Human Genetics in Rheumatoid Arthritis Guides a High-Throughput Drug Screen of the CD40 Signaling Pathway

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Abstract

Although genetic and non-genetic studies in mouse and human implicate the CD40 pathway in rheumatoid arthritis (RA), there are no approved drugs that inhibit CD40 signaling for clinical care in RA or any other disease. Here, we sought to understand the biological consequences of a CD40 risk variant in RA discovered by a previous genome-wide association study (GWAS) and to perform a high-throughput drug screen for modulators of CD40 signaling based on human genetic findings. First, we fine-map the CD40 risk locus in 7,222 seropositive RA patients and 15,870 controls, together with deep sequencing of CD40 coding exons in 500 RA cases and 650 controls, to identify a single SNP that explains the entire signal of association (rs4810485, \( P = 1.4 \times 10^{-22} \)). Second, we demonstrate that subjects homozygous for the RA risk allele have ~33% more CD40 on the surface of primary human CD19+ B lymphocytes than subjects homozygous for the non-risk allele (\( P = 10^{-07} \)), a finding corroborated by expression quantitative trait loci (eQTL) analysis in peripheral blood mononuclear cells from 1,469 healthy control individuals. Third, we use retroviral shRNA infection to perturb the amount of CD40 on the surface of a human B lymphocyte cell line (BL2) and observe a direct correlation between amount of CD40 protein and phosphorylation of RelA (p65), a subunit of the NF-κB transcription factor. Finally, we develop a high-throughput NF-κB luciferase reporter assay in BL2 cells activated with trimerized CD40 ligand (tCD40L) and conduct an HTS of 1,982 chemical compounds and FDA–approved drugs. After a series of counter-screens and testing in primary human CD19+ B cells, we identify 2 novel chemical inhibitors not previously implicated in inflammation or CD40-mediated NF-κB signaling. Our study demonstrates proof-of-concept that human genetics can be used to guide the development of phenotype-based, high-throughput small-molecule screens to identify potential novel therapies in complex traits such as RA.


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Introduction

Rheumatoid arthritis (RA) is a common autoimmune disease for which there is no known cure. A diverse number of pathological pathways are altered in patients with RA, which impinge on a wide-variety of cell types, tissue types and organ systems – innate immune cells (e.g., neutrophils, dendritic cells, mast cells, platelets), adaptive immune cells (e.g., B and T cells), bone, cartilage, synovial fibroblasts, vascular cells, brain, muscle, and fat [1]. Accordingly, the task of sorting through which biological pathways cause disease, as compared to those pathways that are simply a consequence of disease, is a daunting challenge. Without knowing the critical causal pathways, it is very difficult to develop novel therapeutics to treat or cure RA.

There are fundamental principles of human genetics that make it a promising strategy to identify critical biological pathways and novel therapeutic targets in complex traits such as RA [2]. Since risk alleles are randomly assigned at meiosis, are independent of non-genetic confounding, and are unmodified by the disease itself, human genetics can help distinguish between cause and consequence. Moreover, risk alleles indicate if a pathway is up or down regulated in disease – a critical first step in drug development. Risk alleles help calibrate the amount of target modulations that is tolerable in humans, as gain-of-function and loss-of-function mutations in the same gene can be assessed for clinical phenotypes in carriers of these mutations. Consistent with these concepts, known drug targets that are safe and effective in humans appear on the list of genes identified by genome-wide association studies (GWAS) of common diseases [3], which suggests that other GWAS hits represent targets worthy of further investigation [4].

However, there are important challenges in translating SNP associations from human genetics (and GWAS in particular) to novel therapeutics. First, the causal gene must be identified within the risk locus, as there are often multiple genes in the region of linkage disequilibrium. Compounding this challenge, most GWAS hits are to non-coding variants that cannot pinpoint specific genes. Second, the risk allele must be experimentally validated as gain- or loss-of-function in a relevant human tissue, in order to guide whether a drug should inhibit or activate (respectively) the target of interest. Third, the biology of the risk allele should be recapitu-
CD40 on the surface of primary human CD19+ B cells. We demonstrated high reproducibility of the assay on blood samples drawn from the same individual >3 months apart ($r^2 = 0.76$, Figure S2). We measured CD40 protein levels from 90 healthy control subjects. We performed high-density SNP genotyping across the CD40 locus, using the same genotyping array as in our case-control study of RA risk. Strikingly, the strongest signal of association across the CD40 locus was at the RA risk allele ($P = 3.6 \times 10^{-9}$, Table S2). After conditional analysis, no additional SNP was significant (Figure S1B). Healthy control subjects homozygous for RA risk allele have 33% more CD40 on the surface of primary human CD19+ B lymphocytes than subjects homozygous for the non-risk allele (Figure 1C). The RA risk allele (the G allele of rs4810485) explains 31% of variation observed in CD40 protein level in these healthy control subjects, and was the strongest signal among the genome-wide set of SNPs tested for association with CD40 protein levels (Figure S1C).

To complement this finding, we examined CD40 gene expression in peripheral blood mononuclear cells of 1,469 unrelated individuals [30]. As shown in Figure 1D, we found that the RA risk allele was an expression quantitative trait locus (eQTL) on CD40 gene expression ($P = 8.2 \times 10^{-15}$). Similar findings have been reported for the RA risk allele in other immune cell types [31,32].

Taken together, our data demonstrate unequivocally that the RA risk allele (the G allele of rs4810485) is a gain-of-function mutation that leads to increased level of CD40 on the surface of primary human CD19+ B cells (and possibly other immune lineages within PBMC's).

CD40 influences p65 phosphorylation in a B-cell line (BL2)

We next sought to determine the biological consequences of having more CD40 on the surface of B cells, in order to determine the most appropriate assay for a drug screen. Engagement of CD40 by its trimerized ligand (tCD40L) leads to phosphorylation of p65, a subunit of NF-kB (Figure 2A). To determine the effect of p65 phosphorylation in a human B cell line (BL2) with varying levels of CD40 protein, we derived clones in which CD40 mRNA was knocked-down with shRNA [33]. In two independent cell lines, we found that the RA risk allele (G allele of rs4810485) increased p65 phosphorylation in a dose-dependent manner (Figure 2B). These findings suggest that the increased CD40 expression on RA-risk allele carriers may contribute to the pathogenesis of RA through increased p65 phosphorylation and activation of NF-kB.
lines, we observed CD40 protein levels at 40% and 55% compared to the BL2 parent line, respectively (Figure 2B). We used the parent BL2 line and two BL2/shRNA lines to activate the CD40 signaling pathway with tCD40L. In both BL2/shRNA cell lines, we observed a reproducible decrease in phosphorylation of p65 at Ser536 at 15 and 30 minutes following tCD40L activation. The levels of NF-κB p65 phosphorylation, as measured by Western blot, correlated with the levels of CD40 protein across all three B cell lines (Figure 2C). That is, more CD40 on the surface of B cells (as is the case for carriers of the RA risk allele) has increased activation of the classical NF-κB pathway (as measured by phosphorylation of NF-κB p65).

**HTS to identify inhibitors of CD40-mediated NF-κB signaling**

A Western blot is not suitable for a high-throughput screen (HTS). Based on our functional analysis, we developed a luciferase reporter assay that can be used in an HTS to identify inhibitors of CD40 signaling pathway. For this assay, we generated a BL2 cell line (BL2-NFκB-Luc) that was transfected with a luciferase reporter construct driven by a basal promoter element (TATA box) joined to tandem repeats of the NF-κB response element.

To optimize conditions for an HTS, we performed a series of experiments with BL2-NFκB-Luc cells. First, we performed a titration of tCD40L, and found approximately 80% activation at 64 ng/ml tCD40L. Luciferase activity at baseline (i.e., no tCD40L activation) was subtracted from each measurement to plot results. Second, we determined the optimal time course following 64 ng/ml tCD40L activation, and found maximum activation (5.6-fold induction) at 4.5 hours. Third, we performed a titration of a known inhibitor of the classical NF-κB signaling pathway, IKK inhibitor VII (Milipore) (Figure 2E). To confirm that the decrease of NF-κB activity by this inhibitor is not due to cytotoxicity, we used an anti-PARP antibody (116-kDa poly-ADP-ribose nuclear polymerase) to demonstrate by Western blot that the decrease in NF-κB phosphorylation following IKK inhibition was not simply due to cell death (Figure S3). And fourth, we determined the fold-increase and fold-inhibition of luciferase activity following tCD40L activation and IKK inhibition, respectively. We observed robust performance of our assay under a specific set of conditions (Figure 2F), with a Z'-factor of >0.8 (where a Z'-factor of >0.5 is considered appropriate for a small-molecule screen [35]).
We optimized our luciferase assay in a 384-well format. We conducted a pilot screen of 2,240 chemical compounds (of which 1,982 are in PubChem), each assayed in duplicate experiments. The chemical compounds comprise bioactive compounds (including FDA-approved drugs), commercially available drug-like molecules, targeted collections (e.g., biased for kinases), stereochemically-diverse compounds, and purified natural products.

Following normalization of luciferase activity to correct for variability across plates, we determined fold-change in luciferase activity relative to our positive (IKK inhibitor VII) and neutral controls. The red dashed line indicates >2SD from the mean of the neutral controls, which defines our “hit” compounds (n = 81 compounds). Figure 3 shows dose-response curves for two compounds known to inhibit inflammation [CID = 5282230 (tranilast)] or NF-κB signaling [CID = 5282360 (4-hydroxyestradiol)] in the BL2-NFκB-Luc cell lines. Dose-response curves for two compounds not previously implicated in inflammation, NF-κB signaling, CD40 signaling, or other biological pathways related to rheumatoid arthritis: CID = 306804, [4-(1-acetyl-4-oxo-2H-3,1-benzoxazin-2-yl)phenyl] acetate; and CID = 7309015, 8-[[2-(3,4-dimethoxyphenyl)prop-2-enoyl]-7-hydroxy-4-methylchromen-2-one. Red line = cells activated with tCD40L; black line = cells activated with tCD40L or CD40 or LPS (in BL2-TLR4-NFκB-Luc cells); green line = cell toxicity, as measured by CellTiter-Glo.

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that the 2 known inhibitors and the 2 novel compounds identified expression with all 4 compounds (Figure 4). Thus, we confirmed CD40L [43]. We observed dose-dependent decrease in CD86 

Equally important, we discover 2 novel small-molecules that inhibit CD40 signaling through the classical NF-κB pathway in primary CD19+ B cells.

There are few examples where GWAS was used to guide drug discovery. One example is PCSK9, where a loss-of-function variant is associated with lower levels of LDL cholesterol and protection from cardiovascular disease [46–49]. However, the original finding implicating PCSK9 and LDL cholesterol came not from GWAS, but from sequencing in families with autosomal dominant high LDL levels and an increased incidence of coronary heart disease [50]. In 2012, a randomized control trial was published that a monoclonal antibody to PCSK9 significantly reduced LDL cholesterol levels in healthy volunteers and in subjects with hypercholesterolemia [51,52]. Another example is BCL11A and persistence of fetal hemoglobin in sickle cell anemia. In 2008, a GWAS found an association with a common, non-coding variant of the hemoglobin silencing factor gene, BCL11A, and HbF expression [53,54]. Based on these data, together with data from animal models [55], repressors of BCL11A are under development for the treatment of sickle cell disease [56].

Our study illustrates another example, as we demonstrate that genetic findings can be instrumental in developing optimal high-throughput drug screens. In RA, many biological pathways have been implicated. Consequently, identifying relevant pathways is critical for the development of molecules that will be effective in treating the disease. Our strategy successfully links an RA risk allele to a biological process suitable for an HTS. First, we show unequivocally that the RA risk allele leads to increased levels of CD40 protein on the surface of CD19+ B cells, thereby establishing a causal link between increased CD40 protein levels and risk of RA. Second, we establish a direct relationship between amount of CD40 on the surface of B cells and an intracellular biological pathway, NF-κB signaling. In doing so, we recapitulate the effect of the CD40 risk allele in an assay system suitable for an HTS.

There are important limitations of our study. First, the chemical library tested in our study is small relative to libraries in academic centers and industry (which often contain hundreds of thousands to millions of compounds) [57,58]. Second, our screen did not identify inhibitors specific to CD40 signaling. Whether a more selective CD40 inhibitor would be a better therapeutic than a more general inhibitor requires additional studies. That our HTS identified two “known” drugs that inhibit inflammation reinforces that our general strategy is successful. Third, we have not yet tested our compounds in animal models of RA. However, one of our known compounds, tranilast, has been shown by others to inhibit collagen-induced arthritis in the mouse [41]. Fourth, we do not yet know the target of our “novel” small molecule inhibitors of CD40-mediated NF-κB signaling. One of these compounds (CID 7309015) has been annotated in PubChem as an inhibitor of
**Figure 4. Effect of compounds on CD86 expression in primary CD19+ B cells.** Purified human CD19+ primary B cells were incubated with 10 ng/ml IL4 alone ("No activation") or IL4+64 ng/ml tCD40L ("Activation"), together with different concentrations of drugs for 48 hours. CD86 expression was measured by PE GeoMFI on CD19+ gated B cells. The chemical structure of each compound is shown.

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**Table 1. Relative IC_{50} for two “known” and two “novel” compounds in both BL2-NFκB-Luc and Ramos-NFκB-Luc cell lines.**

<table>
<thead>
<tr>
<th>Compound</th>
<th>BL2/ tCD40L</th>
<th>BL2-TLR4/ LPS</th>
<th>Ramos/ tCD40L</th>
<th>Ramos/ TNFa</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;known” compounds</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5282230</td>
<td>3.8</td>
<td>6.3</td>
<td>7.1</td>
<td>8.1</td>
</tr>
<tr>
<td>5282360</td>
<td>4.1</td>
<td>1.8</td>
<td>2.1</td>
<td>1.3</td>
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<tr>
<td>&quot;novel” compounds</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>306804</td>
<td>2.5</td>
<td>1.6</td>
<td>9.4</td>
<td>6.7</td>
</tr>
<tr>
<td>7309015</td>
<td>5.0</td>
<td>3.0</td>
<td>18.3</td>
<td>16.4</td>
</tr>
</tbody>
</table>

Relative IC_{50} is the concentration required to bring the dose-response curve to the halfway point between the top and bottom plateaus of the curve.

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**Table 2. Percent maximum inhibition for two “known” and two “novel” compounds in both BL2-NFκB-Luc and Ramos-NFκB-Luc cell lines.**

<table>
<thead>
<tr>
<th>Compound</th>
<th>BL2/ tCD40L</th>
<th>BL2-TLR4/ LPS</th>
<th>Ramos/ tCD40L</th>
<th>Ramos/ TNFa</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;known” compounds</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5282230</td>
<td>54.7%</td>
<td>73.7%</td>
<td>86.4%</td>
<td>87.4%</td>
</tr>
<tr>
<td>5282360</td>
<td>87.0%</td>
<td>54.1%</td>
<td>95.1%</td>
<td>92.7%</td>
</tr>
<tr>
<td>&quot;novel” compounds</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>306804</td>
<td>83.8%</td>
<td>51.8%</td>
<td>91.7%</td>
<td>90.5%</td>
</tr>
<tr>
<td>7309015</td>
<td>90.2%</td>
<td>63.3%</td>
<td>78.3%</td>
<td>85.7%</td>
</tr>
</tbody>
</table>

For each compound, we calculate the maximum amount of inhibition observed at the highest concentration of drug relative to zero luciferase activity.

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retinoic acid-related orphan receptor (ROR) gamma, a transcription factor that has a central role in the differentiation of CD4+ Th17 cells. However, this PubChem annotation has not yet been linked to a PubMed manuscript. The other compound has not been confirmed as active in any PubMed assay, and therefore represents a novel tool compound for further study.

In conclusion, we demonstrate a strategy to translate GWAS findings into HTS to identify novel small-molecule inhibitors of the CD40 signaling pathway. Given the wealth of GWAS data that has accumulated in recent years, human genetics represents a promising approach to develop safe and effective therapies to treat complex human diseases such as RA.

Materials and Methods

Our study was approved by the institutional review board (IRB) at our institutions.

Genetic analysis of CD40 risk locus in RA case-control samples

Six case-control collections were included for genotyping using the Illumina Immunochip platform (Table S1), as part of the RACI consortium [59]; the GWAS datasets have been previously described, and include 4 collections that did not overlap with the Immunochip dataset [60]. All six Immunochip datasets were clustered together using the Illumina Genome Studio algorithm. Initial data filtering steps in GenomeStudio included: removal of samples with call rate <90% and removal of SNPs with poor clustering quality metrics (call frequency <0.98, cluster separation <0.4). Further quality control was performed in the six individual population datasets separately. First, samples with call rate <90% were excluded. Second, SNPs with call rate <99% in either the RA cases or controls were excluded. To address population stratification, we selected a set of common SNPs (MAF >5%), pruned to remove SNPs in LD. We calculated pairwise identity-by-state (IBS) statistics using PLINK [61], and removed one individual from each pair of individuals who were 2nd degree or closer relatives. Principal components analysis (PCA) was subsequently performed using EIGENSTRAT [62]. After exclusion of individuals of non-European ancestry, as determined by clustering with CEU HapMap (phase II), a second PCA was performed to further remove outliers. Cases with anti-CCP negative or missing anti-CCP status data were removed, leaving 7,222 CCP+ cases and 15,870 controls for association analysis. To avoid duplicate samples, we used IBS estimates to remove related samples between the Immunochip and GWAS collections. Specifically, we selected a set of genotyped SNPs with missing-genotype rate <0.5%, MAF >5% and Hardy-Weinberg equilibrium (HWE) P >10^-3 that were shared across all 10 collections. When related samples were identified (siblings or duplicates), the sample from the GWAS data was removed (to preferentially keep genotyped data rather than imputed data in the subsequent association analyses), bringing the total sample size to 9,785 cases and 15,870 controls (Table S1). Finally, we computed a chi-square test to assess the difference in missingness between cases and controls and removed SNPs with a Pmiss-ing <10^-2, together with SNPs in departure form Hardy-Weinberg equilibrium (P_HWE > 5.7 x 10^-7).

To test for association with risk of RA, we used PLINK to conduct logistic regression analysis of the six Immunochip RA case-control status, including 10 eigenvectors as covariates. We conducted an inverse-variance weighted meta-analysis to combine the results across the 6 collections, for the 156,520 SNPs across the genome with results in one or more collections, including 492 SNPs across the CD40 locus. We also computed Cochran’s Q statistic and I^2 statistic to assess heterogeneity across collections. Meta-analysis and heterogeneity statistics computation was adapted from the MANTEL program.

Sequence data at the CD40 locus was generated as part of a larger experiment to perform pooled sequencing of 25 RA risk genes (Supplementary Material). Using Syzzyg (a pooled variant caller) [63], we estimated the allele frequencies in the overall sample set (500 cases and 650 controls of European ancestry geographically and genetically matched). We observed a strong correlation between genotype frequencies available from our GWAS data and frequencies estimated using the method in Syzzyg indicating accurate experimental recovery of the pool composition. For the CD40 region, we had no coverage of exon 1, but near complete coverage of the remaining eight exons (Figure S4). After stringent quality control [Supplementary Material], we observed 4 coding variants at the CD40 locus: two coding-synonymous SNPs and two missense SNPs. None of the SNPs was associated with RA either in a single-SNP analysis or in a gene-burden test (Table S2B).

Measurement and genetic analysis of CD40 levels

CD40 protein levels on the surface of unstimulated CD19+ B cells were measured in healthy control subjects from the PhenoGenetic Project of Brigham and Women’s Hospital, a living biobank of 1,739 subjects free of chronic inflammatory and infectious diseases recruited from the general population of Boston, MA. Subjects used in this experiment were randomly selected from the biobank. Fresh PBMCs were isolated from 10 ml blood with 5 ml Ficoll Hypaque (GE; Cat.#07908). PBMCs were washed once in 0.1% BSA/PBS and blocked with FcR blocking reagent (Milteyi Biotec; Cat.#120-000-442). After red blood cells were lysed in 10 ml human red blood cell lysis buffer, 0.25 x 10^6 isolated PBMCs were double-labeled with an anti-CD19-FFITC (eBioscience; Cat.#11-0199-73) and anti-iCD40/TNFSF5-PE (R&D; Cat.#FAB6321P). The CD40 levels were measured by FACS analysis with PE-GeoMFI on CD19+ cells. As a negative control, an anti-IgG2B-PE (R&D; Cat.#IC0041P) was used; in addition, we used frozen BL2 cells to normalize for day-to-day variation. In total, 97 subjects had both CD40 protein levels measured and genotyping generated using the Immunochip headset at Yale University. The same initial data-filtering steps described above were performed. Following QC, 90 samples with a call rates >99% were included in the analysis. After HapMap phase III PCA, no sample was removed based on ethnicity. A second PCA was performed to compute eigenvectors to include in the association analysis. We conducted a linear regression analysis to test for CD40 protein level-SNP association (PLINK). Ten eigenvectors were included as covariates in the linear model.

Details of the eQTL analysis have been previously described [30]. In short, we assessed the effect of rs4810483 on CD40 in whole peripheral blood in a collection of 1,469 samples (1,240 samples run on the Illumina HT12v3 platform, 229 samples run on the Illumina Hi1v2 platform). We used a Spearman rank correlation and meta-analysis using a weighted Z-method to calculate statistical significance of the rs4810483 G alleles CD40 gene expression levels.

BL2 cells and shRNA targeting of CD40

BL2 cells were purchased from DSMZ (Germany; Cat.# ACC 625). Both BL2/shRNA cell line and BL2-NFkB-Luc cell line were derived from BL2 cells, as described below. All cells were cultured in RPMI 1640 medium (Life Technologies, Inc) supplemented with 10% FBS. For CD40 activation, cells were...
incubated at 37°C for 15 minutes with 64 ng/ml trimerized CD40 ligand (tCD40L). Two independent BL2 cell lines were generated, in which CD40 was knocked-down using a HuSH shRNA Plasmid, pGFP-V-RS (Origene; Cat. TR39007). A double-stranded DNA olio containing a hairpin structure with sequence specific to human CD40 gene (sequence below) [33] was cloned into the pGFP-V-RS, according to manufacture specifications (Origene).

5’GATCGGCGAATTCCAGACCTGTTTCAGAGAGAACAAGGTTCATGGAATTCCTTGTTAGAAGTC
3’

The plasmid (20 µg) was linearized by ScaI and cotransfected into BL2 cells with a puromycin selection vector by electroporation at 300 V and 950 µF. Transfected cells were cultured in regular medium for 2 hours before they were serially diluted and plated into 96-well plates. For selection, cells were grown in 0.3 µg/ml puromycin. Single colonies were picked two weeks later and CD40 levels were measured by Western blot and FACS analysis.

Analysis of p65 phosphorylation

For the immunoblot detection, 0.25×10⁶ BL2 cells were activated either with or without tCD40L. Whole-cell lysate was prepared with 10 µl RIPA buffer and then subjected to electrophoresis on a 7.5% SDS-PAGE gel under reducing conditions. Proteins were electro-blotted onto a nitrocellulose membrane. The membranes were detected by antibodies for CD40 (Santa Cruz; cat# sc-13120), NF-kB p65 (Cell signaling; cat#: 4767) and phospho-NF-kB p65 (Ser536) (Cell signaling; cat#: 3033).

Luciferase assay to detect the activity of NF-kB in BL2 and Ramos cells

A signal lentivector reporter construct driven by a basal promoter element (TATA box) joined to tandem repeats of the NF-kB response element was infected into BL2 and Ramos RA-1 cells, according to manufacture specifications (Qiagen; Cat.# CLS-013L). We call these two lines as BL2-NFkB-luc and Ramos-NFkB-luc, respectively. Single colonies were selected on 96 well plates with 0.3 µg/ml puromycin. Positive clones were further screened by luciferase assay with Steady-Glo assay system (Promega) after 4 hr activation by 64 ng/ml tCD40L. Since the expression of luciferase gene is controlled by the activity of NF-kB, we were able to measure the activity of NF-kB following activation with tCD40L by measuring the activity of luciferase. For LPS activation in BL2 cells, a BL2-NFkB-luc line was transfected with episomal DNA of TLR4 (pUNO1-hTLR4a, InvivoGen) for high levels of TLR4 expression. We call this line as BL2-TLR4-NFkB-luc.

High-throughput screen for inhibitors and activators for CD40 signaling pathway

The high-throughput screening assay was optimized in 384-well format in collaboration with the Broad Institute Probe Development Center (BIPDc). Briefly, 10 µL BL2-NFkB-luc cells at 25K cells/well were plated into each well on a 384-well plate (Perkin Elmer; Cat.# 6008230) using a Multidrop Combi dispenser (Thermo). For each compound, DMSO or positive control IKK inhibitor VII, 25 nL was transferred using a pin tool (Cybio). The concentrations of drugs in each well of a 24-well plate at 37°C for one hour. Cells were activated with and without 64 ng/ml tCD40L. After 48 hours, cells were stained with anti-CD19-FITC/anti-CD86-PE (Biolengd; Cat#130-091-151). Purified human primary CD19+ B cells (1×10⁵) were pre-incubated with 10 ng/ml IL4 and different concentrations of drugs in each well of a 24-well plate at 37°C for 6 hours before they were serially diluted and plated into 96-well plates. For selection, cells were grown in 0.25%; and IKK inhibitor VII 50 μM to 0.39 μM (2-fold decrease between doses). In addition to screening BL2-NFkB-luc cells activated with tCD40L, we also screened BL2-TLR4-NFkB-luc cells activated with 16 ng/ml LPS (Sigma). We screened an additional B cell line transfected with the same luciferase reporter contract, Ramos-NFkB-luc cells, and activated with 64 ng/ml tCD40L and 64 ng/ml TNFα (eBioscience). Cell viability of both lines was evaluated by adding 5 ul 0.5X CellTiter-glo.

Measurement of CD86 expression in human CD19+ primary B cells

CD86 protein levels were measured in human primary CD19+ B cells from the PhenoGenoProject purified by MACs (Miltenyi Biotec; Cat# 130-091-151). Purified human primary CD19+ B cells (1×10⁵) were pre-incubated with 10 ng/ml IL4 and different concentrations of drugs in each well of a 24-well plate at 37°C for one hour. Cells were activated with and without 64 ng/ml tCD40L. After 48 hours, cells were stained with anti-CD19-FTC/anti-CD86-PE (Biolengd; Cat#305405). CD86 expression was measured by PE GeoMFI on CD19+ gated B cells.

Statistical analysis of compound screening data

The raw signals of each 384-well microtiter wells were normalized using the “Neutral Controls minus Inhibitors” method in Genedata Assay Analyzer (v7.0.3). The median raw signal of the intraplate neutral-control wells was set to a normalized activity value of 0. The median raw signal of the intraplate positive-control wells was set to a normalized absolute activity value of 100. The plate pattern correction algorithm “Assay Median” in Genedata (v7.0.3) was applied to the normalized plate data. We used DMSO neutral controls to define 95% confidence intervals (CI) of our 2K screening compounds. We defined “hits” as those compounds outside of 95% CI in both dimensions of the replicate experiments. This led to 86 compounds that inhibited luciferase activity, consistent with our positive IKK inhibitor control. We defined a compound as promiscuous if it satisfies both of the following two rules: (1) the number of assays in which it has been tested is larger than 50, and (2) the ratio between the number of hits and the number of assays in which it has been screened is larger than 0.25. Based on these criteria, we found 40 promiscuous compounds, 5 of which had >2SD inhibition of luciferase activity, yielding 81 compounds that inhibited luciferase activity. A list of all compounds tested, including the annotation of 40 promiscuous compounds, can be found in Tables S3 and S4.

To calculate relative IC₅₀, the abs function in the R package of stats (2.14 version) was used to fit the four-parameter logistic non-linear (weighted) least-squares estimates of the parameters of a nonlinear model, with the equation (xn is concentration and yn is response):

\[ y_n = \frac{L + h}{1 + e^{-(x_n - z)/\beta}} \]

where \( L \) and \( h \) represent the response at the maximum value at smallest concentration; the starting point of \( h \) is the minimum difference between the minimum value at the largest concentration and the average value at smallest concentration. The starting point of \( z \) and \( \beta \) are 4 and 2, respectively. The R
function smooth.spline was used to smooth the estimated points in the curves. In some cases where a singular gradient happens, the parameters are not estimable; when a plateau was not observed, the curve was smoothed by loess.smooth function in R and the percentage was calculated by the observed values. The 95% confidence interval (CI) was computed based on the observed data and transferred into percentage. To calculate percent maximum inhibition for each compound, we determined the difference between the average activity at the lowest drug concentration and the average activity at the highest drug concentration. The percent maximum inhibition was then obtained by dividing the difference by the average activity at the lowest drug concentration.

Supporting Information

Figure S1 Regional association plot of CD40 locus, following conditional analysis of rs4810485 in (A) case-control study of RA risk, and (B) CD40 protein levels; (C) Manhattan plot of ~140,000 iChip SNPs tested for association with CD40 protein levels. (DOCX)

Figure S2 Correlation between CD40 protein levels measured by flow cytometry in the same individuals at two different points in time (>3 months apart). (DOCX)

Figure S3 BL2 cells were incubated with different concentration of IKK for 1 hr and then activated with 16 ng/ml tCD40L for 15 min. Western blot was probed by anti-phospho-p65, anti-p65 and anti-parp antibodies separately. (DOCX)

Figure S4 Coverage of CD40 exons by our pooled sequencing strategy. (DOCX)

Figure S5 (A) Schematic of compound set enrichment analysis: (i) we used text-mining to annotate each compound with a “Pharmacological Action” MeSH term in PubChem; each Pharmacological Action term set contains multiple compounds; (ii) for each compound, we determine luciferase activity relative to the overall distribution: increased (red), neutral (white), or decreased (blue), where the white areas are defined by corrected values between −1 and 1. (iii) we test sets of compounds, annotated by Pharmacological Action terms, for enrichment of the distribution of compounds within each term set relative to the entire distribution of results. (B) The distribution of enrichment scores for 117 groups of pharmacological action terms with ≥3 compounds. Red indicates positive enrichment and blue indicates negative enrichment relative to all sets tested. The dashed line delineates threshold of statistical significance, given the number of independent hypotheses (i.e., compound sets) tested. The 5 compound sets that surpass this level of significance are labeled. (C) The results of top 5 compound sets from the enrichment analysis. Each strip shows the distribution of all results, with black lines indicating specific compounds within each set. The top 5 compound sets are shown, with the number of compounds that inhibit luciferase activity, total number of compounds with the specific Pharmacological Action term annotation, and P-value for enrichment shown at the top (from the Wilcoxon mean rank test). (DOCX)

Figure S6 Corticosteroid compounds and chemical structure. (A) Core structures of the corticosteroid hits. Chemical similarity of 28 corticosteroids and their analogs. Since there are only 45 corticosteroids among 1,982 compounds tested, this finding represents a significant enrichment among hits (P<10^{-16}); (B) Functional groups of the corticosteroid hits that create rings. (DOCX)

Figure S7 Dose-response curves for two “known” and “unknown” compounds in Ramos-NFkB-Luc cells. (DOCX)

Table S1 Description of samples used in immunochip (iChip) association study of case-control status. (DOCX)

Table S2 List of promiscuous chemical compounds from 2K pilot screen; (B) top 81 hits. (XLSX)

Table S3 Corticosteroid compounds and chemical structure. (DOCX)

Table S4 Percent inhibition of luciferase activity or cell viability at 50 nM compound. (DOCX)

Text S1 A description of additional methods is provided. This includes details on CD40 sequencing and compound set enrichment analysis. (DOCX)

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Author Contributions

Conceived and designed the experiments: GL DD DW JS WD LF FK EJR PAC NT RMP. Performed the experiments: GL DD DW JS WD LF FK EJR GD. Analyzed the data: GL DD DW JS WD LF FK EJR PAC ES NT RMP. Contributed reagents/materials/analysis tools: XZ KL JL PLDJ KAS AZ SR JB SE LP PKG JW NG. Wrote the paper: GL DD DW JS WD LF FK EJR LD CH XZ KL JL PLDJ KAS AZ SR JB SE LP PKG JW NG PAC ES NT RMP.

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GWAS to Small Molecule Screen of the CD40 Pathway
