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Disease activity drives transcriptomic heterogeneity in early untreated rheumatoid synovitis

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ABSTRACT

Objectives Transcriptomic profiling of synovial tissue from patients with early, untreated rheumatoid arthritis (RA) was used to explore the ability of unbiased, data-driven approaches to define clinically relevant subgroups.

Methods RNASeq was performed on 74 samples, with disease activity data collected at inclusion. Principal components analysis (PCA) and unsupervised clustering were used to define patient clusters based on expression of the most variable genes, followed by pathway analysis and inference of relative abundance of immune cell subsets. Histological assessment and multiplex immunofluorescence (for CD45, CD68, CD206) were performed on paraffin sections.

Results PCA on expression of the (n=894) most variable genes across this series did not divide samples into distinct groups, instead yielding a continuum correlated with baseline disease activity. Two patient clusters (PtC1, n=52; PtC2, n=22) were defined based on expression of these genes. PtC1, with significantly higher disease activity and probability of response to methotrexate therapy, showed upregulation of immune system genes; PtC2 showed upregulation of lipid metabolism genes, described to characterise tissue resident or M2-like macrophages. In keeping with these data, M2-like:M1-like macrophage ratios were inversely correlated with disease activity scores and were associated with lower synovial immune infiltration and the presence of thinner, M2-like macrophage-rich synovial lining layers.

Conclusion In this large series of early, untreated RA, we show that the synovial transcriptome closely mirrors clinical disease activity and correlates with synovial inflammation. Intriguingly, lower inflammation and disease activity are associated with higher ratios of M2:M1 macrophages, particularly striking in the synovial lining layer. This may point to a protective role for tissue resident macrophages in RA.

INTRODUCTION

Synovitis is the clinical hallmark of rheumatoid arthritis (RA), and the analysis of synovial tissue from affected joints provides unique insights into mechanisms driving synovial inflammation and disease activity. Classically described as the seat of immune cell infiltration and resident cell hyperplasia, the RA synovium is a highly heterogeneous tissue. Histological as well as bulk transcriptomic

WHAT IS ALREADY KNOWN ON THIS TOPIC

⇒ Synovial transcriptomes of patients with rheumatoid arthritis (RA) are highly heterogeneous, partly due to external factors such as disease duration and ongoing therapy; nevertheless, previous studies have reported such heterogeneity even in early, untreated RA suggesting the existence of distinct synovial pathotypes.

WHAT THIS STUDY ADDS

⇒ Using unbiased analyses of bulk synovial transcriptomic data in a large series of early, untreated RA (ERA), we show that baseline disease activity is the main correlate of transcriptomic heterogeneity.
⇒ Higher disease activity is associated with an immune/inflammatory signature and better response to therapy; intriguingly, lower disease activity is associated with an M2-like macrophage signature and higher M2:M1 ratio, particularly pronounced in the synovial lining layer.

HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY

⇒ Transcriptomic profiling of ERA synovia yielded a continuum of profiles remarkably consistent with disease activity scores.
⇒ Patients with high disease activity and an inflammatory/immune response signature in baseline synovial biopsy, had a higher probability of responding to methotrexate.
⇒ Further studies on the role of CD206⁺ synovial macrophages in modulating tissue inflammation will be of great interest.

studies also show wide variability of features, including the extent and composition of immune cell infiltration, between patients.¹ Extra-synovial factors such as disease duration and treatment contribute to variability in synovial signals.¹ Recent studies have however confirmed wide variations in immune alterations even among patients with untreated, early rheumatoid arthritis (ERA).^{2,3} This has led to a keen interest in exploring the potential of ERA synovial tissue analysis in defining clinically

Early arthritis

relevant patient subgroups; the much sought-after goal is effective patient stratification for truly tailored (type and strength of) therapy.^{4 5} Different patterns of synovial inflammation associated with baseline clinical features have therefore been explored for their ability to earmark different disease mechanisms and/or treatment responses. A current paradigm distinguishes between *lympho-myeloid*, *diffuse-myeloid* and *pauci-immune* subgroups (*pathotypes*), defined based mainly on the relative abundance in synovia of T cells, B cells and macrophages (as assessed by histology and molecular signature), and suggested to predict disease evolution and treatment response.²

Somewhat in contrast with these observations, we previously reported that different disease-modifying antirheumatic drugs (DMARDs) downregulate a robust set of genes in common, notwithstanding their direct targets or mechanisms of action.⁶ This would suggest a high degree of interdependence between the different cell populations and processes in the synovium that therefore exert knock-on effects on each other. The degree of downregulation of these ‘shared’ genes seemed to depend primarily on their pretreatment expression levels, and we could not discern distinct signatures significantly associated with clinical response to any particular DMARD.⁶ The patients in these studies had longstanding disease and undergone multiple, heterogeneous rounds of therapy leading up to the specific DMARD being tested, begging the question of whether biopsies performed early in disease would be more informative. Here, we apply unsupervised clustering to RNASeq data from a large series of ERA synovial biopsies, for a data-driven assessment of (1) the most variable transcriptomic features among patients with untreated RA at early disease stage, (2) their baseline clinical correlates and (3) their ability to define clinically relevant patient subgroups according to response to methotrexate.

MATERIALS AND METHODS

Patients and samples

Patients with active, early (<12 months disease duration) rheumatoid arthritis, naïve to DMARD and steroids, were recruited for this study. All patients met the American College of Rheumatology/European Alliance of Associations for Rheumatology (ACR/EULAR) 2010 RA classification criteria. At inclusion, patients were assessed for disease activity and presence of bone erosions on radiographs. Processing and analysis of biopsies was performed in accordance with EULAR minimal reporting requirements for synovial tissue research.⁷ Synovial tissue from a clinically affected joint was obtained using needle arthroscopy or ultrasound (US)-guided biopsy prior to starting treatment. Three to five synovial fragments were obtained from each joint by knee needle arthroscopy or US-guided small joint biopsy and stored at –80°C after overnight incubation in RNA-Later solution (Invitrogen). Where possible, an additional three to five fragments from the same biopsy were fixed overnight in 10% formalin buffer at pH 7.0 and embedded in paraffin for histology and immunofluorescence (n=36 from knees, 2 from wrists, 1 from metatarsophalangeal joint (MTP), 1 from metacarpophalangeal joint (MCP)). Patients were started on conventional treatment (methotrexate±steroids as bridging therapy, n=51) or on other, heterogeneous treatments (n=23) (table 1) (online supplemental table 1). Effects of therapy on disease activity in methotrexate-treated patients was assessed after 3 months.

Patient and public involvement

Patients and the public were not involved in the design, conduct or reporting of this research.

Table 1 Baseline clinical characteristics of n=74 patients with RA included in the study

Age in years (median±SD)	49.2±15.7
Female	82.4% (61/74)
ACPA and/or RF positivity	66.2% (49/74)
TJC28 (median±SD)	6±6.8
SJC28 (median±SD)	8±5.5
CRP (mg/dL) (median±SD)	1.75±3
PhGA (median±SD)	50±18.8
PtGA (median±SD)	63±25.8
HAQ (median±SD)	1.625±0.74
Disease activity: DAS28CRP (median±SD)	5.26±1.25
High	54% (40/74)
Moderate	38% (28/74)
Low	8% (6/74)
Baseline bone erosions	27% (20/74)
Joint biopsy	
Large joint (knee)	74.3% (55/74)
Small joint (W, MCP, PIP, MTP)	25.7% (10/74; 6/74; 2/74; 1/74)

ACPA, anti-citrullinated peptide antibody; CRP, C reactive protein; DAS28CRP, Disease Activity Score 28-joint count C reactive protein; HAQ, Health Assessment Questionnaire; MCP, Metacarpophalangeal joint; MTP, Metatarsophalangeal joint; PhGA, Physician Global Assessment; PIP, Proximal interphalangeal joint; PtGA, Patient Global Assessment; RF, rheumatoid factor; SJC28, Swollen Joint Count 28; TJC28, Tender Joint Count 28; W, Wrist.

Transcriptomic profiling

Total RNA was extracted from synovial biopsies using the NucleoSpin RNA II extraction kit (Macherey-Nagel) including DNase treatment. RNA quality control was performed on a 2100 Bioanalyser (Agilent). RNASeq was performed on 350 ng of RNA, for all (n=74) samples that yielded a RNA Integrity Number (RIN) of 5 or more. Sequencing was performed by Macrogen Europe using a standardised protocol. Briefly, cDNA libraries were constructed with the TruSeq Stranded mRNA LT Sample Prep Kit and sequenced on an Illumina sequencer. Data were processed using a standard RNAseq analysis pipeline including FastQC-0.11.8 for quality control of raw data, and Trimmomatic-0.38 to remove low quality reads and trim adapters from sequences. Hisat2-2.1.0 was used to align reads to the genome (GRCh38).⁸ Gene expression levels were evaluated using featureCounts from subread-2.0.0⁹ and Homo_sapiens.GRCh38.94.gtf. Sequencing data were deposited in the Gene Expression Omnibus of the National Centre for Biotechnology Information and are accessible through Gene Expression Omnibus accession number GSE225731.

Histological evaluation

Degree of lining layer hyperplasia, inflammatory infiltrate, vascular proliferation and fibrinoid necrosis was graded on a 0 (absent) to 3 (maximum) scale on all H&E-stained sections from (n=39 of) the same biopsies used for RNASeq, by an expert pathologist (CG) blinded to clinical and transcriptomic data.

Multiplex immunofluorescence (IF)

Multiplex IF was performed on 5 µm serial sections from the same (n=39) biopsies as above. After deparaffinisation, tissue sections were processed according to the protocol described in the literature.¹⁰ Briefly, endogenous peroxidases were inhibited with 3% hydrogen peroxide in methanol for 20 min. Antigen retrieval was performed in 10 mM citrate buffer pH 5.7 and blocking in Tris buffered saline (TBS)–5% bovine serum albumin (BSA)–0.1%

Tween20. Sections were incubated in the primary antibody overnight at 4°C (in TBS–1% BSA–0.1% Tween20), followed by the corresponding horseradish peroxidase-conjugated secondary antibody (Envision, Dako) for 1 hour at room temperature, and visualised by tyramide signal amplification using AlexaFluor (AF)-conjugated tyramides (Thermo Fisher Scientific). Antibodies were stripped by incubating in citrate buffer. This protocol was applied sequentially with each of the primary and secondary antibodies, with different AF-tyramides, for a total of three markers: CD45 (1:200, Dako M0701) with AF555 (cat. no. B40955), CD68 (1:500, Dako M0876) with AF488 (cat. no. B40953), CD206 (1:2500, Cell Signaling 91992) with AF647 (cat. no. B40958). After a final wash in phosphate buffered saline (PBS), nuclei were stained with Hoechst 33342 (Thermo Fisher Scientific; in TBS–10% BSA–0.1% Tween 20) and washed in TBS–0.1% Tween20. Sections were mounted with fluorescence mounting medium (Dako). Multispectral image acquisition was performed using an Axioscan.z1 (Zeiss, ×20 objective).

Quantitative and semiquantitative evaluation of multiplex IF

Entire multiplex-stained paraffin sections were quantified using the image analysis tool Author V.2022.01.4 (Visiopharm). Tissue sections were first automatically delineated at low digital magnification (×5). Following cell detection and segmentation at high resolution (×20, based on the Hoechst staining), postprocessing steps were applied to separate unstained and stained cells for each marker (CD45, CD68 and CD206). Results were expressed in terms of proportion of marker-positive cells/total cells (nuclei), or as ratios of different marker-positive cells. Classification of biopsies based on the macrophage composition of the synovial lining, as well as evaluation of synovial lining thickness (visualised using CD68, on a scale of 1 to 3), was performed on Zen lite image analysis software (Zeiss) by two scorers blinded to transcriptomic and clinical data. Samples were classified as having a (CD45⁺CD68⁺CD206[−]) M1-predominant lining (M1L) or a (CD45⁺CD68⁺CD206⁺) M2-predominant lining (M2L) (see online supplemental figure 1A–D).

Statistical analyses

Raw RNASeq read counts were normalised using DESeq2 Bioconductor Package.¹¹ Normalised expression data were log₂-transformed, scaled to a mean of 0 and variance of 1, and imported into Qlucore Omics Explorer for further analysis. We filtered for genes with variance ($\sigma/\sigma_{\max}$) ≥ 0.4. Principal component analysis (PCA) and linear regression analysis were performed and samples and genes were classified into clusters based on the gene expression data using unsupervised agglomerative hierarchical clustering. Differentially expressed genes between patient clusters were calculated using t-tests with correction for multiple testing using false discovery rate (FDR)-adjusted q-values. Pathway enrichment analyses (top 3 with FDR-adjusted q-values (figure 1), top 20 with p values (online supplemental figures)) were performed on Metascape.¹² CibersortX¹³ was used to extrapolate relative abundance of immune cell subsets from gene expression data (using the LM22 reference dataset). Other statistical analyses (Spearman's correlation coefficient, Mann-Whitney, t-tests with Benjamini-Yekutieli correction for multiple testing) were performed on GraphPad Prism V.9.

RESULTS

Heterogeneity of synovial gene expression profile in ERA

RNASeq was performed on synovial biopsies from 74 patients with ERA. Patient and sample characteristics are shown in

table 1 and online supplemental figure 2A–G. We applied variance filtering to identify the genes whose expression showed the greatest variation across the cohort ($\sigma/\sigma_{\max} \geq 0.4$, n=894 most variable genes) (figure 1A,B). PCA based on the expression of these genes yielded a continuous distribution (rather than distinct clusters) of samples, broadly associated with baseline DAS28CRP (figure 1A). Unsupervised clustering was used to demark two patient clusters (PtC): PtC1 (n=52) and PtC2 (n=22) (figure 1B), based on their expression of these 894 genes. Pathway analysis of these genes revealed significant enrichment of immune system genes, in the *inflammatory response* and *rheumatoid arthritis* pathways (gene cluster 1: GC1) and B cell and plasma cell-related pathways (GC2) (figure 1C, online supplemental figure 3A,B, online supplemental table 2), upregulated in PtC1. Almost 50% of genes in GC2 are immunoglobulin (Ig) genes, potentially overwhelming signals from additional pathways. We therefore performed pathway analysis after removing all Ig genes, and found that *B cell activation* remains the most significantly enriched (q-value=10^{−2.3}, not shown). The B cell transcriptomic signature in PtC1 was also confirmed using a validated synovial B cell gene set (online supplemental figure 3D).¹⁴ The third cluster of genes (GC3, figure 1C, online supplemental figure 3C, online supplemental table 2), related to fatty acid metabolism and PPAR signalling, is instead upregulated in PtC2. These pathways have been associated with M2-like (in vitro) or non-conventional tissue resident macrophages (in vivo), described to have anti-inflammatory, pro-homeostatic functions.^{15 16}

Unbiased ERA synovial transcriptome-driven clustering defines two clinically meaningful groups

Having used the most variably expressed genes for unbiased clustering of samples, we set out to explore the differences between the two patient groups thus defined. Interestingly, PtC1 and PtC2 were characterised by distinct clinical features (figures 1B and 2A, and online supplemental figure 4A–G): Patients in PtC1 displayed higher baseline indices of all disease activity score components (resulting in a median DAS28CRP of 5.56 in PtC1 vs 4.09 in PtC2; p value=0.0003) except Patient Global Assessment. They also had higher rates of baseline radiological erosions (erosive disease in 34.6% vs 10%; p value=0.0252) (figure 2A). Notably, ACPA/RF positivity was not significantly different between the groups.

Baseline SJC28 was the most significantly distinct clinical value between PtC1 and PtC2 (online supplemental figure 4A). Genes whose expression correlated (n=572; q-value <0.005 using regression analysis) with SJC28 were highly enriched in *lymphocyte activation* and *adaptive immune response* pathways (online supplemental figure 5 and online supplemental table 3). We previously showed that these pathways are downregulated by multiple DMARDs, including methotrexate.⁶ We therefore assessed for whether PtC1 and PtC2 differ in terms of response to first-line methotrexate treatment (used in n=51 patients) at 3 months. A significant effect of methotrexate was indeed observed in PtC1 but not PtC2 (figure 2B–D). As previously observed by others,¹⁷ however, treatment response is correlated with baseline disease activity, whether in terms of absolute (figure 2E) or relative drop (not shown) in DAS28CRP ($r=-0.67$, $p<0.0001$ and $r=-0.55$, $p<0.0001$, respectively). Notably, the relationship between baseline disease activity and drop in DAS28CRP was similar in PtC1 and PtC2 (Spearman's $r=-0.621$ and -0.593 , respectively). This confirms that the synovial transcriptome in early, untreated RA, like that in later-stage, heterogeneously treated

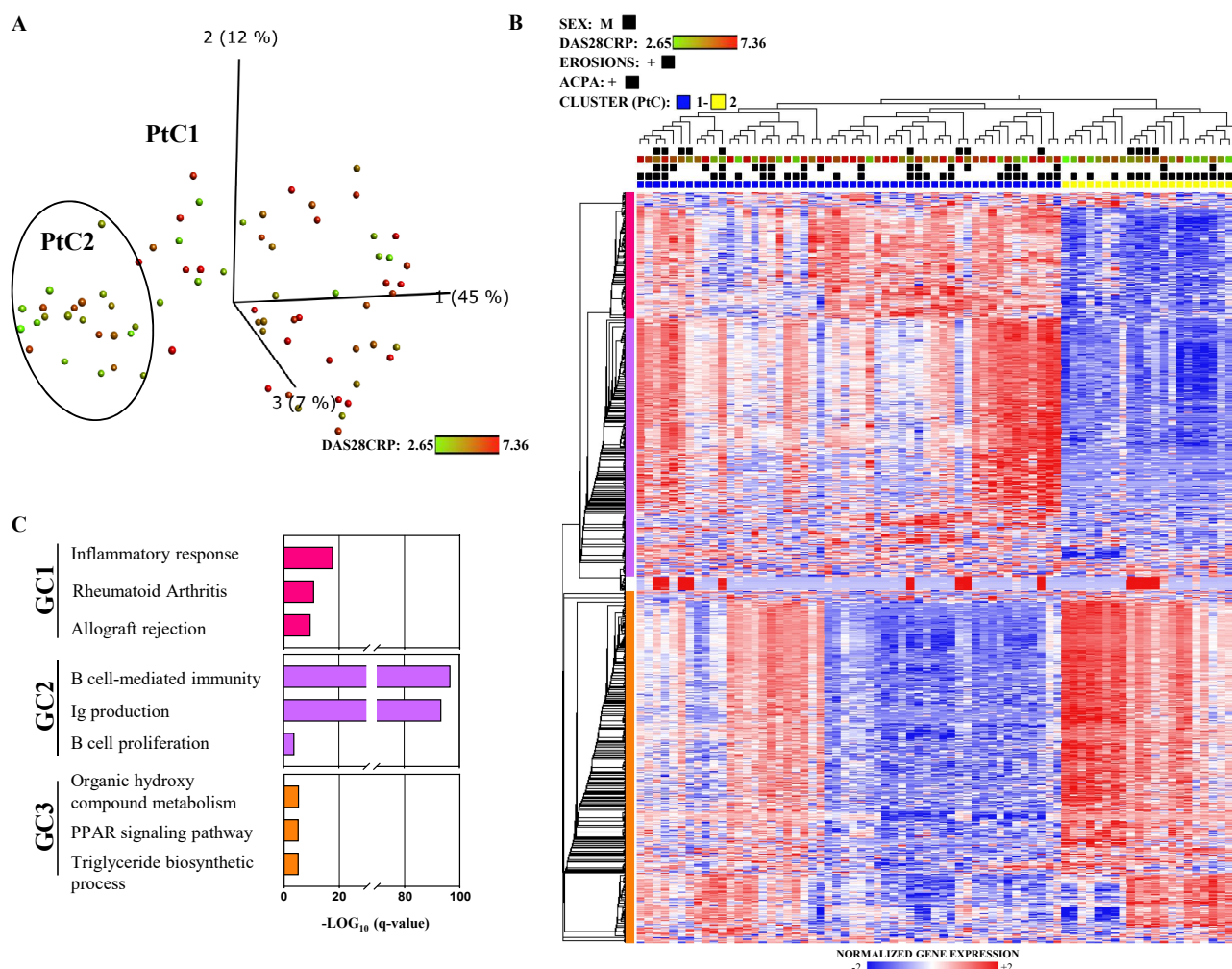


Figure 1 Transcriptomic heterogeneity of synovia from patients with untreated, early rheumatoid arthritis (ERA). (A) Principal components analysis (PCA) plot showing distribution of the 74 samples based on the expression of n=894 most variable genes. Samples are coloured by disease activity score (DAS28CRP colour-scale). Samples in patient cluster 2 (PtC2) from (B) are circled. (B) Heatmap of scaled, normalised expression of the 894 most variable genes across samples. Samples are classified into two patient clusters (PtC): PtC1 (blue) and PtC2 (yellow), using unsupervised clustering (average linking rule). Gender, DAS28CRP, presence of bone erosions at baseline and ACPA seropositivity are indicated above the heatmap. Genes fall into three groups (gene clusters: GC) using unsupervised clustering (average linking rule): GC1 (pink), GC2 (purple) and GC3 (orange); in white: genes located on the Y chromosome, expressed only in male patients across both PtC. These are excluded from pathway analyses. (C) Pathway enrichment analysis using Metascape (top three based on FDR-adjusted q-value) of GC 1–3, coloured as in (B). ACPA, anti-citrullinated peptide antibody; DAS28CRP, Disease Activity Score 28-joint count C reactive protein; FDR, false discovery rate.

disease, is strongly tied to disease activity, a major determinant of treatment response amplitude.

Distinct pathways, histological features and immune cell signatures distinguish the two synovial transcriptome-based ERA groups

We found that the PtC1 and PtC2 groups have significant, clinically relevant characteristics. We therefore set out to perform a detailed supervised analysis of the differentially expressed genes between these two groups (figure 3A). Genes upregulated in PtC1 synovia genes (top 500, ranked by FDR-adjusted q-value) show significant enrichment of pathways related to B cell biology, as well as other immune pathways with critical roles in RA such as *lymphocyte activation*, *TCR signalling* and *cytokine signalling* (figure 3B, online supplemental figure 6A and online supplemental table 4). By contrast, PtC2 is characterised by the upregulation of genes (top 500, ranked by FDR-adjusted q-value) involved in lipid metabolism-related pathways,

although with lower statistical support for pathway enrichment (figure 3C, online supplemental figure 6B and online supplemental table 4). In keeping with the upregulation of immunity/inflammation-related genes in PtC1 synovia, multiple histological features of inflammation were found to be higher in PtC1 synovia than in PtC2 (figure 3D–G), with fibrinoid necrosis being the most pronounced.

M2-like:M1-like macrophage ratio is associated with lower disease activity and synovial inflammation

We next used CibersortX to extrapolate information on the relative proportions of immune cell subpopulations in synovia, from gene expression data.¹³ In line with pathway analyses, PtC1 had a higher transcriptomic signature (inferred relative frequency) of B and plasma cells, T cells and M1-like macrophages than PtC2. PtC2 instead had relatively higher M2-like macrophage and resting mast cell signatures (figure 4A). Accordingly, the M2-like macrophage signature was inversely correlated with

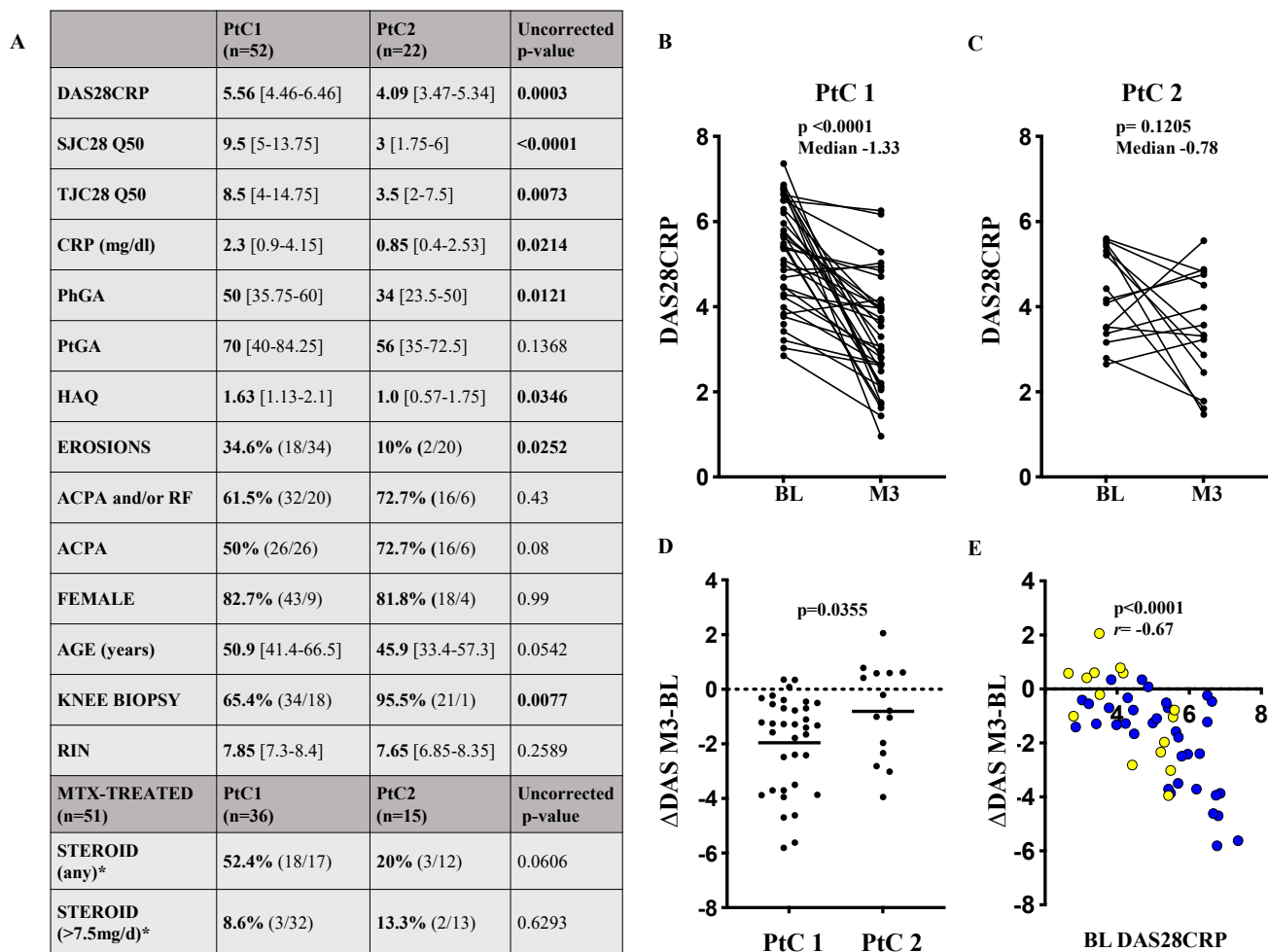


Figure 2 Clinical characteristics and response to treatment of patients in PtC1 and PtC2. (A) Baseline clinical characteristics of patients in PtC1 and PtC2. Values shown are Q50 (Q25-Q75) or percentages. P value of Mann-Whitney or Fisher's exact test are shown. *Data unavailable for one patient from PtC1; assigning this patient to one or the other group (steroid/no steroid) does not modify p value. (B, C) Effect of therapy on DAS28CRP in methotrexate-treated patients from PtC1 (n=35) (B) and PtC2 (n=15) (C); p values (paired Wilcoxon) shown. (D) Change in DAS28CRP from baseline to 3 months (Δ DAS M3-BL) in PtC1 and PtC2; p value (Mann-Whitney) shown. (E) Correlation between baseline (BL) DAS28CRP and delta DAS28CRP from baseline to 3 months (Δ DAS M3-BL) in n=50 patients treated with methotrexate (data unavailable at M3 for one patient in PtC1). Dots coloured according to PtC; p value and Spearman's r are shown. ACPA, anti-citrullinated peptide antibodies; HAQ, Health Assessment Questionnaire; PhGA, Physician Global Assessment; PtGA, Patient Global Assessment; RIN, RNA integrity number; RF, rheumatoid factor; SJC28, Swollen Joint Count across 28 joints; TJC28, Tender Joint Count across 28 joints.

the B cell, T cell and M1-like macrophage signatures (online supplemental figure 7), as well as with clinical indices of baseline disease activity (figure 4B-E and online supplemental figure 7). M2-polarised macrophages have been shown to have a metabolic profile characterised by predominant fatty acid oxidation,¹⁸⁻²⁰ and we indeed found that the M2-like macrophage signature correlated with expression of GC3 genes across samples (online supplemental figure 8A,B).

We used multiplex IF (for CD45, a pan-immune cell marker; CD68, a pan-macrophage marker; CD206, an M2-like macrophage marker) to confirm the inverted M2/M1 ratios suggested to distinguish PtC1 and PtC2 samples by CibersortX. Digitally quantified IF data correlated well with transcriptomic data (M2/M1 ratios, figure 5A), and confirmed the inverse correlation between immune infiltration of the synovium (CD45⁺ fraction by IF) and M2/M1 ratio (figure 5B). Semiquantitative evaluation of multiplex IF added a spatial dimension to our analysis, revealing marked variations in M2 versus M1 content of synovial lining

among samples. Samples were classified as M1L (M1-Lining: predominantly CD206⁻ lining) or M2L (M2-Lining: predominantly CD206⁺ lining) (see the Materials and methods section, figure 5C, online supplemental figure 1A-D). M2L samples had higher M2/M1_{IF} ratios than M1L samples (figure 5D); they also showed significantly lower (CD68⁺) synovial lining thickness on IF (figure 5E).

DISCUSSION

Histological and transcriptomic analyses of synovial biopsies have provided invaluable insights into tissue inflammatory processes in RA. Most studies have focused on established disease^{6 21-23} or have used a priori classification approaches.^{2 4 24} Here, we instead exploited the transcriptional heterogeneity of 74 DMARD-naïve ERA synovial biopsies for unbiased, data-driven clustering of samples. The two groups thus defined (PtC1 and PtC2) showed distinct clinical and histological features,

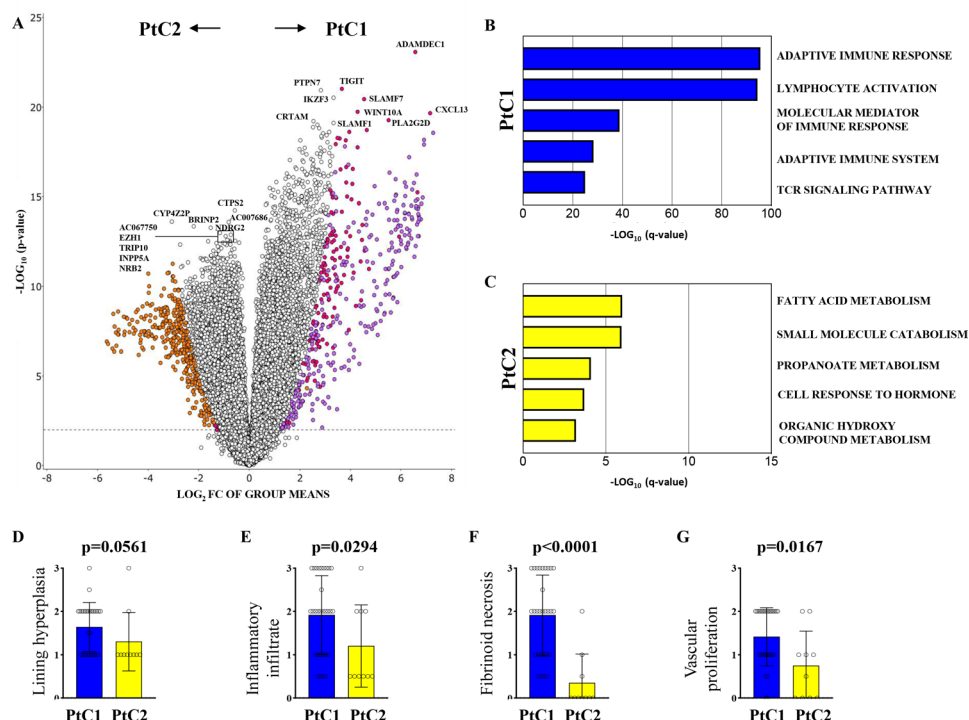


Figure 3 Transcriptomic and histological differences between PtC1 and PtC2. (A) Volcano plot of all differentially expressed genes (no restriction on variance) between PtC1 and PtC2 using t-test. Dashed line: p-value threshold=0.01. Genes belonging to GC 1 (pink), 2 (purple) and 3 (orange) coloured as in figure 1B. Gene symbols of the top 10 upregulated genes in each PtC (based on t-test p values) are shown. (B, C) Pathway enrichment analysis on top 500 upregulated genes based on t-test (with FDR-adjusted q-values), in PtC1 (B) and PtC2 (C). (D–G) Scoring for features of synovial inflammation on H&E sections: lining layer hyperplasia (D), inflammatory infiltrate (E), fibrinoid necrosis (F) and vascular proliferation (G). P values of Mann-Whitney are shown on the graph. FDR, false discovery rate; PtC, patient cluster.

suggesting biologically meaningful clustering. To the question of whether early, treatment-naïve transcriptomes may allow for patient stratification or prediction of treatment response: PtC1 showed a greater decrease in (absolute and relative, ie, baseline-normalised) disease activity 3 months into treatment with methotrexate. Given that the synovial transcriptome correlates strongly with baseline disease activity, we cannot yet conclude the former is an independent (or better) predictor of treatment response.

That the synovial transcriptome captures local (histological) inflammation is not surprising. The degree to which it echoes disease extent (as measured in clinical scores), while not unexpected, is striking. It is also consistent across studies.²³ Increased numbers of tender and swollen joints no doubt tend to be linked to greater local inflammation; nevertheless, the association between synovial transcriptomic profile and global disease activity indices speaks to their robustness and continuing utility. While not designed to specifically address the question, we assessed for previously described pathotype-signatures in our series.² We did not find evidence for distinct (*lymphoid*, *myeloid* and *fibroid*) subgroups.^{24 24} This must be interpreted with some caution: The two studies differ significantly in design and analysis; in particular, unbiased versus hypothesis-driven, reflected in the use of whole transcriptome data (RNASeq) versus a selected gene-panel (NanoString). The former likely entails a far larger cohort for pathotype-defining genes to reach genome-wide significance. Hierarchical clustering based on the expression of published pathotype-gene sets however also resulted in a similar continuum of samples as in our analysis: from fibroid with lower disease activity, to high inflammatory (lymphoid+myeloid) with

higher disease activity, without evident lymphoid vs myeloid clustering (online supplemental figure 9A–C).

Based on the genes differentially expressed between the two groups, synovial biopsies from patients in PtC1 have strong signatures of inflammation and adaptive (particularly B cell lineage) immunity. By contrast, synovia from patients in PtC2, who tend to have less active and erosive disease, have a low inflammatory profile and intriguingly, evidence an M2-like macrophage signature.²² The M2 marker CD206 is expressed by tissue-resident macrophages, thought to play a critical role in maintaining synovial tissue homeostasis.^{25 26} The presence of CD206⁺ macrophages in the synovial lining has indeed been shown to be inversely correlated with clinical parameters of disease activity and histological parameters of synovial hyperplasia and inflammation in long-standing RA.²⁷ These synovial tissue macrophages (STMs) are phenotypically, transcriptionally and metabolically reminiscent of IL4/IL13 polarised, M2-like macrophages, described *in vitro*.¹⁶ Here, we show, in a large series of samples, that (CD206⁺ M1-like vs CD206⁺ M2-like) macrophage composition of the synovial lining is associated with synovial inflammation even in early, untreated RA. Although further mechanistic studies will be required to separate cause from consequence, it is possible that CD206⁺ STMs (or particular subsets thereof²⁷) play an important protective role in dampening synovial inflammation in RA. In this regard, their assessment in unaffected joints of patients with RA, and longitudinally in follow-up biopsies, could be informative. An open question is whether CD206⁺ STMs in healthy synovia are replaced by CD206⁺ macrophages in RA, or whether they are reprogrammed in the inflammatory context—and if so, what

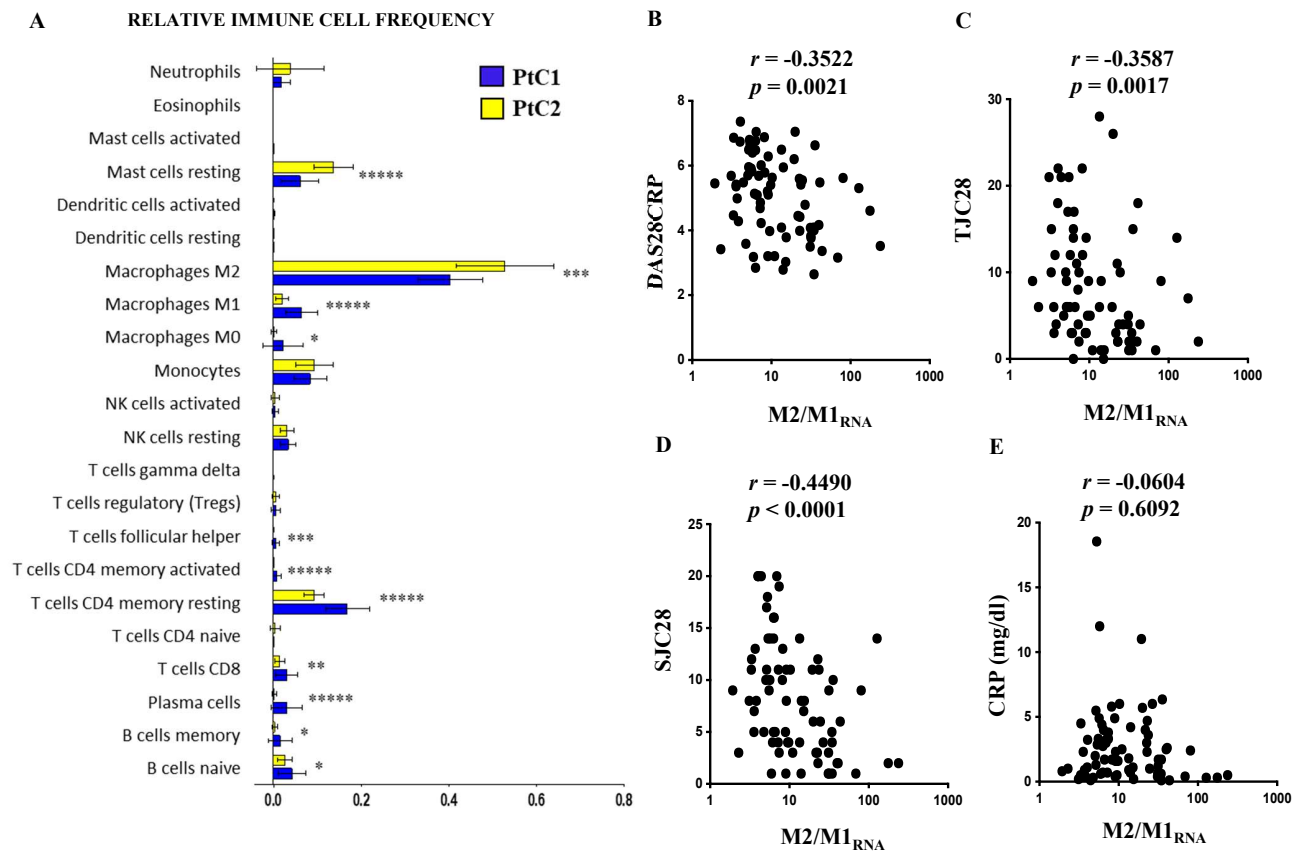


Figure 4 M2:M1 ratios are inversely correlated with clinical disease activity scores. (A) CibersortX-inferred immune cell proportions in samples from PtC1 and PtC2 (mean proportion $\pm$ SD of each immune cell subset). **** $p < 0.000001$, *** $p < 0.00001$, ** $p < 0.0001$, * $p < 0.01$ (unpaired t-tests with 5% FDR (Benjamini-Yekutieli)). (B–E) Correlation between M2/M1_{RNA} (M2:M1 ratio by CibersortX on RNASeq) and baseline clinical disease activity scores (n=74 samples): DAS28CRP (B), Tender Joint Count (C), Swollen Joint Count (D) and CRP (E). P value and Spearman's r are shown. DAS28CRP, Disease Activity Score 28-joint count C reactive protein; FDR, false discovery rate; PtC, patient cluster.

factors may allow for more efficient (or lasting) reversal of this plasticity.

Overall, our data suggest that the synovial immune profile in RA reflects a continuum from high to low inflammatory burden and a corresponding gradient of disease activity; whether one presages the other remains to be determined. It is also possible they reflect different stages of the same, dynamic pathogenic process. While an important strength of our study is the inclusion of only untreated patients with recent onset of RA symptoms (<12 months), it is known that synovial alterations may occur long before the development of clinically overt synovitis.^{28–30} The proportion of knee joints was significantly higher in the PtC2 than in the PtC1 group (table 1), yet it is unlikely that the groups cluster simply based on joint type, as we and others have observed similar patterns of synovial inflammation and gene expression when comparing large versus small joints from the same patients.^{31 32} Moreover, previous studies have not found an enrichment of knee joints in low inflammatory synovitis as assessed by histology.² We applied variance filtering on gene expression exclusively to the (n=55) synovia from knees, and obtained very similar results in terms of both overlap between gene-lists (and therefore, pathway enrichment), and

expression-based unsupervised clustering of samples (data not shown).

We acknowledge several limitations in this study. First, this is an observational cohort in which steroid treatment was not controlled. Longer term follow-up and repeat biopsies, especially in poor responders to methotrexate therapy, would in addition be of great value in determining the clinical relevance of our findings. Consequently, confirmation in a large, controlled, prospective setting is required. While (a minimum of 3) fragments sampled from different locations within joints were used for transcriptional profiling, our methodology may not fully account for intra-joint heterogeneity.³³ The robust correlations observed between RNAseq signatures and histological data (from additional fragments from the same joints) nevertheless support the representativeness of our sampling. In particular, the association of M2-like/tissue resident macrophages with lower disease activity and synovial inflammation is striking and provides an avenue for further mechanistic insights. Spatial single cell transcriptomic profiling will be a powerful starting point, particularly in examining the subphenotypes of STMs,²⁷ their proximal synoviocytes and the interaction between these compartments.

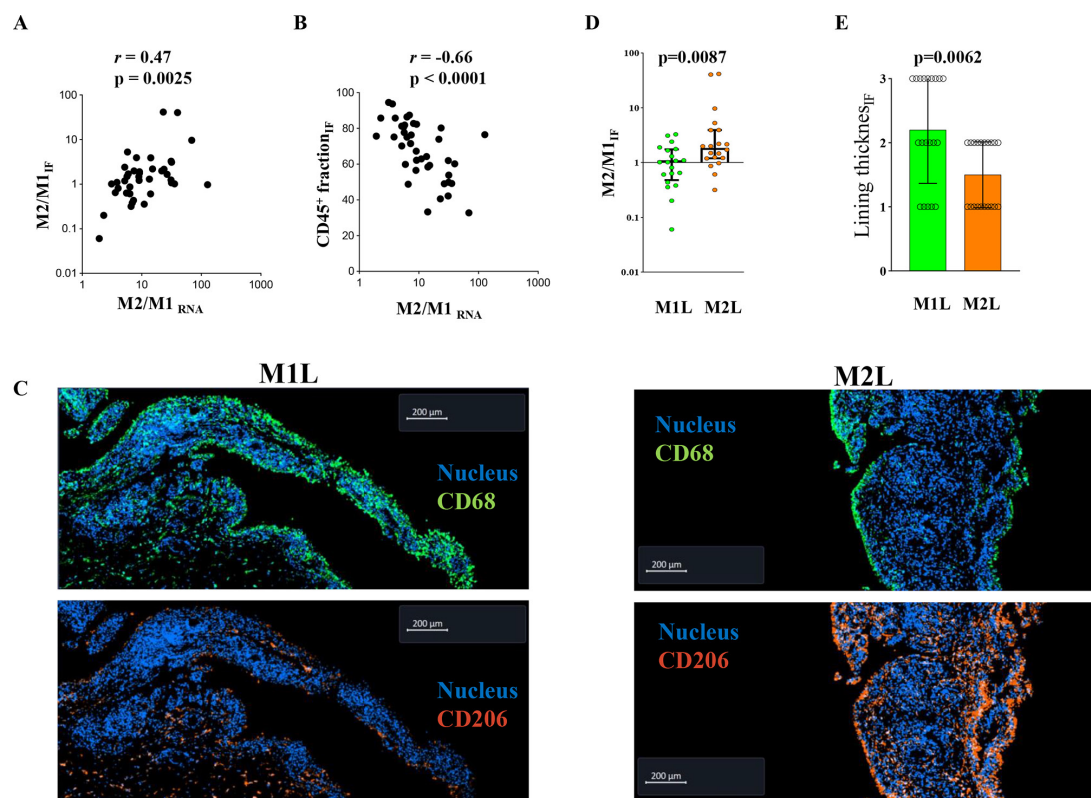


Figure 5 M2:M1 ratios are associated with differences in synovial inflammation, and synovial lining macrophage composition and thickness. (A) Correlation between M2/M1 ratio by CIBERSORTX on RNAseq (M2/M1_{RNA}), and digital quantification of multiplex immunofluorescence (number of CD45⁺CD68⁺CD206⁺ cells/CD45⁺CD68⁺CD206⁻ cells, across entire biopsies) (M2/M1_{IF}). Spearman's r and p value are shown. (B) Correlation between M2/M1_{RNA} ratio and immune cell infiltration based on digital quantification of multiplex immunofluorescence (number of CD45⁺ cells/total cells (nuclei) across entire biopsies) (CD45⁺ fraction_{IF}). Spearman's r and p value are shown. (C) Representative examples of multiplex immunofluorescence images from samples with M1-predominant lining (M1L, left panels) and samples with M2-predominant lining (M2L, right panels). Nuclei in blue, CD68 in green (top panels) and CD206 in orange (bottom panels). (D) M2/M1_{IF} ratio (number of CD45⁺CD68⁺CD206⁺ cells/CD45⁺CD68⁺CD206⁻ cells, across entire biopsies) in M1L and M2L classified samples. Boxplots showing mean and IQR. P value of Mann-Whitney is shown. (E) Semiquantitative scores of CD68⁺ lining of biopsies by immunofluorescence (lining thickness_{IF}) in M1L and M2L classified samples. Bars represent mean and SD. P value of Mann-Whitney is shown.

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Contributors CT, PD, BL and NL designed the study. CT, GT, TS, AL, JM, SDM, AN-T, LMdB, CB, CG and PD participated in data and samples collection. CT, GT, AL, CG, BL and NL analysed and interpreted the data. CT, BL and NL wrote the final manuscript. All authors approved the final manuscript. NL is the guarantor of this study.

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Competing interests BL is currently employed at UCB Pharma, Anderlecht, Belgium.

Patient and public involvement Patients and/or the public were not involved in the design, or conduct, or reporting or dissemination plans of this research.

Patient consent for publication Consent obtained directly from patient(s).

Ethics approval This study involves human participants and was approved by ethics committee of the Université catholique de Louvain (No. 2013/24MAI/293). Participants gave informed consent to participate in the study before taking part.

Provenance and peer review Not commissioned; externally peer reviewed.

Data availability statement Data are available in a public, open access repository. Sequencing data and metadata were deposited in the Gene Expression Omnibus of the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/geo/>), and are freely accessible for public use through Gene Expression Omnibus accession number GSE225731.

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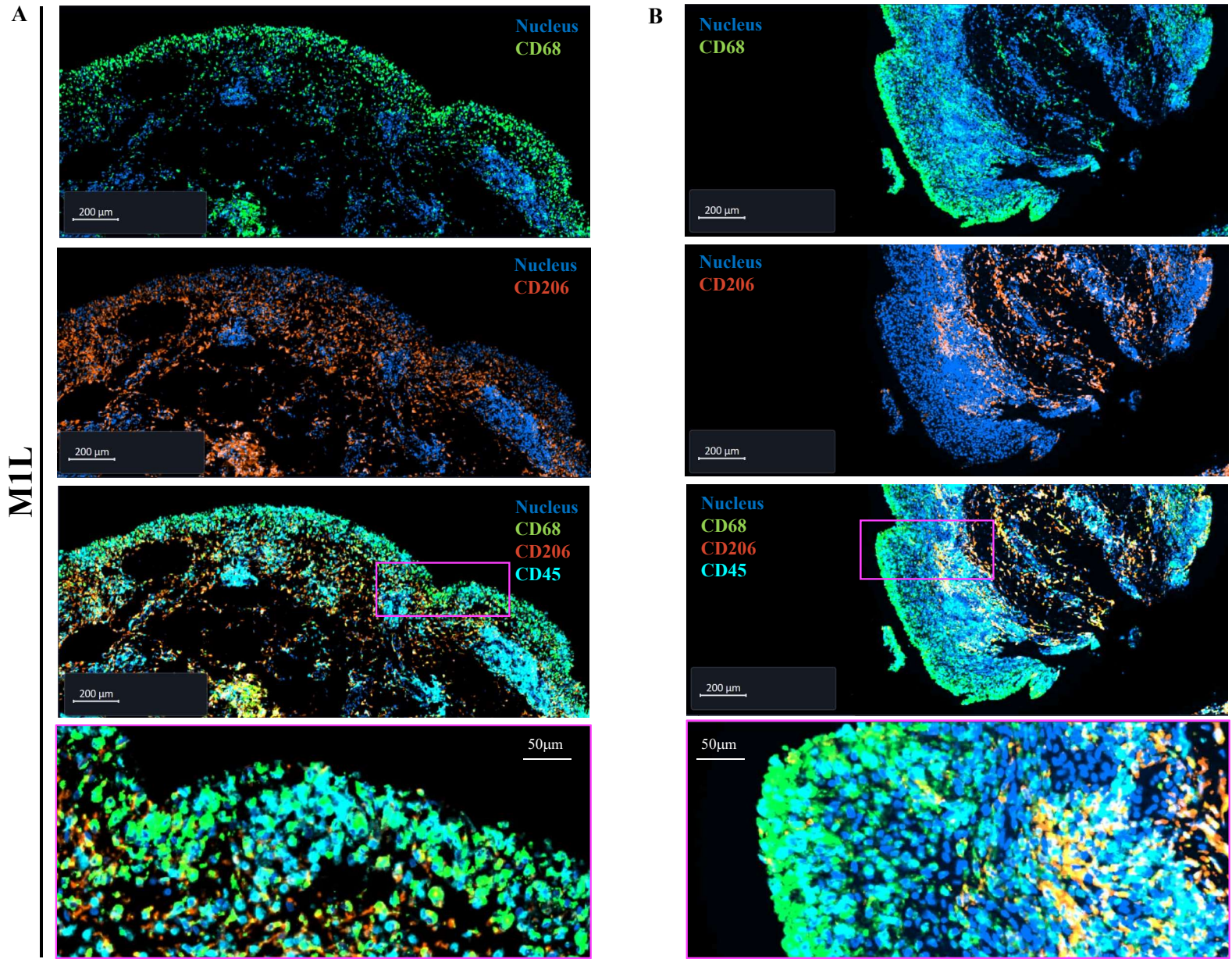
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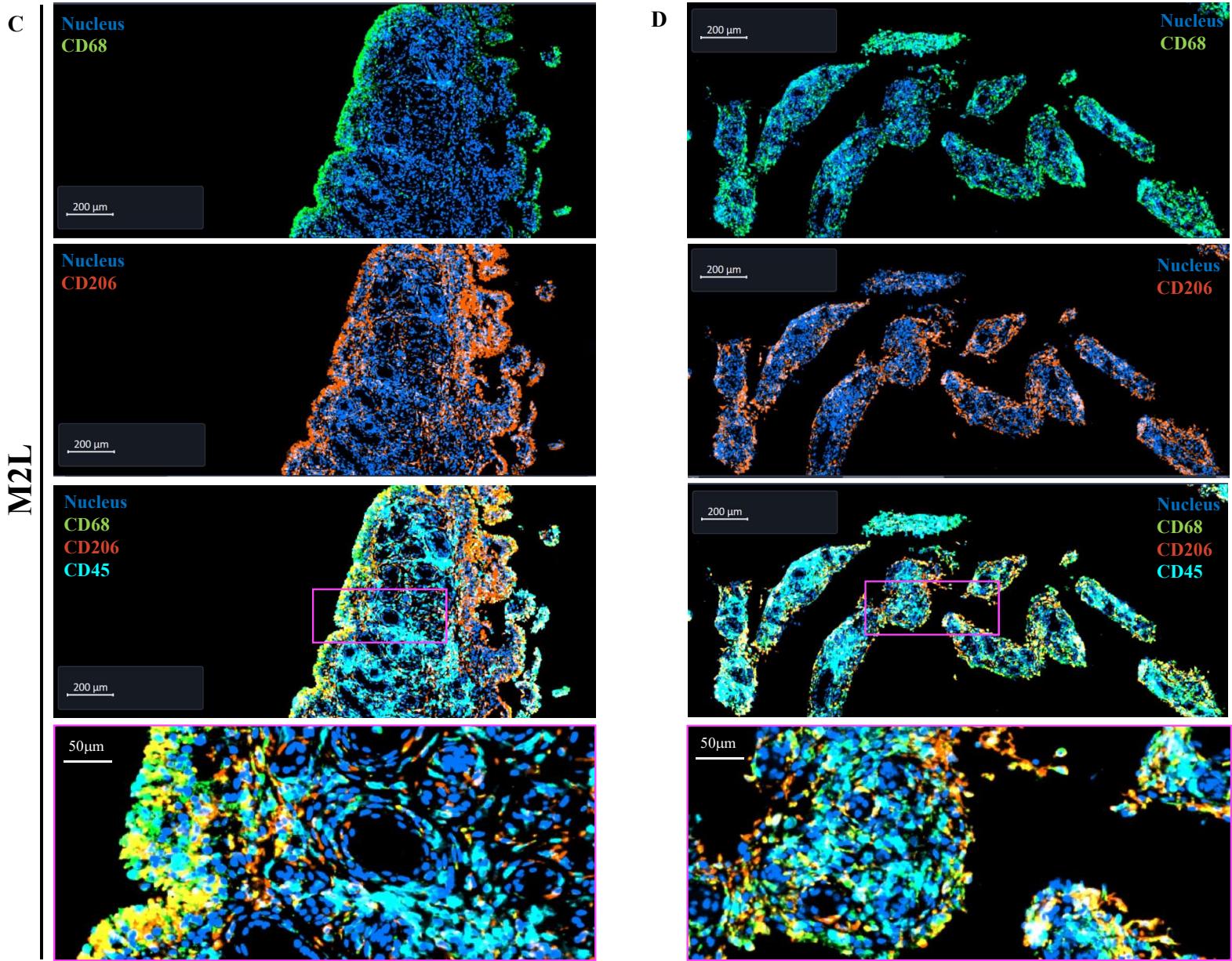
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First-line therapy in n=23 patients excluded from the response to therapy analysis	n of patients
Adalimumab	1
Adalimumab + methotrexate	1
Certolizumab	1
Infliximab	2
Infliximab + methotrexate	1
methotrexate + other csDAMRD	3
Secukinumab	1
Tocilizumab	6
Tocilizumab + methotrexate	5
Unknown	2

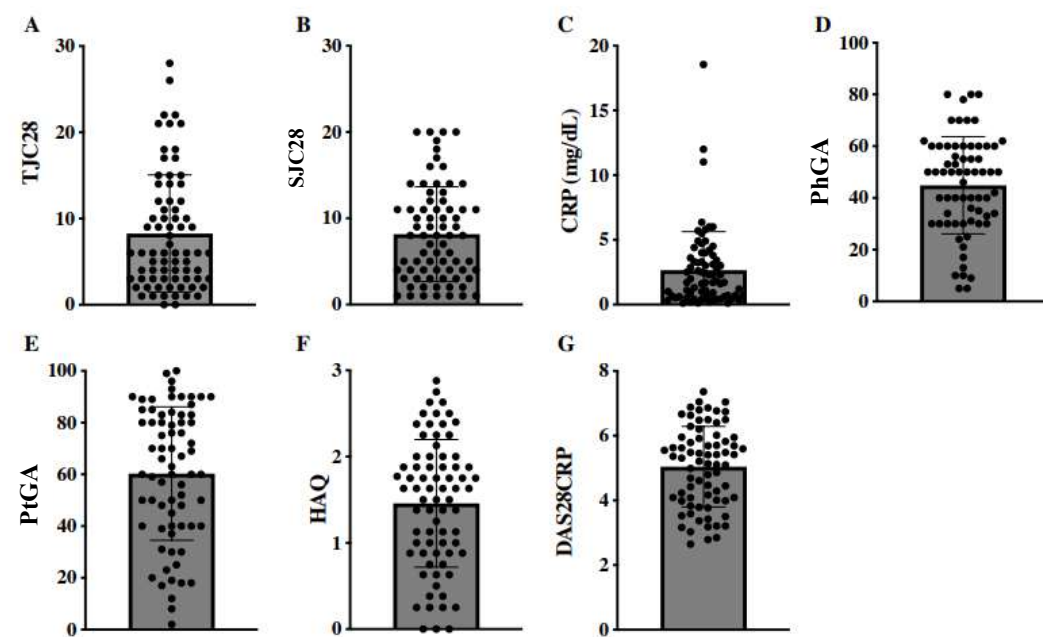
Supplementary Figure 1



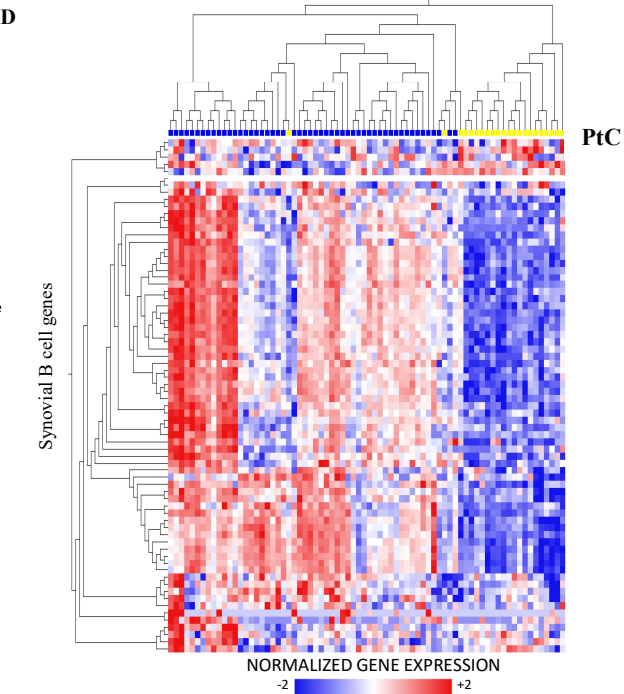
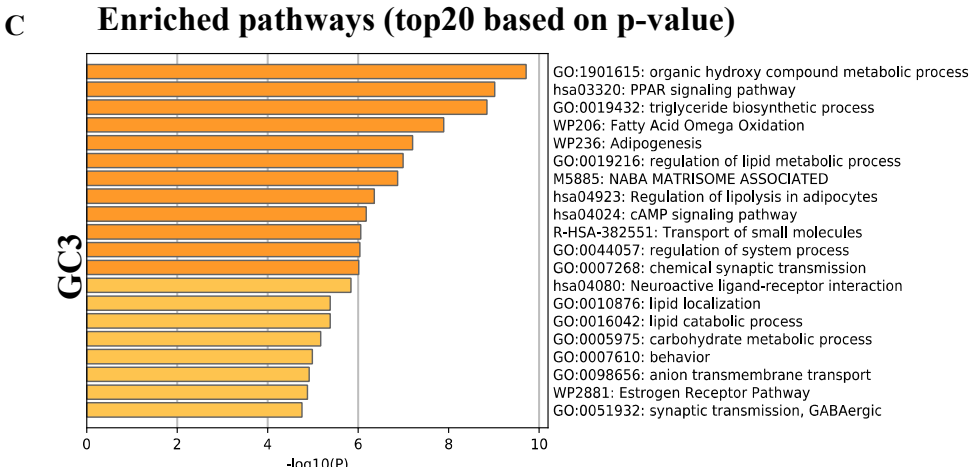
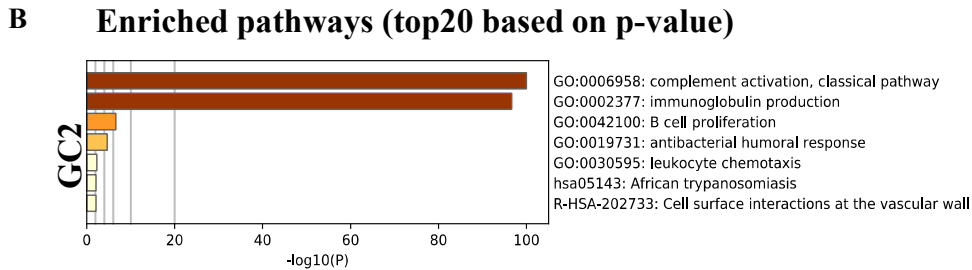
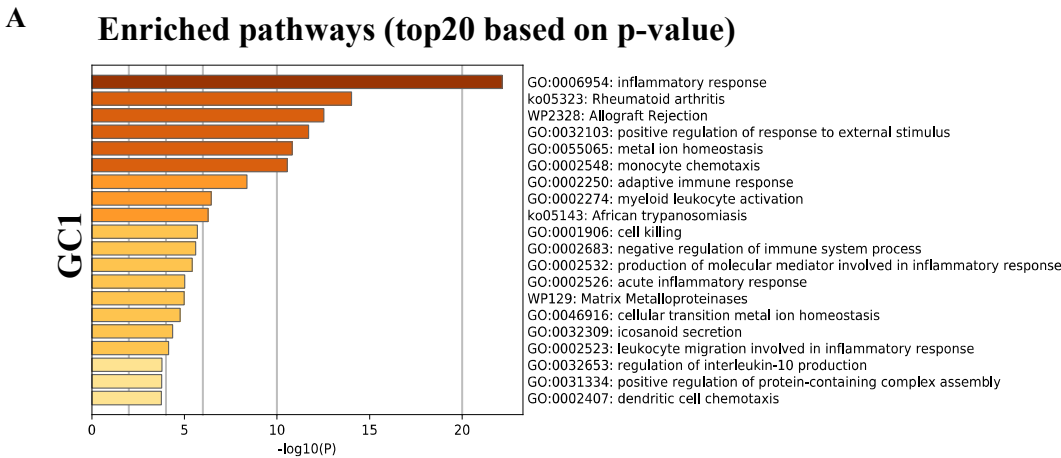
Supplementary Figure 1



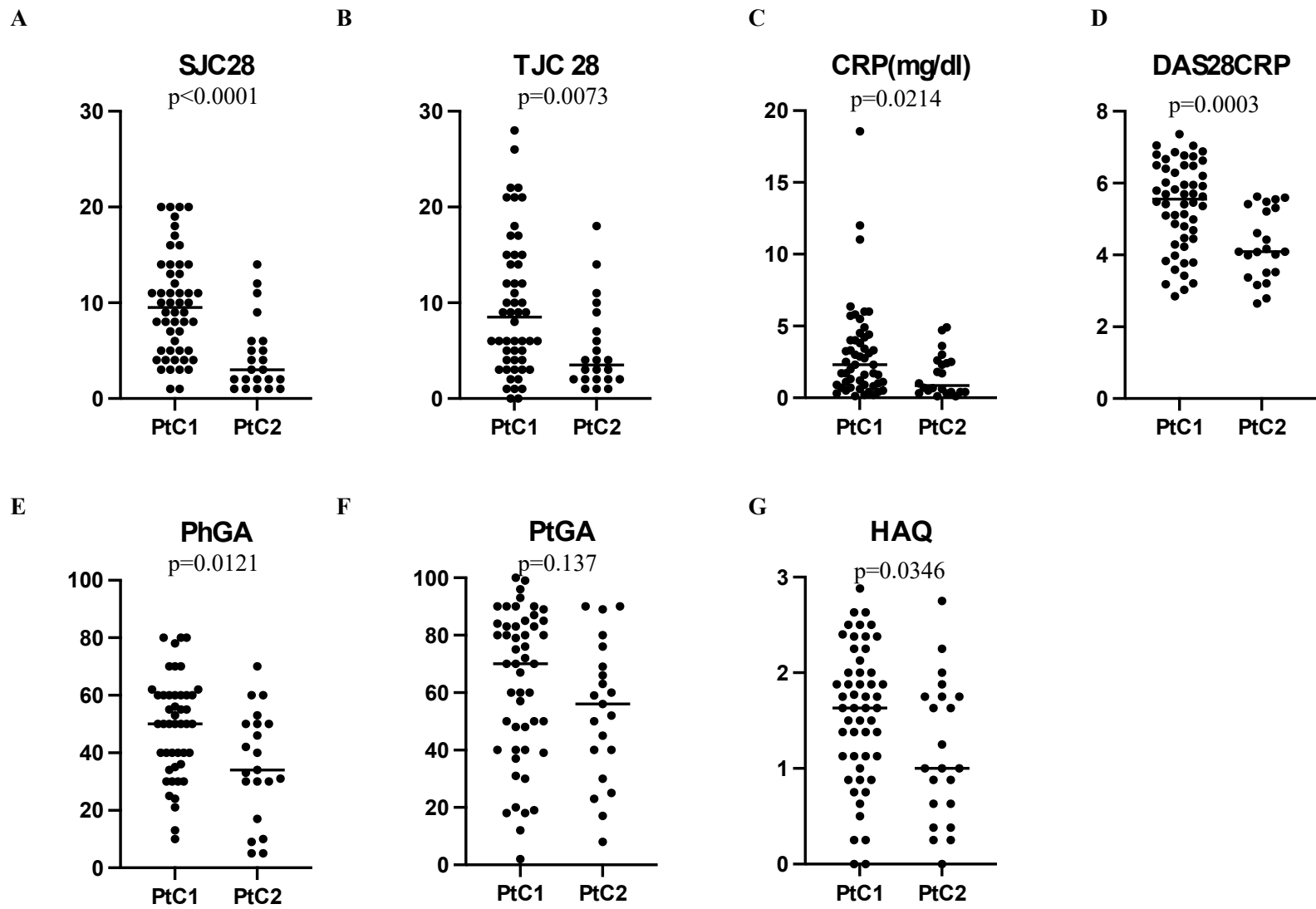
Supplementary Figure 2



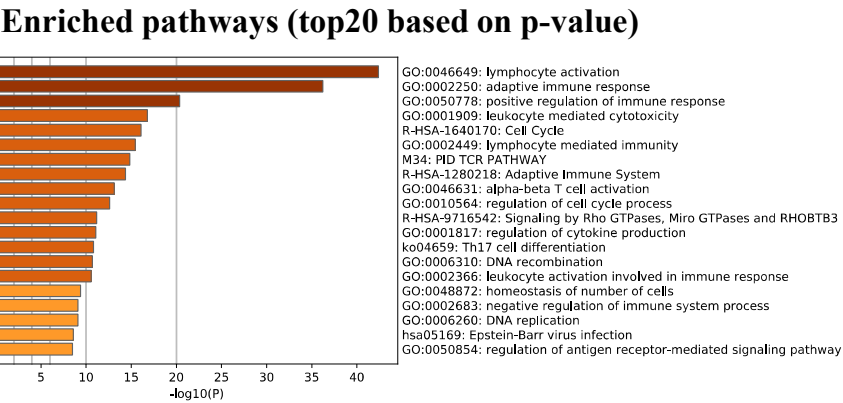
Supplementary Figure 3



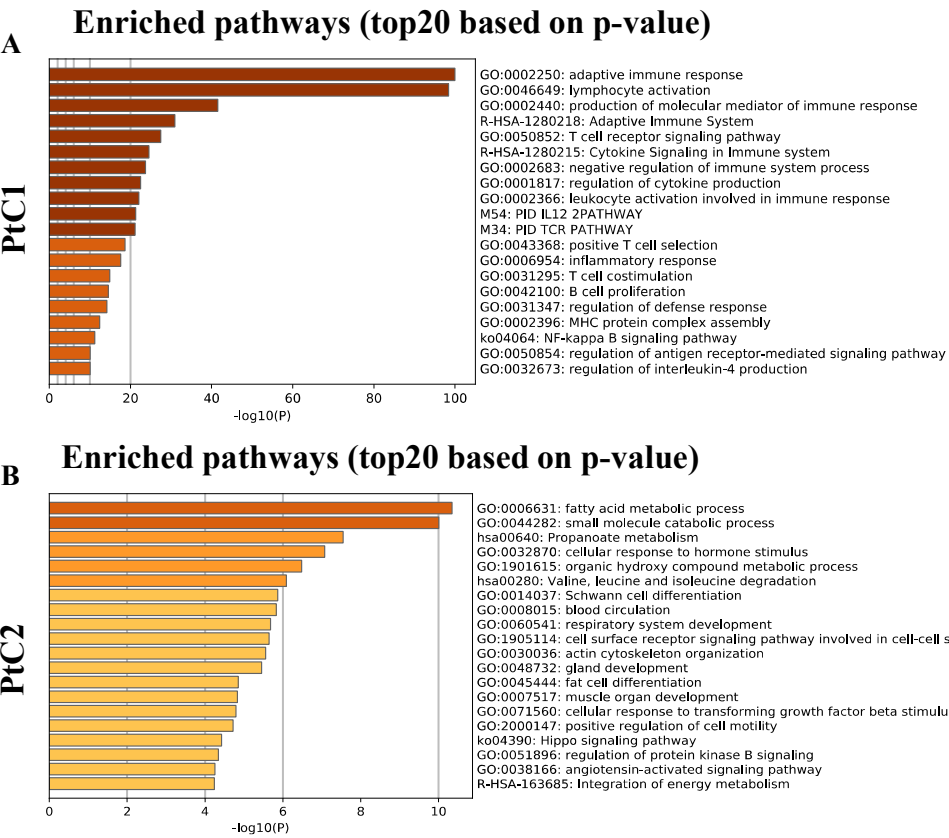
Supplementary Figure 4



Supplementary Figure 5



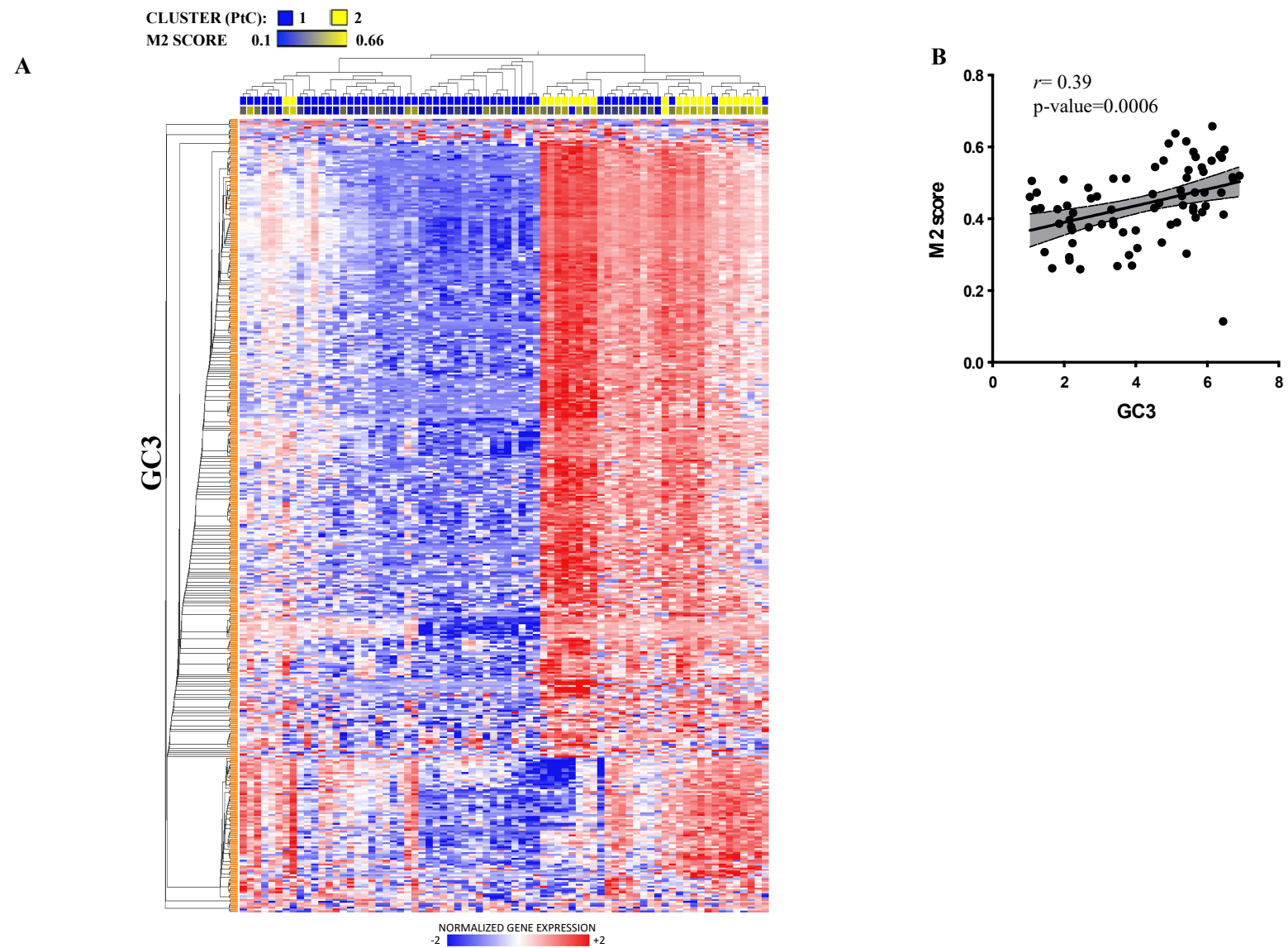
Supplementary Figure 6



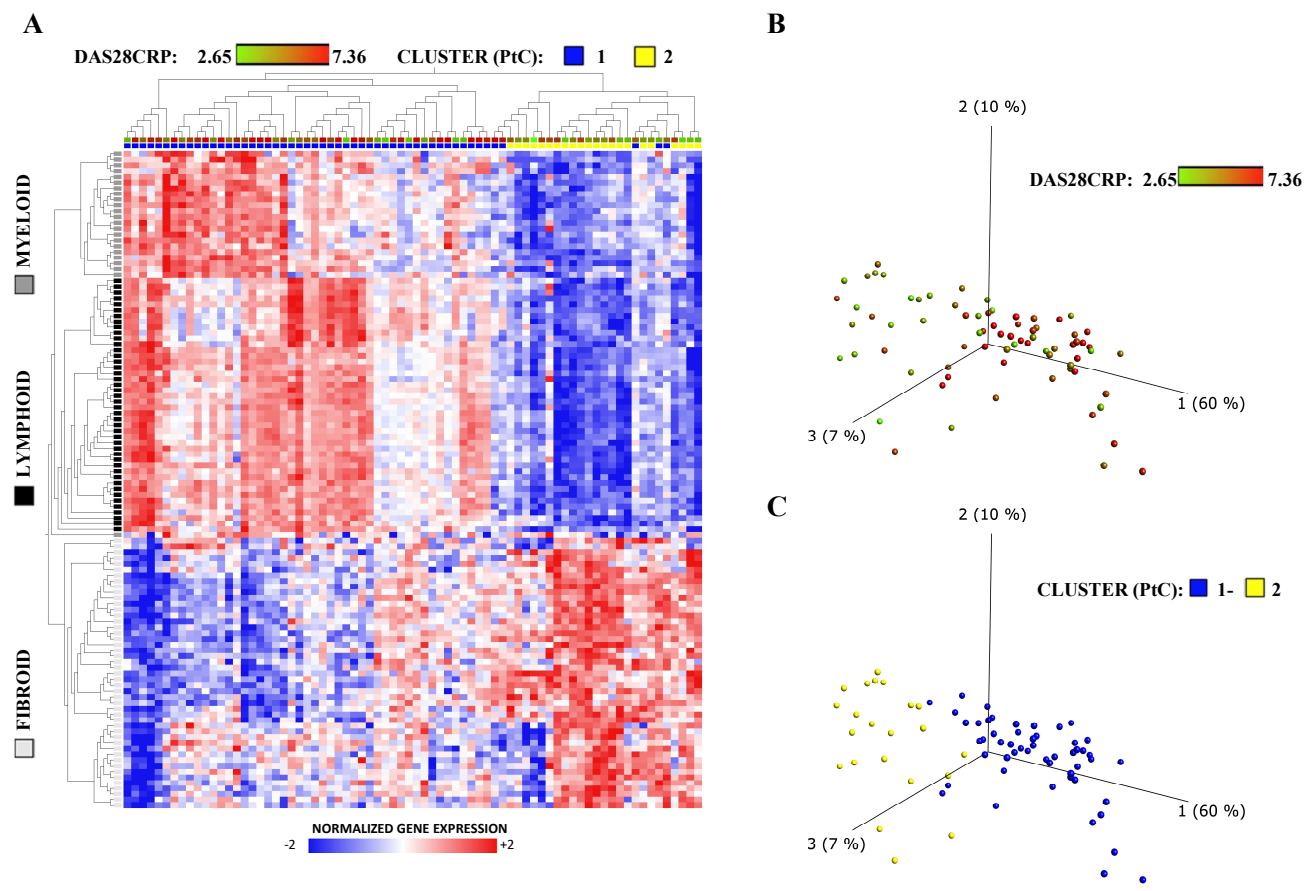
Supplementary Figure 7

	B cells naive	B cells memory	Plasma cells	T cells CD8	T cells CD4 naive	T cells CD4 memory resting	T cells CD4 memory activated	T cells follicular helper	T cells regulatory (Tregs)	T cells gamma delta	NK cells resting	NK cells activated	Monocytes	Macrophages M0	Macrophages M1	Macrophages M2	Dendritic cells resting	Dendritic cells activated	Mast cells resting	Mast cells activated	Neutrophils	tjc28_bl	sjc28_bl	crp_bl (mg/dl)	das28crp_bl
B cells naive	1.00	-0.24	0.46	0.11	0.18	0.10	0.10	0.06	0.14	0.04	0.02	0.03	-0.17	0.04	-0.05	-0.40	0.25	-0.05	0.09	-0.08	0.08	-0.01	0.12	0.15	0.02
B cells memory	-0.24	1.00	0.31	-0.02	-0.18	0.23	0.19	0.23	-0.05	0.08	-0.01		-0.29	0.05	0.09	-0.25	0.06	0.29	-0.16	-0.10	-0.04	-0.07	0.10	-0.05	-0.04
Plasma cells	0.46	0.31	1.00	0.26	-0.14	0.43	0.41	0.36	0.02	-0.08	-0.01	0.11	-0.29	0.02	0.33	-0.66	0.24	0.22	-0.34	0.02	0.05	0.18	0.33	0.29	0.29
T cells CD8	0.11	-0.02	0.26	1.00	-0.13	0.16	0.05	0.38	0.41	-0.18	-0.25	0.35	-0.09	-0.13	0.29	-0.26	0.38	-0.10	-0.09	-0.08	-0.14	0.07	0.13	0.07	0.09
T cells CD4 naive	0.18	-0.18	-0.14	-0.13	1.00	-0.30	-0.04	-0.23	0.18	-0.03	-0.04	0.08	0.19	0.02	-0.19	-0.07	0.11	-0.09	0.10	-0.03	0.36	-0.08	-0.08	0.06	-0.10
T cells CD4 memory resting	0.10	0.23	0.43	0.16	-0.30	1.00	0.57	0.31	-0.29	-0.07	0.28	0.05	-0.08		0.70	-0.59	0.18	0.11	-0.61	-0.08	-0.27	0.24	0.37	0.11	0.33
T cells CD4 memory activated	0.10	0.19	0.41	0.05	-0.04	0.57	1.00	0.19	-0.16	-0.11	0.27	-0.12	0.19	0.09	0.45	-0.54	0.04	0.15	-0.55	0.14	-0.06	0.16	0.34	0.34	0.35
T cells follicular helper	0.06	0.23	0.36	0.38	-0.23	0.31	0.19	1.00	-0.05	-0.09	-0.19	0.29	-0.08	0.06	0.36	-0.49	0.20	0.08	-0.26	-0.09	-0.16	0.30	0.35	-0.01	0.23
T cells regulatory (Tregs)	0.14	-0.05	0.02	0.41	0.18	-0.29	-0.16	-0.05	1.00	0.20	-0.44	0.41	-0.04	-0.04	-0.04	0.01	0.25	-0.19	0.16	-0.10	-0.01	-0.12	-0.13	0.01	-0.13
T cells gamma delta	0.04	0.08	-0.08	-0.18	-0.03	-0.07	-0.11	-0.09	0.20	1.00	-0.16	0.12	-0.20	0.24	-0.11	0.11	-0.06	-0.03	-0.11	-0.01	-0.13	-0.14	-0.18	-0.01	-0.13
NK cells resting	0.02	-0.01	-0.01	-0.25	-0.04	0.29	0.27	-0.19	-0.44	-0.16	1.00	-0.61	0.15	0.10	0.14	-0.16	-0.27	0.14	-0.40	0.17	0.04	0.04	0.21	-0.01	0.10
NK cells activated	0.03		0.11	0.35	0.08	0.05	-0.12	0.29	0.41	0.12	-0.61	1.00	-0.01	-0.25	0.09	-0.17	0.32		0.09	-0.09	0.01	0.08	-0.07	0.04	0.06
Monocytes	-0.17	-0.29	-0.29	-0.09	0.19	-0.08	0.19	-0.08	-0.04	-0.20	0.15	-0.01	1.00	-0.08	0.01	0.05	-0.09	-0.03	-0.19	0.19	0.08	0.04	0.08	0.10	0.15
Macrophages M0	0.04	0.05	0.02	-0.13	0.02		0.09	0.06	-0.04	0.24	0.10	-0.25	-0.06	1.00		-0.23	-0.08	0.02	-0.28	0.23	0.01	-0.06	0.07	0.11	-0.02
Macrophages M1	-0.05	0.09	0.33	0.29	-0.19	0.70	0.45	0.36	-0.04	-0.11	0.14	0.09	0.01		1.00	-0.43	0.26	-0.05	-0.70	-0.15	-0.23	0.33	0.39	0.03	0.32
Macrophages M2	-0.40	-0.25	-0.66	-0.26	-0.07	-0.59	-0.54	-0.49	0.01	0.11	-0.16	-0.17	0.05	-0.23	-0.43	1.00	-0.28	-0.28	0.52	-0.19	-0.05	-0.19	-0.39	-0.21	-0.24
Dendritic cells resting	0.25	0.06	0.24	0.38	0.11	0.18	0.04	0.20	0.25	-0.06	-0.27	0.32	-0.09	-0.08	0.26	-0.28	1.00	-0.14	-0.10	-0.06	0.10	0.09	0.09	-0.03	0.01
Dendritic cells activated	-0.05	0.29	0.22	-0.10	-0.09	0.11	0.15	0.08	-0.19	-0.03	0.14		-0.03	0.02	-0.05	-0.28	-0.14	1.00	-0.14	0.42	-0.07	-0.15	-0.09	-0.03	-0.13
Mast cells resting	0.09	-0.16	-0.34	-0.09	0.10	-0.61	-0.55	-0.26	0.16	-0.11	-0.40	0.09	-0.19	-0.28	-0.70	0.52	-0.10	-0.14	1.00	-0.20	0.06	-0.28	-0.41	-0.22	-0.36
Mast cells activated	-0.08	-0.10	0.02	-0.08	-0.03	-0.08	0.14	-0.09	-0.10	-0.01	0.17	-0.09	0.19	0.23	-0.15	-0.19	-0.06	0.42	-0.20	1.00	0.19	-0.10	-0.12	0.12	-0.06
Neutrophils	0.08	-0.04	0.05	-0.14	0.36	-0.27	-0.06	-0.16	-0.01	-0.13	0.04	0.01	0.08	0.01	-0.23	-0.05	0.10	-0.07	0.06	0.19	1.00	-0.10	-0.10	0.18	-0.03
tjc28_bl	-0.01	-0.07	0.18	0.07	-0.08	0.24	0.16	0.30	-0.12	-0.14	0.04	0.08	0.04	-0.06	0.33	-0.19	0.09	-0.15	-0.28	-0.10	-0.10	1.00	0.61	0.23	0.82
sjc28_bl	0.12	0.10	0.33	0.13	-0.08	0.37	0.34	0.35	-0.13	-0.18	0.21	-0.07	0.08	0.07	0.39	-0.39	0.09	-0.09	-0.41	-0.12	-0.10	0.61	1.00	0.28	0.73
crp_bl (mg/dl)	0.15	-0.05	0.29	0.07	0.06	0.11	0.34	-0.01	0.01	-0.01	0.04	0.10	0.11	0.03	-0.21	-0.03	-0.03	-0.22	0.12	0.18		0.23	0.28	1.00	0.60
das28crp_bl	0.02	-0.04	0.29	0.09	-0.10	0.33	0.35	0.23	-0.13	-0.13	0.10	0.06	0.15	-0.02	0.32	-0.24	0.01	-0.13	-0.36	-0.06	-0.03	0.82	0.73	0.60	1.00

Supplementary Figure 8



Supplementary Figure 9



List of genes in Gene Cluster 1	List of genes in Gene Cluster 32	List of genes in Gene Cluster 3
ENSEMBL_ID	ENSEMBL_ID	ENSEMBL_ID
ENSG00000004809	ENSG00000015413	ENSG00000000005
ENSG00000007171	ENSG00000039068	ENSG000000004776
ENSG00000007908	ENSG00000047936	ENSG000000004846
ENSG00000022556	ENSG00000048462	ENSG000000006047
ENSG00000026751	ENSG00000049247	ENSG000000006071
ENSG00000029559	ENSG00000087250	ENSG000000006128
ENSG00000066279	ENSG00000088340	ENSG000000007174
ENSG00000070915	ENSG00000088882	ENSG000000007314
ENSG00000078081	ENSG00000094796	ENSG000000008323
ENSG00000089012	ENSG00000099958	ENSG000000008394
ENSG00000092345	ENSG00000100433	ENSG000000009950
ENSG00000100453	ENSG00000100985	ENSG000000011677
ENSG00000100721	ENSG00000102854	ENSG000000018625
ENSG00000101188	ENSG00000105369	ENSG000000034971
ENSG00000102794	ENSG00000106178	ENSG000000039537
ENSG00000103522	ENSG00000107159	ENSG000000041515
ENSG00000104951	ENSG00000110777	ENSG000000048540
ENSG00000104970	ENSG00000115884	ENSG000000050628
ENSG00000105048	ENSG00000116147	ENSG000000052850
ENSG00000105251	ENSG00000116748	ENSG000000053438
ENSG00000105697	ENSG00000117322	ENSG000000056998
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Enrichment Analysis GC1

GroupID	Category	Term	Description	LogP	Log(q-value)	InTerm_InList
1_Summary	GO Biological Processes	GO:0006954	inflammatory response	-22,16897207	-17,811	33/778
1_Member	GO Biological Processes	GO:0006954	inflammatory response	-22,16897207	-17,811	33/778
1_Member	Reactome Gene Sets	R-HSA-380108	Chemokine receptors bind chemokine	-20,06340417	-16,006	14/59
1_Member	GO Biological Processes	GO:0070098	chemokine-mediated signaling pathway	-19,12385286	-15,243	15/88
1_Member	GO Biological Processes	GO:1990868	response to chemokine	-18,45048132	-14,791	15/97
1_Member	GO Biological Processes	GO:1990869	cellular response to chemokine	-18,45048132	-14,791	15/97
1_Member	GO Biological Processes	GO:1990266	neutrophil migration	-18,34310022	-14,763	16/124
1_Member	GO Biological Processes	GO:0030593	neutrophil chemotaxis	-18,0389791	-14,593	15/103
1_Member	KEGG Pathway	hsa04060	Cytokine-cytokine receptor interaction	-17,99719297	-14,593	20/270
1_Member	KEGG Pathway	ko04060	Cytokine-cytokine receptor interaction	-17,99719297	-14,593	20/270
1_Member	GO Biological Processes	GO:0097530	granulocyte migration	-17,03129341	-13,673	16/149
1_Member	GO Biological Processes	GO:0097529	myeloid leukocyte migration	-16,98564525	-13,669	18/220
1_Member	GO Biological Processes	GO:0071621	granulocyte chemotaxis	-16,78254975	-13,503	15/124
1_Member	GO Biological Processes	GO:0030595	leukocyte chemotaxis	-16,74228854	-13,498	18/227
1_Member	Canonical Pathways	M5885	NABA MATRISOME ASSOCIATION	-16,22593475	-13,014	27/751
1_Member	GO Biological Processes	GO:0060326	cell chemotaxis	-15,65338531	-12,471	19/307
1_Member	GO Biological Processes	GO:0071222	cellular response to lipopolysaccharide	-15,07848045	-11,924	16/197
1_Member	Reactome Gene Sets	R-HSA-375276	Peptide ligand-binding receptor signaling	-14,93979026	-11,812	16/201
1_Member	Canonical Pathways	M5883	NABA SECRETED FACTORS	-14,77008573	-11,667	19/343
1_Member	GO Biological Processes	GO:0002237	response to molecule of bacterial origin	-14,70112125	-11,621	19/346
1_Member	GO Biological Processes	GO:0071219	cellular response to molecule of bacterial origin	-14,67121708	-11,614	16/209
1_Member	KEGG Pathway	hsa04062	Chemokine signaling pathway	-14,25252747	-11,237	15/182
1_Member	KEGG Pathway	ko04062	Chemokine signaling pathway	-14,25252747	-11,237	15/182
1_Member	GO Biological Processes	GO:0032496	response to lipopolysaccharide	-13,9803101	-11,002	18/326
1_Member	GO Biological Processes	GO:0071216	cellular response to biotic stimulus	-13,92817573	-10,968	16/233
1_Member	GO Biological Processes	GO:0050900	leukocyte migration	-13,73335792	-10,822	21/511
1_Member	GO Biological Processes	GO:0009617	response to bacterium	-13,57993454	-10,684	24/728
1_Member	Reactome Gene Sets	R-HSA-373076	Class A/1 (Rhodopsin-like receptor) signaling	-12,62398796	-9,757	17/335
1_Member	WikiPathways	WP5039	SARS-CoV-2 Innate Immunity	-12,21308986	-9,373	10/68
1_Member	Reactome Gene Sets	R-HSA-500792	GPCR ligand binding	-11,33616374	-8,522	18/467
1_Member	GO Biological Processes	GO:0006935	chemotaxis	-10,86420827	-8,062	20/644
1_Member	GO Biological Processes	GO:0042330	taxis	-10,84010029	-8,050	20/646
1_Member	Reactome Gene Sets	R-HSA-418594	G alpha (i) signalling events	-10,72898591	-7,973	15/318
1_Member	Reactome Gene Sets	R-HSA-372790	Signaling by GPCR	-10,17629977	-7,468	20/704
1_Member	GO Biological Processes	GO:0061844	antimicrobial humoral immunity	-10,05971692	-7,364	9/78
1_Member	WikiPathways	WP3929	Chemokine signaling pathway	-9,570236652	-6,893	11/165
1_Member	Reactome Gene Sets	R-HSA-388396	GPCR downstream signalling	-9,234791544	-6,592	18/629
1_Member	GO Biological Processes	GO:0071396	cellular response to lipid	-9,172899562	-6,547	17/556
1_Member	GO Biological Processes	GO:0019730	antimicrobial humoral response	-8,947160812	-6,338	10/143
1_Member	WikiPathways	WP75	Toll-like Receptor Signaling Pathway	-7,583338381	-5,117	8/104
1_Member	KEGG Pathway	hsa04620	Toll-like receptor signaling pathway	-7,583338381	-5,117	8/104
1_Member	KEGG Pathway	ko04620	Toll-like receptor signaling pathway	-7,583338381	-5,117	8/104
1_Member	GO Biological Processes	GO:0006959	humoral immune response	-6,724122571	-4,315	12/382
1_Member	WikiPathways	WP1449	Regulation of toll-like receptor signaling	-6,461618383	-4,081	8/145
2_Summary	KEGG Pathway	ko05323	Rheumatoid arthritis	-14,03094214	-11,034	12/90
2_Member	KEGG Pathway	ko05323	Rheumatoid arthritis	-14,03094214	-11,034	12/90
2_Member	KEGG Pathway	ko04657	IL-17 signaling pathway	-13,85380126	-10,910	12/93
2_Member	KEGG Pathway	hsa04657	IL-17 signaling pathway	-13,73915461	-10,822	12/95
2_Member	KEGG Pathway	hsa05323	Rheumatoid arthritis	-13,51759221	-10,636	12/99
2_Member	WikiPathways	WP4754	IL-18 signaling pathway	-10,39586958	-7,671	14/279
2_Member	Reactome Gene Sets	R-HSA-6783783	Interleukin-10 signaling	-8,736159289	-6,163	7/47
2_Member	Reactome Gene Sets	R-HSA-449147	Signaling by Interleukins	-8,487235253	-5,928	15/462
2_Member	Reactome Gene Sets	R-HSA-1280215	Cytokine Signaling in Immune System	-8,360624167	-5,828	18/715
2_Member	WikiPathways	WP3617	Photodynamic therapy-induced apoptosis	-7,942599457	-5,442	6/35
2_Member	KEGG Pathway	ko04668	TNF signaling pathway	-6,189006535	-3,843	7/108
2_Member	KEGG Pathway	hsa04668	TNF signaling pathway	-6,004155328	-3,683	7/115
2_Member	KEGG Pathway	ko05132	Salmonella infection	-5,562918156	-3,280	6/86
2_Member	WikiPathways	WP3646	Hepatitis C and Hepatocellular carcinoma	-5,491520446	-3,216	5/50
2_Member	KEGG Pathway	hsa05132	Salmonella infection	-5,310569007	-3,053	6/95
2_Member	Canonical Pathways	M166	PID ATF2 PATHWAY	-5,132279201	-2,894	5/59
2_Member	Reactome Gene Sets	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-4,988710118	-2,792	6/108
2_Member	WikiPathways	WP2431	Spinal Cord Injury	-4,727218422	-2,584	6/120
2_Member	Canonical Pathways	M115	PID REG GR PATHWAY	-4,432120164	-2,339	5/82
2_Member	WikiPathways	WP4891	COVID-19 Adverse Outcome Factors	-4,396909669	-2,315	3/15
2_Member	KEGG Pathway	ko05144	Malaria	-4,132975563	-2,101	4/49
2_Member	KEGG Pathway	ko05146	Amoebiasis	-4,103866787	-2,080	5/96
2_Member	WikiPathways	WP4884	Pathogenesis of SARS-CoV-2 Infection	-3,939734606	-1,935	3/21
2_Member	KEGG Pathway	hsa05144	Malaria	-3,935376293	-1,933	4/55
2_Member	KEGG Pathway	hsa05146	Amoebiasis	-3,880801706	-1,884	5/107
2_Member	KEGG Pathway	ko05202	Transcriptional misregulation in cancer	-3,748341866	-1,779	6/180
2_Member	Canonical Pathways	M167	PID AP1 PATHWAY	-3,528709382	-1,598	4/70
2_Member	KEGG Pathway	hsa05202	Transcriptional misregulation in cancer	-3,456256929	-1,536	6/204
2_Member	Canonical Pathways	M65	PID FRA PATHWAY	-3,196221751	-1,311	3/37
2_Member	KEGG Pathway	hsa04621	NOD-like receptor signaling pathway	-2,958796497	-1,129	5/170
2_Member	KEGG Pathway	ko04621	NOD-like receptor signaling pathway	-2,958796497	-1,129	5/170
2_Member	KEGG Pathway	ko05142	Chagas disease (American trypanosomiasis)	-2,911236841	-1,087	4/102
2_Member	KEGG Pathway	hsa05142	Chagas disease (American trypanosomiasis)	-2,834449344	-1,029	4/107
2_Member	WikiPathways	WP615	Senescence and Autophagy in Cancer	-2,819571931	-1,017	4/108
2_Member	KEGG Pathway	ko05134	Legionellosis	-2,693611102	-0,913	3/55
2_Member	KEGG Pathway	hsa05134	Legionellosis	-2,606219889	-0,836	3/59
2_Member	WikiPathways	WP3865	Novel intracellular components of SARS-CoV-2	-2,564905532	-0,801	3/61
2_Member	WikiPathways	WP3624	Lung fibrosis	-2,525039243	-0,772	3/63
2_Member	WikiPathways	WP4329	miRNAs involvement in the inflammatory response	-2,525039243	-0,772	3/63
2_Member	WikiPathways	WP4341	Non-genomic actions of 1,25-dihydroxyvitamin D3	-2,378334616	-0,644	3/71
2_Member	KEGG Pathway	ko05164	Influenza A	-2,089756352	-0,403	4/173
2_Member	KEGG Pathway	hsa05164	Influenza A	-2,014385262	-0,334	4/182
3_Summary	WikiPathways	WP2328	Allograft Rejection	-12,52487854	-9,672	11/89
3_Member	WikiPathways	WP2328	Allograft Rejection	-12,52487854	-9,672	11/89
3_Member	GO Biological Processes	GO:0002694	regulation of leukocyte activation	-9,631558659	-6,945	18/594
3_Member	GO Biological Processes	GO:0050865	regulation of cell activation	-9,191088519	-6,557	18/633
3_Member	GO Biological Processes	GO:1903037	regulation of leukocyte cell-cell interactions	-8,406270418	-5,857	13/330

3_Member	GO Biological Processes	GO:0030155	regulation of cell adhesion	-8,184246147	-5,658	18/734
3_Member	GO Biological Processes	GO:0007159	leukocyte cell-cell adhesion	-7,87101019	-5,376	13/366
3_Member	GO Biological Processes	GO:0022407	regulation of cell-cell adhesion	-7,851299912	-5,362	14/439
3_Member	GO Biological Processes	GO:0050863	regulation of T cell activation	-7,455934852	-4,995	12/327
3_Member	GO Biological Processes	GO:0022409	positive regulation of cell-cell adhesion	-7,236458059	-4,787	11/276
3_Member	GO Biological Processes	GO:0045785	positive regulation of cell adhesion	-7,111898218	-4,673	13/425
3_Member	GO Biological Processes	GO:0051249	regulation of lymphocyte activation	-7,065477446	-4,631	14/508
3_Member	GO Biological Processes	GO:1903039	positive regulation of leukocyte activation	-6,904084131	-4,480	10/234
3_Member	GO Biological Processes	GO:0002696	positive regulation of leukocyte activation	-6,49906188	-4,109	12/401
3_Member	GO Biological Processes	GO:0046649	lymphocyte activation	-6,465405205	-4,081	16/754
3_Member	GO Biological Processes	GO:0050867	positive regulation of cell activation	-6,374342582	-4,007	12/412
3_Member	GO Biological Processes	GO:0050870	positive regulation of T cell activation	-6,239711426	-3,890	9/212
3_Member	GO Biological Processes	GO:0032611	interleukin-1 beta production	-6,161811328	-3,825	7/109
3_Member	Canonical Pathways	M196	PID IL23 PATHWAY	-6,157687634	-3,825	5/37
3_Member	GO Biological Processes	GO:0042110	T cell activation	-5,727990627	-3,423	12/475
3_Member	GO Biological Processes	GO:0043367	CD4-positive, alpha-beta T cell activation	-5,715841509	-3,417	6/81
3_Member	GO Biological Processes	GO:0032612	interleukin-1 production	-5,714205524	-3,417	7/127
3_Member	GO Biological Processes	GO:0032731	positive regulation of interleukin production	-5,245028436	-2,994	5/56
3_Member	GO Biological Processes	GO:0035710	CD4-positive, alpha-beta T cell activation	-5,181390643	-2,940	6/100
3_Member	GO Biological Processes	GO:0032651	regulation of interleukin-1 beta production	-5,083024316	-2,852	6/104
3_Member	GO Biological Processes	GO:0046632	alpha-beta T cell differentiation	-5,011925891	-2,797	6/107
3_Member	GO Biological Processes	GO:0032732	positive regulation of interleukin production	-4,957476728	-2,763	5/64
3_Member	GO Biological Processes	GO:0042129	regulation of T cell proliferation	-4,912383271	-2,724	7/168
3_Member	GO Biological Processes	GO:0002294	CD4-positive, alpha-beta T cell activation	-4,89165374	-2,715	5/66
3_Member	GO Biological Processes	GO:0002287	alpha-beta T cell activation	-4,859547047	-2,694	5/67
3_Member	GO Biological Processes	GO:0002293	alpha-beta T cell differentiation	-4,859547047	-2,694	5/67
3_Member	GO Biological Processes	GO:0032652	regulation of interleukin-1 production	-4,727218422	-2,584	6/120
3_Member	GO Biological Processes	GO:1903131	mononuclear cell differentiation	-4,705262038	-2,564	10/412
3_Member	GO Biological Processes	GO:0002292	T cell differentiation involved in	-4,677194691	-2,542	5/73
3_Member	WikiPathways	WP619	Type II interferon signaling (IFN-γ)	-4,620910155	-2,488	4/37
3_Member	WikiPathways	WP4484	Control of immune tolerance	-4,595664355	-2,467	3/13
3_Member	GO Biological Processes	GO:0002521	leukocyte differentiation	-4,52849378	-2,409	11/526
3_Member	GO Biological Processes	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	-4,524114911	-2,409	7/193
3_Member	GO Biological Processes	GO:0042098	T cell proliferation	-4,481362085	-2,371	7/196
3_Member	GO Biological Processes	GO:0050729	positive regulation of inflammation	-4,474610346	-2,367	6/133
3_Member	KEGG Pathway	hsa05332	Graft-versus-host disease	-4,441374714	-2,343	4/41
3_Member	KEGG Pathway	ko05332	Graft-versus-host disease	-4,441374714	-2,343	4/41
3_Member	GO Biological Processes	GO:0051251	positive regulation of lymphocyte activation	-4,420887352	-2,332	9/356
3_Member	GO Biological Processes	GO:0032642	regulation of chemokine production	-4,260939356	-2,208	5/89
3_Member	GO Biological Processes	GO:0046631	alpha-beta T cell activation	-4,198879192	-2,152	6/149
3_Member	GO Biological Processes	GO:0050670	regulation of lymphocyte proliferation	-4,151663226	-2,111	7/221
3_Member	GO Biological Processes	GO:0032944	regulation of mononuclear cell proliferation	-4,127146337	-2,098	7/223
3_Member	GO Biological Processes	GO:0032602	chemokine production	-4,125523935	-2,098	5/95
3_Member	GO Biological Processes	GO:0070661	leukocyte proliferation	-4,017759845	-2,002	8/313
3_Member	GO Biological Processes	GO:0070663	regulation of leukocyte proliferation	-3,917275036	-1,917	7/241
3_Member	GO Biological Processes	GO:0030217	T cell differentiation	-3,862180247	-1,869	7/246
3_Member	GO Biological Processes	GO:0002286	T cell activation involved in	-3,805885173	-1,824	5/111
3_Member	GO Biological Processes	GO:0032722	positive regulation of chemokine production	-3,78772008	-1,813	4/60
3_Member	GO Biological Processes	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	-3,694269569	-1,730	7/262
3_Member	GO Biological Processes	GO:0042093	T-helper cell differentiation	-3,678872076	-1,720	4/64
3_Member	WikiPathways	WP530	Cytokines and Inflammatory Response	-3,655826002	-1,701	3/26
3_Member	KEGG Pathway	ko05321	Inflammatory bowel disease	-3,652810055	-1,701	4/65
3_Member	GO Biological Processes	GO:0030098	lymphocyte differentiation	-3,619745059	-1,673	8/358
3_Member	KEGG Pathway	hsa05321	Inflammatory bowel disease	-3,601965978	-1,660	4/67
3_Member	GO Biological Processes	GO:0042531	positive regulation of tyrosine phosphorylation	-3,528709382	-1,598	4/70
3_Member	GO Biological Processes	GO:0046651	lymphocyte proliferation	-3,491289389	-1,566	7/283
3_Member	GO Biological Processes	GO:0032943	mononuclear cell proliferation	-3,463749384	-1,542	7/286
3_Member	GO Biological Processes	GO:0002335	mature B cell differentiation	-3,425275553	-1,508	3/31
3_Member	GO Biological Processes	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell activation	-3,383963885	-1,478	3/32
3_Member	GO Biological Processes	GO:0032755	positive regulation of interleukin production	-3,188267444	-1,306	4/86
3_Member	GO Biological Processes	GO:0042509	regulation of tyrosine phosphorylation	-3,188267444	-1,306	4/86
3_Member	GO Biological Processes	GO:0032760	positive regulation of tumor necrosis factor production	-3,169343486	-1,291	4/87
3_Member	KEGG Pathway	hsa05330	Allograft rejection	-3,161944768	-1,288	3/38
3_Member	KEGG Pathway	ko05330	Allograft rejection	-3,161944768	-1,288	3/38
3_Member	GO Biological Processes	GO:0007260	tyrosine phosphorylation of Src family tyrosine kinase	-3,132202831	-1,265	4/89
3_Member	GO Biological Processes	GO:0032660	regulation of interleukin-17 production	-3,128620939	-1,264	3/39
3_Member	GO Biological Processes	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	-3,128620939	-1,264	3/39
3_Member	GO Biological Processes	GO:1903557	positive regulation of tumor necrosis factor production	-3,113975381	-1,251	4/90
3_Member	GO Biological Processes	GO:0032680	regulation of tumor necrosis factor production	-3,07643525	-1,222	5/160
3_Member	GO Biological Processes	GO:0032635	interleukin-6 production	-3,052246197	-1,200	5/162
3_Member	GO Biological Processes	GO:0032640	tumor necrosis factor production	-3,052246197	-1,200	5/162
3_Member	GO Biological Processes	GO:1903555	regulation of tumor necrosis factor production	-3,016595314	-1,173	5/165
3_Member	GO Biological Processes	GO:0032620	interleukin-17 production	-3,003919452	-1,165	3/43
3_Member	KEGG Pathway	hsa04940	Type I diabetes mellitus	-3,003919452	-1,165	3/43
3_Member	KEGG Pathway	ko04940	Type I diabetes mellitus	-3,003919452	-1,165	3/43
3_Member	GO Biological Processes	GO:0007259	receptor signaling pathway via	-2,993237817	-1,156	5/167
3_Member	GO Biological Processes	GO:0071706	tumor necrosis factor superfamily	-2,981679013	-1,146	5/168
3_Member	GO Biological Processes	GO:0150076	neuroinflammatory response	-2,974687448	-1,140	3/44
3_Member	GO Biological Processes	GO:0042102	positive regulation of T cell proliferation	-2,959346103	-1,129	4/99
3_Member	GO Biological Processes	GO:0045619	regulation of lymphocyte differentiation	-2,902918806	-1,081	5/175
3_Member	GO Biological Processes	GO:0097696	receptor signaling pathway via	-2,891963979	-1,074	5/176
3_Member	GO Biological Processes	GO:0051607	defense response to virus	-2,88961552	-1,074	6/262
3_Member	GO Biological Processes	GO:0140546	defense response to symbiont	-2,88961552	-1,074	6/262
3_Member	GO Biological Processes	GO:0009615	response to virus	-2,870342942	-1,057	7/361
3_Member	GO Biological Processes	GO:0046638	positive regulation of alpha-beta T cell activation	-2,838502367	-1,030	3/49
3_Member	KEGG Pathway	ko04659	Th17 cell differentiation	-2,834449344	-1,029	4/107
3_Member	GO Biological Processes	GO:0018108	peptidyl-tyrosine phosphorylation	-2,809386502	-1,009	7/370
3_Member	GO Biological Processes	GO:0018212	peptidyl-tyrosine modification	-2,789477111	-0,991	7/373
3_Member	GO Biological Processes	GO:0043370	regulation of CD4-positive, alpha-beta T cell activation	-2,78817109	-0,991	3/51
3_Member	KEGG Pathway	hsa04659	Th17 cell differentiation	-2,761564432	-0,965	4/112
3_Member	GO Biological Processes	GO:0002285	lymphocyte activation involved in	-2,745759768	-0,951	5/190
3_Member	WikiPathways	WP1533	Vitamin B12 Metabolism	-2,739926588	-0,950	3/53
3_Member	GO Biological Processes	GO:1902105	regulation of leukocyte differentiation	-2,735729982	-0,947	6/281

3_Member	GO Biological Processes	GO:0050671	positive regulation of lympho	-2,467784395	-0,722	4/135
3_Member	GO Biological Processes	GO:0046635	positive regulation of alpha-b	-2,467755841	-0,722	3/66
3_Member	GO Biological Processes	GO:0032946	positive regulation of monon	-2,456326674	-0,712	4/136
3_Member	GO Biological Processes	GO:0046637	regulation of alpha-beta T cel	-2,44929101	-0,707	3/67
3_Member	GO Biological Processes	GO:2000514	regulation of CD4-positive, al	-2,44929101	-0,707	3/67
3_Member	GO Biological Processes	GO:0098586	cellular response to virus	-2,361279706	-0,630	3/72
3_Member	GO Biological Processes	GO:0045580	regulation of T cell differentia	-2,346797471	-0,621	4/146
3_Member	WikiPathways	WP176	Folate Metabolism	-2,344483081	-0,621	3/73
3_Member	GO Biological Processes	GO:0070665	positive regulation of leukocy	-2,325926644	-0,605	4/148
3_Member	GO Biological Processes	GO:1902107	positive regulation of leukocy	-2,24558842	-0,536	4/156
3_Member	GO Biological Processes	GO:1903708	positive regulation of hemopo	-2,24558842	-0,536	4/156
3_Member	KEGG Pathway	hsa04630	Jak-STAT signaling pathway	-2,24558842	-0,536	4/156
3_Member	KEGG Pathway	ko04630	Jak-STAT signaling pathway	-2,24558842	-0,536	4/156
3_Member	GO Biological Processes	GO:0032675	regulation of interleukin-6 pr	-2,226249288	-0,519	4/158
3_Member	WikiPathways	WP4298	Viral Acute Myocarditis	-2,132923087	-0,442	3/87
3_Member	GO Biological Processes	GO:0045582	positive regulation of T cell di	-2,119282982	-0,429	3/88
3_Member	WikiPathways	WP15	Selenium Micronutrient Netw	-2,066403131	-0,382	3/92
4_Summary	GO Biological Processes	GO:0032103	positive regulation of respons	-11,70857086	-8,882	19/509
4_Member	GO Biological Processes	GO:0032103	positive regulation of respons	-11,70857086	-8,882	19/509
4_Member	GO Biological Processes	GO:0031347	regulation of defense respons	-9,379726295	-6,719	19/697
4_Member	GO Biological Processes	GO:0001817	regulation of cytokine produc	-9,377973288	-6,719	20/782
4_Member	GO Biological Processes	GO:0001819	positive regulation of cytokin	-8,814169744	-6,234	15/437
4_Member	GO Biological Processes	GO:0031349	positive regulation of defense	-6,988399357	-4,559	12/361
4_Member	GO Biological Processes	GO:0050727	regulation of inflammatory re	-6,885688361	-4,467	12/369
4_Member	GO Biological Processes	GO:0045088	regulation of innate immune	-6,6587826	-4,255	11/315
4_Member	GO Biological Processes	GO:0050778	positive regulation of immuno	-6,412108344	-4,040	16/761
4_Member	GO Biological Processes	GO:0002831	regulation of response to biot	-6,286048155	-3,928	12/420
4_Member	GO Biological Processes	GO:0002699	positive regulation of immuno	-6,105392995	-3,776	9/220
4_Member	GO Biological Processes	GO:0002833	positive regulation of respons	-5,534659315	-3,255	9/258
4_Member	GO Biological Processes	GO:0045089	positive regulation of innate i	-5,064086511	-2,836	8/223
4_Member	GO Biological Processes	GO:0002697	regulation of immune effecto	-5,004789118	-2,793	11/467
4_Member	GO Biological Processes	GO:0002228	natural killer cell mediated im	-4,827954977	-2,671	5/68
4_Member	GO Biological Processes	GO:0042267	natural killer cell mediated cy	-3,652810055	-1,701	4/65
4_Member	GO Biological Processes	GO:0002705	positive regulation of leukocy	-3,565428811	-1,627	5/125
4_Member	GO Biological Processes	GO:0002717	positive regulation of natural	-3,425275553	-1,508	3/31
4_Member	GO Biological Processes	GO:0002703	regulation of leukocyte medic	-3,400375855	-1,489	6/209
4_Member	GO Biological Processes	GO:0002367	cytokine production involved	-3,043234247	-1,194	4/94
4_Member	GO Biological Processes	GO:0002715	regulation of natural killer cel	-2,864505269	-1,054	3/48
4_Member	GO Biological Processes	GO:0002708	positive regulation of lympho	-2,819571931	-1,017	4/108
4_Member	GO Biological Processes	GO:0002720	positive regulation of cytokin	-2,739926588	-0,950	3/53
4_Member	GO Biological Processes	GO:0002706	regulation of lymphocyte me	-2,235883033	-0,527	4/157
4_Member	GO Biological Processes	GO:0002449	lymphocyte mediated immun	-2,204654616	-0,501	6/361
4_Member	GO Biological Processes	GO:0002718	regulation of cytokine produc	-2,174915173	-0,476	3/84
5_Summary	GO Biological Processes	GO:0055065	metal ion homeostasis	-10,81607824	-8,037	20/648
5_Member	GO Biological Processes	GO:0055065	metal ion homeostasis	-10,81607824	-8,037	20/648
5_Member	GO Biological Processes	GO:0055080	cation homeostasis	-10,77682987	-8,010	21/730
5_Member	GO Biological Processes	GO:0098771	inorganic ion homeostasis	-10,66710585	-7,921	21/740
5_Member	GO Biological Processes	GO:0050801	ion homeostasis	-10,17364775	-7,468	21/787
5_Member	GO Biological Processes	GO:0030003	cellular cation homeostasis	-8,956358102	-6,338	18/655
5_Member	GO Biological Processes	GO:0006875	cellular metal ion homeostasi	-8,941010287	-6,338	17/576
5_Member	GO Biological Processes	GO:0006873	cellular ion homeostasis	-8,821958627	-6,234	18/668
5_Member	GO Biological Processes	GO:0072507	divalent inorganic cation hom	-6,306583331	-3,944	13/500
5_Member	GO Biological Processes	GO:0072503	cellular divalent inorganic cat	-5,671770692	-3,382	12/481
5_Member	GO Biological Processes	GO:0055074	calcium ion homeostasis	-5,110608837	-2,876	11/455
5_Member	GO Biological Processes	GO:0051209	release of sequestered calcium	-4,898146037	-2,715	6/112
5_Member	GO Biological Processes	GO:0007204	positive regulation of cytosoli	-4,892440303	-2,715	9/310
5_Member	GO Biological Processes	GO:0051283	negative regulation of seques	-4,876058749	-2,705	6/113
5_Member	GO Biological Processes	GO:0051282	regulation of sequestering of	-4,832520803	-2,673	6/115
5_Member	GO Biological Processes	GO:0051208	sequestering of calcium ion	-4,747888051	-2,599	6/119
5_Member	GO Biological Processes	GO:0051480	regulation of cytosolic calcium	-4,526850661	-2,409	9/345
5_Member	GO Biological Processes	GO:0051281	positive regulation of release	-4,484430773	-2,372	4/40
5_Member	GO Biological Processes	GO:0097553	calcium ion transmembrane i	-4,456321043	-2,353	6/134
5_Member	GO Biological Processes	GO:0006874	cellular calcium ion homeosta	-4,438137779	-2,342	10/443
5_Member	Canonical Pathways	M222	PID CXCR3 PATHWAY	-4,35856756	-2,288	4/43
5_Member	GO Biological Processes	GO:1904064	positive regulation of cation t	-4,332391431	-2,266	6/141
5_Member	GO Biological Processes	GO:0060402	calcium ion transport into cyt	-4,150862716	-2,111	6/152
5_Member	GO Biological Processes	GO:0010524	positive regulation of calcium	-3,998545529	-1,990	4/53
5_Member	GO Biological Processes	GO:0060401	cytosolic calcium ion transpo	-3,841984798	-1,853	6/173
5_Member	GO Biological Processes	GO:0051928	positive regulation of calcium	-3,681697584	-1,720	5/118
5_Member	GO Biological Processes	GO:1904427	positive regulation of calcium	-3,528709382	-1,598	4/70
5_Member	GO Biological Processes	GO:0034764	positive regulation of transme	-3,422540988	-1,508	6/207
5_Member	GO Biological Processes	GO:0034767	positive regulation of ion tran	-3,422540988	-1,508	6/207
5_Member	GO Biological Processes	GO:0051651	maintenance of location in ce	-3,400375855	-1,489	6/209
5_Member	GO Biological Processes	GO:0051279	regulation of release of seques	-3,391929905	-1,482	4/76
5_Member	GO Biological Processes	GO:0051235	maintenance of location	-3,181852379	-1,301	7/319
5_Member	GO Biological Processes	GO:0098662	inorganic cation transmembr	-3,102422062	-1,241	11/769
5_Member	GO Biological Processes	GO:0043270	positive regulation of ion tran	-3,050696332	-1,200	10/660
5_Member	GO Biological Processes	GO:0010522	regulation of calcium ion tran	-3,026067648	-1,178	4/95
5_Member	GO Biological Processes	GO:1904062	regulation of cation transme	-3,020199847	-1,175	7/340
5_Member	GO Biological Processes	GO:0070588	calcium ion transmembrane t	-2,565515226	-0,801	6/304
5_Member	GO Biological Processes	GO:0006816	calcium ion transport	-2,565234437	-0,801	7/409
5_Member	GO Biological Processes	GO:0034765	regulation of ion transmembr	-2,382196717	-0,646	8/560
5_Member	GO Biological Processes	GO:0034762	regulation of transmembrane	-2,359238872	-0,629	8/565
5_Member	GO Biological Processes	GO:1903169	regulation of calcium ion tran	-2,35735682	-0,628	4/145
5_Member	GO Biological Processes	GO:0051924	regulation of calcium ion tran	-2,326657878	-0,605	5/238
5_Member	GO Biological Processes	GO:0010959	regulation of metal ion transp	-2,259350379	-0,545	5/247
5_Member	GO Biological Processes	GO:0030001	metal ion transport	-2,16103862	-0,466	7/486
6_Summary	GO Biological Processes	GO:0002548	monocyte chemotaxis	-10,55239756	-7,817	9/69
6_Member	GO Biological Processes	GO:0002548	monocyte chemotaxis	-10,55239756	-7,817	9/69
6_Member	GO Biological Processes	GO:0048247	lymphocyte chemotaxis	-9,28235867	-6,632	8/64
6_Member	GO Biological Processes	GO:0071674	mononuclear cell migration	-8,893805943	-6,299	11/191
6_Member	GO Biological Processes	GO:0002685	regulation of leukocyte migra	-8,548079354	-5,982	11/206
6_Member	GO Biological Processes	GO:0002688	regulation of leukocyte chem	-8,402947398	-5,857	9/119

6_Member	GO Biological Processes	GO:0071346	cellular response to interferon	-8,04980082	-5,530	10/177
6_Member	GO Biological Processes	GO:0002690	positive regulation of leukocy	-8,043492911	-5,530	8/91
6_Member	GO Biological Processes	GO:0002687	positive regulation of leukocy	-7,976871042	-5,470	9/133
6_Member	GO Biological Processes	GO:0034341	response to interferon-gamm	-7,606419337	-5,123	10/197
6_Member	GO Biological Processes	GO:0070555	response to interleukin-1	-7,422852285	-4,968	10/206
6_Member	GO Biological Processes	GO:0072676	lymphocyte migration	-7,153053645	-4,708	8/118
6_Member	GO Biological Processes	GO:0071347	cellular response to interleuk	-6,839905451	-4,426	9/180
6_Member	GO Biological Processes	GO:0050921	positive regulation of chemot	-6,602329416	-4,203	8/139
6_Member	GO Biological Processes	GO:0034612	response to tumor necrosis fa	-6,590634587	-4,196	11/320
6_Member	GO Biological Processes	GO:2000403	positive regulation of lympho	-6,157687634	-3,825	5/37
6_Member	GO Biological Processes	GO:0050920	regulation of chemotaxis	-6,040270678	-3,715	9/224
6_Member	GO Biological Processes	GO:0071356	cellular response to tumor ne	-5,968138226	-3,651	10/296
6_Member	GO Biological Processes	GO:1902622	regulation of neutrophil migr	-5,823104845	-3,510	5/43
6_Member	GO Biological Processes	GO:0090023	positive regulation of neutroph	-5,394517027	-3,126	4/24
6_Member	KEGG Pathway	ko04064	NF-kappa B signaling pathway	-5,310569007	-3,053	6/95
6_Member	GO Biological Processes	GO:1901623	regulation of lymphocyte che	-5,249303575	-2,995	4/26
6_Member	GO Biological Processes	GO:0010818	T cell chemotaxis	-5,181196334	-2,940	4/27
6_Member	GO Biological Processes	GO:0071624	positive regulation of granulo	-5,181196334	-2,940	4/27
6_Member	GO Biological Processes	GO:1902624	positive regulation of neutroph	-5,052848373	-2,828	4/29
6_Member	KEGG Pathway	hsa04064	NF-kappa B signaling pathway	-5,011925891	-2,797	6/107
6_Member	GO Biological Processes	GO:2000406	positive regulation of T cell m	-4,992228596	-2,792	4/30
6_Member	GO Biological Processes	GO:0071677	positive regulation of mononu	-4,991227892	-2,792	5/63
6_Member	GO Biological Processes	GO:2000401	regulation of lymphocyte mig	-4,991227892	-2,792	5/63
6_Member	GO Biological Processes	GO:0071675	regulation of mononuclear ce	-4,920450731	-2,729	6/111
6_Member	GO Biological Processes	GO:0072678	T cell migration	-4,89165374	-2,715	5/66
6_Member	GO Biological Processes	GO:0090022	regulation of neutrophil chem	-4,877294423	-2,705	4/32
6_Member	GO Biological Processes	GO:2000404	regulation of T cell migration	-4,358556756	-2,288	4/43
6_Member	GO Biological Processes	GO:0030335	positive regulation of cell mig	-4,353149453	-2,285	11/550
6_Member	GO Biological Processes	GO:0010819	regulation of T cell chemotaxi	-4,308177949	-2,251	3/16
6_Member	GO Biological Processes	GO:2000147	positive regulation of cell mo	-4,187074632	-2,143	11/574
6_Member	GO Biological Processes	GO:0071622	regulation of granulocyte che	-4,132975563	-2,101	4/49
6_Member	GO Biological Processes	GO:0051272	positive regulation of cellular	-4,107269799	-2,081	11/586
6_Member	GO Biological Processes	GO:0040017	positive regulation of locomo	-4,100712513	-2,079	11/587
6_Member	GO Biological Processes	GO:0140131	positive regulation of lympho	-4,005237914	-1,993	3/20
6_Member	GO Biological Processes	GO:0070374	positive regulation of ERK1 ar	-3,346020774	-1,444	6/214
6_Member	GO Biological Processes	GO:0043547	positive regulation of GTPase	-2,553516227	-0,791	7/411
6_Member	GO Biological Processes	GO:0070372	regulation of ERK1 and ERK2 c	-2,544479616	-0,785	6/307
6_Member	GO Biological Processes	GO:0043410	positive regulation of MAPK c	-2,540959385	-0,782	8/527
6_Member	GO Biological Processes	GO:0051345	positive regulation of hydrola	-2,522344354	-0,770	10/779
6_Member	GO Biological Processes	GO:0070371	ERK1 and ERK2 cascade	-2,410451911	-0,672	6/327
6_Member	GO Biological Processes	GO:0043087	regulation of GTPase activity	-2,156354746	-0,463	7/487
7_Summary	GO Biological Processes	GO:0002250	adaptive immune response	-8,379514735	-5,841	18/713
7_Member	GO Biological Processes	GO:0002250	adaptive immune response	-8,379514735	-5,841	18/713
8_Summary	GO Biological Processes	GO:0002274	myeloid leukocyte activation	-6,452431408	-4,076	15/661
8_Member	GO Biological Processes	GO:0002274	myeloid leukocyte activation	-6,452431408	-4,076	15/661
8_Member	GO Biological Processes	GO:0002366	leukocyte activation involved	-4,592196274	-2,467	13/720
8_Member	GO Biological Processes	GO:0002263	cell activation involved in imm	-4,567300553	-2,444	13/724
8_Member	GO Biological Processes	GO:0002275	myeloid cell activation involv	-3,024233429	-1,178	9/550
8_Member	GO Biological Processes	GO:0002444	myeloid leukocyte mediated i	-3,00774189	-1,165	9/553
8_Member	GO Biological Processes	GO:0002446	neutrophil mediated immunit	-2,681012999	-0,901	8/500
8_Member	GO Biological Processes	GO:0042119	neutrophil activation	-2,675650014	-0,898	8/501
8_Member	GO Biological Processes	GO:0036230	granulocyte activation	-2,64904363	-0,876	8/506
9_Summary	KEGG Pathway	ko05143	African trypanosomiasis	-6,282519781	-3,928	5/35
9_Member	KEGG Pathway	ko05143	African trypanosomiasis	-6,282519781	-3,928	5/35
9_Member	KEGG Pathway	hsa05143	African trypanosomiasis	-5,772296061	-3,463	5/44
9_Member	GO Biological Processes	GO:1901606	alpha-amino acid catabolic pr	-4,284476472	-2,229	5/88
9_Member	GO Biological Processes	GO:0009074	aromatic amino acid family ca	-4,005237914	-1,993	3/20
9_Member	GO Biological Processes	GO:0009063	cellular amino acid catabolic p	-3,900014066	-1,901	5/106
9_Member	WikiPathways	WP5044	Kynurenine Pathway and link	-3,818253789	-1,833	3/23
9_Member	GO Biological Processes	GO:0032615	interleukin-12 production	-3,78772008	-1,813	4/60
9_Member	GO Biological Processes	GO:0032655	regulation of interleukin-12 p	-3,78772008	-1,813	4/60
9_Member	GO Biological Processes	GO:0009072	aromatic amino acid family m	-3,383963885	-1,478	3/32
9_Member	GO Biological Processes	GO:0032735	positive regulation of interleu	-3,096200657	-1,240	3/40
9_Member	KEGG Pathway	hsa00380	Tryptophan metabolism	-3,096200657	-1,240	3/40
9_Member	KEGG Pathway	ko00380	Tryptophan metabolism	-3,096200657	-1,240	3/40
9_Member	GO Biological Processes	GO:1901605	alpha-amino acid metabolic p	-2,725898698	-0,940	5/192
9_Member	GO Biological Processes	GO:0046395	carboxylic acid catabolic proc	-2,281451026	-0,566	5/244
9_Member	GO Biological Processes	GO:0016054	organic acid catabolic process	-2,174113241	-0,476	5/259
10_Summary	GO Biological Processes	GO:0001906	cell killing	-5,69744609	-3,404	8/183
10_Member	GO Biological Processes	GO:0001906	cell killing	-5,69744609	-3,404	8/183
10_Member	GO Biological Processes	GO:0001909	leukocyte mediated cytotoxic	-4,854184943	-2,692	6/114
10_Member	GO Biological Processes	GO:0051709	regulation of killing of cells of	-4,308177949	-2,251	3/16
10_Member	GO Biological Processes	GO:0031341	regulation of cell killing	-3,999167377	-1,990	5/101
10_Member	GO Biological Processes	GO:0031640	killing of cells of other organi	-3,601965978	-1,660	4/67
10_Member	GO Biological Processes	GO:0001910	regulation of leukocyte medic	-3,327890249	-1,432	4/79
10_Member	Canonical Pathways	M54	PID IL12 2PATHWAY	-2,544797347	-0,785	3/62
10_Member	GO Biological Processes	GO:0031343	positive regulation of cell killi	-2,525039243	-0,772	3/63
11_Summary	GO Biological Processes	GO:0002683	negative regulation of immu	-5,610980951	-3,324	11/403
11_Member	GO Biological Processes	GO:0002683	negative regulation of immu	-5,610980951	-3,324	11/403
11_Member	GO Biological Processes	GO:0002695	negative regulation of leukoc	-4,687548298	-2,549	7/182
11_Member	GO Biological Processes	GO:0050866	negative regulation of cell act	-4,425496667	-2,334	7/200
11_Member	GO Biological Processes	GO:1903038	negative regulation of leukoc	-4,384648209	-2,305	6/138
11_Member	GO Biological Processes	GO:0051250	negative regulation of lympho	-4,135092427	-2,101	6/153
11_Member	GO Biological Processes	GO:0031295	T cell costimulation	-3,874638893	-1,880	4/57
11_Member	GO Biological Processes	GO:0031294	lymphocyte costimulation	-3,81616084	-1,833	4/59
11_Member	GO Biological Processes	GO:0050868	negative regulation of T cell a	-3,664625119	-1,708	5/119
11_Member	GO Biological Processes	GO:0022408	negative regulation of cell-cel	-3,633854966	-1,684	6/189
11_Member	GO Biological Processes	GO:0042130	negative regulation of T cell p	-3,627179117	-1,679	4/66
11_Member	GO Biological Processes	GO:0007162	negative regulation of cell ad	-3,38314742	-1,478	7/295
11_Member	GO Biological Processes	GO:0050672	negative regulation of lympho	-3,286656527	-1,395	4/81
11_Member	GO Biological Processes	GO:0032945	negative regulation of monor	-3,266455466	-1,376	4/82
11_Member	GO Biological Processes	GO:0045066	regulatory T cell differentiat	-3,231505698	-1,343	3/36
11_Member	GO Biological Processes	GO:0008285	negative regulation of cell po	-3,170373722	-1,297	11/753

11_Member	GO Biological Processes	GO:0070664	negative regulation of leukocyte chemotaxis	-3,150657105	-1,279	4/88
11_Member	WikiPathways	WP4559	Interactions between immune cells	-3,096200657	-1,240	3/40
11_Member	Canonical Pathways	M60	PID NFAT TFPATHWAY	-2,946160747	-1,118	3/45
11_Member	KEGG Pathway	hsa05320	Autoimmune thyroid disease	-2,739926588	-0,950	3/53
11_Member	KEGG Pathway	ko05320	Autoimmune thyroid disease	-2,739926588	-0,950	3/53
11_Member	KEGG Pathway	hsa04514	Cell adhesion molecules (CAMs)	-2,368000336	-0,636	4/144
11_Member	KEGG Pathway	ko04514	Cell adhesion molecules (CAMs)	-2,368000336	-0,636	4/144
12_Summary	GO Biological Processes	GO:0002532	production of molecular mediators	-5,419364654	-3,147	6/91
12_Member	GO Biological Processes	GO:0002532	production of molecular mediators	-5,419364654	-3,147	6/91
12_Member	GO Biological Processes	GO:0042742	defense response to bacterium	-5,341339447	-3,076	10/348
12_Member	KEGG Pathway	ko05133	Pertussis	-4,592019809	-2,467	5/76
12_Member	KEGG Pathway	hsa05133	Pertussis	-4,457868783	-2,353	5/81
12_Member	WikiPathways	WP4136	Fibrin Complement Receptor	-4,399434907	-2,315	4/42
12_Member	GO Biological Processes	GO:1900015	regulation of cytokine production	-3,57715796	-1,637	4/68
12_Member	GO Biological Processes	GO:0002534	cytokine production involved	-3,552742953	-1,616	4/69
12_Member	GO Biological Processes	GO:0050829	defense response to Gram-negative bacterium	-3,150657105	-1,279	4/88
13_Summary	GO Biological Processes	GO:0002526	acute inflammatory response	-5,011925891	-2,797	6/107
13_Member	GO Biological Processes	GO:0002526	acute inflammatory response	-5,011925891	-2,797	6/107
13_Member	GO Biological Processes	GO:0045124	regulation of bone resorption	-4,31868958	-2,255	4/44
13_Member	GO Biological Processes	GO:0034103	regulation of tissue remodeling	-4,308307317	-2,251	5/87
13_Member	GO Biological Processes	GO:0006953	acute-phase response	-4,241802834	-2,191	4/46
13_Member	GO Biological Processes	GO:0046850	regulation of bone remodeling	-4,064339629	-2,046	4/51
13_Member	GO Biological Processes	GO:0042116	macrophage activation	-3,978910846	-1,973	5/102
13_Member	GO Biological Processes	GO:0043030	regulation of macrophage activation	-3,81616084	-1,833	4/59
13_Member	GO Biological Processes	GO:0045453	bone resorption	-3,732345756	-1,767	4/62
13_Member	GO Biological Processes	GO:0046849	bone remodeling	-3,132202831	-1,265	4/89
13_Member	GO Biological Processes	GO:0001894	tissue homeostasis	-2,906590856	-1,083	6/260
13_Member	GO Biological Processes	GO:0048771	tissue remodeling	-2,891963979	-1,074	5/176
13_Member	Canonical Pathways	M183	PID IL6 7 PATHWAY	-2,891098352	-1,074	3/47
13_Member	GO Biological Processes	GO:0002673	regulation of acute inflammation	-2,864505269	-1,054	3/48
13_Member	GO Biological Processes	GO:0046883	regulation of hormone secretion	-2,146770749	-0,455	5/263
13_Member	GO Biological Processes	GO:0048871	multicellular organismal homeostasis	-2,02591921	-0,344	7/516
14_Summary	WikiPathways	WP129	Matrix Metalloproteinases	-4,992228596	-2,792	4/30
14_Member	WikiPathways	WP129	Matrix Metalloproteinases	-4,992228596	-2,792	4/30
14_Member	Reactome Gene Sets	R-HSA-1592389	Activation of Matrix Metalloproteinases	-4,822706053	-2,668	4/33
14_Member	GO Biological Processes	GO:0022617	extracellular matrix disassembly	-4,406711054	-2,320	5/83
14_Member	GO Biological Processes	GO:0030574	collagen catabolic process	-4,204698374	-2,156	4/47
14_Member	GO Biological Processes	GO:0032963	collagen metabolic process	-3,84296411	-1,853	5/109
14_Member	Reactome Gene Sets	R-HSA-1442490	Collagen degradation	-3,678872076	-1,720	4/64
14_Member	Reactome Gene Sets	R-HSA-1474228	Degradation of the extracellular matrix	-3,33904564	-1,439	5/140
14_Member	GO Biological Processes	GO:0030198	extracellular matrix organization	-3,335292241	-1,436	8/395
14_Member	GO Biological Processes	GO:0043062	extracellular structure organization	-3,328062524	-1,432	8/396
14_Member	GO Biological Processes	GO:0045229	external encapsulating structure	-3,313670485	-1,419	8/398
14_Member	Reactome Gene Sets	R-HSA-1474244	Extracellular matrix organization	-2,586807871	-0,818	6/301
14_Member	Reactome Gene Sets	R-HSA-2022090	Assembly of collagen fibrils and fibers	-2,564905532	-0,801	3/61
14_Member	WikiPathways	WP2324	AGE/RAGE pathway	-2,467755841	-0,722	3/66
14_Member	WikiPathways	WP2374	Oncostatin M Signaling Pathway	-2,467755841	-0,722	3/66
14_Member	Canonical Pathways	M3468	NABA ECM REGULATORS	-2,326657878	-0,605	5/238
14_Member	Reactome Gene Sets	R-HSA-1474290	Collagen formation	-2,092514533	-0,404	3/90
15_Summary	GO Biological Processes	GO:0046916	cellular transition metal ion homeostasis	-4,768749716	-2,617	6/118
15_Member	GO Biological Processes	GO:0046916	cellular transition metal ion homeostasis	-4,768749716	-2,617	6/118
15_Member	GO Biological Processes	GO:0055076	transition metal ion homeostasis	-4,367090127	-2,290	6/139
15_Member	GO Biological Processes	GO:0010043	response to zinc ion	-2,649084107	-0,876	3/57
15_Member	GO Biological Processes	GO:0098754	detoxification	-2,433697348	-0,694	4/138
15_Member	GO Biological Processes	GO:0006879	cellular iron ion homeostasis	-2,395655255	-0,658	3/70
15_Member	GO Biological Processes	GO:0055072	iron ion homeostasis	-2,146739107	-0,455	3/86
16_Summary	GO Biological Processes	GO:0032309	icosanoid secretion	-4,358556756	-2,288	4/43
16_Member	GO Biological Processes	GO:0032309	icosanoid secretion	-4,358556756	-2,288	4/43
16_Member	GO Biological Processes	GO:0071715	icosanoid transport	-4,064339629	-2,046	4/51
16_Member	GO Biological Processes	GO:0140353	lipid export from cell	-3,286656527	-1,395	4/81
16_Member	GO Biological Processes	GO:0015718	monocarboxylic acid transport	-2,87026829	-1,057	5/178
16_Member	GO Biological Processes	GO:0010876	lipid localization	-2,628005445	-0,856	8/510
16_Member	GO Biological Processes	GO:0015908	fatty acid transport	-2,305378824	-0,586	4/150
16_Member	GO Biological Processes	GO:0006869	lipid transport	-2,282487432	-0,566	7/461
16_Member	GO Biological Processes	GO:0032370	positive regulation of lipid transport	-2,160735214	-0,466	3/85
16_Member	GO Biological Processes	GO:0046942	carboxylic acid transport	-2,005065669	-0,326	5/285
17_Summary	GO Biological Processes	GO:0002523	leukocyte migration involved	-4,147564784	-2,109	3/18
17_Member	GO Biological Processes	GO:0002523	leukocyte migration involved	-4,147564784	-2,109	3/18
17_Member	GO Biological Processes	GO:1904994	regulation of leukocyte adhesion	-3,196221751	-1,311	3/37
17_Member	GO Biological Processes	GO:0061756	leukocyte adhesion to vascular cells	-2,716536875	-0,933	3/54
18_Summary	GO Biological Processes	GO:0032653	regulation of interleukin-10 production	-3,78772008	-1,813	4/60
18_Member	GO Biological Processes	GO:0032653	regulation of interleukin-10 production	-3,78772008	-1,813	4/60
18_Member	GO Biological Processes	GO:0032613	interleukin-10 production	-3,732345756	-1,767	4/62
18_Member	GO Biological Processes	GO:0032733	positive regulation of interleukin-10 production	-3,161944768	-1,288	3/38
19_Summary	GO Biological Processes	GO:0031334	positive regulation of protein transport	-3,766215578	-1,793	7/255
19_Member	GO Biological Processes	GO:0031334	positive regulation of protein transport	-3,766215578	-1,793	7/255
19_Member	GO Biological Processes	GO:0044089	positive regulation of cellular transport	-2,530963091	-0,774	8/529
19_Member	GO Biological Processes	GO:0043254	regulation of protein-containing complex assembly	-2,34914005	-0,621	7/448
20_Summary	GO Biological Processes	GO:0002407	dendritic cell chemotaxis	-3,761704463	-1,791	3/24
20_Member	GO Biological Processes	GO:0002407	dendritic cell chemotaxis	-3,761704463	-1,791	3/24
20_Member	GO Biological Processes	GO:0036336	dendritic cell migration	-3,512355213	-1,584	3/29
20_Member	GO Biological Processes	GO:2000107	negative regulation of leukocyte chemotaxis	-2,918307599	-1,091	3/46
20_Member	GO Biological Processes	GO:0071887	leukocyte apoptotic process	-2,911236841	-1,087	4/102
20_Member	GO Biological Processes	GO:0043123	positive regulation of I-kappaB activation	-2,827710355	-1,023	5/182
20_Member	GO Biological Processes	GO:0048260	positive regulation of receptor activity	-2,78817109	-0,991	3/51
20_Member	GO Biological Processes	GO:0007249	I-kappaB kinase/NF-kappaB activation	-2,727980937	-0,940	6/282
20_Member	GO Biological Processes	GO:0032874	positive regulation of stress-activated kinase activity	-2,705832229	-0,924	4/116
20_Member	GO Biological Processes	GO:0070304	positive regulation of stress-activated kinase activity	-2,6787698	-0,900	4/118
20_Member	GO Biological Processes	GO:0002573	myeloid leukocyte differentiation	-2,602438078	-0,833	5/205
20_Member	GO Biological Processes	GO:0045860	positive regulation of protein transport	-2,525983745	-0,772	8/530
20_Member	GO Biological Processes	GO:0045859	regulation of protein kinase activity	-2,448361838	-0,707	10/798
20_Member	GO Biological Processes	GO:0043122	regulation of I-kappaB kinase activity	-2,281451026	-0,566	5/244
20_Member	GO Biological Processes	GO:2000106	regulation of leukocyte apoptosis	-2,233574008	-0,525	3/80

20_Member	GO Biological Processes	GO:0033674	positive regulation of kinase i	-2,193372271	-0,492 8/603
20_Member	GO Biological Processes	GO:0046330	positive regulation of JNK cas	-2,17491573	-0,476 3/84
20_Member	GO Biological Processes	GO:0071900	regulation of protein serine/t	-2,110216036	-0,421 7/497
20_Member	GO Biological Processes	GO:0051897	positive regulation of protein	-2,072612237	-0,387 4/175

Enrichment Analysis GC2						
GroupID	Category	Term	Description	LogP	Log(q-value)	InTerm_InList
1_Summary	GO Biological Processes	GO:0006958	complement activation, c	-100	-96,787	90/141
1_Member	GO Biological Processes	GO:0006958	complement activation, c	-100	-96,787	90/141
1_Member	GO Biological Processes	GO:0002455	humoral immune respons	-100	-96,787	90/156
1_Member	GO Biological Processes	GO:0006956	complement activation	-100	-96,787	91/179
1_Member	GO Biological Processes	GO:0016064	immunoglobulin mediate	-100	-96,787	91/223
1_Member	GO Biological Processes	GO:0019724	B cell mediated immunity	-100	-96,787	91/226
1_Member	GO Biological Processes	GO:0006959	humoral immune respons	-100	-96,787	98/382
1_Member	GO Biological Processes	GO:0002449	lymphocyte mediated im	-100	-96,787	91/361
1_Member	GO Biological Processes	GO:0002460	adaptive immune respons	-100	-96,787	91/369
1_Member	GO Biological Processes	GO:0006909	phagocytosis	-100	-96,787	90/382
1_Member	GO Biological Processes	GO:0002429	immune response-activat	-100	-96,787	98/481
1_Member	GO Biological Processes	GO:0002757	immune response-activat	-100	-96,787	98/481
1_Member	GO Biological Processes	GO:0002768	immune response-regulat	-100	-96,787	98/515
1_Member	GO Biological Processes	GO:0002764	immune response-regulat	-100	-96,787	98/518
1_Member	GO Biological Processes	GO:0002250	adaptive immune respons	-100	-96,787	133/713
1_Member	GO Biological Processes	GO:0002253	activation of immune resp	-97,79090591	-94,608	98/573
1_Member	GO Biological Processes	GO:0030449	regulation of complemen	-89,84884899	-86,720	59/116
1_Member	GO Biological Processes	GO:0050853	B cell receptor signaling p	-89,03867904	-85,935	61/134
1_Member	GO Biological Processes	GO:0006910	phagocytosis, recognition	-86,91351701	-83,833	55/98
1_Member	GO Biological Processes	GO:0050778	positive regulation of imm	-86,60132629	-83,543	99/761
1_Member	GO Biological Processes	GO:0006897	endocytosis	-84,10373022	-81,067	94/684
1_Member	GO Biological Processes	GO:0002920	regulation of humoral im	-83,71304977	-80,696	59/139
1_Member	GO Biological Processes	GO:0002431	Fc receptor mediated stim	-80,36111352	-77,382	58/145
1_Member	GO Biological Processes	GO:0002433	immune response-regulat	-79,71180118	-76,767	57/139
1_Member	GO Biological Processes	GO:0038096	Fc-gamma receptor signal	-79,71180118	-76,767	57/139
1_Member	GO Biological Processes	GO:0038094	Fc-gamma receptor signal	-79,4878074	-76,560	57/140
1_Member	GO Biological Processes	GO:0006911	phagocytosis, engulfment	-78,74755288	-75,835	55/126
1_Member	GO Biological Processes	GO:0050871	positive regulation of B ce	-77,35773442	-74,461	57/150
1_Member	GO Biological Processes	GO:0050864	regulation of B cell activat	-77,07765579	-74,195	61/193
1_Member	GO Biological Processes	GO:0099024	plasma membrane invagin	-76,64569023	-73,778	55/135
1_Member	GO Biological Processes	GO:0010324	membrane invagination	-74,92781907	-72,074	55/143
1_Member	GO Biological Processes	GO:0042113	B cell activation	-72,41902202	-69,578	68/326
1_Member	GO Biological Processes	GO:0038095	Fc-epsilon receptor signal	-68,28454393	-65,457	54/169
1_Member	GO Biological Processes	GO:0038093	Fc receptor signaling path	-65,56089345	-62,746	58/239
1_Member	GO Biological Processes	GO:0050851	antigen receptor-mediate	-64,88365949	-62,081	63/323
1_Member	GO Biological Processes	GO:0008037	cell recognition	-62,96777553	-60,177	56/233
1_Member	GO Biological Processes	GO:0050900	leukocyte migration	-59,79962177	-57,020	69/511
1_Member	GO Biological Processes	GO:0042742	defense response to bacte	-56,78916337	-54,021	59/348
1_Member	GO Biological Processes	GO:0006898	receptor-mediated endoc	-56,50682757	-53,749	58/333
1_Member	GO Biological Processes	GO:0002697	regulation of immune effe	-54,31697897	-51,570	63/467
1_Member	GO Biological Processes	GO:0051251	positive regulation of lym	-53,30971878	-50,574	57/356
1_Member	GO Biological Processes	GO:0051249	regulation of lymphocyte	-50,67801869	-47,952	62/508
1_Member	GO Biological Processes	GO:0002696	positive regulation of leu	-50,25865451	-47,543	57/401
1_Member	GO Biological Processes	GO:0050867	positive regulation of cell	-49,57172977	-46,866	57/412
1_Member	GO Biological Processes	GO:0046649	lymphocyte activation	-48,15874149	-45,462	69/754
1_Member	GO Biological Processes	GO:0002694	regulation of leukocyte ac	-47,69513529	-45,008	63/594
1_Member	GO Biological Processes	GO:0050865	regulation of cell activati	-45,97845555	-43,300	63/633
1_Member	GO Biological Processes	GO:0009617	response to bacterium	-43,38499716	-40,716	64/728
2_Summary	GO Biological Processes	GO:0002377	immunoglobulin producti	-96,63845907	-93,483	72/199
2_Member	GO Biological Processes	GO:0002377	immunoglobulin producti	-96,63845907	-93,483	72/199
2_Member	GO Biological Processes	GO:0002440	production of molecular r	-83,15248295	-80,155	72/288
3_Summary	GO Biological Processes	GO:0042100	B cell proliferation	-6,605824311	-3,945	9/96
3_Member	GO Biological Processes	GO:0042100	B cell proliferation	-6,605824311	-3,945	9/96
3_Member	KEGG Pathway	hsa05340	Primary immunodeficien	-4,679845711	-2,036	5/37
3_Member	KEGG Pathway	ko05340	Primary immunodeficien	-4,679845711	-2,036	5/37
3_Member	KEGG Pathway	hsa04672	Intestinal immune netwo	-4,077639165	-1,489	5/49
3_Member	KEGG Pathway	ko04672	Intestinal immune netwo	-4,077639165	-1,489	5/49
3_Member	GO Biological Processes	GO:0050855	regulation of B cell recept	-3,932742805	-1,351	4/28
3_Member	GO Biological Processes	GO:0030888	regulation of B cell prolif	-3,622148608	-1,048	5/61
3_Member	GO Biological Processes	GO:0070661	leukocyte proliferation	-3,187784133	-0,628	10/313
3_Member	GO Biological Processes	GO:0046651	lymphocyte proliferation	-2,907505433	-0,361	9/283
3_Member	GO Biological Processes	GO:0032943	mononuclear cell prolif	-2,875880811	-0,336	9/286
3_Member	GO Biological Processes	GO:0030183	B cell differentiation	-2,781272675	-0,248	6/137
3_Member	KEGG Pathway	hsa04640	Hematopoietic cell lineag	-2,702741406	-0,182	5/97
3_Member	KEGG Pathway	ko04640	Hematopoietic cell lineag	-2,702741406	-0,182	5/97
3_Member	Reactome Gene Sets	R-HSA-983695	Antigen activates B Cell R	-2,51372342	-0,006	3/32
3_Member	GO Biological Processes	GO:0050854	regulation of antigen rece	-2,503813362	-0,002	4/66
3_Member	KEGG Pathway	hsa04662	B cell receptor signaling p	-2,389451367	0,000	4/71
3_Member	KEGG Pathway	ko04662	B cell receptor signaling p	-2,389451367	0,000	4/71
4_Summary	GO Biological Processes	GO:0019731	antibacterial humoral res	-4,660845218	-2,026	6/62
4_Member	GO Biological Processes	GO:0019731	antibacterial humoral res	-4,660845218	-2,026	6/62
4_Member	GO Biological Processes	GO:0019730	antimicrobial humoral res	-4,275038122	-1,648	8/143
4_Member	GO Biological Processes	GO:0060267	positive regulation of resp	-4,217621044	-1,599	3/9
4_Member	GO Biological Processes	GO:0003094	glomerular filtration	-4,205139972	-1,594	4/24
4_Member	GO Biological Processes	GO:0097205	renal filtration	-4,132534825	-1,529	4/25
4_Member	GO Biological Processes	GO:0060263	regulation of respiratory l	-3,414268746	-0,847	3/16
4_Member	GO Biological Processes	GO:0001895	retina homeostasis	-3,076650923	-0,523	5/80
4_Member	GO Biological Processes	GO:0001894	tissue homeostasis	-2,553232194	-0,039	8/260
4_Member	GO Biological Processes	GO:0045730	respiratory burst	-2,367141465	0,000	3/36
5_Summary	GO Biological Processes	GO:0030595	leukocyte chemotaxis	-2,3008245	0,000	7/227
5_Member	GO Biological Processes	GO:0030595	leukocyte chemotaxis	-2,3008245	0,000	7/227
6_Summary	KEGG Pathway	hsa05143	African trypanosomiasis	-2,122025668	0,000	3/44
6_Member	KEGG Pathway	hsa05143	African trypanosomiasis	-2,122025668	0,000	3/44
7_Summary	Reactome Gene Sets	R-HSA-202733	Cell surface interactions a	-2,066631172	0,000	5/137
7_Member	Reactome Gene Sets	R-HSA-202733	Cell surface interactions a	-2,066631172	0,000	5/137

Enrichment Analysis GC3						
GroupID	Category	Term	Description	LogP	Log(q-value)	InTerm_InList
1_Summary	GO Biological Processes	GO:1901615	organic hydroxy compound metabolic process	-9.709573784	-5.350	28/555
1_Member	GO Biological Processes	GO:1901615	organic hydroxy compound metabolic process	-9.709573784	-5.350	28/555
1_Member	GO Biological Processes	GO:0001523	retinoid metabolic process	-9.216121316	-5.265	13/108
1_Member	GO Biological Processes	GO:0016101	diterpenoid metabolic process	-8.920931891	-5.265	13/114
1_Member	GO Biological Processes	GO:0006721	terpenoid metabolic process	-8.466959416	-4.953	13/124
1_Member	GO Biological Processes	GO:0042572	retinol metabolic process	-8.383861175	-4.928	9/47
1_Member	GO Biological Processes	GO:0006066	alcohol metabolic process	-8.23729675	-4.853	21/373
1_Member	GO Biological Processes	GO:0010817	regulation of hormone levels	-7.763926504	-4.565	24/513
1_Member	GO Biological Processes	GO:0006720	isoprenoid metabolic process	-7.711701137	-4.556	13/143
1_Member	GO Biological Processes	GO:0034308	primary alcohol metabolism	-6.708248374	-3.711	10/94
1_Member	GO Biological Processes	GO:0042445	hormone metabolic process	-6.365168331	-3.444	14/218
1_Member	KEGG Pathway	hsa00350	Tyrosine metabolism	-5.4682663	-2.825	6/35
1_Member	KEGG Pathway	ko00350	Tyrosine metabolism	-5.4682663	-2.825	6/35
1_Member	GO Biological Processes	GO:0034754	cellular hormone metabolism	-4.398214824	-2.012	9/136
1_Member	GO Biological Processes	GO:0006069	ethanol oxidation	-3.462353733	-1.346	3/12
1_Member	Reactome Gene Sets	R-HSA-71384	Ethanol oxidation	-3.462353733	-1.346	3/12
1_Member	WikiPathways	WP3925	Amino Acid metabolism	-3.098373174	-1.078	6/91
1_Member	KEGG Pathway	hsa00010	Glycolysis / Gluconeogenesis	-2.901805076	-0.932	5/67
1_Member	KEGG Pathway	ko00010	Glycolysis / Gluconeogenesis	-2.901805076	-0.932	5/67
1_Member	KEGG Pathway	hsa00071	Fatty acid metabolism	-2.726964837	-0.831	4/44
1_Member	KEGG Pathway	ko00071	Fatty acid degradation	-2.726964837	-0.831	4/44
1_Member	GO Biological Processes	GO:0006067	ethanol metabolic process	-2.65575865	-0.795	3/22
1_Member	GO Biological Processes	GO:0042573	retinoic acid metabolic process	-2.148491109	-0.452	3/33
2_Summary	KEGG Pathway	hsa03320	PPAR signaling pathway	-9.015157364	-5.265	11/72
2_Member	KEGG Pathway	hsa03320	PPAR signaling pathway	-9.015157364	-5.265	11/72
2_Member	KEGG Pathway	ko03320	PPAR signaling pathway	-9.015157364	-5.265	11/72
2_Member	WikiPathways	WP3942	PPAR signaling pathway	-6.978441521	-3.941	9/67
2_Member	GO Biological Processes	GO:0048871	multicellular organismal homeostasis	-5.878503661	-3.110	21/516
2_Member	GO Biological Processes	GO:0001659	temperature homeostasis	-4.362854814	-1.986	10/171
2_Member	GO Biological Processes	GO:0106106	cold-induced thermogenesis	-4.204345779	-1.854	9/144
2_Member	GO Biological Processes	GO:0120161	regulation of cold-induced thermogenesis	-4.204345779	-1.854	9/144
2_Member	GO Biological Processes	GO:1990845	adaptive thermogenesis	-4.001433536	-1.715	9/153
2_Member	GO Biological Processes	GO:0120162	positive regulation of cold-induced thermogenesis	-3.772732342	-1.566	7/97
3_Summary	GO Biological Processes	GO:0019432	triglyceride biosynthetic process	-8.846189224	-5.265	9/42
3_Member	GO Biological Processes	GO:0019432	triglyceride biosynthetic process	-8.846189224	-5.265	9/42
3_Member	GO Biological Processes	GO:0006641	triglyceride metabolic process	-8.150010151	-4.853	12/108
3_Member	GO Biological Processes	GO:0046460	neutral lipid biosynthetic process	-8.133053696	-4.853	9/50
3_Member	GO Biological Processes	GO:0046463	acylglycerol biosynthetic process	-8.133053696	-4.853	9/50
3_Member	WikiPathways	WP325	Triacylglyceride Synthesis	-7.7480153	-4.565	7/26
3_Member	GO Biological Processes	GO:0006638	neutral lipid metabolic process	-7.020000268	-3.941	12/136
3_Member	GO Biological Processes	GO:0006639	acylglycerol metabolic process	-7.020000268	-3.941	12/136
3_Member	Reactome Gene Sets	R-HSA-8979227	Triglyceride metabolism	-6.602547499	-3.623	7/37
3_Member	GO Biological Processes	GO:0006651	diacylglycerol biosynthetic process	-5.61605701	-2.919	4/9
3_Member	GO Biological Processes	GO:0006071	glycerol metabolic process	-5.496725348	-2.836	5/20
3_Member	GO Biological Processes	GO:0019400	alditol metabolic process	-5.173008889	-2.575	5/23
3_Member	GO Biological Processes	GO:0046339	diacylglycerol metabolic process	-4.983176856	-2.430	5/25
3_Member	Reactome Gene Sets	R-HSA-75109	Triglyceride biosynthesis	-4.878595015	-2.352	4/13
3_Member	KEGG Pathway	hsa00561	Glycerolipid metabolism	-4.129605015	-1.791	6/59
3_Member	KEGG Pathway	ko00561	Glycerolipid metabolism	-4.129605015	-1.791	6/59
3_Member	GO Biological Processes	GO:0046486	glycerolipid metabolic process	-3.591946317	-1.434	15/433
3_Member	GO Biological Processes	GO:0019751	polyol metabolic process	-3.003054051	-1.005	7/130
3_Member	GO Biological Processes	GO:0055089	fatty acid homeostasis	-2.991547561	-1.005	3/17
3_Member	GO Biological Processes	GO:0045017	glycerolipid biosynthetic process	-2.833100136	-0.902	10/266
3_Member	WikiPathways	WP4722	Glycerolipids and Glycerol	-2.544741876	-0.712	3/24
4_Summary	WikiPathways	WP206	Fatty Acid Omega Oxidation	-7.891559149	-4.646	6/15
4_Member	WikiPathways	WP206	Fatty Acid Omega Oxidation	-7.891559149	-4.646	6/15
4_Member	Reactome Gene Sets	R-HSA-211945	Phase I - Functionalization	-6.216329346	-3.319	10/106
4_Member	KEGG Pathway	hsa00982	Drug metabolism - cytochrome P450	-5.717459192	-2.992	8/70
4_Member	KEGG Pathway	ko00982	Drug metabolism - cytochrome P450	-5.717459192	-2.992	8/70
4_Member	WikiPathways	WP2882	Nuclear Receptors Metabolism	-5.699326784	-2.983	16/322
4_Member	KEGG Pathway	hsa00980	Metabolism of xenobiotics	-5.532306578	-2.854	8/74
4_Member	KEGG Pathway	ko00980	Metabolism of xenobiotics	-5.532306578	-2.854	8/74
4_Member	Reactome Gene Sets	R-HSA-211859	Biological oxidations	-5.506727645	-2.838	13/222
4_Member	KEGG Pathway	ko05204	Chemical carcinogenesis	-5.194511269	-2.583	8/82
4_Member	KEGG Pathway	hsa05204	Chemical carcinogenesis	-4.928982608	-2.382	8/89
4_Member	WikiPathways	WP702	Metapathway biotransformation	-4.81003505	-2.296	11/185
4_Member	KEGG Pathway	hsanan01	drug metabolism	-4.06983489	-1.753	8/117
4_Member	GO Biological Processes	GO:0006805	xenobiotic metabolic process	-3.992592125	-1.712	8/120
4_Member	KEGG Pathway	hsa00830	Retinol metabolism	-3.892503457	-1.640	6/65
4_Member	KEGG Pathway	ko00830	Retinol metabolism	-3.892503457	-1.640	6/65
4_Member	GO Biological Processes	GO:0071466	cellular response to xenobiotic stimulus	-3.868912929	-1.630	8/125
4_Member	GO Biological Processes	GO:0009410	response to xenobiotic stimulus	-3.728218611	-1.536	8/131
4_Member	GO Biological Processes	GO:0001676	long-chain fatty acid metabolism	-3.208485063	-1.167	7/120
4_Member	WikiPathways	WP43	Oxidation by Cytochrome P450	-3.022917089	-1.018	5/63
4_Member	GO Biological Processes	GO:0042493	response to drug	-2.851668315	-0.909	12/359
4_Member	WikiPathways	WP697	Estrogen metabolism	-2.84542875	-0.908	3/19
4_Member	GO Biological Processes	GO:0019373	epoxygenase P450 pathway	-2.77869226	-0.867	3/20
4_Member	WikiPathways	WP691	Tamoxifen metabolism	-2.715587753	-0.827	3/21
4_Member	Reactome Gene Sets	R-HSA-211981	Xenobiotics	-2.493057576	-0.678	3/25
4_Member	GO Biological Processes	GO:0042759	long-chain fatty acid biosynthesis	-2.148491109	-0.452	3/33
4_Member	Reactome Gene Sets	R-HSA-211897	Cytochrome P450 - arrangement	-2.090964615	-0.413	4/66
5_Summary	WikiPathways	WP236	Adipogenesis	-7.200589459	-4.072	12/131
5_Member	WikiPathways	WP236	Adipogenesis	-7.200589459	-4.072	12/131
5_Member	WikiPathways	WP2895	Differentiation of white adipocytes	-4.983176856	-2.430	5/25
5_Member	KEGG Pathway	ko04152	AMPK signaling pathway	-4.830988216	-2.310	9/120
5_Member	GO Biological Processes	GO:0009743	response to carbohydrate	-4.778164414	-2.270	12/222
5_Member	GO Biological Processes	GO:0032870	cellular response to hormone	-4.651034902	-2.179	21/621
5_Member	KEGG Pathway	hsa04152	AMPK signaling pathway	-4.579575939	-2.134	9/129
5_Member	Reactome Gene Sets	R-HSA-381340	Transcriptional regulation	-4.167982466	-1.821	7/84
5_Member	GO Biological Processes	GO:0043434	response to peptide hormone	-4.069673864	-1.753	16/437
5_Member	GO Biological Processes	GO:0034284	response to monosaccharide	-3.850922788	-1.625	10/197

5_Member	WikiPathways	WP1403	AMP-activated Protein Kinase	-3,783289104	-1,570 6/68
5_Member	GO Biological Processes	GO:0009749	response to glucose	-3,368127779	-1,269 9/186
5_Member	GO Biological Processes	GO:0042593	glucose homeostasis	-3,298816459	-1,225 10/231
5_Member	GO Biological Processes	GO:0009746	response to hexose	-3,28468009	-1,219 9/191
5_Member	GO Biological Processes	GO:0033500	carbohydrate homeostasis	-3,284215107	-1,219 10/232
5_Member	GO Biological Processes	GO:0032868	response to insulin	-3,219659325	-1,172 11/280
5_Member	GO Biological Processes	GO:0071375	cellular response to peptide	-3,199806521	-1,161 12/327
5_Member	GO Biological Processes	GO:1901652	response to peptide	-3,174613124	-1,142 16/526
5_Member	GO Biological Processes	GO:1901653	cellular response to peptide	-2,973420462	-0,989 13/396
5_Member	GO Biological Processes	GO:0097305	response to alcohol	-2,668559706	-0,798 9/234
5_Member	WikiPathways	WP3599	Transcription factor regulation	-2,65575865	-0,795 3/22
5_Member	GO Biological Processes	GO:0050873	brown fat cell differentiation	-2,655154727	-0,795 4/46
5_Member	GO Biological Processes	GO:0045471	response to ethanol	-2,363778682	-0,586 6/127
5_Member	GO Biological Processes	GO:0015850	organic hydroxy compound	-2,250641431	-0,517 9/271
5_Member	GO Biological Processes	GO:0032869	cellular response to insulin	-2,192769141	-0,478 8/228
5_Member	GO Biological Processes	GO:0009062	fatty acid catabolic process	-2,044341953	-0,382 5/106
5_Member	GO Biological Processes	GO:0014823	response to activity	-2,024040267	-0,369 4/69
5_Member	KEGG Pathway	hsa04920	Adipocytokine signaling pathway	-2,024040267	-0,369 4/69
5_Member	KEGG Pathway	ko04920	Adipocytokine signaling pathway	-2,024040267	-0,369 4/69
6_Summary	GO Biological Processes	GO:0019216	regulation of lipid metabolism	-6,989046854	-3,941 20/402
6_Member	GO Biological Processes	GO:0019216	regulation of lipid metabolism	-6,989046854	-3,941 20/402
6_Member	GO Biological Processes	GO:0032787	monocarboxylic acid metabolism	-6,498595049	-3,550 25/645
6_Member	GO Biological Processes	GO:0006631	fatty acid metabolic process	-6,49481305	-3,550 19/392
6_Member	GO Biological Processes	GO:0046890	regulation of lipid biosynthesis	-5,938616884	-3,151 13/203
6_Member	GO Biological Processes	GO:0008610	lipid biosynthetic process	-4,567062635	-2,127 23/729
6_Member	Reactome Gene Sets	R-HSA-556833	Metabolism of lipids	-4,466977701	-2,047 23/740
6_Member	GO Biological Processes	GO:0044283	small molecule biosynthesis	-4,43202548	-2,033 22/693
6_Member	GO Biological Processes	GO:0006633	fatty acid biosynthetic process	-4,42816536	-2,033 10/168
6_Member	GO Biological Processes	GO:0008203	cholesterol metabolic process	-4,067399688	-1,753 9/150
6_Member	GO Biological Processes	GO:0072330	monocarboxylic acid biosynthesis	-4,051740781	-1,745 11/224
6_Member	GO Biological Processes	GO:0090181	regulation of cholesterol metabolism	-4,007733695	-1,717 6/62
6_Member	GO Biological Processes	GO:1902625	secondary alcohol metabolism	-3,874184865	-1,630 9/159
6_Member	GO Biological Processes	GO:0016125	sterol metabolic process	-3,733089021	-1,536 9/166
6_Member	GO Biological Processes	GO:0046394	carboxylic acid biosynthesis	-3,188200504	-1,151 12/328
6_Member	GO Biological Processes	GO:0008202	steroid metabolic process	-3,17664428	-1,142 12/329
6_Member	GO Biological Processes	GO:0019218	regulation of steroid metabolism	-3,165741073	-1,138 7/122
6_Member	GO Biological Processes	GO:0016053	organic acid biosynthetic process	-3,097119204	-1,078 12/336
6_Member	GO Biological Processes	GO:0062012	regulation of small molecule metabolism	-3,048734694	-1,036 14/438
6_Member	Reactome Gene Sets	R-HSA-8978868	Fatty acid metabolism	-2,86262765	-0,911 8/177
6_Member	GO Biological Processes	GO:0006637	acyl-CoA metabolic process	-2,776000487	-0,867 6/105
6_Member	GO Biological Processes	GO:0035383	thioester metabolic process	-2,776000487	-0,867 6/105
6_Member	WikiPathways	WP1982	Steroid Regulatory Element	-2,735271955	-0,835 5/73
6_Member	GO Biological Processes	GO:1902930	regulation of alcohol biosynthesis	-2,657991224	-0,795 5/76
6_Member	GO Biological Processes	GO:0045540	regulation of cholesterol metabolism	-2,55393122	-0,714 4/49
6_Member	GO Biological Processes	GO:0106118	regulation of sterol biosynthesis	-2,55393122	-0,714 4/49
6_Member	GO Biological Processes	GO:0009150	purine ribonucleotide metabolism	-2,390191855	-0,605 12/409
6_Member	GO Biological Processes	GO:0050810	regulation of steroid biosynthesis	-2,299920193	-0,545 5/92
6_Member	GO Biological Processes	GO:0009259	ribonucleotide metabolic process	-2,252415376	-0,517 12/426
6_Member	GO Biological Processes	GO:0019693	ribose phosphate metabolism	-2,175341056	-0,466 12/436
6_Member	GO Biological Processes	GO:0033865	nucleoside bisphosphate	-2,160576485	-0,458 6/140
6_Member	GO Biological Processes	GO:0033875	ribonucleoside bisphosphate	-2,160576485	-0,458 6/140
6_Member	GO Biological Processes	GO:0034032	purine nucleoside bisphosphate	-2,160576485	-0,458 6/140
6_Member	GO Biological Processes	GO:0006163	purine nucleotide metabolism	-2,130434822	-0,437 12/442
6_Member	GO Biological Processes	GO:0006694	steroid biosynthetic process	-2,076743638	-0,400 7/191
6_Member	GO Biological Processes	GO:0072521	purine-containing compound	-2,001427097	-0,353 12/460
7_Summary	Canonical Pathways	M5885	NABA MATRISOME ASSOCIATION	-6,870052458	-3,853 28/751
7_Member	Canonical Pathways	M5885	NABA MATRISOME ASSOCIATION	-6,870052458	-3,853 28/751
7_Member	Canonical Pathways	M5883	NABA SECRETED FACTORS	-6,004102496	-3,201 17/343
7_Member	GO Biological Processes	GO:0071363	cellular response to growth factor	-2,267717113	-0,523 17/707
7_Member	GO Biological Processes	GO:0070848	response to growth factor	-2,101591896	-0,420 17/736
7_Member	GO Biological Processes	GO:0090287	regulation of cellular response	-2,002973479	-0,353 9/297
8_Summary	KEGG Pathway	hsa04923	Regulation of lipolysis in adipocytes	-6,355776225	-3,444 8/58
8_Member	KEGG Pathway	hsa04923	Regulation of lipolysis in adipocytes	-6,355776225	-3,444 8/58
8_Member	WikiPathways	WP4746	Thyroid hormones production	-3,000428055	-1,005 6/95
8_Member	Reactome Gene Sets	R-HSA-163560	Triglyceride catabolism	-2,544741876	-0,712 3/24
8_Member	WikiPathways	WP3965	Lipid Metabolism Pathway	-2,307325667	-0,549 3/29
8_Member	WikiPathways	WP4321	Thermogenesis	-2,011299062	-0,358 5/108
9_Summary	KEGG Pathway	hsa04024	cAMP signaling pathway	-6,176586669	-3,294 14/226
9_Member	KEGG Pathway	hsa04024	cAMP signaling pathway	-6,176586669	-3,294 14/226
9_Member	KEGG Pathway	ko04024	cAMP signaling pathway	-6,06061487	-3,201 13/198
9_Member	GO Biological Processes	GO:0050805	negative regulation of synaptic transmission	-3,855458533	-1,625 6/66
9_Member	KEGG Pathway	ko05031	Amphetamine addiction	-3,783289104	-1,570 6/68
9_Member	KEGG Pathway	hsa05031	Amphetamine addiction	-3,679549715	-1,505 6/71
9_Member	KEGG Pathway	ko05030	Cocaine addiction	-3,530257557	-1,391 5/49
9_Member	WikiPathways	WP4222	Phosphodiesterases in neurobiology	-3,331727254	-1,246 5/54
9_Member	KEGG Pathway	hsa05030	Cocaine addiction	-3,294566382	-1,225 5/55
9_Member	Reactome Gene Sets	R-HSA-112316	Neuronal System	-2,838560974	-0,906 13/410
9_Member	WikiPathways	WP2636	Common Pathways Underlying	-2,802627593	-0,878 4/42
9_Member	Reactome Gene Sets	R-HSA-112315	Transmission across Chemical Synapses	-2,785230765	-0,867 10/270
9_Member	Reactome Gene Sets	R-HSA-9620244	Long-term potentiation	-2,544741876	-0,712 3/24
9_Member	GO Biological Processes	GO:0099601	regulation of neurotransmission	-2,536973946	-0,705 5/81
9_Member	Reactome Gene Sets	R-HSA-112314	Neurotransmitter receptors	-2,466831417	-0,657 8/205
9_Member	GO Biological Processes	GO:0035235	ionotropic glutamate receptor activity	-2,396318613	-0,610 3/27
9_Member	KEGG Pathway	ko04728	Dopaminergic synapse	-2,314578797	-0,552 6/130
9_Member	KEGG Pathway	hsa04728	Dopaminergic synapse	-2,282579825	-0,533 6/132
9_Member	GO Biological Processes	GO:0060292	long-term synaptic depression	-2,265389523	-0,523 3/30
9_Member	KEGG Pathway	hsa04720	Long-term potentiation	-2,068256983	-0,395 4/67
9_Member	KEGG Pathway	ko04720	Long-term potentiation	-2,068256983	-0,395 4/67
10_Summary	Reactome Gene Sets	R-HSA-382551	Transport of small molecules	-6,054032981	-3,201 26/729
10_Member	Reactome Gene Sets	R-HSA-382551	Transport of small molecules	-6,054032981	-3,201 26/729
11_Summary	GO Biological Processes	GO:0044057	regulation of system process	-6,039083293	-3,201 23/592
11_Member	GO Biological Processes	GO:0044057	regulation of system process	-6,039083293	-3,201 23/592
11_Member	GO Biological Processes	GO:0007588	excretion	-5,130752116	-2,542 7/60

11_Member	GO Biological Processes	GO:0003012	muscle system process	-4,421366862	-2,030 17/453
11_Member	GO Biological Processes	GO:0045822	negative regulation of he	-3,751704191	-1,551 4/24
11_Member	GO Biological Processes	GO:1903523	negative regulation of blo	-3,680080596	-1,505 4/25
11_Member	GO Biological Processes	GO:0010459	negative regulation of he	-3,583429653	-1,428 3/11
11_Member	GO Biological Processes	GO:0008217	regulation of blood press	-3,525855469	-1,389 9/177
11_Member	GO Biological Processes	GO:0006936	muscle contraction	-3,446954692	-1,336 13/352
11_Member	GO Biological Processes	GO:0003014	renal system process	-3,252115176	-1,199 7/118
11_Member	GO Biological Processes	GO:0003013	circulatory system proces	-2,913577972	-0,938 17/611
11_Member	GO Biological Processes	GO:0006939	smooth muscle contractic	-2,88479263	-0,925 6/100
11_Member	GO Biological Processes	GO:0008015	blood circulation	-2,719972387	-0,827 15/528
11_Member	GO Biological Processes	GO:0055078	sodium ion homeostasis	-2,400243901	-0,610 4/54
11_Member	GO Biological Processes	GO:0006940	regulation of smooth mus	-2,26236422	-0,522 4/59
11_Member	GO Biological Processes	GO:0098801	regulation of renal system	-2,186069515	-0,474 3/32
11_Member	GO Biological Processes	GO:0060047	heart contraction	-2,161104	-0,458 9/280
11_Member	GO Biological Processes	GO:0003015	heart process	-2,066423627	-0,395 9/290
11_Member	GO Biological Processes	GO:1903522	regulation of blood circula	-2,057220542	-0,390 9/291
11_Member	GO Biological Processes	GO:0008016	regulation of heart contra	-2,003948315	-0,353 8/246
12_Summary	GO Biological Processes	GO:0007268	chemical synaptic transm	-6,009540459	-3,201 25/686
12_Member	GO Biological Processes	GO:0007268	chemical synaptic transm	-6,009540459	-3,201 25/686
12_Member	GO Biological Processes	GO:0098916	anterograde trans-synapt	-6,009540459	-3,201 25/686
12_Member	GO Biological Processes	GO:0099537	trans-synaptic signaling	-5,930205781	-3,151 25/693
12_Member	GO Biological Processes	GO:0099536	synaptic signaling	-5,688238702	-2,982 25/715
12_Member	GO Biological Processes	GO:0050804	modulation of chemical s	-4,458731804	-2,044 16/405
12_Member	GO Biological Processes	GO:0099177	regulation of trans-synap	-4,445929591	-2,036 16/406
12_Member	GO Biological Processes	GO:0048167	regulation of synaptic pla	-2,878272636	-0,922 8/176
12_Member	GO Biological Processes	GO:0055080	cation homeostasis	-2,854814235	-0,909 19/730
12_Member	GO Biological Processes	GO:0050801	ion homeostasis	-2,853609601	-0,909 20/787
12_Member	GO Biological Processes	GO:0098771	inorganic ion homeostasi	-2,787733298	-0,867 19/740
12_Member	GO Biological Processes	GO:0050806	positive regulation of syn	-2,746486877	-0,845 7/144
12_Member	GO Biological Processes	GO:0055065	metal ion homeostasis	-2,645584121	-0,789 17/648
12_Member	GO Biological Processes	GO:0051480	regulation of cytosolic cal	-2,501414866	-0,678 11/345
12_Member	GO Biological Processes	GO:0072503	cellular divalent inorganic	-2,249422547	-0,516 13/481
12_Member	GO Biological Processes	GO:0006873	cellular ion homeostasis	-2,149220532	-0,452 16/668
12_Member	GO Biological Processes	GO:0006874	cellular calcium ion home	-2,12304544	-0,431 12/443
12_Member	GO Biological Processes	GO:0072507	divalent inorganic cation	-2,114642832	-0,429 13/500
12_Member	GO Biological Processes	GO:0055074	calcium ion homeostasis	-2,036428224	-0,376 12/455
13_Summary	KEGG Pathway	hsa04080	Neuroactive ligand-recept	-5,837689134	-3,091 15/277
13_Member	KEGG Pathway	hsa04080	Neuroactive ligand-recept	-5,837689134	-3,091 15/277
13_Member	KEGG Pathway	ko04080	Neuroactive ligand-recept	-5,837689134	-3,091 15/277
13_Member	GO Biological Processes	GO:0007218	neuropeptide signaling p	-3,534378654	-1,392 7/106
13_Member	WikiPathways	WP455	GPCRs, Class A Rhodopsin	-2,931897592	-0,953 10/258
13_Member	WikiPathways	WP24	Peptide GPCRs	-2,68334096	-0,807 5/75
13_Member	GO Biological Processes	GO:0007631	feeding behavior	-2,260547279	-0,522 5/94
13_Member	Reactome Gene Sets	R-HSA-373076	Class A/1 (Rhodopsin-like	-2,126514745	-0,434 10/335
13_Member	GO Biological Processes	GO:0007200	phospholipase C-activatin	-2,095412722	-0,415 5/103
13_Member	Reactome Gene Sets	R-HSA-388396	GPCR downstream signal	-2,030467745	-0,371 15/629
14_Summary	GO Biological Processes	GO:0010876	lipid localization	-5,383852111	-2,753 20/510
14_Member	GO Biological Processes	GO:0010876	lipid localization	-5,383852111	-2,753 20/510
14_Member	GO Biological Processes	GO:0051051	negative regulation of tra	-3,020439058	-1,017 14/441
14_Member	GO Biological Processes	GO:0006869	lipid transport	-2,838963457	-0,906 14/461
14_Member	GO Biological Processes	GO:1903792	negative regulation of ani	-2,318835176	-0,552 8/217
14_Member	GO Biological Processes	GO:0032387	negative regulation of int	-2,315804915	-0,552 4/57
14_Member	GO Biological Processes	GO:0043271	negative regulation of ion	-2,260963424	-0,522 10/320
15_Summary	GO Biological Processes	GO:0016042	lipid catabolic process	-5,380335932	-2,753 16/341
15_Member	GO Biological Processes	GO:0016042	lipid catabolic process	-5,380335932	-2,753 16/341
15_Member	GO Biological Processes	GO:0019433	triglyceride catabolic pro	-5,25073195	-2,632 6/38
15_Member	GO Biological Processes	GO:0019915	lipid storage	-5,077593406	-2,496 8/85
15_Member	GO Biological Processes	GO:0046461	neutral lipid catabolic pro	-4,646528958	-2,179 6/48
15_Member	GO Biological Processes	GO:0046464	acylglycerol catabolic pro	-4,646528958	-2,179 6/48
15_Member	GO Biological Processes	GO:0010883	regulation of lipid storage	-4,258845365	-1,899 6/56
15_Member	GO Biological Processes	GO:1905952	regulation of lipid localiza	-3,998908664	-1,715 10/189
15_Member	GO Biological Processes	GO:0010890	positive regulation of seq	-3,868901911	-1,630 3/9
15_Member	GO Biological Processes	GO:0046503	glycerolipid catabolic pro	-3,580814127	-1,428 6/74
15_Member	GO Biological Processes	GO:0034389	lipid droplet organization	-3,546083431	-1,402 4/27
15_Member	GO Biological Processes	GO:0010884	positive regulation of lipic	-3,483228945	-1,354 4/28
15_Member	GO Biological Processes	GO:0044242	cellular lipid catabolic pro	-3,298816459	-1,225 10/231
15_Member	GO Biological Processes	GO:0010889	regulation of sequesterin	-3,251393874	-1,199 3/14
15_Member	GO Biological Processes	GO:0030730	sequestering of triglyceric	-2,991547561	-1,005 3/17
15_Member	GO Biological Processes	GO:0045833	negative regulation of lipi	-2,88479263	-0,925 6/100
15_Member	GO Biological Processes	GO:0051235	maintenance of location	-2,763514277	-0,859 11/319
15_Member	GO Biological Processes	GO:1905954	positive regulation of lipic	-2,653566831	-0,795 6/111
15_Member	GO Biological Processes	GO:0050995	negative regulation of lipi	-2,493057576	-0,678 3/25
15_Member	GO Biological Processes	GO:0050994	regulation of lipid catabol	-2,236439834	-0,509 4/60
15_Member	WikiPathways	WP143	Fatty Acid Beta Oxidation	-2,112185798	-0,429 3/34
16_Summary	GO Biological Processes	GO:0005975	carbohydrate metabolic p	-5,17051149	-2,575 22/620
16_Member	GO Biological Processes	GO:0005975	carbohydrate metabolic p	-5,17051149	-2,575 22/620
16_Member	GO Biological Processes	GO:0016051	carbohydrate biosynthesi	-5,020060544	-2,446 12/210
16_Member	GO Biological Processes	GO:0006094	gluconeogenesis	-4,039061693	-1,740 7/88
16_Member	GO Biological Processes	GO:0019319	hexose biosynthetic proce	-3,946827812	-1,681 7/91
16_Member	GO Biological Processes	GO:0046364	monosaccharide biosynth	-3,772732342	-1,566 7/97
16_Member	GO Biological Processes	GO:0044262	cellular carbohydrate met	-3,681120352	-1,505 12/289
16_Member	GO Biological Processes	GO:0019318	hexose metabolic process	-3,634638533	-1,466 11/250
16_Member	GO Biological Processes	GO:0006006	glucose metabolic process	-3,626147197	-1,460 10/210
16_Member	GO Biological Processes	GO:0062013	positive regulation of sma	-3,510474346	-1,376 8/141
16_Member	GO Biological Processes	GO:0045913	positive regulation of carl	-3,456243912	-1,342 6/78
16_Member	GO Biological Processes	GO:0005996	monosaccharide metabol	-3,324231005	-1,241 11/272
16_Member	GO Biological Processes	GO:0051591	response to cAMP	-3,024441439	-1,018 6/94
16_Member	GO Biological Processes	GO:0045821	positive regulation of glyc	-2,544741876	-0,712 3/24
16_Member	GO Biological Processes	GO:0006109	regulation of carbohydrat	-2,454050924	-0,647 8/206
16_Member	GO Biological Processes	GO:0046683	response to organophosph	-2,298500896	-0,544 6/131
16_Member	GO Biological Processes	GO:0043255	regulation of carbohydrat	-2,222196201	-0,503 5/96
16_Member	GO Biological Processes	GO:0010675	regulation of cellular carb	-2,102926717	-0,420 6/144
16_Member	GO Biological Processes	GO:0014074	response to purine-contai	-2,088841749	-0,412 6/145

17_Summary	GO Biological Processes	GO:0007610	behavior	-4,983847402	-2,430	20/543
17_Member	GO Biological Processes	GO:0007610	behavior	-4,983847402	-2,430	20/543
17_Member	GO Biological Processes	GO:0007616	long-term memory	-4,434347543	-2,033	5/32
17_Member	GO Biological Processes	GO:0007613	memory	-4,345605546	-1,973	8/107
17_Member	GO Biological Processes	GO:0007614	short-term memory	-4,041123598	-1,740	3/8
17_Member	GO Biological Processes	GO:0050890	cognition	-3,271427554	-1,209	11/276
17_Member	GO Biological Processes	GO:0007611	learning or memory	-3,24090916	-1,191	10/235
17_Member	GO Biological Processes	GO:0014072	response to isoquinoline	-2,307325667	-0,549	3/29
17_Member	GO Biological Processes	GO:0043278	response to morphine	-2,307325667	-0,549	3/29
17_Member	GO Biological Processes	GO:0008306	associative learning	-2,045952905	-0,382	4/68
18_Summary	GO Biological Processes	GO:0098656	anion transmembrane tra	-4,914812393	-2,375	20/549
18_Member	GO Biological Processes	GO:0098656	anion transmembrane tra	-4,914812393	-2,375	20/549
18_Member	GO Biological Processes	GO:0046323	glucose import	-4,524544504	-2,089	7/74
18_Member	GO Biological Processes	GO:0072073	kidney epithelium develo	-3,728218611	-1,536	8/131
18_Member	GO Biological Processes	GO:1904659	glucose transmembrane t	-3,436147654	-1,330	7/110
18_Member	GO Biological Processes	GO:0008645	hexose transmembrane t	-3,388643213	-1,287	7/112
18_Member	GO Biological Processes	GO:0008643	carbohydrate transport	-3,349635628	-1,255	8/149
18_Member	GO Biological Processes	GO:0015749	monosaccharide transme	-3,342160431	-1,252	7/114
18_Member	GO Biological Processes	GO:0001656	metanephros developme	-3,338994265	-1,251	6/82
18_Member	GO Biological Processes	GO:0034219	carbohydrate transmembr	-3,296662658	-1,225	7/116
18_Member	GO Biological Processes	GO:0046324	regulation of glucose imp	-3,153381629	-1,128	5/59
18_Member	GO Biological Processes	GO:0046326	positive regulation of gluc	-2,967141966	-0,984	4/38
18_Member	GO Biological Processes	GO:0034765	regulation of ion transme	-2,890884682	-0,925	16/560
18_Member	GO Biological Processes	GO:0034762	regulation of transmembr	-2,851441773	-0,909	16/565
18_Member	GO Biological Processes	GO:0072009	nephron epithelium deve	-2,755003899	-0,852	6/106
18_Member	GO Biological Processes	GO:0010828	positive regulation of gluc	-2,690600563	-0,811	4/45
18_Member	GO Biological Processes	GO:1903959	regulation of anion transr	-2,653566831	-0,795	6/111
18_Member	GO Biological Processes	GO:0010827	regulation of glucose tran	-2,633037219	-0,777	5/77
18_Member	GO Biological Processes	GO:0072001	renal system developmen	-2,570730274	-0,726	10/289
18_Member	GO Biological Processes	GO:0072202	cell differentiation involv	-2,493057576	-0,678	3/25
18_Member	GO Biological Processes	GO:0061326	renal tubule developmen	-2,340361173	-0,569	5/90
18_Member	GO Biological Processes	GO:0061005	cell differentiation involv	-2,288812975	-0,538	4/58
18_Member	GO Biological Processes	GO:0001655	urogenital system develop	-2,251708515	-0,517	10/321
18_Member	GO Biological Processes	GO:1903961	positive regulation of anik	-2,211021959	-0,495	4/61
18_Member	GO Biological Processes	GO:0072006	nephron development	-2,175326024	-0,466	6/139
19_Summary	WikiPathways	WP2881	Estrogen Receptor Pathw	-4,878595015	-2,352	4/13
19_Member	WikiPathways	WP2881	Estrogen Receptor Pathw	-4,878595015	-2,352	4/13
19_Member	GO Biological Processes	GO:0070365	hepatocyte differentiation	-3,072016988	-1,057	3/16
19_Member	KEGG Pathway	hsa04964	Proximal tubule bicarbon	-2,598898475	-0,751	3/23
19_Member	KEGG Pathway	ko04964	Proximal tubule bicarbon	-2,598898475	-0,751	3/23
20_Summary	GO Biological Processes	GO:0051932	synaptic transmission, GA	-4,755106123	-2,253	6/46
20_Member	GO Biological Processes	GO:0051932	synaptic transmission, GA	-4,755106123	-2,253	6/46
20_Member	GO Biological Processes	GO:0002675	positive regulation of acu	-2,396318613	-0,610	3/27
20_Member	GO Biological Processes	GO:0032228	regulation of synaptic tra	-2,225004856	-0,503	3/31

Genes with expression correlated with SJC28 at baseline

ENSEMBL [variables]	FDR-adjusted q-value
ENSG00000002549	0.00414919475561402
ENSG00000004468	0.004248047418364367
ENSG00000005844	0.004080585840262999
ENSG00000006555	0.004080585840262999
ENSG00000007968	0.0039147146522488605
ENSG00000009790	0.0041266177632112615
ENSG00000010803	0.004169010830118809
ENSG00000012171	0.0039147146522488605
ENSG00000012822	0.0039147146522488605
ENSG00000013725	0.004080585840262999
ENSG00000013810	0.004258459988454249
ENSG00000019144	0.00464319485595346
ENSG00000020633	0.0039147146522488605
ENSG00000023445	0.004248047418364367
ENSG00000023892	0.0039147146522488605
ENSG00000023902	0.004248047418364367
ENSG00000028116	0.004080585840262999
ENSG00000030110	0.004080585840262999
ENSG00000035141	0.004610758843514008
ENSG00000042088	0.004080585840262999
ENSG00000048140	0.0043136902499363436
ENSG00000049768	0.004372319581974301
ENSG00000049769	0.004169010830118809
ENSG00000051341	0.004248047418364367
ENSG00000054967	0.004851884001031491
ENSG00000060656	0.00409451459487538
ENSG00000063978	0.004258459988454249
ENSG00000064012	0.004080585840262999
ENSG00000065328	0.004080585840262999
ENSG00000065675	0.004080585840262999
ENSG00000065717	0.0039147146522488605
ENSG00000065923	0.004258459988454249
ENSG00000066382	0.004080585840262999
ENSG00000068489	0.004080585840262999
ENSG00000070190	0.0039147146522488605
ENSG00000072786	0.004248047418364367
ENSG00000072832	0.004080585840262999
ENSG00000073614	0.004610758843514008
ENSG00000073861	0.004258459988454249
ENSG00000074706	0.004633085620710771
ENSG00000075702	0.0039147146522488605
ENSG00000075884	0.004258524485784959
ENSG00000076641	0.0039147146522488605
ENSG00000077152	0.00495505112699003
ENSG00000077942	0.004248047418364367
ENSG00000078081	0.004080585840262999
ENSG00000078246	0.0039147146522488605

ENSG00000078295	0.004248047418364367
ENSG00000078589	0.004248047418364367
ENSG00000079337	0.004080585840262999
ENSG00000080839	0.0039147146522488605
ENSG00000080986	0.0039147146522488605
ENSG00000081237	0.0039147146522488605
ENSG00000081818	0.00495505112699003
ENSG00000083799	0.00393958538218559
ENSG00000084090	0.0039147146522488605
ENSG00000084764	0.0039147146522488605
ENSG00000085840	0.0043136902499363436
ENSG00000087586	0.00396897380222318
ENSG00000088280	0.004248047418364367
ENSG00000088876	0.0043136902499363436
ENSG00000088888	0.0039147146522488605
ENSG00000089094	0.0043136902499363436
ENSG00000089639	0.004372319581974301
ENSG00000090382	0.004080585840262999
ENSG00000092096	0.004248047418364367
ENSG00000092470	0.00484823766791225
ENSG00000092607	0.00475540639524063
ENSG00000092853	0.00464319485595346
ENSG00000093009	0.004080585840262999
ENSG00000095066	0.00484823766791225
ENSG00000096996	0.004169010830118809
ENSG00000100297	0.004248047418364367
ENSG00000100385	0.0039147146522488605
ENSG00000100453	0.004169010830118809
ENSG00000100749	0.00025995469911404927
ENSG00000100842	0.0039147146522488605
ENSG00000101057	0.004896518635144914
ENSG00000101082	0.0039147146522488605
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ENSG00000272506	0.0045830727819521164
ENSG00000272674	0.004372319581974301
ENSG00000272692	0.0039147146522488605
ENSG00000272797	0.004248047418364367
ENSG00000273729	0.004080585840262999
ENSG00000275004	0.004248047418364367
ENSG00000275302	0.00495505112699003
ENSG00000275791	0.00484823766791225
ENSG00000276223	0.004093168047804151
ENSG00000276293	0.0039147146522488605
ENSG00000276557	0.0039147146522488605
ENSG00000277559	0.004080585840262999
ENSG00000278071	0.004276992175209103
ENSG00000279275	0.004080585840262999
ENSG00000280332	0.004258459988454249
ENSG00000281103	0.0039147146522488605
ENSG00000282556	0.004080585840262999
ENSG00000282939	0.0039147146522488605
ENSG00000283063	0.004258459988454249
ENSG00000284681	0.004248047418364367
ENSG00000284954	0.004248047418364367
ENSG00000285804	0.004248047418364367
[variables end]	

Genes enriched in PtC1 (Top 500 based on q-value)			Genes enriched in PtC2 (Top 500 based on q-value)	
ENSEMBL	p-value	q-value	ENSEMBL	p-value
ENSG00000134028	8,87E-24	5,21E-19	ENSG00000040204	1,14E-21
ENSG00000181847	9,40E-22	2,23E-17	ENSG00000150001	1,14E-21
ENSG00000143851	1,14E-21	2,23E-17	ENSG00000027007	1,14E-21
ENSG00000161405	3,06E-21	4,24E-17	ENSG00000019009	1,14E-21
ENSG00000026751	3,61E-21	4,24E-17	ENSG00000160001	1,14E-21
ENSG00000135925	1,88E-20	1,81E-16	ENSG00000027007	1,14E-21
ENSG00000156234	2,15E-20	1,81E-16	ENSG00000010000	1,14E-21
ENSG00000117215	5,38E-20	3,94E-16	ENSG00000012002	1,14E-21
ENSG00000109943	6,03E-20	3,94E-16	ENSG00000006006	1,14E-21
ENSG00000117090	7,74E-20	4,55E-16	ENSG00000018008	1,14E-21
ENSG00000132182	1,00E-19	5,35E-16	ENSG00000012002	1,14E-21
ENSG00000162739	1,33E-19	6,51E-16	ENSG00000014004	1,14E-21
ENSG00000160185	1,54E-19	6,95E-16	ENSG00000013003	1,14E-21
ENSG00000269404	1,91E-19	8,01E-16	ENSG00000016006	1,14E-21
ENSG00000042980	2,41E-19	9,04E-16	ENSG00000010000	1,14E-21
ENSG00000103522	2,46E-19	9,04E-16	ENSG00000010000	1,14E-21
ENSG00000211964	2,74E-19	9,47E-16	ENSG00000007007	1,14E-21
ENSG00000124203	2,97E-19	9,68E-16	ENSG00000017009	1,14E-21
ENSG00000183813	3,69E-19	1,14E-15	ENSG00000017009	1,14E-21
ENSG00000100385	4,22E-19	1,24E-15	ENSG00000019009	1,14E-21
ENSG00000135127	5,16E-19	1,39E-15	ENSG00000029009	1,14E-21
ENSG00000172215	5,21E-19	1,39E-15	ENSG00000026006	1,14E-21
ENSG00000150337	5,78E-19	1,48E-15	ENSG00000011001	1,14E-21
ENSG00000211943	6,87E-19	1,67E-15	ENSG00000012002	1,14E-21
ENSG00000158714	7,22E-19	1,67E-15	ENSG00000017009	1,14E-21
ENSG00000188042	7,40E-19	1,67E-15	ENSG00000001000	1,14E-21
ENSG00000225783	8,92E-19	1,94E-15	ENSG00000029009	1,14E-21
ENSG00000089012	1,15E-18	2,42E-15	ENSG00000028008	1,14E-21
ENSG00000211956	1,23E-18	2,48E-15	ENSG00000010000	1,14E-21
ENSG00000285417	1,55E-18	3,03E-15	ENSG00000021001	1,14E-21
ENSG00000147138	1,77E-18	3,29E-15	ENSG00000011001	1,14E-21
ENSG00000163599	1,79E-18	3,29E-15	ENSG00000018008	1,14E-21
ENSG00000006555	1,90E-18	3,33E-15	ENSG00000012002	1,14E-21
ENSG00000155307	1,93E-18	3,33E-15	ENSG00000001000	1,14E-21
ENSG00000178199	2,27E-18	3,81E-15	ENSG00000014004	1,14E-21
ENSG00000186810	2,70E-18	4,40E-15	ENSG00000018008	1,14E-21
ENSG00000158050	3,36E-18	5,34E-15	ENSG00000014004	1,14E-21
ENSG00000172578	3,54E-18	5,42E-15	ENSG00000012002	1,14E-21
ENSG00000177272	3,60E-18	5,42E-15	ENSG00000001000	1,14E-21
ENSG00000103257	3,87E-18	5,69E-15	ENSG00000007007	1,14E-21
ENSG00000113088	4,24E-18	6,08E-15	ENSG00000001000	1,14E-21
ENSG00000027869	4,48E-18	6,27E-15	ENSG00000016006	1,14E-21
ENSG00000278030	5,47E-18	7,47E-15	ENSG00000028008	1,14E-21
ENSG00000163508	5,86E-18	7,82E-15	ENSG00000016006	1,14E-21

ENSG00000211666	6,29E-18	8,20E-15	ENSG0000016
ENSG00000162676	8,02E-18	1,02E-14	ENSG0000018
ENSG00000116824	8,93E-18	1,10E-14	ENSG0000007
ENSG00000105122	8,95E-18	1,10E-14	ENSG0000018
ENSG00000091490	9,67E-18	1,16E-14	ENSG0000013
ENSG00000163600	1,09E-17	1,28E-14	ENSG0000017
ENSG00000122224	1,13E-17	1,30E-14	ENSG0000016
ENSG00000167208	1,17E-17	1,32E-14	ENSG0000008
ENSG00000198851	1,60E-17	1,78E-14	ENSG0000014
ENSG00000128165	1,67E-17	1,81E-14	ENSG0000012
ENSG00000188389	1,91E-17	2,04E-14	ENSG0000010
ENSG00000117009	1,98E-17	2,08E-14	ENSG0000011
ENSG00000147570	2,28E-17	2,35E-14	ENSG0000016
ENSG00000146232	2,35E-17	2,38E-14	ENSG0000017
ENSG00000133805	2,83E-17	2,71E-14	ENSG0000010
ENSG00000105639	2,87E-17	2,71E-14	ENSG0000016
ENSG00000005844	2,89E-17	2,71E-14	ENSG0000014
ENSG00000224557	2,89E-17	2,71E-14	ENSG0000026
ENSG00000186891	2,91E-17	2,71E-14	ENSG0000016
ENSG00000078081	3,05E-17	2,80E-14	ENSG0000027
ENSG00000115232	3,15E-17	2,85E-14	ENSG0000017
ENSG00000113263	3,52E-17	3,13E-14	ENSG0000007
ENSG00000127152	3,70E-17	3,25E-14	ENSG0000017
ENSG00000168421	3,91E-17	3,37E-14	ENSG0000017
ENSG00000197471	4,18E-17	3,56E-14	ENSG0000016
ENSG00000159618	4,40E-17	3,69E-14	ENSG0000011
ENSG00000211597	4,55E-17	3,76E-14	ENSG0000016
ENSG00000156127	4,62E-17	3,77E-14	ENSG0000013
ENSG00000204252	4,70E-17	3,78E-14	ENSG0000019
ENSG00000124508	5,08E-17	4,03E-14	ENSG0000014
ENSG00000153563	5,21E-17	4,05E-14	ENSG0000016
ENSG00000196735	5,24E-17	4,05E-14	ENSG0000000
ENSG00000110448	5,40E-17	4,12E-14	ENSG0000025
ENSG00000188263	5,47E-17	4,12E-14	ENSG0000016
ENSG00000139626	5,56E-17	4,14E-14	ENSG0000009
ENSG00000169442	5,80E-17	4,26E-14	ENSG0000016
ENSG00000211598	6,03E-17	4,37E-14	ENSG0000016
ENSG00000160791	6,11E-17	4,38E-14	ENSG0000024
ENSG00000188452	6,25E-17	4,42E-14	ENSG0000009
ENSG00000163568	6,85E-17	4,79E-14	ENSG0000010
ENSG00000211787	7,36E-17	5,09E-14	ENSG0000009
ENSG00000205744	7,76E-17	5,30E-14	ENSG0000018
ENSG00000122122	8,66E-17	5,85E-14	ENSG0000027
ENSG00000164430	1,02E-16	6,81E-14	ENSG0000008
ENSG00000143297	1,10E-16	7,25E-14	ENSG0000015
ENSG00000231389	1,15E-16	7,51E-14	ENSG0000012

ENSG00000159753	1,22E-16	7,85E-14	ENSG0000014
ENSG00000164483	1,40E-16	8,94E-14	ENSG0000011
ENSG00000182866	1,49E-16	9,34E-14	ENSG0000023
ENSG00000093072	1,50E-16	9,34E-14	ENSG0000027
ENSG00000121966	1,51E-16	9,34E-14	ENSG0000008
ENSG00000125354	1,58E-16	9,65E-14	ENSG0000016
ENSG00000147168	1,62E-16	9,73E-14	ENSG0000013
ENSG00000159166	1,64E-16	9,73E-14	ENSG0000027
ENSG00000186265	1,66E-16	9,73E-14	ENSG0000014
ENSG00000242534	1,67E-16	9,73E-14	ENSG0000002
ENSG00000172575	1,69E-16	9,73E-14	ENSG0000014
ENSG00000224650	1,70E-16	9,73E-14	ENSG0000015
ENSG00000173578	1,71E-16	9,73E-14	ENSG0000014
ENSG00000223865	1,78E-16	1,01E-13	ENSG0000008
ENSG00000266088	1,92E-16	1,07E-13	ENSG0000018
ENSG00000204287	1,95E-16	1,08E-13	ENSG0000016
ENSG00000197299	2,00E-16	1,10E-13	ENSG0000015
ENSG00000248099	2,18E-16	1,18E-13	ENSG0000014
ENSG00000167286	2,19E-16	1,18E-13	ENSG0000016
ENSG00000263528	2,22E-16	1,19E-13	ENSG0000018
ENSG00000211752	2,52E-16	1,33E-13	ENSG0000011
ENSG00000145649	2,58E-16	1,35E-13	ENSG0000022
ENSG00000110777	2,60E-16	1,35E-13	ENSG0000022
ENSG00000076641	2,65E-16	1,37E-13	ENSG0000022
ENSG00000185101	2,78E-16	1,41E-13	ENSG0000018
ENSG00000078589	2,79E-16	1,41E-13	ENSG0000017
ENSG00000211897	2,81E-16	1,41E-13	ENSG0000012
ENSG00000168685	2,83E-16	1,41E-13	ENSG0000010
ENSG00000123610	3,18E-16	1,57E-13	ENSG0000008
ENSG00000135838	3,44E-16	1,67E-13	ENSG0000021
ENSG00000211772	3,44E-16	1,67E-13	ENSG0000016
ENSG00000171792	3,48E-16	1,68E-13	ENSG0000010
ENSG00000163519	3,95E-16	1,88E-13	ENSG0000007
ENSG00000211659	3,96E-16	1,88E-13	ENSG0000023
ENSG00000155660	4,22E-16	1,98E-13	ENSG0000015
ENSG00000101082	4,34E-16	2,02E-13	ENSG0000008
ENSG00000211790	4,49E-16	2,08E-13	ENSG0000013
ENSG00000242574	4,57E-16	2,09E-13	ENSG0000011
ENSG00000211788	4,60E-16	2,09E-13	ENSG0000013
ENSG00000119714	4,95E-16	2,23E-13	ENSG0000025
ENSG00000013725	5,14E-16	2,30E-13	ENSG0000011
ENSG00000211751	5,28E-16	2,35E-13	ENSG0000027
ENSG00000175354	5,38E-16	2,38E-13	ENSG0000012
ENSG00000196611	5,66E-16	2,48E-13	ENSG0000006
ENSG00000214900	6,18E-16	2,69E-13	ENSG0000020
ENSG00000020633	6,42E-16	2,77E-13	ENSG0000011

ENSG00000117091	6,54E-16	2,80E-13	ENSG0000019
ENSG00000160856	6,58E-16	2,80E-13	ENSG0000012
ENSG00000131242	6,86E-16	2,90E-13	ENSG0000016
ENSG00000163739	7,25E-16	3,02E-13	ENSG0000017
ENSG00000119866	7,26E-16	3,02E-13	ENSG0000012
ENSG00000156711	7,71E-16	3,19E-13	ENSG0000002
ENSG00000241294	7,86E-16	3,23E-13	ENSG0000018
ENSG00000167984	7,95E-16	3,24E-13	ENSG0000011
ENSG00000110848	8,11E-16	3,28E-13	ENSG0000018
ENSG00000211900	8,77E-16	3,53E-13	ENSG0000016
ENSG00000179051	9,00E-16	3,59E-13	ENSG0000019
ENSG00000115919	9,16E-16	3,62E-13	ENSG0000008
ENSG00000211955	9,19E-16	3,62E-13	ENSG0000018
ENSG00000237989	9,45E-16	3,70E-13	ENSG0000027
ENSG00000275302	9,52E-16	3,70E-13	ENSG0000019
ENSG00000104814	9,66E-16	3,73E-13	ENSG0000007
ENSG00000065675	9,82E-16	3,77E-13	ENSG0000014
ENSG00000121594	1,02E-15	3,89E-13	ENSG0000010
ENSG00000271856	1,05E-15	3,97E-13	ENSG0000014
ENSG00000023445	1,06E-15	3,97E-13	ENSG0000007
ENSG00000167642	1,06E-15	3,97E-13	ENSG0000027
ENSG00000128815	1,07E-15	3,99E-13	ENSG0000014
ENSG00000241351	1,11E-15	4,09E-13	ENSG0000027
ENSG00000181467	1,15E-15	4,18E-13	ENSG0000016
ENSG00000109684	1,16E-15	4,18E-13	ENSG0000013
ENSG00000226979	1,16E-15	4,18E-13	ENSG0000018
ENSG00000178860	1,17E-15	4,18E-13	ENSG0000017
ENSG00000277734	1,17E-15	4,18E-13	ENSG0000019
ENSG00000139572	1,23E-15	4,37E-13	ENSG0000029
ENSG00000172673	1,30E-15	4,59E-13	ENSG0000008
ENSG00000128340	1,34E-15	4,73E-13	ENSG0000019
ENSG00000244437	1,43E-15	5,01E-13	ENSG0000016
ENSG00000131401	1,46E-15	5,09E-13	ENSG0000011
ENSG00000104951	1,47E-15	5,10E-13	ENSG0000018
ENSG00000281103	1,59E-15	5,46E-13	ENSG0000028
ENSG00000136250	1,75E-15	5,96E-13	ENSG0000026
ENSG00000211938	1,77E-15	5,97E-13	ENSG0000013
ENSG00000170476	1,77E-15	5,97E-13	ENSG0000010
ENSG00000108950	1,85E-15	6,22E-13	ENSG0000024
ENSG00000107742	1,88E-15	6,29E-13	ENSG0000009
ENSG00000271503	2,01E-15	6,67E-13	ENSG0000014
ENSG00000198821	2,06E-15	6,79E-13	ENSG0000017
ENSG00000168995	2,07E-15	6,79E-13	ENSG0000016
ENSG00000239713	2,13E-15	6,94E-13	ENSG0000019
ENSG00000196189	2,19E-15	7,11E-13	ENSG0000026
ENSG00000115085	2,25E-15	7,27E-13	ENSG0000017

ENSG00000242472	2,32E-15	7,44E-13	ENSG0000026
ENSG00000166920	2,33E-15	7,44E-13	ENSG0000016
ENSG00000143870	2,41E-15	7,67E-13	ENSG0000015
ENSG00000211669	2,49E-15	7,88E-13	ENSG0000014
ENSG00000211893	2,53E-15	7,94E-13	ENSG0000016
ENSG00000135052	2,61E-15	8,15E-13	ENSG0000010
ENSG00000118705	2,83E-15	8,81E-13	ENSG0000011
ENSG00000151790	2,94E-15	9,04E-13	ENSG0000013
ENSG00000136295	2,95E-15	9,04E-13	ENSG0000010
ENSG00000150637	2,96E-15	9,04E-13	ENSG0000011
ENSG00000211933	2,97E-15	9,05E-13	ENSG0000006
ENSG00000211949	3,16E-15	9,57E-13	ENSG0000013
ENSG00000211637	3,36E-15	1,01E-12	ENSG0000026
ENSG00000160654	3,43E-15	1,03E-12	ENSG0000023
ENSG00000030110	3,50E-15	1,04E-12	ENSG0000006
ENSG00000142512	3,70E-15	1,10E-12	ENSG0000017
ENSG00000164543	3,82E-15	1,12E-12	ENSG0000017
ENSG00000242076	3,82E-15	1,12E-12	ENSG0000017
ENSG00000007968	3,94E-15	1,15E-12	ENSG0000013
ENSG00000211966	4,20E-15	1,22E-12	ENSG0000011
ENSG00000237111	4,24E-15	1,23E-12	ENSG0000005
ENSG00000181026	4,27E-15	1,23E-12	ENSG0000026
ENSG00000138964	4,43E-15	1,27E-12	ENSG0000010
ENSG00000234745	4,56E-15	1,30E-12	ENSG0000010
ENSG00000211947	4,67E-15	1,32E-12	ENSG0000012
ENSG00000119686	4,96E-15	1,40E-12	ENSG0000011
ENSG00000125430	4,97E-15	1,40E-12	ENSG0000011
ENSG00000187583	4,99E-15	1,40E-12	ENSG0000019
ENSG00000211796	5,34E-15	1,48E-12	ENSG0000027
ENSG00000049249	5,35E-15	1,48E-12	ENSG0000003
ENSG00000143119	5,38E-15	1,48E-12	ENSG0000016
ENSG00000211592	5,38E-15	1,48E-12	ENSG0000024
ENSG00000136167	5,59E-15	1,53E-12	ENSG0000016
ENSG00000043462	5,62E-15	1,53E-12	ENSG0000015
ENSG00000126882	5,78E-15	1,56E-12	ENSG0000011
ENSG00000151136	5,85E-15	1,57E-12	ENSG0000016
ENSG00000079931	6,40E-15	1,71E-12	ENSG0000011
ENSG00000019582	6,46E-15	1,72E-12	ENSG0000000
ENSG00000102096	6,55E-15	1,73E-12	ENSG0000017
ENSG00000189233	6,56E-15	1,73E-12	ENSG0000016
ENSG00000160326	6,63E-15	1,73E-12	ENSG0000015
ENSG00000256262	6,63E-15	1,73E-12	ENSG0000015
ENSG00000070915	6,73E-15	1,74E-12	ENSG0000015
ENSG00000211970	6,74E-15	1,74E-12	ENSG0000010
ENSG00000168081	7,07E-15	1,82E-12	ENSG0000010
ENSG00000141505	7,26E-15	1,86E-12	ENSG0000014

ENSG00000100453	7,44E-15	1,90E-12	ENSG0000013
ENSG00000163564	7,49E-15	1,90E-12	ENSG0000024
ENSG00000230099	7,64E-15	1,93E-12	ENSG0000017
ENSG00000211899	7,64E-15	1,93E-12	ENSG0000014
ENSG00000131323	7,71E-15	1,94E-12	ENSG0000018
ENSG00000125245	7,80E-15	1,95E-12	ENSG0000006
ENSG00000163874	8,01E-15	1,99E-12	ENSG0000012
ENSG00000239951	8,06E-15	2,00E-12	ENSG0000013
ENSG00000171310	8,18E-15	2,01E-12	ENSG0000019
ENSG00000211747	8,19E-15	2,01E-12	ENSG0000017
ENSG00000224137	8,60E-15	2,10E-12	ENSG0000000
ENSG00000197057	8,76E-15	2,14E-12	ENSG0000021
ENSG00000243466	8,84E-15	2,15E-12	ENSG0000018
ENSG00000135047	8,97E-15	2,17E-12	ENSG0000019
ENSG00000211648	9,08E-15	2,18E-12	ENSG0000013
ENSG00000244116	9,36E-15	2,24E-12	ENSG0000013
ENSG00000261594	9,54E-15	2,28E-12	ENSG0000018
ENSG00000137078	9,86E-15	2,34E-12	ENSG0000010
ENSG00000154978	9,87E-15	2,34E-12	ENSG0000023
ENSG00000174500	9,97E-15	2,35E-12	ENSG0000010
ENSG00000132465	1,01E-14	2,38E-12	ENSG0000019
ENSG00000023892	1,05E-14	2,45E-12	ENSG0000008
ENSG00000120280	1,07E-14	2,48E-12	ENSG0000008
ENSG00000122188	1,07E-14	2,48E-12	ENSG0000026
ENSG00000111796	1,12E-14	2,60E-12	ENSG0000016
ENSG00000171208	1,15E-14	2,66E-12	ENSG0000016
ENSG00000141968	1,19E-14	2,73E-12	ENSG0000012
ENSG00000211945	1,19E-14	2,73E-12	ENSG0000014
ENSG00000162894	1,20E-14	2,73E-12	ENSG0000013
ENSG00000096996	1,20E-14	2,73E-12	ENSG0000022
ENSG00000135905	1,24E-14	2,81E-12	ENSG0000013
ENSG00000104894	1,26E-14	2,84E-12	ENSG0000013
ENSG00000138795	1,29E-14	2,89E-12	ENSG0000012
ENSG00000049768	1,34E-14	3,00E-12	ENSG0000000
ENSG00000118503	1,38E-14	3,08E-12	ENSG0000014
ENSG00000211640	1,39E-14	3,09E-12	ENSG0000012
ENSG00000185811	1,40E-14	3,10E-12	ENSG0000019
ENSG00000211670	1,62E-14	3,56E-12	ENSG0000016
ENSG00000179583	1,65E-14	3,62E-12	ENSG0000019
ENSG00000048462	1,68E-14	3,66E-12	ENSG0000019
ENSG00000241755	1,68E-14	3,66E-12	ENSG0000019
ENSG00000137101	1,70E-14	3,68E-12	ENSG0000017
ENSG00000224373	1,80E-14	3,88E-12	ENSG0000016
ENSG00000211663	1,84E-14	3,96E-12	ENSG0000021
ENSG00000187764	1,86E-14	3,99E-12	ENSG0000018
ENSG00000181896	1,90E-14	4,05E-12	ENSG0000016

ENSG00000198019	1,90E-14	4,05E-12	ENSG0000017
ENSG00000211895	1,96E-14	4,15E-12	ENSG0000017
ENSG00000211935	2,00E-14	4,22E-12	ENSG0000018
ENSG00000131746	2,03E-14	4,27E-12	ENSG0000011
ENSG00000211677	2,07E-14	4,35E-12	ENSG0000007
ENSG00000143390	2,18E-14	4,55E-12	ENSG0000016
ENSG00000197646	2,19E-14	4,55E-12	ENSG0000011
ENSG00000160991	2,23E-14	4,63E-12	ENSG0000027
ENSG00000169679	2,28E-14	4,72E-12	ENSG0000016
ENSG00000090339	2,30E-14	4,73E-12	ENSG0000014
ENSG00000139193	2,43E-14	4,96E-12	ENSG0000015
ENSG00000163376	2,44E-14	4,97E-12	ENSG0000020
ENSG00000077984	2,45E-14	4,97E-12	ENSG0000012
ENSG00000211973	2,45E-14	4,97E-12	ENSG0000021
ENSG00000009790	2,65E-14	5,33E-12	ENSG0000019
ENSG00000204257	2,74E-14	5,49E-12	ENSG0000028
ENSG00000249096	2,75E-14	5,49E-12	ENSG0000014
ENSG00000186074	2,76E-14	5,49E-12	ENSG0000014
ENSG00000125637	2,84E-14	5,64E-12	ENSG0000014
ENSG00000105374	3,16E-14	6,25E-12	ENSG0000018
ENSG00000137309	3,24E-14	6,39E-12	ENSG0000028
ENSG00000140968	3,34E-14	6,57E-12	ENSG0000025
ENSG00000251546	3,49E-14	6,84E-12	ENSG0000011
ENSG00000259834	3,57E-14	6,97E-12	ENSG0000015
ENSG00000187951	3,65E-14	7,10E-12	ENSG0000007
ENSG00000237988	3,67E-14	7,10E-12	ENSG0000010
ENSG00000099958	3,72E-14	7,19E-12	ENSG0000014
ENSG00000121895	3,78E-14	7,27E-12	ENSG0000010
ENSG00000211896	3,84E-14	7,38E-12	ENSG0000027
ENSG00000164733	4,26E-14	8,15E-12	ENSG0000019
ENSG00000211653	4,28E-14	8,16E-12	ENSG0000017
ENSG00000276557	4,30E-14	8,17E-12	ENSG0000019
ENSG00000123975	4,35E-14	8,25E-12	ENSG0000011
ENSG00000082074	4,38E-14	8,27E-12	ENSG0000025
ENSG00000204475	4,49E-14	8,45E-12	ENSG0000013
ENSG00000270550	4,64E-14	8,68E-12	ENSG0000012
ENSG00000047365	4,66E-14	8,69E-12	ENSG0000016
ENSG00000167895	4,85E-14	9,01E-12	ENSG0000007
ENSG00000128438	4,92E-14	9,12E-12	ENSG0000018
ENSG00000070882	4,96E-14	9,16E-12	ENSG0000026
ENSG00000116990	5,01E-14	9,23E-12	ENSG0000009
ENSG00000181284	5,03E-14	9,23E-12	ENSG0000004
ENSG00000211706	5,14E-14	9,41E-12	ENSG0000015
ENSG00000225079	5,19E-14	9,47E-12	ENSG0000018
ENSG00000101057	5,37E-14	9,76E-12	ENSG0000013
ENSG00000057657	5,42E-14	9,78E-12	ENSG0000016

ENSG00000090104	5,42E-14	9,78E-12	ENSG00000014
ENSG00000069424	5,44E-14	9,78E-12	ENSG00000016
ENSG00000065923	5,46E-14	9,78E-12	ENSG00000010
ENSG00000240535	5,47E-14	9,78E-12	ENSG00000028
ENSG00000211673	5,96E-14	1,06E-11	ENSG00000012
ENSG00000159958	6,04E-14	1,07E-11	ENSG00000019
ENSG00000136040	6,17E-14	1,09E-11	ENSG00000010
ENSG00000127507	6,65E-14	1,17E-11	ENSG00000026
ENSG00000211967	6,84E-14	1,20E-11	ENSG00000024
ENSG00000117560	6,91E-14	1,21E-11	ENSG00000022
ENSG00000159322	6,92E-14	1,21E-11	ENSG00000011
ENSG00000206503	7,17E-14	1,25E-11	ENSG00000011
ENSG00000213024	7,25E-14	1,26E-11	ENSG00000018
ENSG00000101310	7,60E-14	1,32E-11	ENSG00000016
ENSG00000240382	7,90E-14	1,36E-11	ENSG00000014
ENSG00000121152	7,99E-14	1,38E-11	ENSG00000029
ENSG00000226012	8,12E-14	1,39E-11	ENSG00000021
ENSG00000228863	8,15E-14	1,40E-11	ENSG00000009
ENSG00000276043	8,20E-14	1,40E-11	ENSG00000023
ENSG00000266094	8,26E-14	1,41E-11	ENSG00000017
ENSG00000211625	8,64E-14	1,47E-11	ENSG00000002
ENSG00000132704	8,81E-14	1,49E-11	ENSG00000023
ENSG00000104972	8,83E-14	1,49E-11	ENSG00000016
ENSG00000110031	9,14E-14	1,54E-11	ENSG00000022
ENSG00000185527	9,22E-14	1,55E-11	ENSG00000009
ENSG00000229961	9,27E-14	1,55E-11	ENSG00000017
ENSG00000211660	9,51E-14	1,59E-11	ENSG00000018
ENSG00000139618	9,58E-14	1,59E-11	ENSG00000022
ENSG00000113532	9,74E-14	1,62E-11	ENSG00000013
ENSG00000117650	1,05E-13	1,73E-11	ENSG00000017
ENSG00000140379	1,06E-13	1,75E-11	ENSG00000017
ENSG00000186818	1,09E-13	1,79E-11	ENSG00000009
ENSG00000277632	1,11E-13	1,81E-11	ENSG00000014
ENSG00000102879	1,11E-13	1,81E-11	ENSG00000011
ENSG00000148773	1,13E-13	1,84E-11	ENSG00000027
ENSG00000102245	1,16E-13	1,87E-11	ENSG00000013
ENSG00000154127	1,21E-13	1,97E-11	ENSG00000013
ENSG00000238121	1,24E-13	2,00E-11	ENSG00000011
ENSG00000140030	1,32E-13	2,13E-11	ENSG00000018
ENSG00000211651	1,33E-13	2,13E-11	ENSG00000023
ENSG00000154451	1,33E-13	2,13E-11	ENSG00000008
ENSG00000211795	1,39E-13	2,22E-11	ENSG00000018
ENSG00000121807	1,40E-13	2,22E-11	ENSG00000016
ENSG00000066279	1,41E-13	2,24E-11	ENSG00000012
ENSG00000276775	1,42E-13	2,24E-11	ENSG00000010
ENSG00000240041	1,44E-13	2,27E-11	ENSG00000014

ENSG00000022556	1,49E-13	2,34E-11	ENSG0000018
ENSG00000140511	1,50E-13	2,35E-11	ENSG0000016
ENSG00000188011	1,57E-13	2,45E-11	ENSG0000015
ENSG00000211937	1,58E-13	2,45E-11	ENSG0000010
ENSG00000151651	1,58E-13	2,45E-11	ENSG0000013
ENSG00000211941	1,60E-13	2,47E-11	ENSG0000025
ENSG00000138684	1,61E-13	2,49E-11	ENSG0000016
ENSG00000136490	1,64E-13	2,53E-11	ENSG0000022
ENSG00000004468	1,66E-13	2,54E-11	ENSG0000008
ENSG00000149968	1,71E-13	2,62E-11	ENSG0000024
ENSG00000162892	1,72E-13	2,63E-11	ENSG0000016
ENSG00000187808	1,74E-13	2,65E-11	ENSG0000013
ENSG00000105369	1,78E-13	2,69E-11	ENSG0000017
ENSG00000081237	1,81E-13	2,74E-11	ENSG0000006
ENSG00000204525	1,81E-13	2,74E-11	ENSG0000025
ENSG00000104856	1,83E-13	2,75E-11	ENSG0000018
ENSG00000285744	1,83E-13	2,75E-11	ENSG0000010
ENSG00000211810	1,84E-13	2,76E-11	ENSG0000015
ENSG00000166002	1,87E-13	2,79E-11	ENSG0000016
ENSG00000179750	1,87E-13	2,79E-11	ENSG0000012
ENSG00000033100	1,91E-13	2,83E-11	ENSG0000020
ENSG00000090382	1,91E-13	2,83E-11	ENSG0000013
ENSG00000197540	1,92E-13	2,84E-11	ENSG0000012
ENSG00000211817	1,95E-13	2,87E-11	ENSG0000025
ENSG00000079263	1,96E-13	2,88E-11	ENSG0000024
ENSG00000114013	2,01E-13	2,95E-11	ENSG0000010
ENSG00000071073	2,09E-13	3,06E-11	ENSG0000027
ENSG00000123338	2,10E-13	3,07E-11	ENSG0000027
ENSG00000231475	2,11E-13	3,08E-11	ENSG0000013
ENSG00000164620	2,19E-13	3,19E-11	ENSG0000019
ENSG00000171848	2,22E-13	3,21E-11	ENSG0000007
ENSG00000065600	2,26E-13	3,27E-11	ENSG0000022
ENSG00000213186	2,33E-13	3,36E-11	ENSG0000013
ENSG00000211593	2,39E-13	3,44E-11	ENSG0000014
ENSG00000186517	2,44E-13	3,50E-11	ENSG0000026
ENSG00000101160	2,46E-13	3,52E-11	ENSG0000027
ENSG00000206337	2,48E-13	3,54E-11	ENSG0000020
ENSG00000164611	2,50E-13	3,56E-11	ENSG0000016
ENSG00000231131	2,59E-13	3,68E-11	ENSG0000005
ENSG00000255282	2,60E-13	3,68E-11	ENSG0000010
ENSG00000177494	2,65E-13	3,75E-11	ENSG0000011
ENSG00000239975	2,70E-13	3,81E-11	ENSG0000025
ENSG00000116852	2,73E-13	3,83E-11	ENSG0000026
ENSG00000149428	2,83E-13	3,96E-11	ENSG0000016
ENSG00000100647	2,92E-13	4,05E-11	ENSG0000007
ENSG00000051523	2,92E-13	4,05E-11	ENSG0000016

ENSG00000126246	2,94E-13	4,06E-11	ENSG0000013
ENSG00000271605	2,99E-13	4,12E-11	ENSG0000019
ENSG00000102524	3,10E-13	4,26E-11	ENSG0000022
ENSG00000167618	3,14E-13	4,30E-11	ENSG0000023
ENSG00000121797	3,15E-13	4,31E-11	ENSG0000020
ENSG00000106683	3,18E-13	4,34E-11	ENSG0000023
ENSG00000124256	3,23E-13	4,38E-11	ENSG0000013
ENSG00000067606	3,23E-13	4,38E-11	ENSG0000025
ENSG00000189159	3,24E-13	4,38E-11	ENSG0000012
ENSG00000163734	3,28E-13	4,43E-11	ENSG0000027
ENSG00000166598	3,35E-13	4,52E-11	ENSG0000014
ENSG00000117676	3,41E-13	4,58E-11	ENSG0000014
ENSG00000226660	3,45E-13	4,62E-11	ENSG0000013
ENSG00000100526	3,46E-13	4,62E-11	ENSG0000026
ENSG00000283063	3,47E-13	4,62E-11	ENSG0000008
ENSG00000188820	3,49E-13	4,64E-11	ENSG0000014
ENSG00000211777	3,52E-13	4,67E-11	ENSG0000018
ENSG00000111348	3,55E-13	4,70E-11	ENSG0000027
ENSG00000104970	3,57E-13	4,71E-11	ENSG0000025
ENSG00000242371	3,58E-13	4,71E-11	ENSG0000011
ENSG00000154310	3,66E-13	4,79E-11	ENSG0000025
ENSG00000211679	3,66E-13	4,79E-11	ENSG0000016
ENSG00000167483	3,74E-13	4,88E-11	ENSG0000025
ENSG00000156738	3,89E-13	5,05E-11	ENSG0000018
ENSG00000115956	3,90E-13	5,05E-11	ENSG0000010
ENSG00000179344	3,94E-13	5,09E-11	ENSG0000019
ENSG00000139192	3,98E-13	5,13E-11	ENSG0000012
ENSG00000160255	3,99E-13	5,13E-11	ENSG0000011
ENSG00000211749	4,12E-13	5,29E-11	ENSG0000013
ENSG00000111424	4,17E-13	5,33E-11	ENSG0000024
ENSG00000113368	4,21E-13	5,37E-11	ENSG0000026
ENSG00000280135	4,26E-13	5,41E-11	ENSG0000027
ENSG00000196126	4,33E-13	5,49E-11	ENSG0000011
ENSG00000179218	4,34E-13	5,50E-11	ENSG0000016
ENSG00000278196	4,48E-13	5,65E-11	ENSG0000018
ENSG00000162511	4,58E-13	5,77E-11	ENSG0000014
ENSG00000070190	4,61E-13	5,80E-11	ENSG0000014
ENSG00000211965	4,69E-13	5,87E-11	ENSG0000016
ENSG00000211793	4,69E-13	5,87E-11	ENSG0000018
ENSG00000077150	4,73E-13	5,89E-11	ENSG0000017
ENSG00000198502	4,78E-13	5,93E-11	ENSG0000016
ENSG00000182162	4,92E-13	6,10E-11	ENSG0000011
ENSG00000184661	5,02E-13	6,20E-11	ENSG0000014
ENSG00000104774	5,05E-13	6,22E-11	ENSG0000024
ENSG00000167461	5,20E-13	6,40E-11	ENSG0000022
ENSG00000275004	5,37E-13	6,58E-11	ENSG0000014

ENSG00000211662	5,56E-13	6,80E-11	ENSG0000010
ENSG00000144136	5,68E-13	6,92E-11	ENSG0000016
ENSG00000146094	5,69E-13	6,92E-11	ENSG0000007
ENSG00000087085	5,70E-13	6,92E-11	ENSG0000010
ENSG00000110756	5,70E-13	6,92E-11	ENSG0000027
ENSG00000128285	6,07E-13	7,33E-11	ENSG0000016
ENSG00000188822	6,08E-13	7,33E-11	ENSG0000022
ENSG00000275385	6,21E-13	7,48E-11	ENSG0000022
ENSG00000211746	6,24E-13	7,50E-11	ENSG0000024
ENSG00000163013	6,29E-13	7,53E-11	ENSG0000011
ENSG00000234663	6,30E-13	7,53E-11	ENSG0000016
ENSG00000137812	6,41E-13	7,65E-11	ENSG0000026
ENSG00000101265	6,51E-13	7,76E-11	ENSG0000007
ENSG00000104081	6,53E-13	7,76E-11	ENSG0000013
ENSG00000231925	6,68E-13	7,92E-11	ENSG0000008
ENSG00000211962	6,71E-13	7,94E-11	ENSG0000011
ENSG00000243290	6,80E-13	8,03E-11	ENSG0000015
ENSG00000146386	6,90E-13	8,12E-11	ENSG0000014
ENSG00000180535	6,93E-13	8,14E-11	ENSG0000017
ENSG00000136379	6,96E-13	8,15E-11	ENSG0000011
ENSG00000166710	7,09E-13	8,29E-11	ENSG0000017
ENSG00000167004	7,20E-13	8,40E-11	ENSG0000014
ENSG00000216490	7,21E-13	8,41E-11	ENSG0000016
ENSG00000105251	7,53E-13	8,73E-11	ENSG0000016
ENSG00000130816	7,54E-13	8,73E-11	ENSG0000007
ENSG00000143226	7,60E-13	8,79E-11	ENSG0000016
ENSG00000142765	7,63E-13	8,81E-11	ENSG0000011
ENSG00000240864	7,84E-13	9,03E-11	ENSG0000013
ENSG00000118193	7,93E-13	9,12E-11	ENSG0000012
ENSG00000211734	8,13E-13	9,32E-11	ENSG0000016
ENSG00000135074	8,15E-13	9,33E-11	ENSG0000021
ENSG00000072786	8,19E-13	9,35E-11	ENSG0000015
ENSG00000130487	8,32E-13	9,47E-11	ENSG0000025
ENSG00000140451	8,77E-13	9,96E-11	ENSG0000006
ENSG00000138821	8,79E-13	9,97E-11	ENSG0000008
ENSG00000198286	8,86E-13	1,00E-10	ENSG0000005
ENSG00000051341	8,90E-13	1,00E-10	ENSG0000014
ENSG00000167077	9,02E-13	1,02E-10	ENSG0000017
ENSG00000226777	9,18E-13	1,03E-10	ENSG0000028
ENSG00000183943	9,29E-13	1,04E-10	ENSG0000020
ENSG00000100721	9,30E-13	1,04E-10	ENSG0000015
ENSG00000129667	9,42E-13	1,05E-10	ENSG0000009

and in PtC2 (Top 500 based on q-value)

p-value	q-value
5,69E-15	1,54E-12
2,40E-14	4,93E-12
2,61E-14	5,26E-12
4,52E-14	8,49E-12
5,48E-14	9,78E-12
1,04E-13	1,73E-11
1,35E-13	2,15E-11
1,57E-13	2,45E-11
2,63E-13	3,73E-11
2,79E-13	3,91E-11
2,88E-13	4,02E-11
2,91E-13	4,04E-11
3,12E-13	4,28E-11
3,46E-13	4,62E-11
3,60E-13	4,73E-11
3,78E-13	4,92E-11
3,94E-13	5,09E-11
4,17E-13	5,33E-11
4,68E-13	5,87E-11
4,74E-13	5,89E-11
4,99E-13	6,17E-11
5,96E-13	7,21E-11
6,88E-13	8,12E-11
7,43E-13	8,64E-11
8,29E-13	9,46E-11
8,89E-13	1,00E-10
1,02E-12	1,12E-10
1,05E-12	1,16E-10
1,46E-12	1,54E-10
1,55E-12	1,62E-10
1,60E-12	1,66E-10
1,87E-12	1,92E-10
2,00E-12	2,03E-10
2,08E-12	2,10E-10
2,13E-12	2,13E-10
2,57E-12	2,50E-10
2,59E-12	2,52E-10
2,63E-12	2,53E-10
2,67E-12	2,57E-10
2,74E-12	2,61E-10
2,75E-12	2,62E-10
2,85E-12	2,70E-10
2,91E-12	2,75E-10
2,97E-12	2,80E-10

3,00E-12	2,82E-10
3,02E-12	2,84E-10
3,19E-12	2,98E-10
3,37E-12	3,12E-10
3,79E-12	3,45E-10
3,88E-12	3,52E-10
3,94E-12	3,56E-10
4,06E-12	3,64E-10
4,39E-12	3,91E-10
4,51E-12	4,01E-10
4,53E-12	4,01E-10
4,58E-12	4,05E-10
4,82E-12	4,22E-10
5,00E-12	4,35E-10
5,47E-12	4,70E-10
5,65E-12	4,84E-10
5,83E-12	4,96E-10
5,88E-12	4,99E-10
5,97E-12	5,05E-10
6,08E-12	5,12E-10
6,65E-12	5,55E-10
7,18E-12	5,92E-10
7,33E-12	6,03E-10
7,44E-12	6,10E-10
7,54E-12	6,17E-10
7,99E-12	6,44E-10
8,28E-12	6,64E-10
8,38E-12	6,71E-10
8,91E-12	7,09E-10
8,94E-12	7,10E-10
9,14E-12	7,22E-10
9,28E-12	7,31E-10
9,50E-12	7,47E-10
9,69E-12	7,57E-10
9,86E-12	7,65E-10
1,02E-11	7,83E-10
1,03E-11	7,91E-10
1,03E-11	7,91E-10
1,05E-11	8,02E-10
1,07E-11	8,10E-10
1,15E-11	8,70E-10
1,15E-11	8,70E-10
1,17E-11	8,78E-10
1,19E-11	8,92E-10
1,20E-11	9,02E-10
1,22E-11	9,12E-10

1,26E-11	9,41E-10
1,28E-11	9,47E-10
1,30E-11	9,60E-10
1,31E-11	9,63E-10
1,33E-11	9,77E-10
1,34E-11	9,79E-10
1,44E-11	1,05E-09
1,45E-11	1,06E-09
1,47E-11	1,07E-09
1,56E-11	1,12E-09
1,60E-11	1,15E-09
1,61E-11	1,15E-09
1,63E-11	1,16E-09
1,66E-11	1,18E-09
1,67E-11	1,18E-09
1,71E-11	1,21E-09
1,75E-11	1,23E-09
1,75E-11	1,23E-09
1,76E-11	1,24E-09
1,78E-11	1,25E-09
1,83E-11	1,27E-09
1,83E-11	1,27E-09
1,83E-11	1,27E-09
1,84E-11	1,28E-09
1,92E-11	1,33E-09
2,07E-11	1,42E-09
2,08E-11	1,43E-09
2,19E-11	1,49E-09
2,21E-11	1,50E-09
2,23E-11	1,51E-09
2,24E-11	1,51E-09
2,26E-11	1,52E-09
2,37E-11	1,58E-09
2,44E-11	1,62E-09
2,49E-11	1,65E-09
2,53E-11	1,67E-09
2,63E-11	1,72E-09
2,73E-11	1,78E-09
2,73E-11	1,78E-09
2,74E-11	1,78E-09
2,76E-11	1,80E-09
2,77E-11	1,80E-09
2,79E-11	1,81E-09
2,82E-11	1,83E-09
2,94E-11	1,90E-09
2,99E-11	1,91E-09

3,01E-11	1,92E-09
3,16E-11	2,00E-09
3,28E-11	2,07E-09
3,39E-11	2,13E-09
3,57E-11	2,23E-09
3,61E-11	2,25E-09
3,62E-11	2,25E-09
3,62E-11	2,25E-09
3,63E-11	2,26E-09
3,74E-11	2,30E-09
3,78E-11	2,32E-09
3,79E-11	2,33E-09
3,83E-11	2,35E-09
3,98E-11	2,43E-09
4,03E-11	2,45E-09
4,04E-11	2,46E-09
4,14E-11	2,50E-09
4,22E-11	2,54E-09
4,26E-11	2,56E-09
4,29E-11	2,57E-09
4,36E-11	2,61E-09
4,47E-11	2,66E-09
4,50E-11	2,67E-09
4,53E-11	2,69E-09
4,54E-11	2,69E-09
4,62E-11	2,72E-09
4,69E-11	2,75E-09
4,72E-11	2,76E-09
4,82E-11	2,80E-09
4,95E-11	2,86E-09
4,97E-11	2,87E-09
5,15E-11	2,95E-09
5,53E-11	3,12E-09
5,62E-11	3,16E-09
5,63E-11	3,17E-09
5,64E-11	3,17E-09
6,30E-11	3,49E-09
6,30E-11	3,49E-09
6,32E-11	3,50E-09
6,59E-11	3,64E-09
6,66E-11	3,67E-09
6,68E-11	3,68E-09
6,77E-11	3,71E-09
6,85E-11	3,76E-09
6,93E-11	3,80E-09
7,20E-11	3,93E-09

7,42E-11	4,03E-09
7,51E-11	4,07E-09
7,58E-11	4,10E-09
7,80E-11	4,21E-09
8,25E-11	4,43E-09
8,38E-11	4,50E-09
8,48E-11	4,54E-09
8,53E-11	4,56E-09
8,83E-11	4,71E-09
8,85E-11	4,71E-09
9,08E-11	4,83E-09
9,14E-11	4,85E-09
9,23E-11	4,89E-09
9,30E-11	4,92E-09
9,47E-11	5,00E-09
9,47E-11	5,00E-09
9,63E-11	5,08E-09
9,74E-11	5,14E-09
9,95E-11	5,23E-09
1,00E-10	5,27E-09
1,09E-10	5,68E-09
1,13E-10	5,85E-09
1,14E-10	5,88E-09
1,15E-10	5,92E-09
1,15E-10	5,94E-09
1,18E-10	6,06E-09
1,19E-10	6,14E-09
1,21E-10	6,21E-09
1,22E-10	6,25E-09
1,23E-10	6,29E-09
1,23E-10	6,30E-09
1,24E-10	6,33E-09
1,24E-10	6,33E-09
1,26E-10	6,42E-09
1,26E-10	6,42E-09
1,28E-10	6,51E-09
1,31E-10	6,63E-09
1,32E-10	6,66E-09
1,33E-10	6,70E-09
1,35E-10	6,79E-09
1,36E-10	6,85E-09
1,38E-10	6,89E-09
1,39E-10	6,90E-09
1,40E-10	6,95E-09
1,40E-10	6,96E-09
1,40E-10	6,96E-09

1,44E-10	7,13E-09
1,45E-10	7,14E-09
1,47E-10	7,23E-09
1,47E-10	7,25E-09
1,47E-10	7,25E-09
1,48E-10	7,25E-09
1,50E-10	7,33E-09
1,51E-10	7,37E-09
1,52E-10	7,43E-09
1,52E-10	7,43E-09
1,53E-10	7,44E-09
1,54E-10	7,48E-09
1,54E-10	7,49E-09
1,56E-10	7,60E-09
1,56E-10	7,60E-09
1,57E-10	7,60E-09
1,58E-10	7,65E-09
1,59E-10	7,67E-09
1,59E-10	7,69E-09
1,61E-10	7,73E-09
1,62E-10	7,77E-09
1,63E-10	7,83E-09
1,64E-10	7,87E-09
1,67E-10	8,01E-09
1,69E-10	8,09E-09
1,71E-10	8,19E-09
1,78E-10	8,46E-09
1,81E-10	8,56E-09
1,82E-10	8,61E-09
1,86E-10	8,77E-09
1,87E-10	8,80E-09
1,87E-10	8,83E-09
1,88E-10	8,86E-09
1,89E-10	8,92E-09
1,92E-10	9,03E-09
1,98E-10	9,26E-09
2,03E-10	9,43E-09
2,10E-10	9,72E-09
2,16E-10	9,99E-09
2,20E-10	1,01E-08
2,23E-10	1,02E-08
2,32E-10	1,06E-08
2,40E-10	1,09E-08
2,42E-10	1,10E-08
2,44E-10	1,11E-08
2,47E-10	1,12E-08

2,57E-10	1,16E-08
2,58E-10	1,17E-08
2,62E-10	1,18E-08
2,64E-10	1,19E-08
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2,69E-10	1,20E-08
2,70E-10	1,21E-08
2,77E-10	1,23E-08
2,81E-10	1,25E-08
2,85E-10	1,26E-08
2,85E-10	1,26E-08
2,87E-10	1,27E-08
2,90E-10	1,28E-08
2,90E-10	1,28E-08
2,93E-10	1,29E-08
3,01E-10	1,32E-08
3,03E-10	1,32E-08
3,11E-10	1,35E-08
3,13E-10	1,36E-08
3,17E-10	1,38E-08
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3,18E-10	1,38E-08
3,20E-10	1,39E-08
3,22E-10	1,39E-08
3,22E-10	1,39E-08
3,27E-10	1,41E-08
3,28E-10	1,42E-08
3,32E-10	1,43E-08
3,34E-10	1,44E-08
3,36E-10	1,44E-08
3,41E-10	1,46E-08
3,41E-10	1,46E-08
3,42E-10	1,46E-08
3,46E-10	1,48E-08
3,62E-10	1,54E-08
3,65E-10	1,55E-08
3,65E-10	1,55E-08
3,67E-10	1,56E-08
3,67E-10	1,56E-08
3,82E-10	1,61E-08
3,89E-10	1,64E-08
4,02E-10	1,69E-08
4,07E-10	1,71E-08
4,09E-10	1,72E-08
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4,20E-10	1,76E-08

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4,24E-10	1,77E-08
4,30E-10	1,79E-08
4,33E-10	1,80E-08
4,33E-10	1,80E-08
4,36E-10	1,81E-08
4,41E-10	1,83E-08
4,44E-10	1,84E-08
4,51E-10	1,86E-08
4,51E-10	1,87E-08
4,56E-10	1,88E-08
4,56E-10	1,88E-08
4,58E-10	1,89E-08
4,60E-10	1,90E-08
4,67E-10	1,92E-08
4,80E-10	1,97E-08
4,86E-10	1,99E-08
4,87E-10	1,99E-08
4,87E-10	1,99E-08
4,96E-10	2,02E-08
4,99E-10	2,03E-08
5,04E-10	2,05E-08
5,09E-10	2,07E-08
5,16E-10	2,09E-08
5,19E-10	2,11E-08
5,38E-10	2,17E-08
5,40E-10	2,18E-08
5,47E-10	2,20E-08
5,53E-10	2,22E-08
5,58E-10	2,24E-08
5,65E-10	2,26E-08
5,69E-10	2,27E-08
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5,74E-10	2,29E-08
5,76E-10	2,29E-08
5,76E-10	2,29E-08
5,85E-10	2,33E-08
5,86E-10	2,33E-08
5,89E-10	2,34E-08
6,02E-10	2,39E-08
6,15E-10	2,44E-08
6,20E-10	2,45E-08
6,24E-10	2,47E-08
6,25E-10	2,47E-08
6,27E-10	2,47E-08

6,29E-10	2,48E-08
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6,30E-10	2,48E-08
6,37E-10	2,51E-08
6,41E-10	2,52E-08
6,45E-10	2,53E-08
6,52E-10	2,55E-08
6,62E-10	2,58E-08
6,66E-10	2,59E-08
6,71E-10	2,61E-08
6,74E-10	2,62E-08
6,80E-10	2,64E-08
6,85E-10	2,66E-08
6,94E-10	2,69E-08
6,99E-10	2,70E-08
7,12E-10	2,75E-08
7,16E-10	2,76E-08
7,30E-10	2,81E-08
7,32E-10	2,81E-08
7,37E-10	2,83E-08
7,40E-10	2,84E-08
7,41E-10	2,84E-08
7,44E-10	2,84E-08
7,46E-10	2,85E-08
7,50E-10	2,86E-08
7,61E-10	2,89E-08
7,65E-10	2,91E-08
7,66E-10	2,91E-08
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7,70E-10	2,92E-08
7,72E-10	2,93E-08
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7,80E-10	2,95E-08
7,88E-10	2,98E-08
7,94E-10	3,00E-08
8,06E-10	3,03E-08
8,19E-10	3,08E-08
8,23E-10	3,08E-08
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8,57E-10	3,19E-08
8,58E-10	3,19E-08
8,58E-10	3,19E-08
8,62E-10	3,20E-08
8,64E-10	3,21E-08
8,71E-10	3,23E-08

8,75E-10	3,24E-08
8,75E-10	3,24E-08
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8,87E-10	3,27E-08
8,96E-10	3,30E-08
8,99E-10	3,31E-08
9,03E-10	3,32E-08
9,07E-10	3,34E-08
9,09E-10	3,34E-08
9,21E-10	3,38E-08
9,32E-10	3,41E-08
9,38E-10	3,42E-08
9,39E-10	3,43E-08
9,42E-10	3,44E-08
9,43E-10	3,44E-08
9,43E-10	3,44E-08
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9,50E-10	3,46E-08
9,58E-10	3,48E-08
9,62E-10	3,49E-08
9,73E-10	3,53E-08
9,95E-10	3,60E-08
1,01E-09	3,66E-08
1,02E-09	3,66E-08
1,02E-09	3,67E-08
1,02E-09	3,68E-08
1,04E-09	3,74E-08
1,05E-09	3,77E-08
1,06E-09	3,81E-08
1,06E-09	3,81E-08
1,06E-09	3,81E-08
1,07E-09	3,83E-08
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1,10E-09	3,91E-08
1,12E-09	3,97E-08
1,12E-09	3,97E-08
1,12E-09	3,97E-08
1,13E-09	4,01E-08
1,14E-09	4,03E-08
1,14E-09	4,03E-08
1,14E-09	4,03E-08
1,14E-09	4,04E-08
1,15E-09	4,06E-08
1,15E-09	4,06E-08

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1,21E-09	4,24E-08
1,21E-09	4,25E-08
1,21E-09	4,26E-08
1,21E-09	4,26E-08
1,24E-09	4,33E-08
1,24E-09	4,33E-08
1,24E-09	4,34E-08
1,24E-09	4,34E-08
1,25E-09	4,35E-08
1,26E-09	4,38E-08
1,31E-09	4,56E-08
1,32E-09	4,58E-08
1,33E-09	4,61E-08
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1,46E-09	4,99E-08
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1,47E-09	5,01E-08
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1,49E-09	5,08E-08
1,50E-09	5,10E-08
1,51E-09	5,14E-08
1,52E-09	5,18E-08
1,53E-09	5,20E-08
1,55E-09	5,24E-08
1,57E-09	5,32E-08
1,58E-09	5,35E-08
1,60E-09	5,41E-08
1,60E-09	5,42E-08
1,62E-09	5,47E-08
1,65E-09	5,54E-08
1,65E-09	5,55E-08
1,68E-09	5,63E-08
1,68E-09	5,64E-08