGCTTCAGCATCTTTTTTCTTCGGCGTTTCCTGCTCCTTTGTTTTCAAGG TCACTCTGTCCTGCCTGCCCCACTCTGGGCCAAGCTTACCCAAG
All Non-Risk	TCTGAGAGGTACCCATGGCTCCAGGTCACACAGCCCAAAGCCTTGGCCTGTTTTGTA CGTGGACGGGGCAAAGAGAACACCCTCGCCGCTTCTCTCTGCCTTTAGCAGGGCTGT AGGAAACCCCCACCAGAGACCTCCAGCTTGGAGAGGAAAGAGTGGAACAGCCCTCT GGAAGCAAGTTACCCACAGGTTTAGTTTGCCTGGAGAGAAACAGGC**C**GGAGAGAGAC TGCGGCCTCCCTAGGGTCTTCTGACGGCAAATTCCTCCAGCTCAGTGGCTGCTGGG**C** AGCAGCACAGCCGGTTTCTCTCAAGGGCACACCCCACACACCGCGTCACTGTGCACT AGCCTCAGATGACAGACAAGCCTTTCACAAGACTTTTGTGGCACTGTTCATTTCTGAG ACCTTCTCTATGATGAGCTCAAACTGCTTACCTCAGAGAAGAAACTGCGTGCACAGAA AGCTGCTGAGGCCAGCTTGGGGCCCCTTCTTTCCTGTCCCTGGGCACTTCCC**T**GGCT GCTCTCTTTCCCCACTGCCCAGCCCAAGGAGTCCCCTCTGCAGCTGACCCGGGTTCA GCCTCCAGAACAGCGAGTTCCACAGCCCTGAAGCCTGGCCATCGTCCCTTTTCTGGA CACTGGACTGGTTCATAGGGCTCAGTGCCCTGCGGCTTTCTCCTCCCCACCACAGGC CTGGGAGGGGCAAGAAGCAAGCTTACCAGTT Red=rs4936443_Non-risk (C) Green=rs4938572_Non-risk (C) Blue=rs7117261_Non-risk (T)

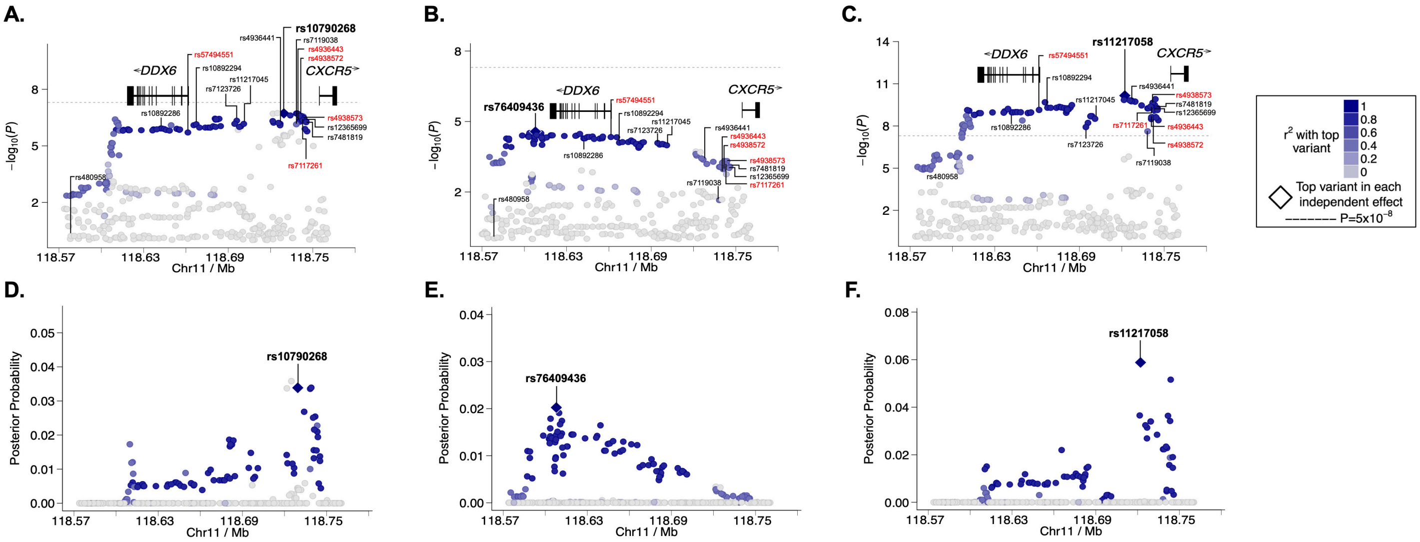
Supplementary Table 4 Continued

All Risk	TCTGAGAGGTACCCATGGCTCCAGGTCACACAGCCCAAAGCCTTGGCCTGTTTTGTA CGTGGACGGGGCAAAGAGAACACCCTCGCCGCTTCTCTCTGCCTTTAGCAGGGCTGT AGGAAACCCCCACCAGAGACCTCCAGCTTGGAGAGGAAAGAGTGGAACAGCCCTCT GGAAGCAAGTTACCCACAGGTTTAGTTTGCCTGGAGAGAAACAGGC**T**GGAGAGAGAC TGCGGCCTCCCTAGGGTCTTCTGACGGCAAATTCCTCCAGCTCAGTGGCTGCTGGG**T** AGCAGCACAGCCGGTTTCTCTCAAGGGCACACCCCACACACCGCGTCACTGTGCACT AGCCTCAGATGACAGACAAGCCTTTCACAAGACTTTTGTGGCACTGTTCATTTCTGAG ACCTTCTCTATGATGAGCTCAAACTGCTTACCTCAGAGAAGAAACTGCGTGCACAGAA AGCTGCTGAGGCCAGCTTGGGGCCCCTTCTTTCCTGTCCCTGGGCACTTCCC**C**GGCT GCTCTCTTTCCCCACTGCCCAGCCCAAGGAGTCCCCTCTGCAGCTGACCCGGGTTCA GCCTCCAGAACAGCGAGTTCCACAGCCCTGAAGCCTGGCCATCGTCCCTTTTCTGGA CACTGGACTGGTTCATAGGGCTCAGTGCCCTGCGGCTTTCTCCTCCCCACCACAGGC CTGGGAGGGGCAAGAAGCAAGCTTACCAGTT Red=rs4936443_Risk (T) Green=rs4938572_Risk (T) Blue=rs7117261_Risk (C)

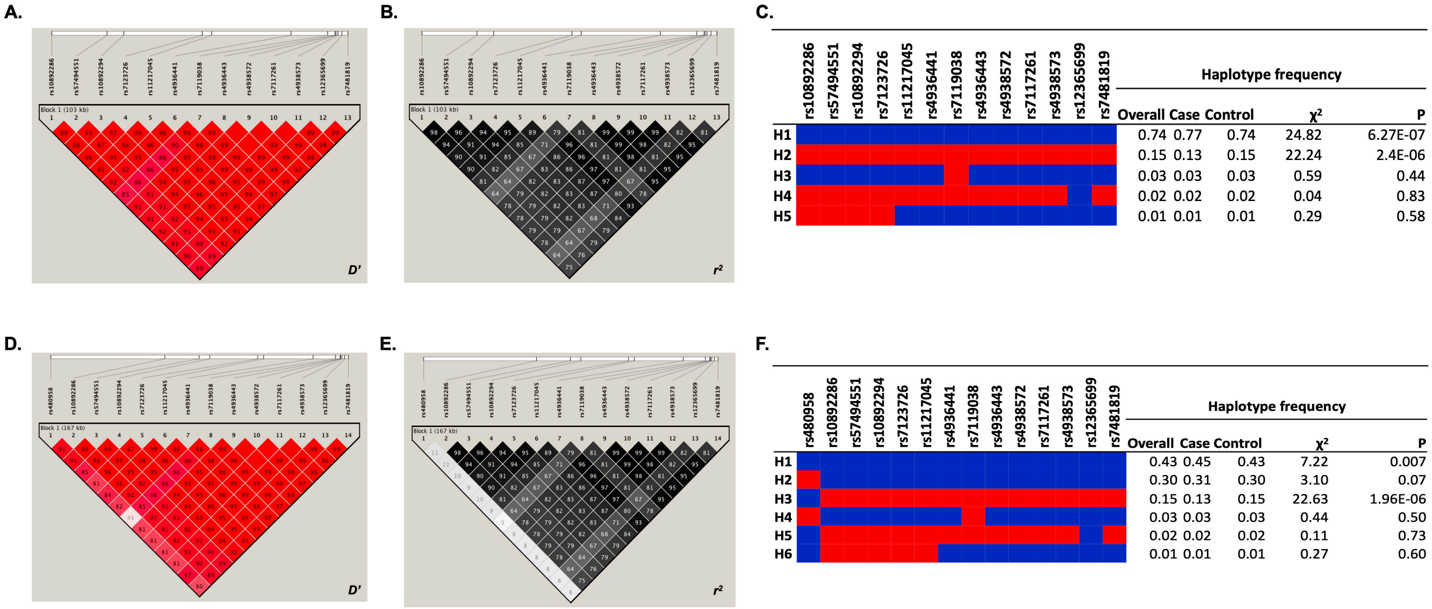
Supplemental Table 5: 3C-qPCR Primers

Primer Name	**Primer Sequence**
rs57494551 Anchor	CTCCACTCAAGATGGCGAAA
1-rs57494551 3C Short Range Primer Control	ACTGAAGAAAGTAGGGGCGG
2-rs57494551	GACACAGGAAACCTGAGGGA
3-rs57494551	GTGCATTCATGATTGTTGCC
4-rs57494551	TTGGTGAGCTGTGATTGAGC
5-rs57494551	AGTCCCTTCCAGAGGGTTTT
6-rs57494551	TTGGTTACAGATTACACCTTGT
7-rs57494551	TCCTTCCTGATCAATGTCCC
8-rs57494551	TGAAGGTAACAGTGGCCCTT
9-rs57494551	AGGTGCATGTTGCTGTCAAG
10-rs57494551	CAAGGCTCTGGGAGAGAGG
11-rs57494551	CAAGGCTCTGGGAGAGAGG
12-rs57494551	TTAGCGTGGGATACAAAGCC
13-rs57494551	TTCCTGTATTCCAATTTCCCC
14-rs57494551	TTCTCCACTCACCCCAAACT
15-rs57494551	GAGGTGCTGGAGTATCTGGG
rs4938572 Anchor	TGTAATGGGGTGTTGGGTCC
1-rs4938572 3C Short Range Primer Control	TCCTTCCTGATCAATGTCCC
2-rs4938572	TGACTTTGTGATCCAGCTGC
3-rs4938572	CTCCACTCAAGATGGCGAAA
4-rs4938572	CAAGGCTCTGGGAGAGAGG
5-rs4938572	TTTCCCTTCAAGAGAGCCAG
6-rs4938572	GCATAGAAAGGTGCTTTGGG
7-rs4938572	CTCTCCCCACTGAGTCCTCA
8-rs4938572	GAGGTGCTGGAGTATCTGGG
9-rs4938572	AAATCTTCCTTCCCAGCCTG
10-rs4938572	GTCTGAGGGTTCCTGAAGGA
11-rs4938572	CATATCCTGGGCCTTCACTG
12-rs4938572	AGGACAGTCAGAGAGCGTCAG

SUPPLEMENTAL FIGURES & LEGENDS



Supplemental Figure 1. Fine mapping of the *DDX6-CXCR5* region in SjD and SLE Immunochip data after imputation. (A-C) Logistic regression analysis was performed on **(A)** DS3-SjD (1916 SjD cases; 6194 controls), **(B)** DS4-SLE (3762 SLE cases; 6194 controls), and **(C)** DS3+DS4 (merged SjD and SLE) after quality control and imputation, identifying the top SNPs (e.g., index SNPs indicated in bold) of the *DDX6-CXCR5* association. SNPs prioritized for bioinformatic screening in this study are indicated in black; five SNPs prioritized for functional characterized are labeled in red. **(D-F)** Posterior probability distributions of SNPs in the *DDX6-CXCR5* region of **(D)** DS3, **(E)** DS4, and **(F)** DS3+DS4. SNPs with highest posterior probability are indicated. Pairwise (r^2) analysis for DS3-SjD **(A, D)** was based on the second most significant SNP because the most significant SNP was not in linkage disequilibrium (LD) with the haplotype.



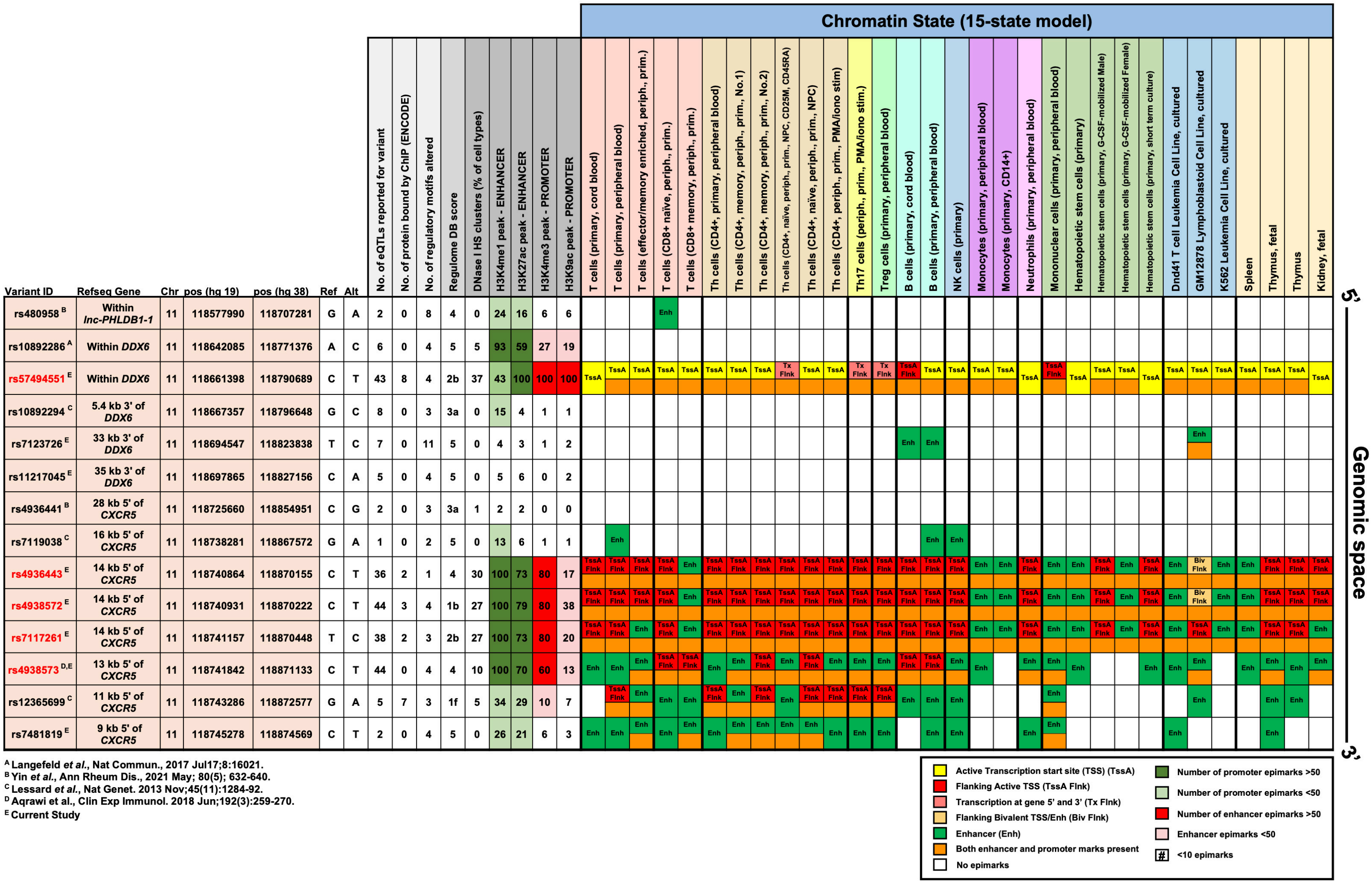
C.

														Haplotype frequency				
	rs10892286	rs57494551	rs10892294	rs7123726	rs11217045	rs4936441	rs7119038	rs4936443	rs4938572	rs7117261	rs4938573	rs12365699	rs7481819	Overall	Case	Control	χ²	P
H1	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	0.74	0.77	0.74	24.82	6.27E-07
H2	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	0.15	0.13	0.15	22.24	2.4E-06
H3	🟦	🟦	🟦	🟦	🟦	🟦	🟥	🟦	🟦	🟦	🟦	🟦	🟦	0.03	0.03	0.03	0.59	0.44
H4	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟦	🟥	0.02	0.02	0.02	0.04	0.83
H5	🟥	🟥	🟥	🟥	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	0.01	0.01	0.01	0.29	0.58

F.

															Haplotype frequency				
	rs480958	rs10892286	rs57494551	rs10892294	rs7123726	rs11217045	rs4936441	rs7119038	rs4936443	rs4938572	rs7117261	rs4938573	rs12365699	rs7481819	Overall	Case	Control	χ²	P
H1	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	0.43	0.45	0.43	7.22	0.007
H2	🟥	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	0.30	0.31	0.30	3.10	0.07
H3	🟦	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	0.15	0.13	0.15	22.63	1.96E-06
H4	🟥	🟦	🟦	🟦	🟦	🟦	🟦	🟥	🟦	🟦	🟦	🟦	🟦	🟦	0.03	0.03	0.03	0.44	0.50
H5	🟦	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟦	🟥	0.02	0.02	0.02	0.11	0.73
H6	🟦	🟥	🟥	🟥	🟥	🟥	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦	0.01	0.01	0.01	0.27	0.60

Supplemental Figure 2. Haplotype frequency of the *DDX6-CXCR5* risk region in SjD. (A,D) Co-inheritance (D') and **(B,E)** pairwise linkage disequilibrium (r^2) were assessed across the *DDX6-CXCR5* risk haplotype of SjD without **(A-C)** or with **(D-F)** rs480958. **(C,F)** Haplotype organization and frequencies of the index SNPs from the meta-analyses, SNPs previously reported as associated with SjD and/or SLE, and SNPs with strong bioinformatic functional evidence are shown.

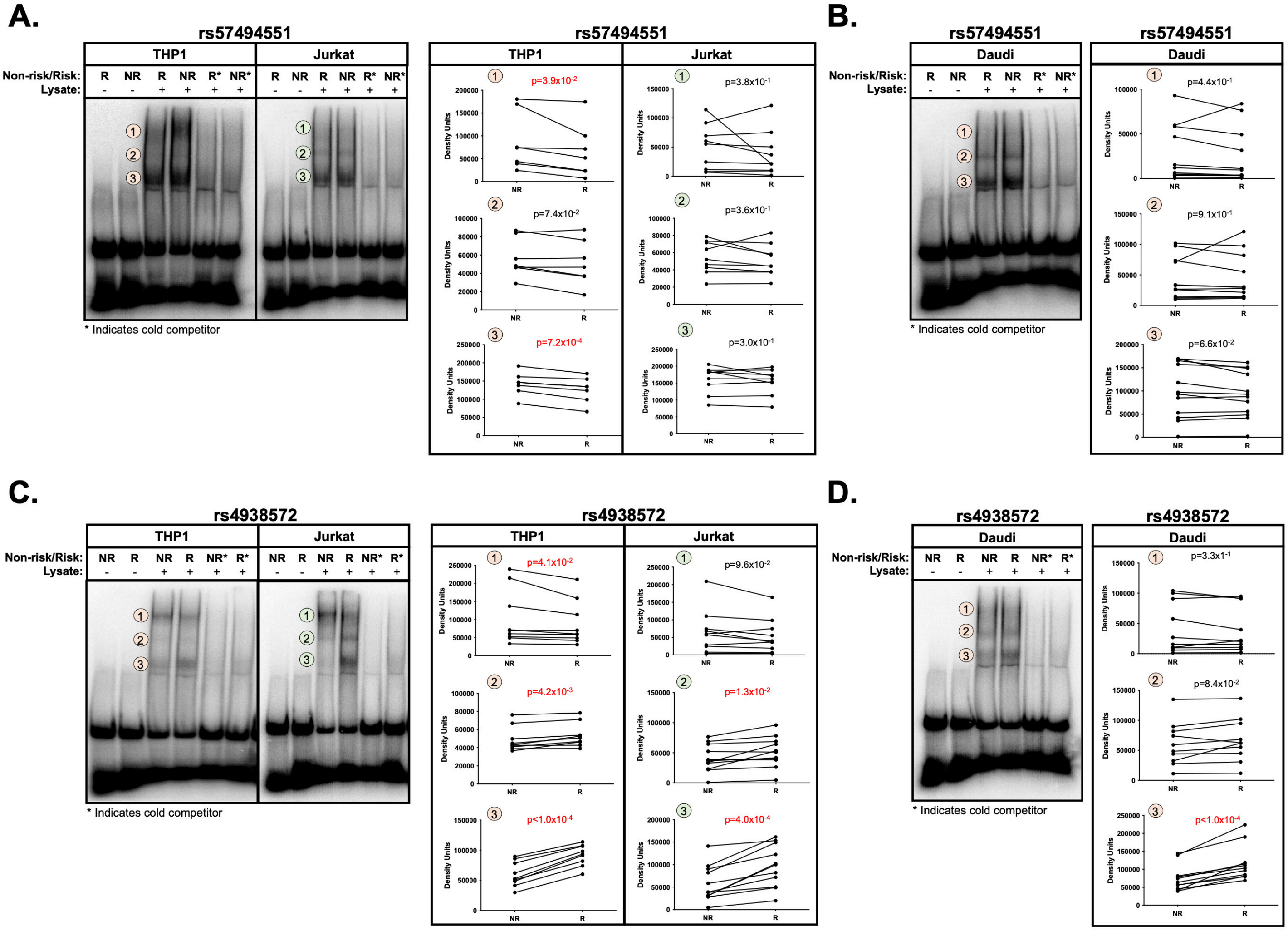


																Chromatin State (15-state model)																														
Variant ID	Refseq Gene	Chr	pos (hg 19)	pos (hg 38)	Ref	Alt	No. of eQTLs reported for variant	No. of protein bound by ChIP (ENCODE)	No. of regulatory motifs altered	Regulome DB score	DNase I HS clusters (% of cell types)	H3K4me1 peak - ENHANCER	H3K27ac peak - ENHANCER	H3K4me3 peak - PROMOTER	H3K9ac peak - PROMOTER	T cells (primary, cord blood)	T cells (primary, peripheral blood)	T cells (effector/memory enriched, periph., prim.)	T cells (CD8+ naïve, periph., prim.)	T cells (CD8+ memory, periph., prim.)	Th cells (CD4+, primary, peripheral blood)	Th cells (CD4+, memory, periph., prim., No.1)	Th cells (CD4+, memory, periph., prim., No.2)	Th cells (CD4+, naïve, periph., prim., NPC, CD25M, CD45RA)	Th cells (CD4+, naïve, periph., prim., NPC)	Th cells (CD4+, periph., prim., PMA/iono stim)	Th17 cells (periph., prim., PMA/iono stim.)	Treg cells (primary, peripheral blood)	B cells (primary, cord blood)	B cells (primary, peripheral blood)	NK cells (primary)	Monocytes (primary, peripheral blood)	Monocytes (primary, CD14+)	Neutrophils (primary, peripheral blood)	Mononuclear cells (primary, peripheral blood)	Hematopoietic stem cells (primary)	Hematopoietic stem cells (primary, G-CSF-mobilized Male)	Hematopoietic stem cells (primary, G-CSF-mobilized Female)	Hematopoietic stem cells (primary, short term culture)	Dnd41 T cell Leukemia Cell Line, cultured	GM12878 Lymphoblastoid Cell Line, cultured	K562 Leukemia Cell Line, cultured	Spleen	Thymus, fetal	Thymus	Kidney, fetal
rs480958 [B]	Within *lnc-PHLDB1-1*	11	118577990	118707281	G	A	2	0	8	4	0	24	16	6	6				Enh																											
rs10892286 [A]	Within *DDX6*	11	118642085	118771376	A	C	6	0	4	5	5	93	59	27	19																															
rs57494551 [E]	Within *DDX6*	11	118661398	118790689	C	T	43	8	4	2b	37	43	100	100	100	TssA	TssA	TssA	TssA	TssA	TssA	TssA	TssA	Tx Flnk	TssA	TssA	Tx Flnk	Tx Flnk	TssA Flnk	TssA	TssA	TssA	TssA	TssA	TssA Flnk	TssA	TssA	TssA	TssA	TssA	TssA	TssA	TssA	TssA	TssA	TssA
rs10892294 [C]	5.4 kb 3' of *DDX6*	11	118667357	118796648	G	C	8	0	3	3a	0	15	4	1	1																															
rs7123726 [E]	33 kb 3' of *DDX6*	11	118694547	118823838	T	C	7	0	11	5	0	4	3	1	2														Enh	Enh											Enh					
rs11217045 [E]	35 kb 3' of *DDX6*	11	118697865	118827156	C	A	5	0	4	5	0	5	6	0	2																															
rs4936441 [B]	28 kb 5' of *CXCR5*	11	118725660	118854951	C	G	2	0	3	3a	1	2	2	0	0																															
rs7119038 [C]	16 kb 5' of *CXCR5*	11	118738281	118867572	G	A	1	0	2	5	0	13	6	1	1		Enh													Enh	Enh															
rs4936443 [E]	14 kb 5' of *CXCR5*	11	118740864	118870155	C	T	36	2	1	4	30	100	73	80	17	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	Enh	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	Enh	Enh	TssA Flnk	Enh	Enh	TssA Flnk	Enh	TssA Flnk	Enh	Biv Flnk	Enh	Enh	TssA Flnk	TssA Flnk	TssA Flnk
rs4938572 [E]	14 kb 5' of *CXCR5*	11	118740931	118870222	C	T	44	3	4	1b	27	100	79	80	38	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	Enh	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	Enh	Enh	TssA Flnk	Enh	Enh	TssA Flnk	Enh	TssA Flnk	Enh	Biv Flnk	Enh	Enh	TssA Flnk	TssA Flnk	TssA Flnk
rs7117261 [E]	14 kb 5' of *CXCR5*	11	118741157	118870448	T	C	38	2	3	2b	27	100	73	80	20	TssA Flnk	TssA Flnk	Enh	TssA Flnk	Enh	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	Enh	Enh	TssA Flnk	Enh	Enh	TssA Flnk	Enh	TssA Flnk	Enh	TssA Flnk	Enh	Enh	TssA Flnk	TssA Flnk	Enh
rs4938573 [D,E]	13 kb 5' of *CXCR5*	11	118741842	118871133	C	T	44	0	4	4	10	100	70	60	13	Enh	Enh	Enh	TssA Flnk	TssA Flnk	Enh	Enh	TssA Flnk	Enh	TssA Flnk	Enh	Enh	Enh	TssA Flnk	TssA Flnk	Enh	Enh		Enh	Enh	Enh			Enh	Enh	Enh		Enh	Enh	Enh	Enh
rs12365699 [C]	11 kb 5' of *CXCR5*	11	118743286	118872577	G	A	5	7	3	1f	5	34	29	10	7		TssA Flnk	Enh	Enh	Enh	TssA Flnk	Enh	TssA Flnk	Enh	TssA Flnk	TssA Flnk	TssA Flnk	TssA Flnk	Enh	Enh	Enh				Enh						Enh			Enh	Enh	
rs7481819 [E]	9 kb 5' of *CXCR5*	11	118745278	118874569	C	T	2	0	4	5	0	26	21	6	3	Enh	Enh	Enh	Enh	Enh	Enh	Enh	Enh	Enh	Enh	Enh	Enh	Enh		Enh	Enh			Enh	Enh					Enh				Enh		

[A] Langefeld *et al.*, Nat Commun., 2017 Jul17;8:16021.
[B] Yin *et al.*, Ann Rheum Dis., 2021 May; 80(5); 632-640.
[C] Lessard *et al.*, Nat Genet. 2013 Nov;45(11):1284-92.
[D] Aqrawi et al., Clin Exp Immunol. 2018 Jun;192(3):259-270.
[E] Current Study

🟨	Active Transcription start site (TSS) (TssA)	🟩	Number of promoter epimarks >50
🟥	Flanking Active TSS (TssA Flnk)	🟩	Number of promoter epimarks <50
🟥	Transcription at gene 5' and 3' (Tx Flnk)	🟥	Number of enhancer epimarks >50
🟧	Flanking Bivalent TSS/Enh (Biv Flnk)	🟥	Enhancer epimarks <50
🟩	Enhancer (Enh)	#	<10 epimarks
🟧	Both enhancer and promoter marks present		
☐	No epimarks		

Supplemental Figure 3. Functional bioinformatic analyses of putative functional SNPs in the *DDX6-CXCR5* risk region. RegulomeDB, HaploReg 4.1, UCSC genome browser, GTEx, and ENCODE were used to assess the predicted histone marks and regulatory elements positioned at the indicated SNPs in 31 cell types and tissues. Total number of enhancer marks (H3K4me1, H3K27ac) or promoter marks (H3K4me3, H3K9ac) are also indicated. RegulomeDB scores, total number of eQTLs, proteins bound by ChIP, altered regulatory motifs, and DNase I HS clusters from HaploReg are depicted. White boxes indicate that no epimarks were found. Five SNPs (red) exhibit compounding bioinformatic evidence of function and were prioritized for functional interrogation.



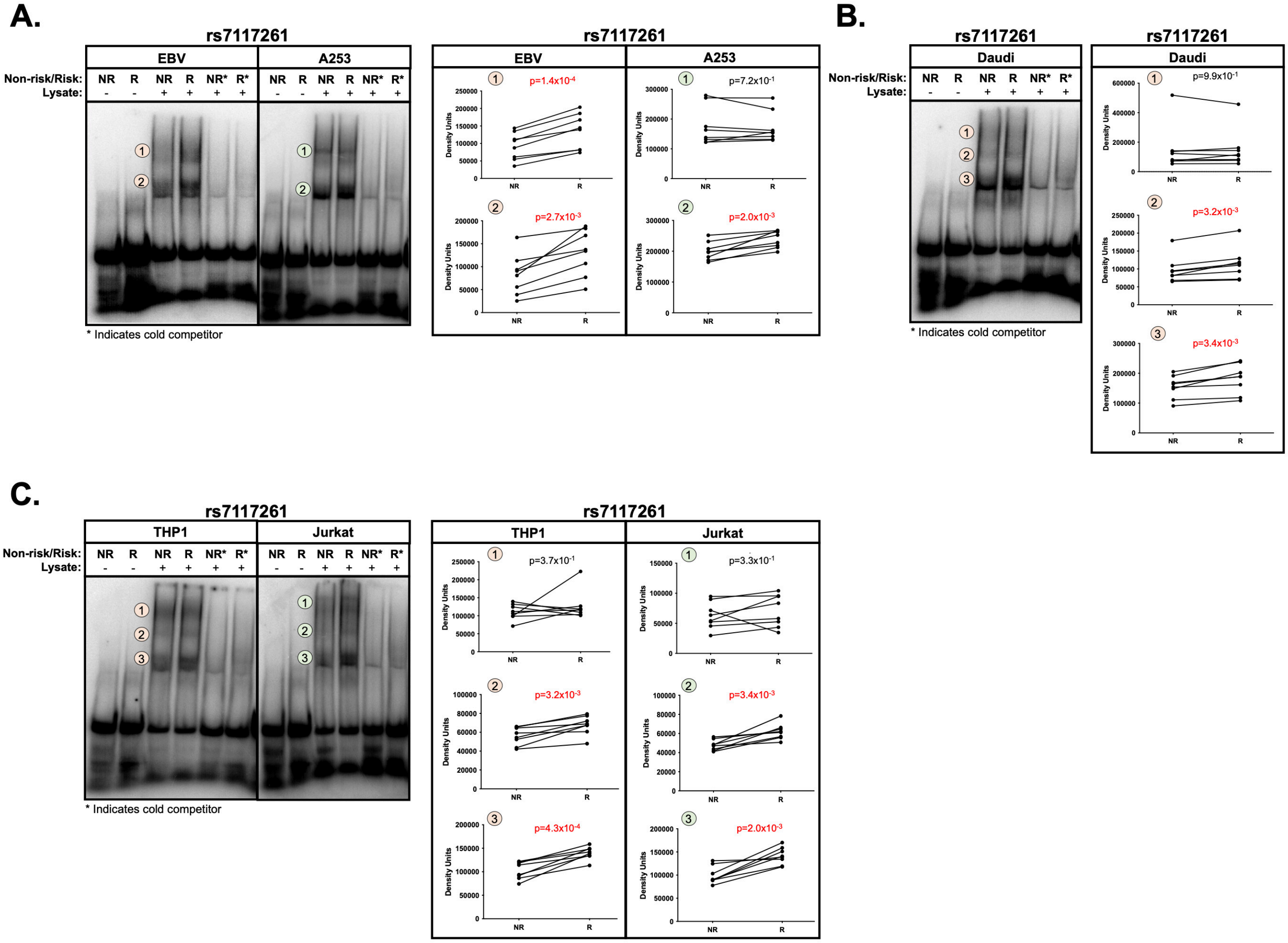
* Indicates cold competitor

* Indicates cold competitor

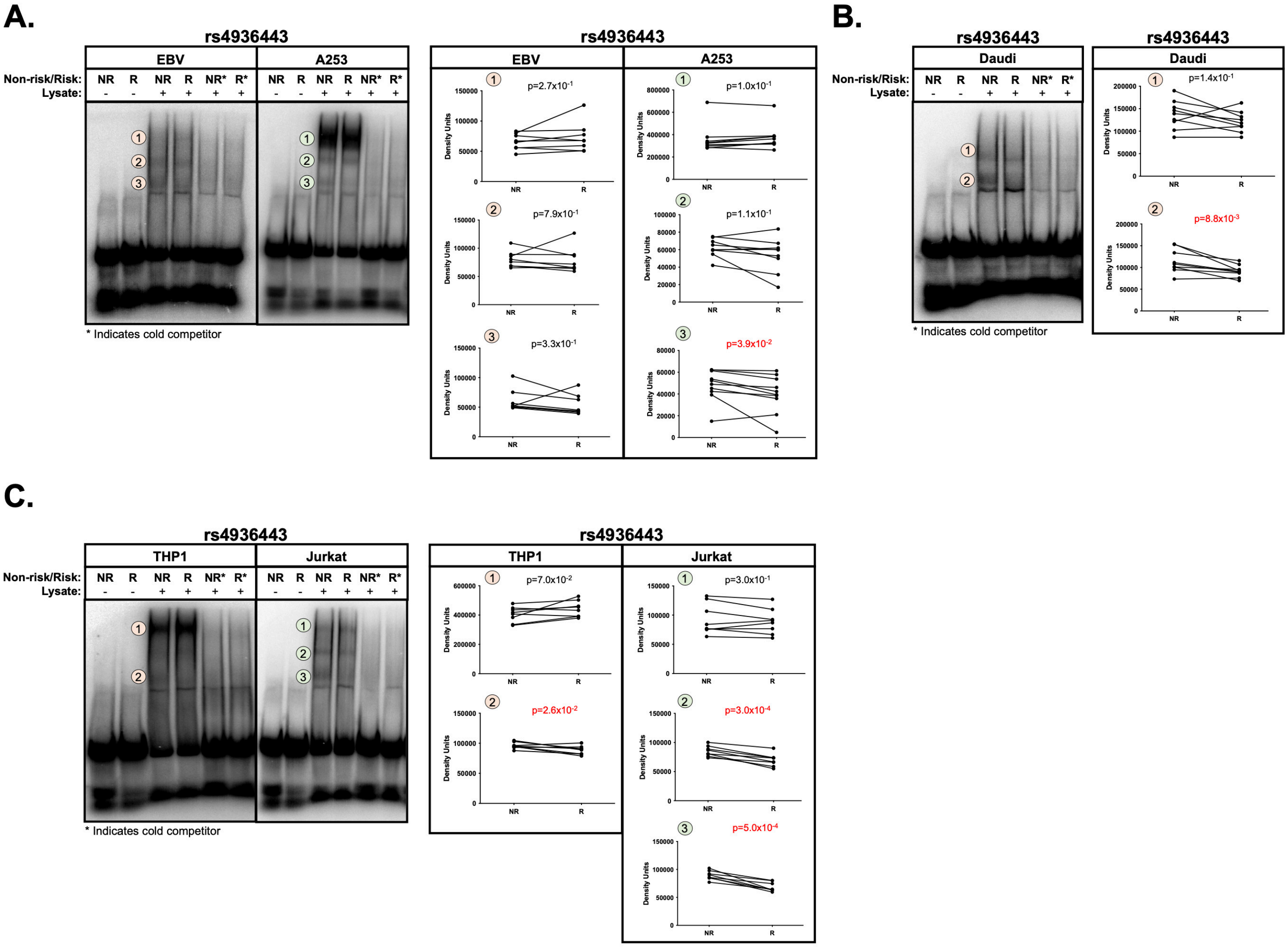
* Indicates cold competitor

* Indicates cold competitor

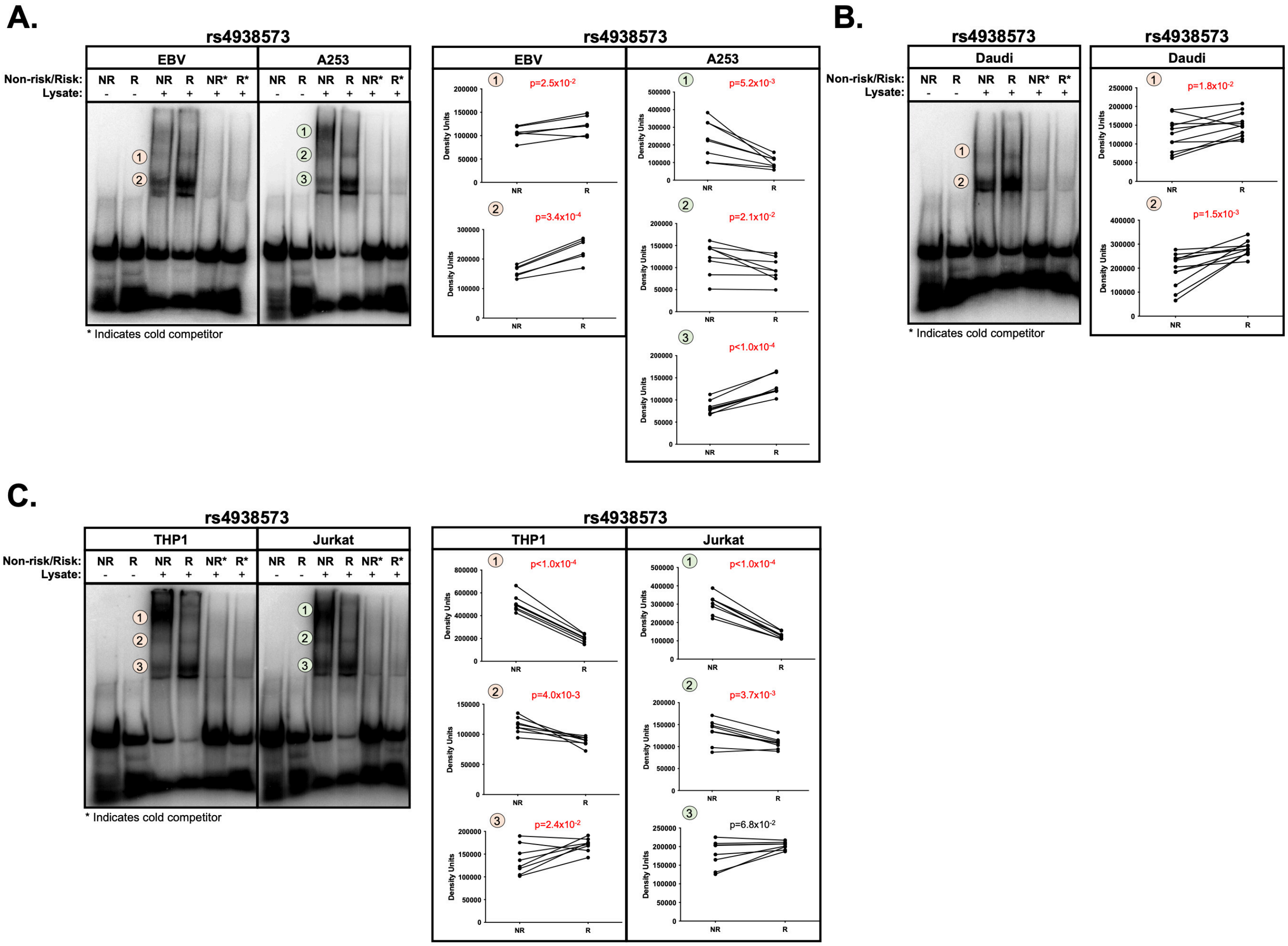
Supplemental Figure 4. Allele- and cell-type specific differential nuclear protein affinities of SNPs rs57494551 and rs4938572. (A-B) Radiolabeled electromobility shift assays (EMSA) were performed using oligonucleotides containing the non-risk (NR) or risk (R) allele of rs57494551 and nuclear extracts from **(A)** THP1 and Jurkat cells or **(B)** Daudi cells. **(C-D)** Radiolabeled EMSAs were performed using oligonucleotides containing the NR or R allele of rs4938572 and nuclear extracts from **(A)** THP1 and Jurkat cells or **(B)** Daudi cells. For all panels, probes incubated in the absence of nuclear lysate were used as negative control (Lanes 1, 2). Cold competitors were used to assess non-specific binding (Lanes 5, 6). Images are representative of n>6 biological replicates. Bands indicated by numbered orange or green circles were quantified by densitometry and analyzed using paired t-test; p-values are indicated.



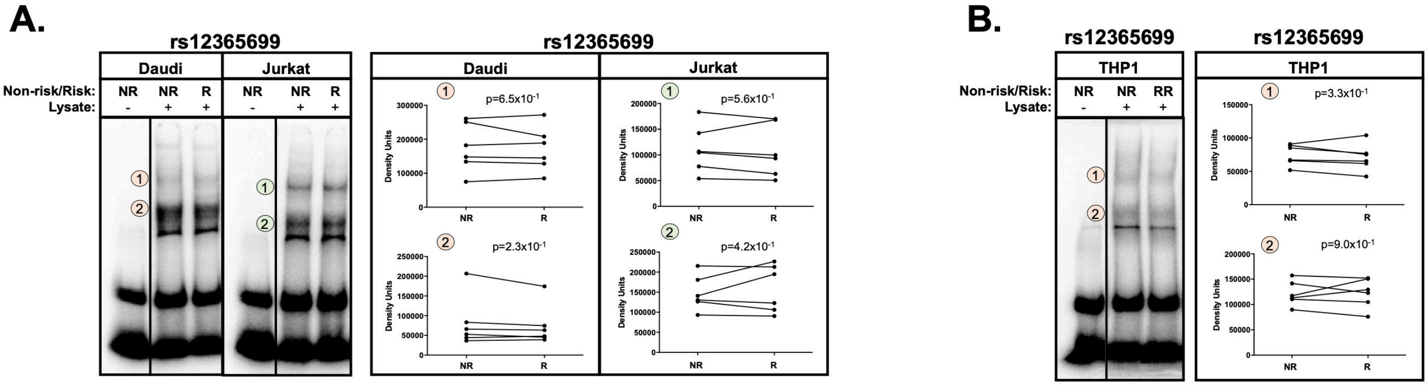
Supplemental Figure 5. Allele- and cell-type specific differential nuclear protein affinities of SNPs rs7117261. (A-C) Radiolabeled electromobility shift assays (EMSA) were performed using oligonucleotides containing the non-risk (NR) or risk (R) allele of rs7117261 and nuclear extracts from **(A)** EBV B and A253 cells, **(B)** Daudi cells, or **(C)** THP1 and Jurkat cells. For all panels, probes incubated in the absence of nuclear lysate were used as negative control (Lanes 1, 2). Cold competitors were used to assess non-specific binding (Lanes 5, 6). Images are representative of n>6 biological replicates. Bands indicated by numbered orange or green circles were quantified by densitometry and analyzed using paired t-test; p-values are indicated.



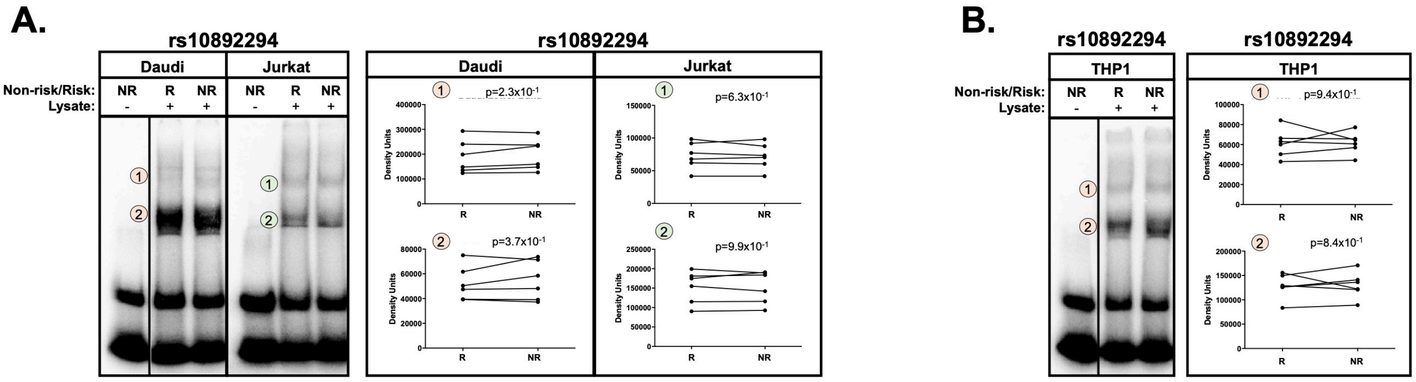
Supplemental Figure 6. Allele- and cell-type specific differential nuclear protein affinities of SNPs rs4936443. (A-C) Radiolabeled electromobility shift assays (EMSA) were performed using oligonucleotides containing the non-risk (NR) or risk (R) allele of rs4936443 and nuclear extracts from **(A)** EBV B and A253 cells, **(B)** Daudi cells, or **(C)** THP1 and Jurkat cells. For all panels, probes incubated in the absence of nuclear lysate were used as negative control (Lanes 1, 2). Cold competitors were used to assess non-specific binding (Lanes 5, 6). Images are representative of n>6 biological replicates. Bands indicated by numbered orange or green circles were quantified by densitometry and analyzed using paired t-test; p-values are indicated.



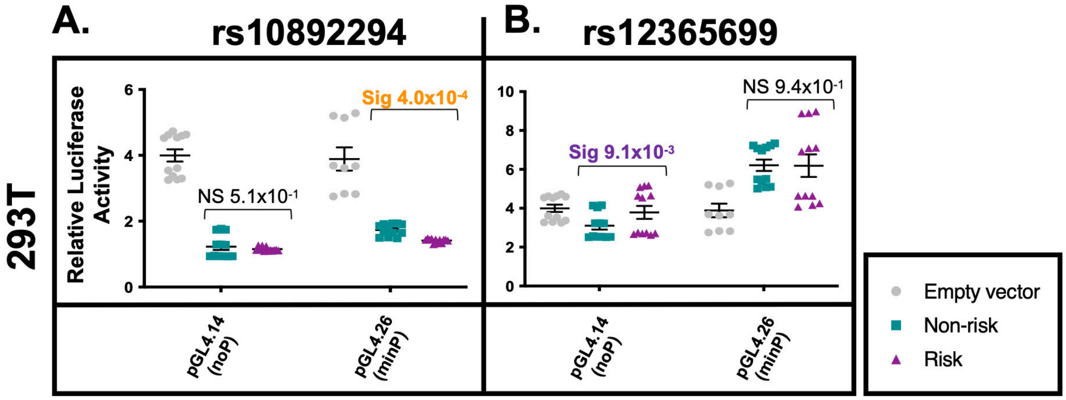
Supplemental Figure 7. Allele- and cell-type specific differential nuclear protein affinities of SNPs rs4938573. (A-C) Radiolabeled electromobility shift assays (EMSA) were performed using oligonucleotides containing the non-risk (NR) or risk (R) allele of rs4938573 and nuclear extracts from **(A)** EBV B and A253 cells, **(B)** Daudi cells, or **(C)** THP1 and Jurkat cells. For all panels, probes incubated in the absence of nuclear lysate were used as negative control (Lanes 1, 2). Cold competitors were used to assess non-specific binding (Lanes 5, 6). Images are representative of n>6 biological replicates. Bands indicated by numbered orange or green circles were quantified by densitometry and analyzed using paired t-test; p-values are indicated.



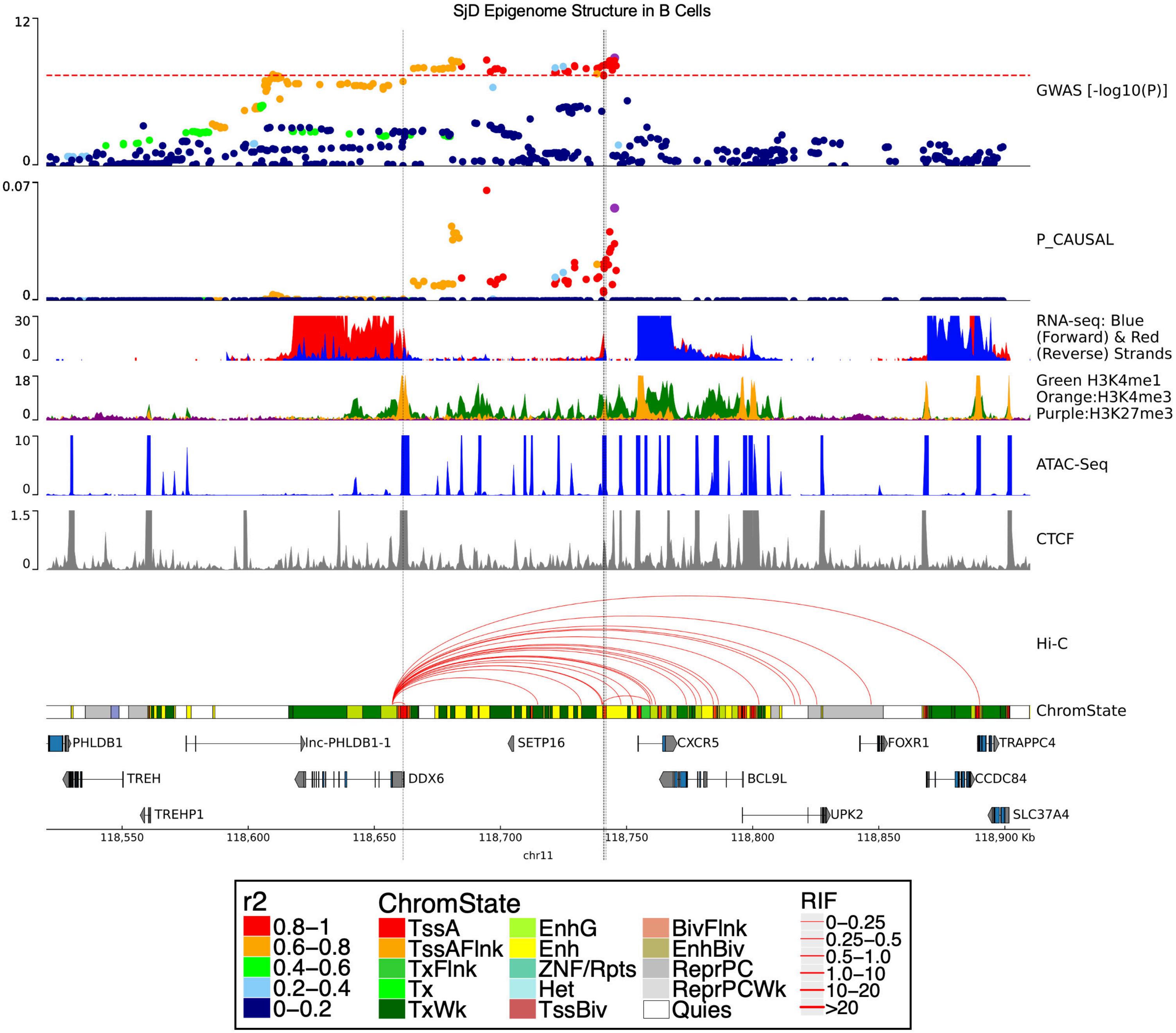
Supplemental Figure 8. Allele- and cell-type specific differential nuclear protein affinities of SNPs rs12365699. (A-B) Radiolabeled electromobility shift assays (EMSA) were performed using oligonucleotides containing the non-risk (NR) or risk (R) allele of rs12365699 and nuclear extracts from **(A)** Daudi and Jurkat cells or **(B)** THP 1. For all panels, probes incubated in the absence of nuclear lysate were used as negative control (Lanes 1). Images are representative of n>6 biological replicates. Bands indicated by numbered orange or green circles were quantified by densitometry and analyzed using paired t-test; p-values are indicated.



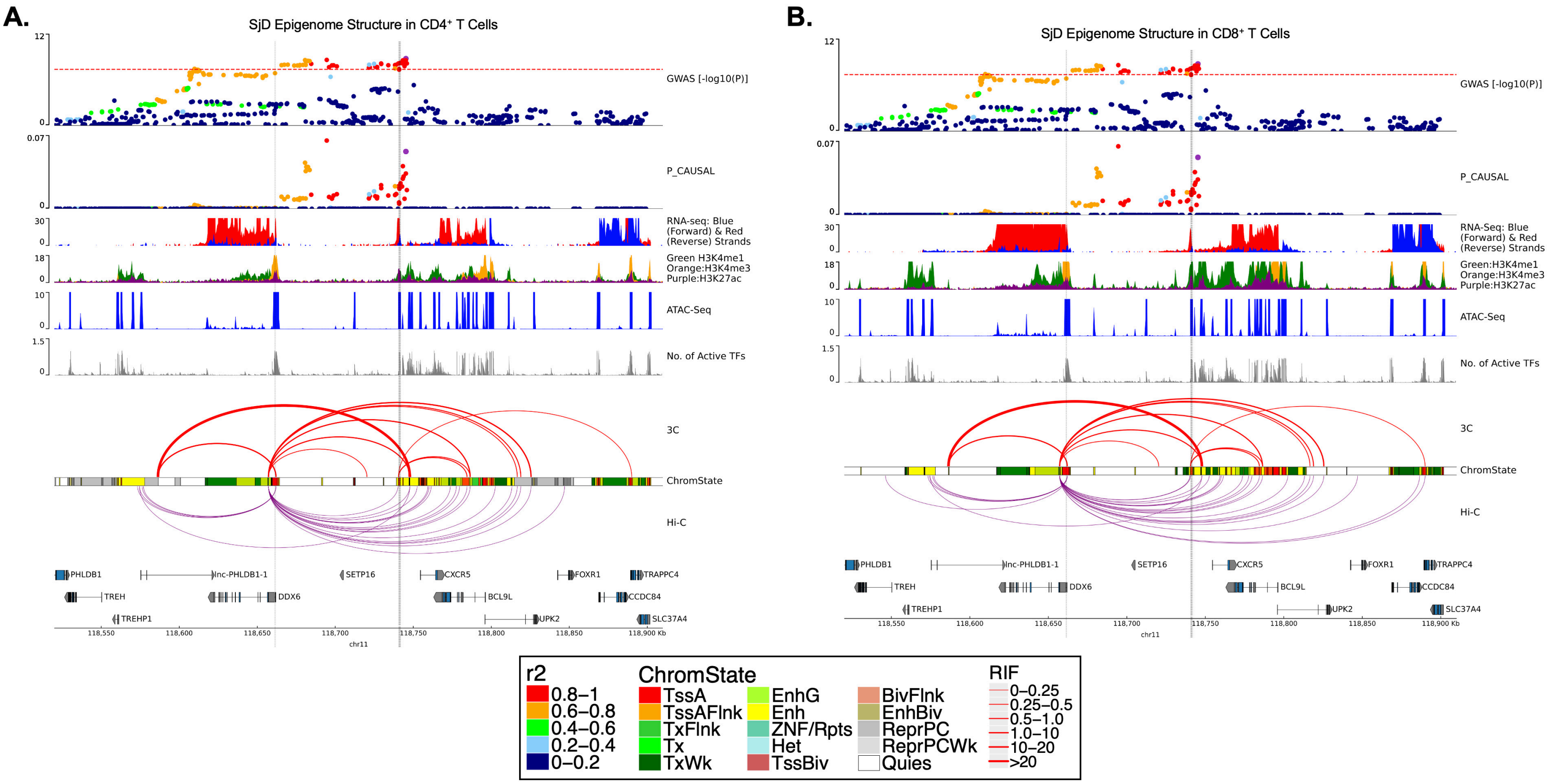
Supplemental Figure 9. Allele- and cell-type specific differential nuclear protein affinities of SNPs rs10892294. (A-B) Radiolabeled electromobility shift assays (EMSA) were performed using oligonucleotides containing the non-risk (NR) or risk (R) allele of rs10892294 and nuclear extracts from **(A)** Daudi and Jurkat cells or **(B)** THP1 cells. For all panels, probes incubated in the absence of nuclear lysate were used as negative control (Lanes 1). Images are representative of n>6 biological replicates. Bands indicated by numbered orange or green circles were quantified by densitometry and analyzed using paired t-test; p-values are indicated.



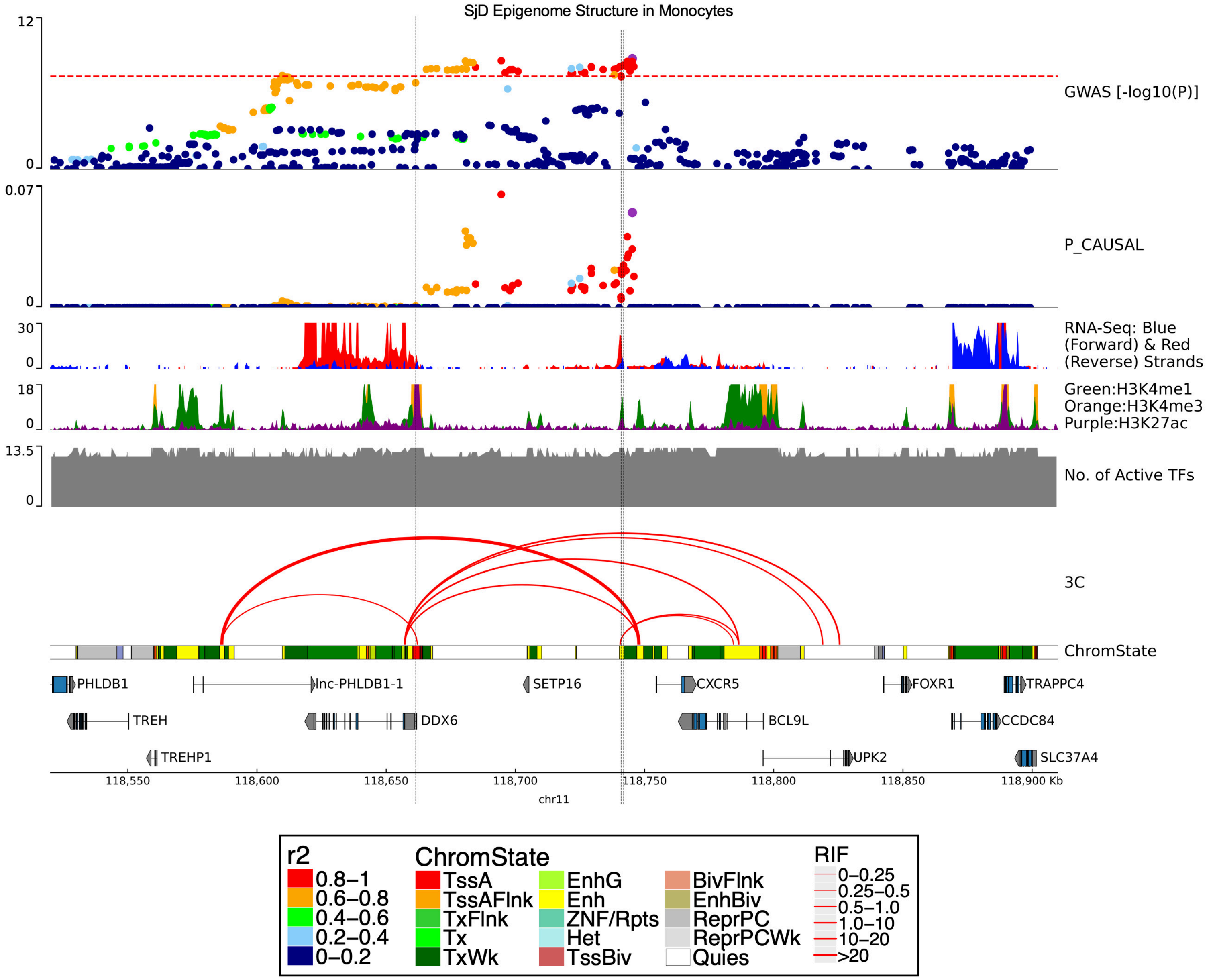
Supplemental Figure 10. Allele-specific promoter and enhancer activity of rs10892294 and rs12365699 on the *DDX6-CXCR5* region in 293T cells. gBlocks carrying the non-risk or risk alleles of **(A)** rs10892294 or **(B)** rs12365699 were cloned into a promoter-less (pGL4.14; noP) or minimal promoter (pGL4.26; minP) luciferase vector. Plasmids were transfected into 293T cells. Luciferase activity was measured after 24 hours and normalized to the Renilla transfection control and then the vector-only control; reported as Relative Luciferase Activity. Statistical comparisons were performed using a paired t-test; p-values are indicated.



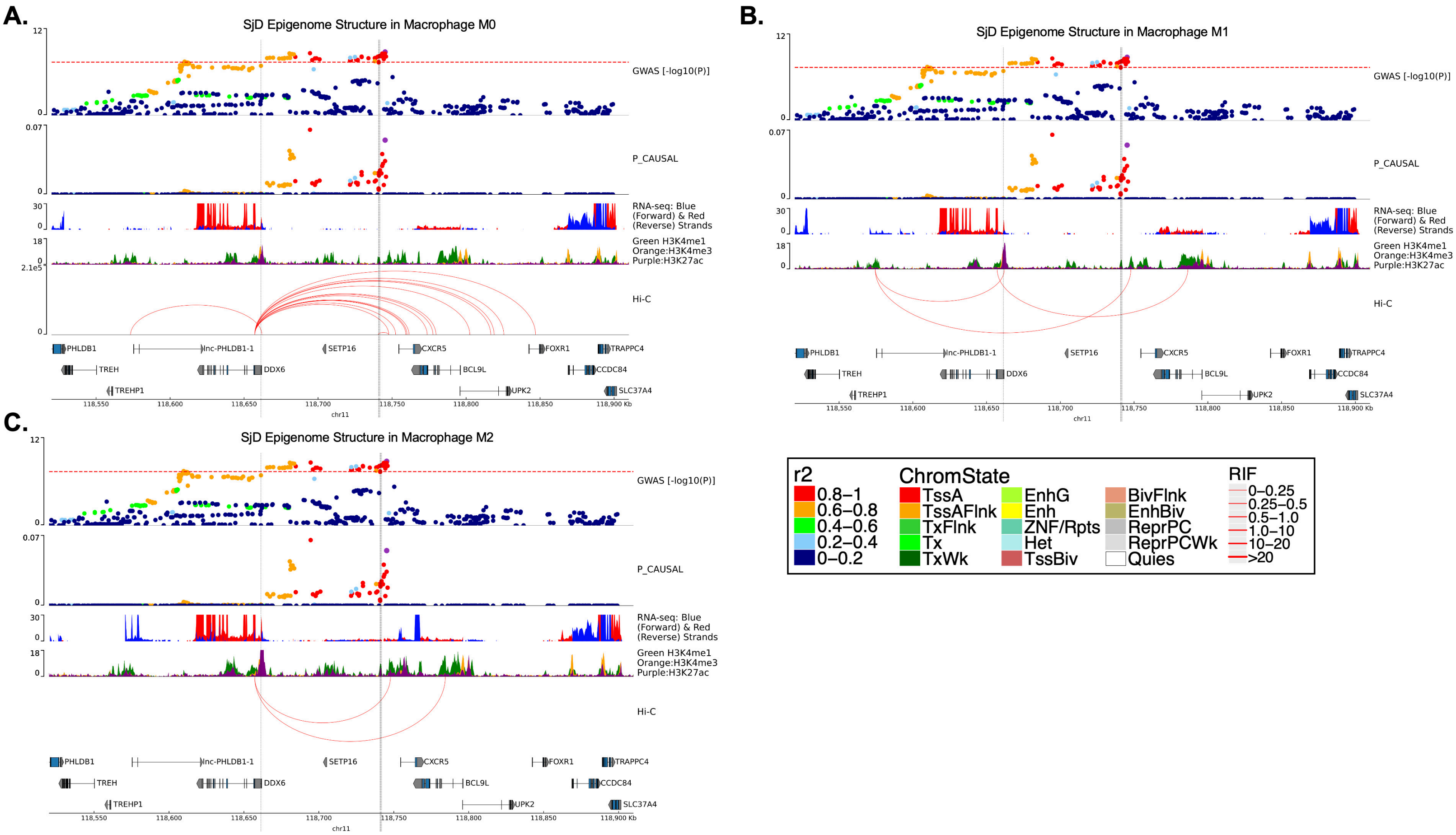
Supplemental Figure 11. Complex chromatin architecture revealed across the *DDX6-CXCR5* region in human primary B cells. SjD GWAS association (top panel), publicly available epigenomic enrichment, and promoter-capture Hi-C looping data (red lines) across the *DDX6-CXCR5* region in human primary B cells are shown. Vertical grey lines indicate the locations of rs57494551 or rs4938572, respectively.



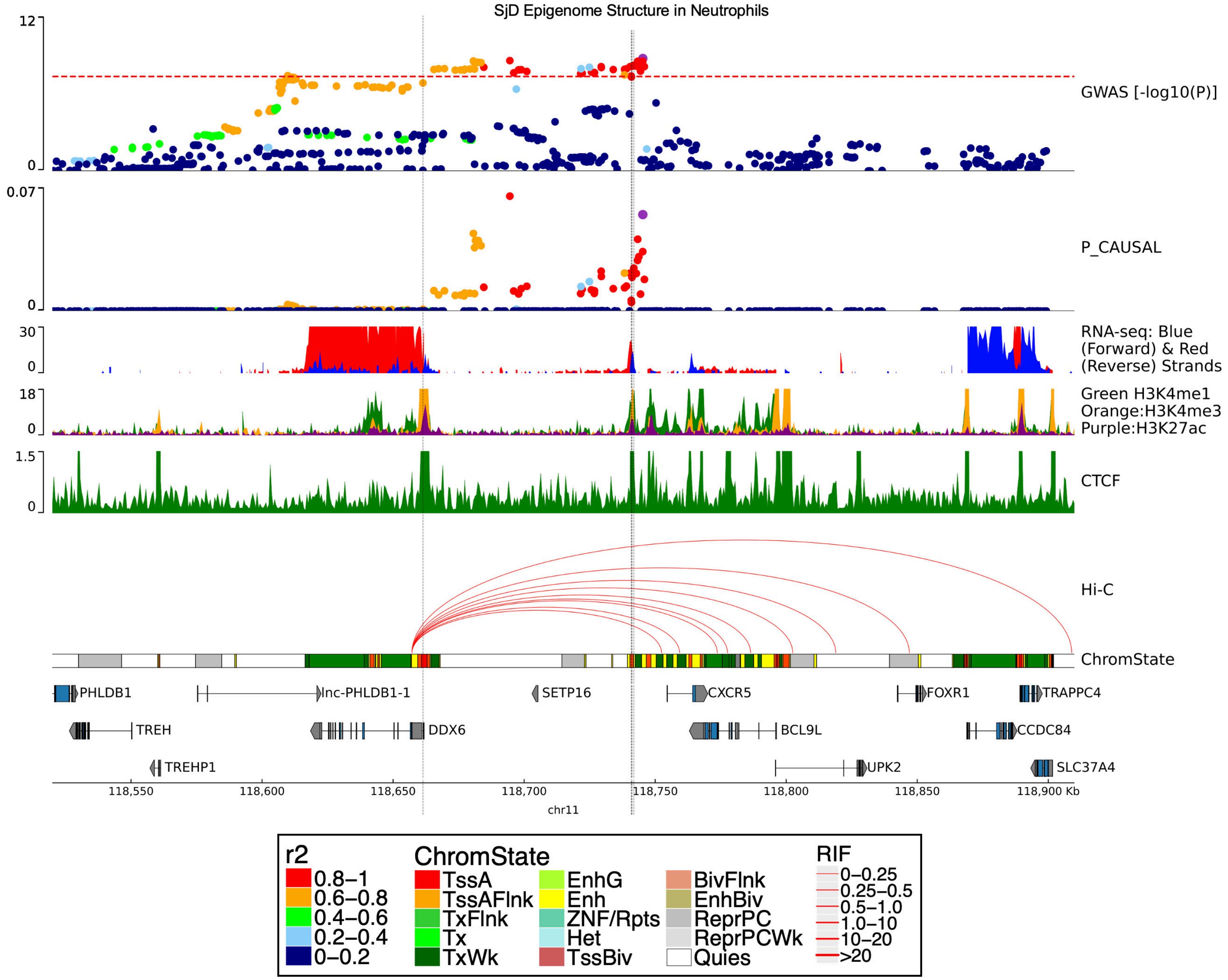
Supplemental Figure 12. Complex chromatin architecture revealed across the *DDX6-CXCR5* region in primary human T cells. SjD GWAS association (top panel) and publicly available epigenomic enrichment across the *DDX6-CXCR5* region in human primary **(A)** CD4$^+$ T cells and **(B)** CD8$^+$ T cells. Vertical grey lines indicate the locations of rs57494551 or rs4938572, respectively. Promoter-capture Hi-C looping (purple lines) contrasts the summary 3C-qPCR results reported in Figure 6 (red lines); 3C-qPCR line thickness indicates relative interaction frequency (RIF).



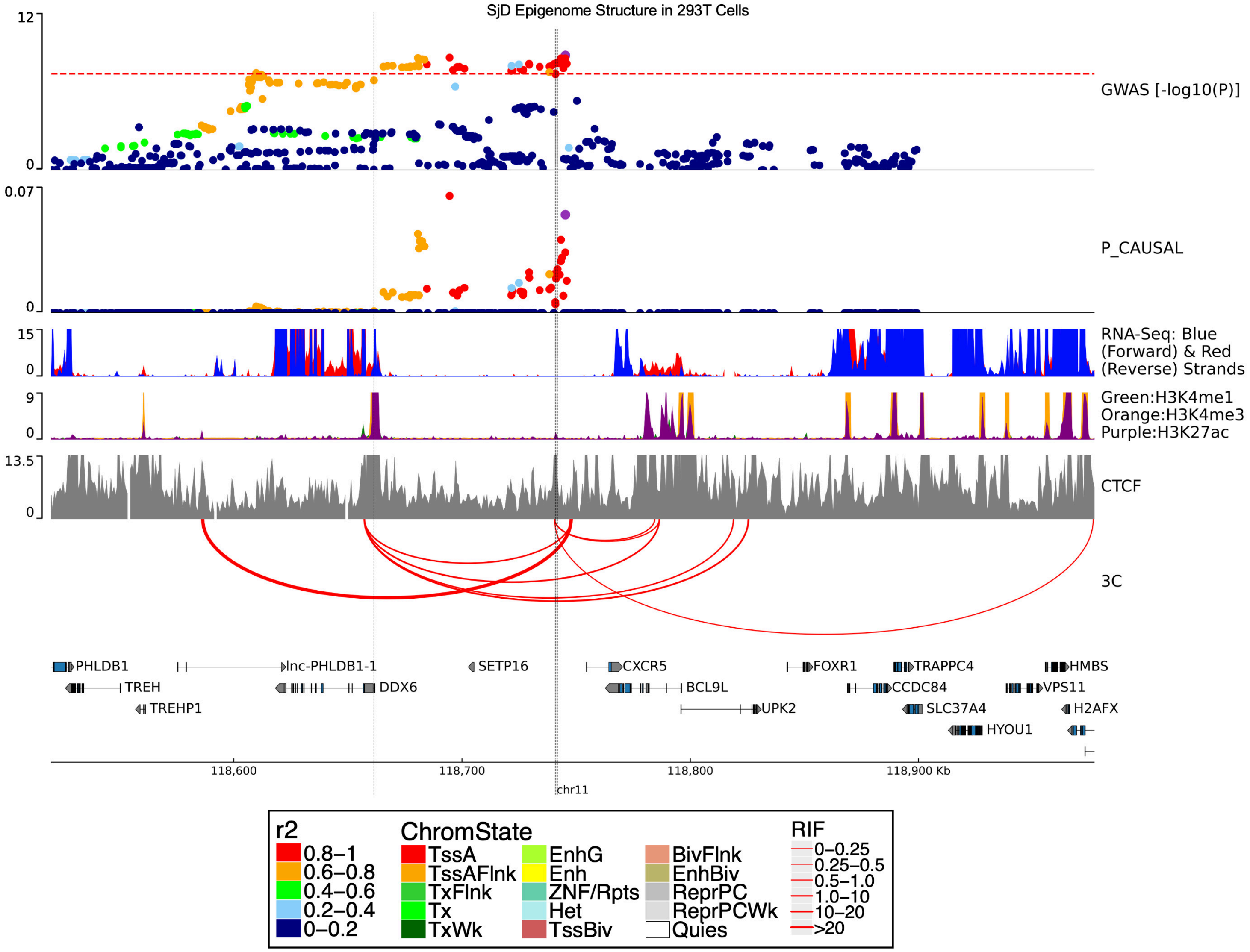
Supplemental Figure 13. Complex chromatin architecture revealed across the *DDX6-CXCR5* region in human primary monocytes. SjD GWAS association (top panel) and publicly available epigenomic enrichment across the *DDX6-CXCR5* region in human primary monocytes. Vertical grey lines indicate the locations of rs57494551 or rs4938572, respectively. Summary 3C-qPCR results reported in Figure 6 are also shown (red lines); line thickness indicates relative interaction frequency (RIF).



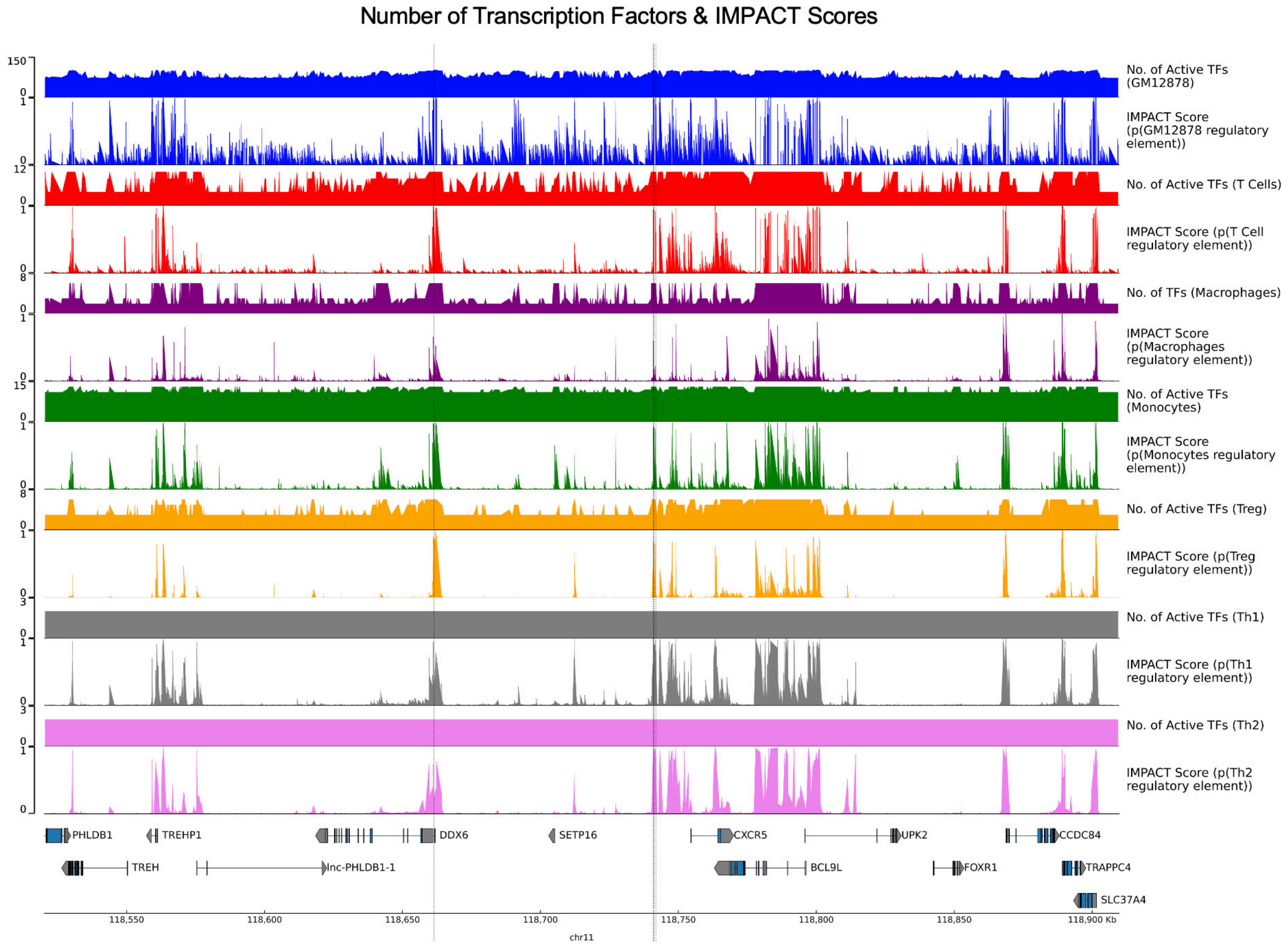
Supplemental Figure 14. Complex chromatin architecture revealed across the *DDX6-CXCR5* region in human primary macrophages. SjD GWAS association (top panel), publicly available epigenomic enrichment, and promoter-capture Hi-C looping data (red lines) across the *DDX6-CXCR5* region in human primary **(A)** M0, **(B)** M1, and **(C)** M2 macrophages. Vertical grey lines indicate the locations of rs57494551 or rs4938572, respectively.



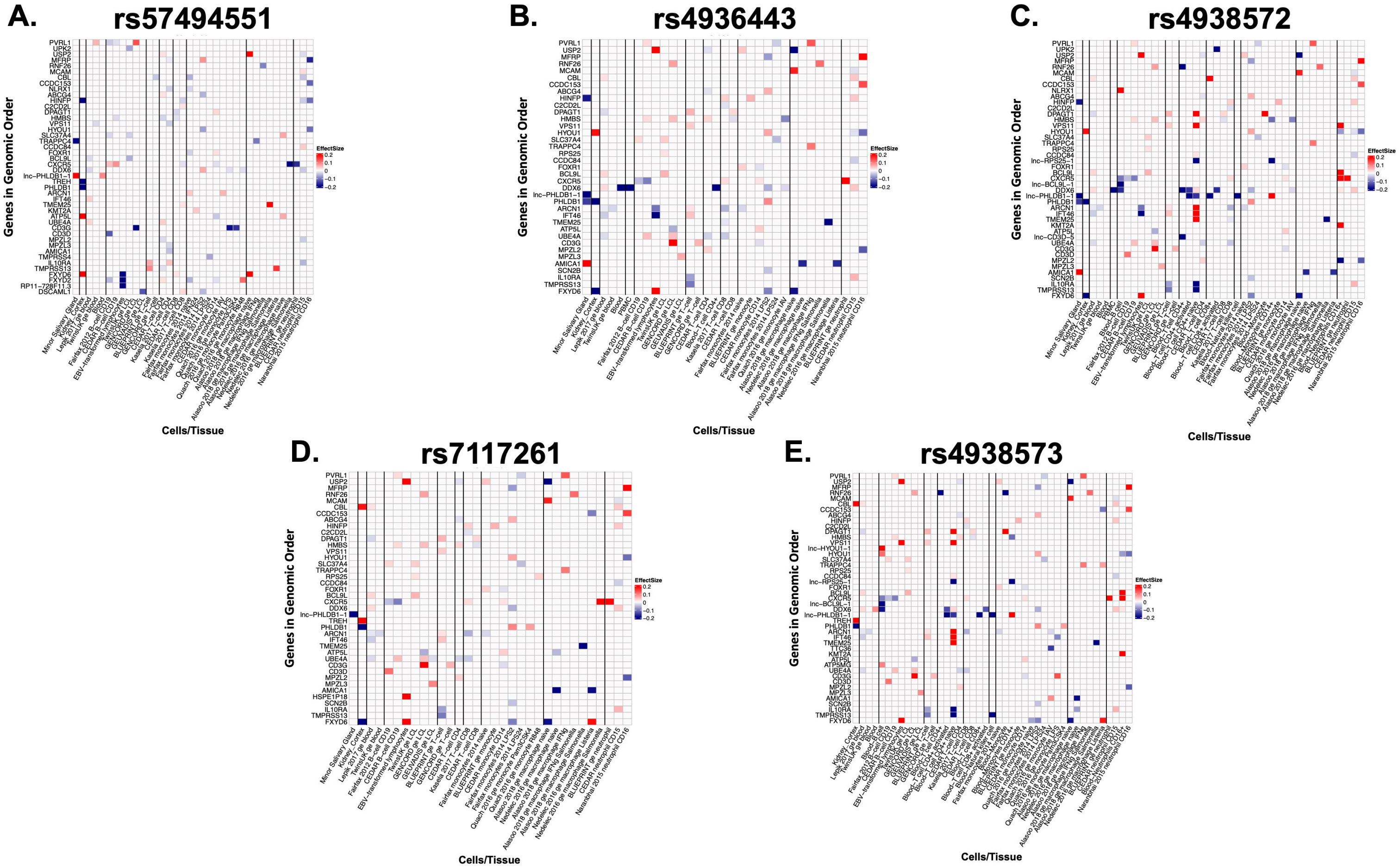
Supplemental Figure 15. Complex chromatin architecture revealed across the *DDX6-CXCR5* region in human primary neutrophils. SjD GWAS association (top panel), publicly available epigenomic enrichment, and promoter-capture Hi-C looping data (red lines) across the *DDX6-CXCR5* region in human neutrophils. Vertical grey lines indicate the locations of rs57494551 or rs4938572, respectively.



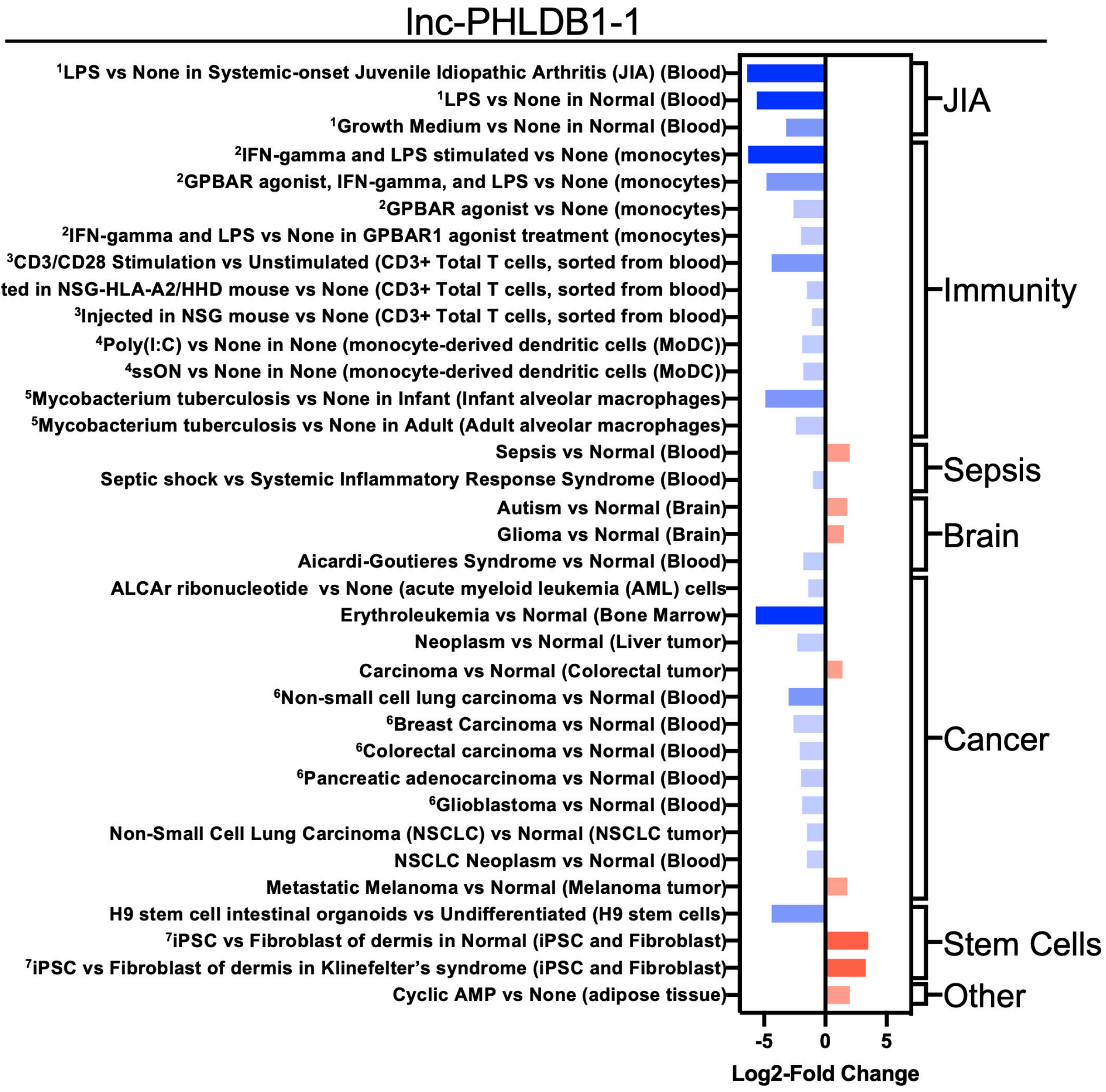
Supplemental Figure 16. Complex chromatin architecture revealed across the *DDX6-CXCR5* region in human 293T cells. SjD GWAS association (top panel) and publicly available epigenomic enrichment across the *DDX6-CXCR5* region in 293T cells. Vertical grey lines indicate the locations of rs57494551 or rs4938572, respectively. Summary 3C-qPCR results reported in Figure 6 are also shown (red lines); line thickness indicates relative interaction frequency (RIF).



Supplemental Figure 17. IMPACT regulatory element probabilities and corresponding transcription factor elements in immune cells. IMPACT uses transcription factor binding sites (TF) to predict the locations of regulatory sites across the genome. Image shows predicted IMPACT regulatory elements for GM12878 B cell line and primary human T cells, macrophages, monocytes, regulatory T cells (Treg), Th1 cells, and Th2 cells. The location of the rs57494551 and rs4938572 are indicates as vertical grey lines.



Supplemental Figure 18. eQTLs for five prioritized SNPs across blood, salivary and kidney tissue, and immune cells. eQTL values from GTEx in minor salivary gland, blood, kidney tissue, EBV B cells, and human primary immune cells in genes upstream and downstream of the *DDX6-CXCR5* interval for **(A)** rs57494551, **(B)** rs4936443, **(C)** rs4938572, **(D)** rs7117261, **(E)** rs4938573. Vertical lines separate different cell types. Horizontal lines highlight interesting genes such as *CXCR5*, *DDX6*, *lnc-PHLDB1-1*, *TRAPPC4*, and *IL10RA*.



Supplemental Figure 19. Expression Atlas results for lnc-PHLDB1-1 (ENSG00000255422). RNA-seq results from Expression Atlas (https://www.ebi.ac.uk/gxa/home) published studies where increases in *lnc-PHLDB1-1* (ENSG00000255422) expression are in red and decreased expression are in blue. Superscripts are used to depict experiments with multiple plotted conditions.