Supplemental Materials and Methods

Evaluating Eosinophilic Colitis as a Unique Disease using Colonic Molecular Profiles: A Multi-Site Study

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*The list of participants is provided in this article's Supplementary Material

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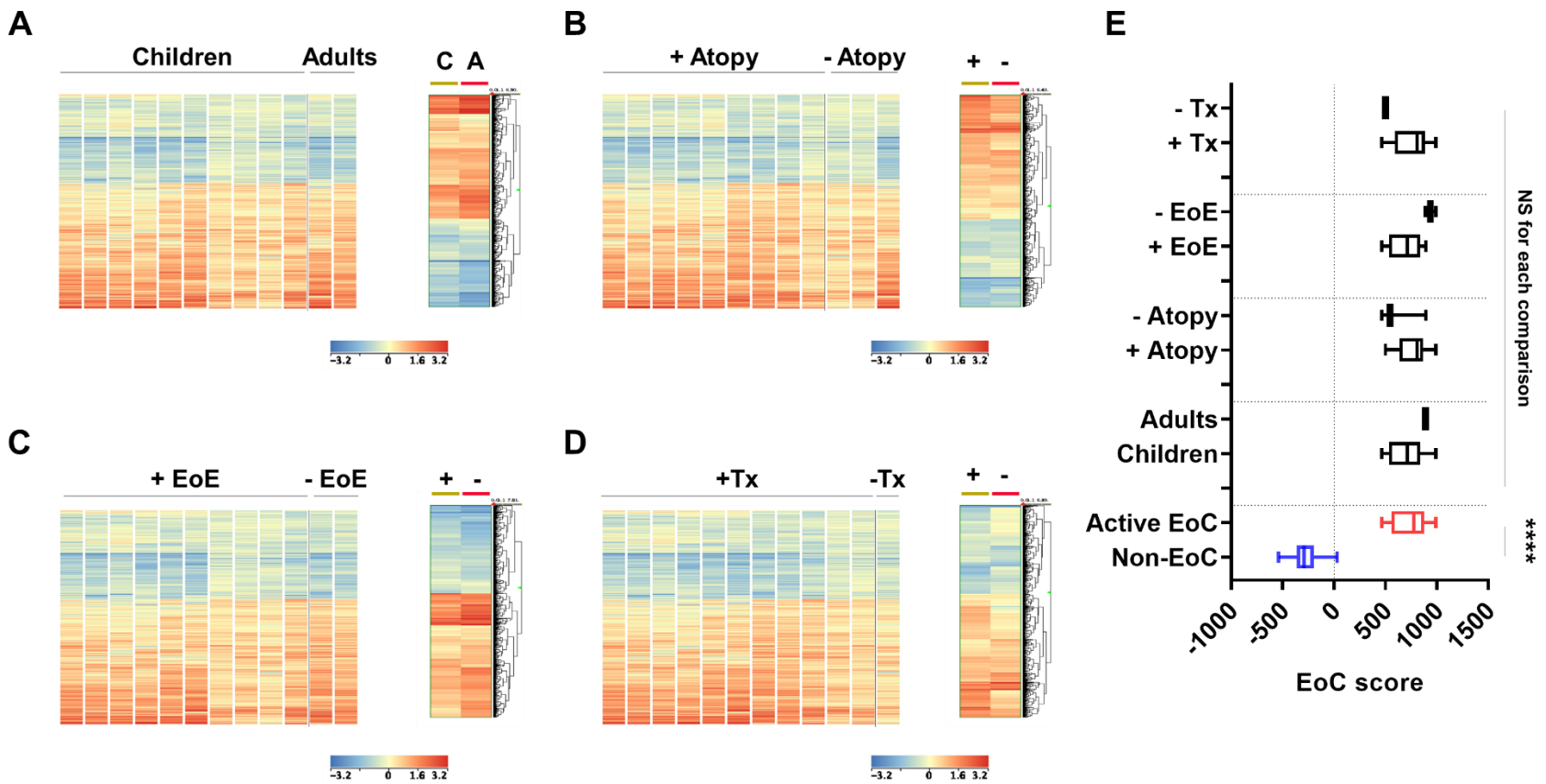
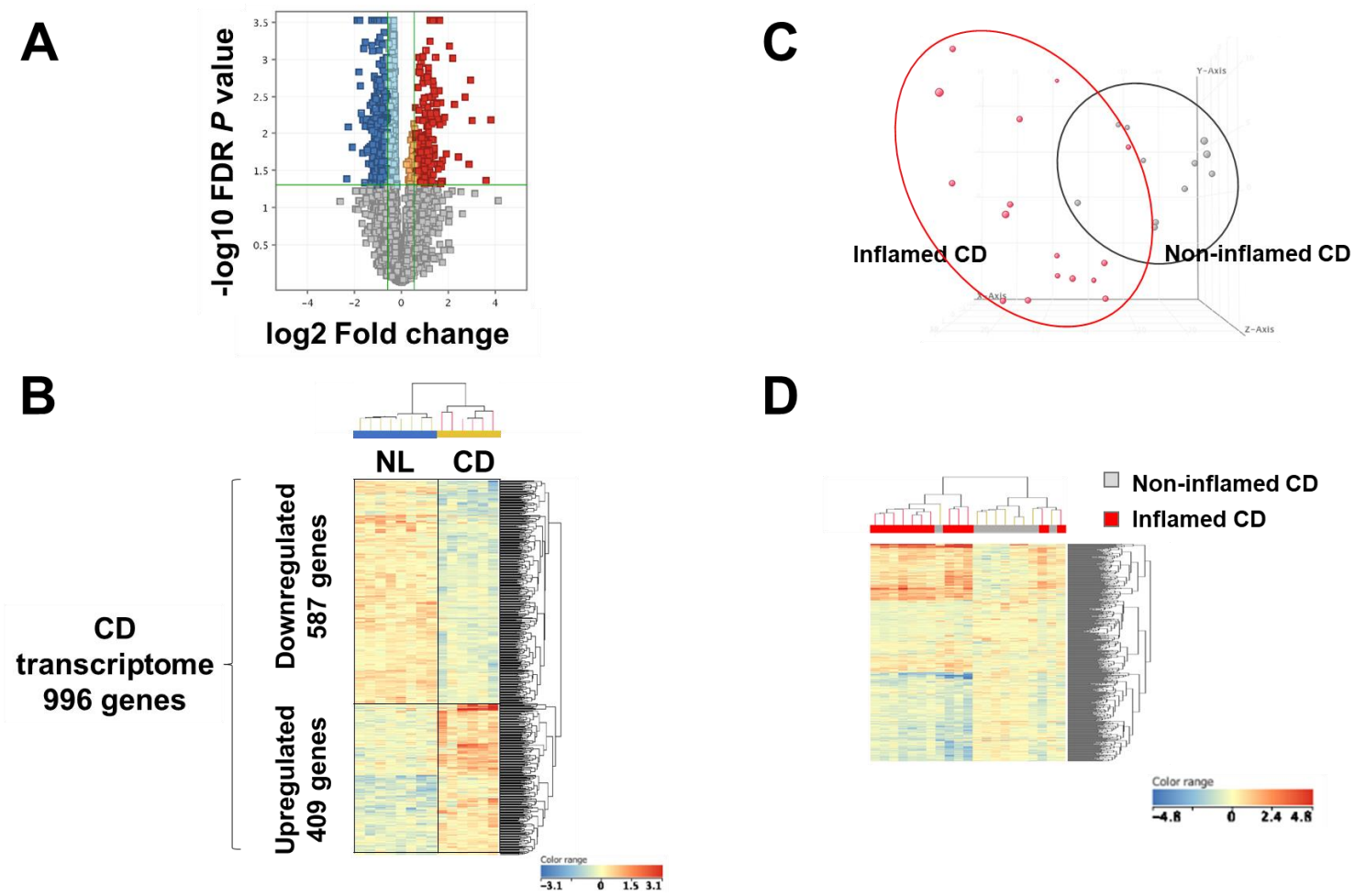
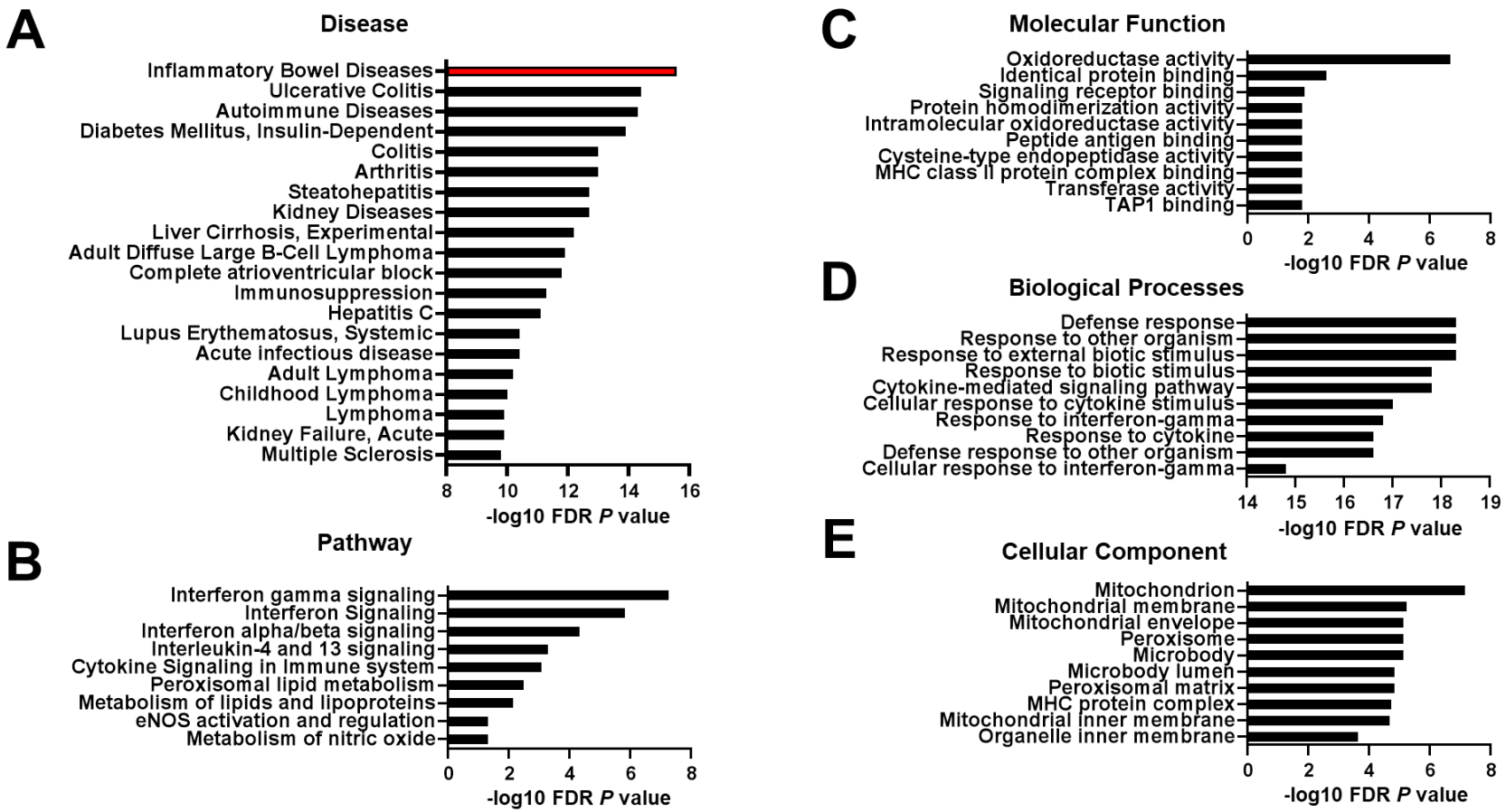
Overview of Contents



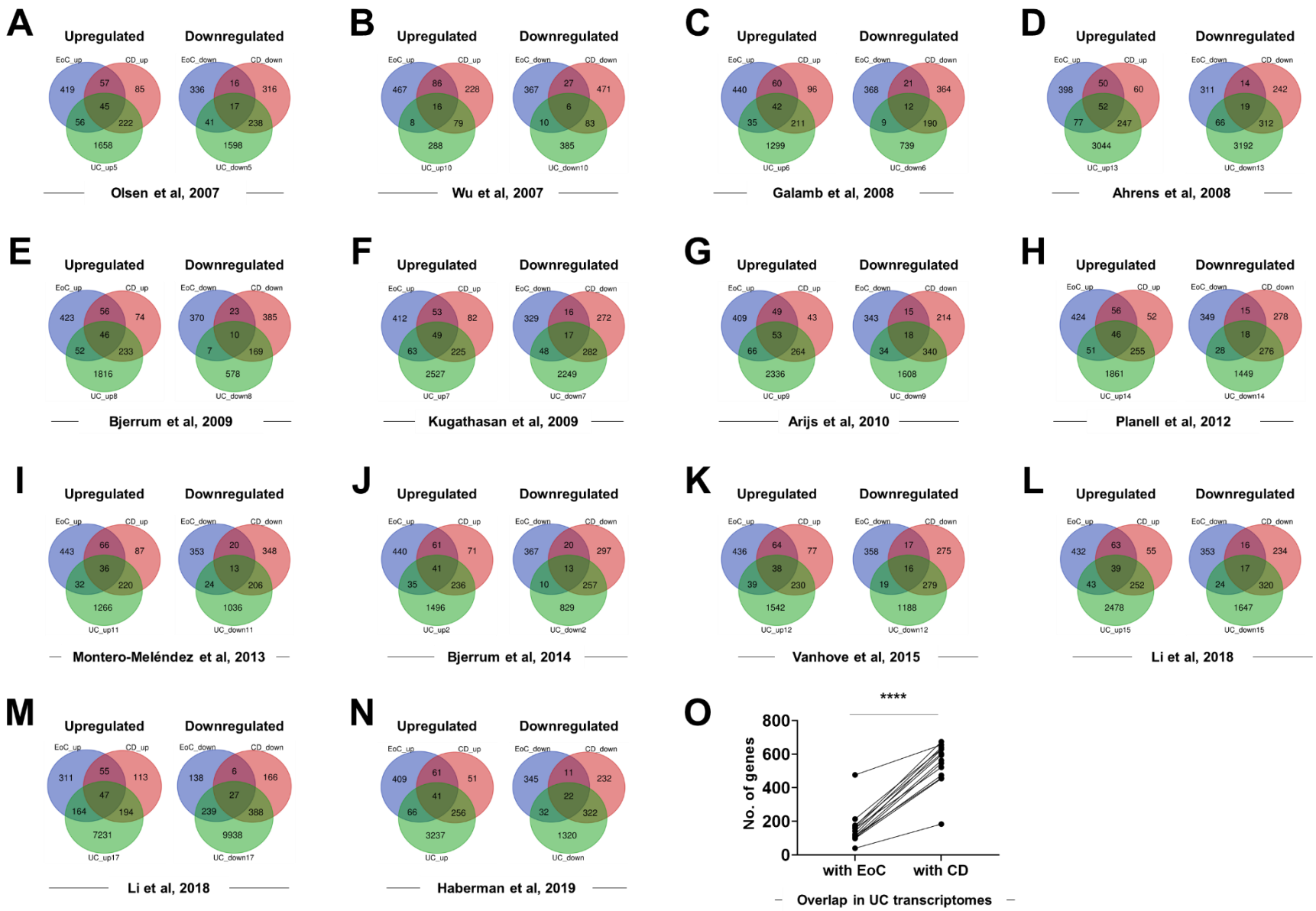
Supplementary Figure 1. Molecular comparisons among active EoC by clinical heterogeneity. A-D, Heatmap based on the EoC transcriptome by indicated groups. Heatmap was depicted by each individual (left) and averaged (right) for Age [children (C) vs. adults (A)] (A), Atopy [subjects having atopy (+ atopy) vs. subjects not having atopy (- atopy)] (B), EoE [subjects having EoE (+EoE) vs. subjects not having EoE (-EoE)] (C), and treatment [treated subjects (+Tx) vs. untreated subjects (-Tx)] (D). **E**, EoC score by indicated groups. Data are mean ± SEM. NS, not significant, using Mann–Whitney U test. EoC, eosinophilic colitis; EoE, eosinophilic esophagitis; Treatment, Tx.



Supplementary Figure 2. Identification of a conserved pattern of gene expression from colonic tissue of subjects with CD. A, Volcano plot (*red*, upregulated; *blue*, downregulated) of expression profiles of differentially dysregulated genes between normal controls (NL) and subjects with inflamed CD (FDR $P < .05$, ≥1.5-fold change). **B,** Clustering analysis was performed on the basis of 996 differentially expressed genes (CD transcriptome); each column represents an individual subject or control. **C-D,** Unsupervised analyses [principal component analysis (C), clustering analysis (D)] of the CD transcriptome showed separation of subjects with noninflamed CD *(gray)* and subjects with inflamed CD (*red*). CD, Crohn disease; EoC, eosinophilic colitis; FDR, false discovery rate.



Supplementary Figure 3. Functional enrichment analysis of the CD transcriptome. A, Functional enrichment analysis in the Disease category using ToppGene (https://toppgene.cchmc.org/). CD transcriptome shows enrichment in Inflammatory Bowel Disease (IBD)–relevant disease pathways (*red*). **B–E**, Shown are the 10 most significant terms identified for the CD transcriptome by functional enrichment analysis in the following categories: Pathway (B), Molecular Function (C), Biological Processes (D), and Cellular Component (E). CD, Crohn disease; FDR, false discovery rate.


A
Upregulated
Downregulated
EoC_up
CD_up
EoC_down
CD_down
419
57
85
45
56
222
1658
UC_up5
336
16
316
17
41
238
1598
UC_down5
Olsen et al, 2007
B
Upregulated
Downregulated
467
86
228
16
8
79
288
UC_up10
367
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471
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10
83
385
UC_down10
Wu et al, 2007
C
Upregulated
Downregulated
440
60
96
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35
211
1299
UC_up6
368
21
364
12
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190
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UC_down6
Galamb et al, 2008
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Upregulated
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398
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60
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3044
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19
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312
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Downregulated
423
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74
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1816
UC_up8
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10
7
169
578
UC_down8
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Downregulated
412
53
82
49
63
225
2527
UC_up7
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17
48
282
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UC_down7
Kugathasan et al, 2009
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Upregulated
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2336
UC_up9
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UC_down9
Arijs et al, 2010
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Upregulated
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1861
UC_up14
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UC_down14
Planell et al, 2012
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443
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87
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UC_up11
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UC_up2
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UC_down2
Bjerrum et al, 2014
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Upregulated
Downregulated
436
64
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UC_up12
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1188
UC_down12
Vanhove et al, 2015
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Upregulated
Downregulated
432
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2478
UC_up15
353
16
234
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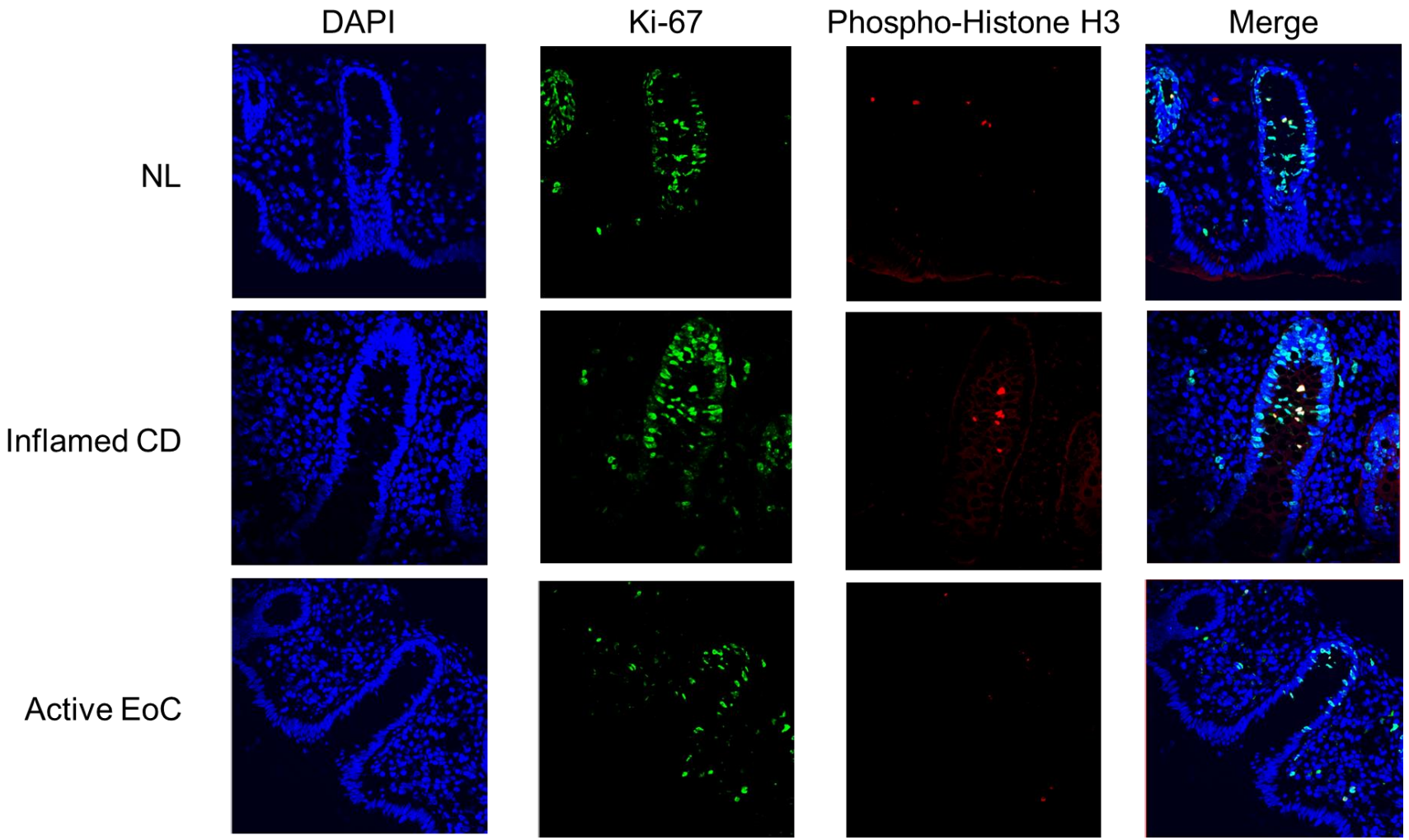
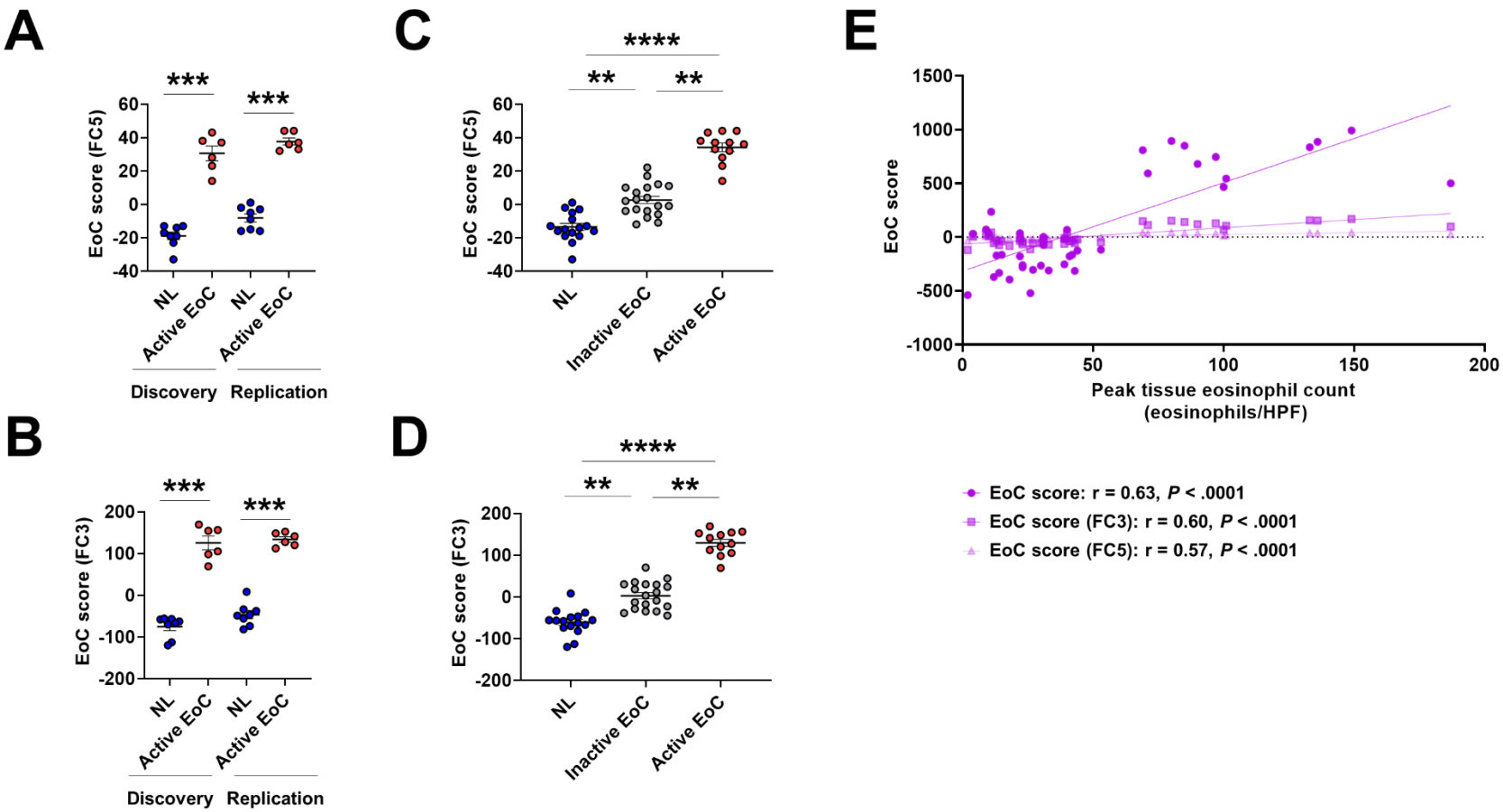
24
320
1647
UC_down15
Li et al, 2018
M
Upregulated
Downregulated
311
55
113
47
164
194
7231
UC_up17
138
6
166
27
239
388
9938
UC_down17
Li et al, 2018
N
Upregulated
Downregulated
409
61
51
41
66
256
3237
UC_up
345
11
232
22
32
322
1320
UC_down
Haberman et al, 2019
O
****
No. of genes
800
600
400
200
0
with EoC
with CD
Overlap in UC transcriptomes

Supplementary Figure 4. Comparisons of EoC and CD to several different UC datasets. A-N, Venn diagrams of the number of genes dysregulated in EoC (blue) and CD (red) transcriptomes to several different pediatric UC transcriptome data from the previously published studies (green). A, GSE9452; B, GSE6731; C, GSE10714; D, GSE10191; E, GSE13367; F, GSE10616; G, GSE14580; H, GSE38713; I, GSE36807; J, GSE47908; K, GSE59071; L, GSE87473; M, GSE87473; N, GSE109142. O, Comparison of EoC and CD transcriptomes to publicly available UC transcriptomes. ****P < .0001, using Wilcoxon matched-pairs signed rank test. EoC, eosinophilic colitis; CD, Crohn disease; UC, ulcerative colitis.



Supplementary Figure 5. Immunofluorescence staining of colonic biopsy. Representative images of colonic biopsy sections for Ki-67 (cyan) and Phospho-Histone H3 (red) with DAPI–stained nuclei (blue); sections from normal control individuals (NL) (N = 7), patients with inflamed CD (N = 6), and patients with active EoC (N = 8). CD, Crohn disease; DAPI, 4',6-diamidino-2-phenylindole; EoC, eosinophilic colitis; NL, normal controls.



Supplementary Figure 6. EoC scores by several cut-offs. A–B, Discovery and replication of the EoC score with independent patients and from different colon sites (discovery: ascending, replication: descending/sigmoid colon). EoC score based on FC >3 (A) and FC >5 (B) are shown. Data are mean ± SEM. ***P < .001, using Mann–Whitney U test. **C–D,** EoC score as a function of disease activity in EoC. EoC score based on FC >3 (C) and FC >5 (D) are shown. Data are mean ± SEM. **P < .01, ***P < .001, and ****P < .0001, using Kruskal-Wallis test followed by Dunn multiple-comparison test. **E,** Spearman correlation plots for peak colonic eosinophil count and EoC scores. EoC, eosinophilic colitis; CD, Crohn disease; NL, normal; HPF, high-power microscopic field; SEM, standard error of mean, FC; fold change.

Supplementary Materials and Methods

Study Design and Participants

This study was conducted in the Consortium of Eosinophilic Gastrointestinal Diseases Researchers (CEGIR),[1] a national collaborative network of academic centers caring for and researching adults and children with Eosinophilic gastrointestinal diseases (EGIDs). The CEGIR observational study, Outcome Measures in Eosinophilic Gastrointestinal disorders Across the ages (OMEGA), is a longitudinal cohort study aimed at understanding the natural history of eosinophilic esophagitis (EoE), eosinophilic gastritis (EoG), eosinophilic duodenitis (EoD), eosinophilic gastroenteritis (EGE), and eosinophilic colitis (EoC) during routine clinical care. Demographic, clinical, endoscopic, and histologic data and gastrointestinal (GI) tissue and peripheral blood samples, were prospectively collected starting from 2015; all samples from any CEGIR site that contributed subjects with EoC were used (n = 5 sample-providing institutions). The clinical features of subjects were determined during a standard-of-care evaluation using standardized intake forms. All subjects' clinical data were stored at the Rare Diseases Clinical Research Network (RDCRN) Data Management and Coordinating Center (University of South Florida in Tampa, FL [2015-2019] and Cincinnati Children's Hospital Medical Center [CCHMC; 2020–2024]).

Pediatric subjects were defined as having an age of less than 18 years. Atopy was defined on the basis of self-report of allergic rhinitis, atopic dermatitis, asthma, or food allergy. Subjects were defined as having EoC if they had a history of colonic eosinophilia (ascending colon ≥100 eosinophils/high-power field [HPF], descending colon ≥85 eosinophils/HPF, and/or sigmoid colon ≥65 eosinophils/HPF) without other known causes of GI eosinophilia; negative tests typically included stool culture for pathogenic bacteria or parasites, viral antibody titers and/or PCR, and Celiac and inflammatory bowel disease serology.[2] A 2X the upper limit of normal for each anatomic site in normal biopsies was used as the thresholds for the definitions of colonic eosinophilia.[2-5] Active EoC was defined as colonic biopsies that met the above criteria, and inactive EoC was defined as <100 eosinophils/HPF for ascending colon, <85 eosinophils/HPF in descending colon and/or <65 eosinophils/HPF for sigmoid colon in subjects with a previous history of EoC. Subjects with EoC with GI eosinophilia outside of the colon (esophagus: ≥15 eosinophils/HPF, stomach: ≥30 eosinophils/HPF in at least 5 HPF) were included.

Non-EoC control subjects (normal [NL], Crohn disease [CD]) from the Cincinnati Center for Eosinophilic Disorders (CCED) EGID database between 2015–2019 included children and adults who had undergone endoscopy, had no history of EoC nor pathologic evidence of EoC surveyed during the index endoscopy, and had colonic biopsies collected for research purposes during the index endoscopy. NL were not healthy volunteers, but instead were patients who underwent endoscopic examination due to digestive symptoms but did not show colonic eosinophilia. NL subjects having treatments because of concomitant diseases [e.g., gastroesophageal reflux disease (GERD) and IgE-mediated food allergy] were not excluded. A diagnosis of CD for this study was made using previously published guidelines.[6] Features may include a variable combination of the following: (1) Clinical signs and symptoms including abdominal pain, diarrhea, rectal bleeding, growth delay, and pubertal delay; (2) Physical findings including abdominal tenderness, perirectal skin tags, perirectal fistula, and erythema nodosum; (3) Endoscopic findings of aphthous, linear or stellate ulcerations, cobble stoning, skip lesions, and strictures in the ileum or colon; (4) Histologic findings including ulceration, crypt abscesses, non-caseating granuloma, focal changes within biopsy, and patchy inflammation, and (5) Cross-sectional imaging findings including mural thickening, hyperemia, abnormal luminal caliber, altered peristalsis, fibro-fatty proliferation, regional lymphadenopathy, and sinus tracts/fistulae. Diagnosis and disease activity of CD was based on a combination of the clinical, endoscopic, and histologic characteristics by gastroenterologists and pathologists at CCHMC. The inflammation status of subjects (inflamed or non-inflamed) was defined by the assessment of histologic features of chronicity and quantitated acute inflammation. A subset of patients with CD who also had a high peak colonic eosinophils/HPF (≥65 eosinophils/HPF) was defined as CD-high colonic eosinophils.

This study was approved by the institutional review boards of the participating institutions via a central institutional review board at CCHMC. An informed consent/assent form was signed by the subjects and/or their legal guardians per institutional guidelines prior to inclusion in the study. Study participants were also made aware that their involvement in the study was voluntary and that their declination to participate did not interfere with their standard of care.

Molecular Evaluation

Fresh biopsy specimens collected from subjects with EoC and controls were stored in RNAlater until they were subjected to RNA isolation using the miRNeasy kit (Qiagen, Valencia, Calif) per the manufacturer's instructions. The RNA concentration was measured by Nanodrop, and the RNA integrity number (RIN) was determined by the Gene Expression Core at CCHMC using the Agilent Bioanalyzer. Samples for RNA sequencing were selected from the total cohort on the basis of RNA quality and quantity. RNA sequencing was performed with high-quality RNA (RIN > 8) using the QuantSeq 3' mRNA Seq Library Prep Kit FWD for Illumina (Lexogen). Libraries were subjected to quality control and concentration measurements at the Gene Expression Core at CCHMC. Libraries were diluted to a final concentration of 5 nM and sequenced on a HiSeq 4000 Illumina sequencing machine at the Genomics & Cell Characterization Core Facility at the University of Oregon with single reads of 100–150 bp. Data were aligned to the GRCh37 build of the human genome using the Ensembl annotations. Data analyses, including principal component analysis (PCA) and hierarchical clustering, were performed using DESeq2 in CLC Genomics Workbench software (CLC bio, Waltham, MA, USA) and GeneSpring software ver. 14.9 (Agilent Technologies). Transcripts per kilobase million (TPM) were assessed for statistical significance using a Welch *t* test with Benjamini–Hochberg false-discovery rate (FDR), threshold of $P < .05$, and 1.5-fold–change cut-off filter. Data are available at EGIDExpress (https://egidexpress.research.cchmc.org/data/).

Gene ontology enrichment analysis was performed with the ToppGene suite and CluGO.[7, 8] Cell type enrichment analysis was performed with xCell.[9] EoC score was calculated by summing the normalized expression values of the dysregulated genes of the EoC transcriptomes, respectively. Of note, the EoC score calculated from the EoC transcriptome positively correlated with disease severity.

A real-time reverse-transcription quantitative polymerase chain reaction (RT-qPCR) array platform was performed to determine mucosal expression of genes associated with type 2 inflammation in patients with EGIDs. As type 2 inflammation, 7 genes [eosinophils (*CLC*), mast cells (*HPGDS*), chemokines/cytokines (*CCL11, CCL26, IL13, IL4, IL5*)] were assessed. Patients' biopsies [esophagus (EoE n=82, NL n=50),[10] stomach (EoG n=21, NL n=20),[11] colon (EoC n=12, NL n=16)] were assessed by the EoE Diagnostic Panel (EDP)[10] or EoG Diagnostic Panel (EGDP)[11]

with normalization to the housekeeping gene glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*).

As another relevant disease control, publicly available colonic transcriptome datasets from patients with ulcerative colitis (UC) having active colitis and patient clinical data were comprehensively searched and obtained by the BaseSpace correlation engine (Illumina Inc., San Diego, CA, USA).[12]

Histologic Features

Colonic biopsies were assessed for the peak eosinophil counts and other histologic features of EoC. Hematoxylin and eosin (H&E)–stained biopsy slides from NL, CD, and EoC were blindly reviewed by CEGIR pathologists (M.H.C., K.E.C., G.Y.). Standardization across centers was performed. CEGIR central review pathologists reviewed images of slides that had been scanned (Aperio scanner) at 40X magnification. Each pathologist used the same annotation to count eosinophils/hpf. The annotation was created for the purpose of counting eosinophils in a view finder that mimicked a round high-power field and measured 0.27 mm^2, an area that is commonly covered at 40X magnification. Histologic features in images of all submitted colon biopsies were as follows: acute crypt abscess, acute cryptitis, acute inflammation, crypt architectural abnormalities, crypt dropout/loss, crypt epithelial injury, crypts partly destroyed by eosinophilic inflammation, eosinophil crypt abscess, eosinophil cryptitis, eosinophils in muscularis mucosa/submucosa, eosinophils in surface epithelium, granulomas, lamina propria eosinophil sheets, lymphocytes in surface epithelium, overall eosinophilic inflammation, pericryptal circumferential eosinophil collars, subcryptal eosinophil aggregates, subcryptal lymphoplasmacytes, and surface epithelial injury. Each feature was scored using a 3-point scale (0 = absent, 1 = mild/moderate, 2 = marked) (Supplementary Table S3).

Immunohistochemical and immunofluorescent staining

Immunohistochemical stains with the Ki-67 (a proliferation marker, 790-4286, Roche) or cleaved caspase-3 (an apoptotic marker, ab2302, Abcam) in colonic biopsies were performed at the Pathology Research Core at CCHMC using the Ventana BenchMark XT automated immunostainer

(Ventana Medical Systems, Inc., Tuscon, AZ). No signal was observed in biopsies stained with negative control IgG antibodies. Stained biopsy slides from NL, CD, and EoC were blindly reviewed by an expert pathologist (M.H.C.). Immunofluorescent staining was performed as previously described,[13] using the following primary antibodies (1:100 dilution): Ki67 (MA5-14520; Invitrogen) and phospho-histone H3 (#9706; Cell Signaling Technology). The nuclei were stained with DAPI. The slides were blocked with PBS with 10% donkey serum. The secondary antibodies (1:400 dilution) used were donkey anti-mouse Alexa Fluor 570 or donkey anti-rabbit Alexa Fluor 488 (Invitrogen). Imaging was performed with a Nikon A1 inverted confocal microscope.

Statistical Analysis

Statistical analyses were performed using the JMP v13.2.1 (SAS Institute, Cary, NC), CLC Genomics Workbench software (CLC bio, Waltham, MA, USA), GeneSpring GX 14.9 (Agilent Technologies, Santa Clara, CA), and GraphPad Prism 9 (GraphPad Software, Inc., San Diego, CA). Data are presented as n (%) or median (interquartile range [IQR]) unless otherwise stated. Missing data were excluded from all formal statistical analyses. Nonparametric correlation analysis was performed using Spearman's rank correlation coefficient. For continuous data, statistical significance comparing 2 different groups was determined by the Mann-Whitney *U* test (nonparametric test, 2 groups) or the Kruskal-Wallis test followed by a Dunn multiple-comparison test (nonparametric test, 3 groups or more). Benjamini–Hochberg correction was applied for multiple testing to control the FDR. For categorical data, the chi-square test was used to ascertain differences. A significant *P* value was defined as less than 0.05.

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Author names in bold designate shared co-first authorship.

Supplementary Table 1. Number of subjects with EoC from each site

Number of samples	Total N = 31	Inactive EoC N = 19	Active EoC N = 12
Children's Hospital Colorado	7	6	1
Cincinnati Children's Hospital Medical Center	20	10	10
National Institutes of Health	1	1	0
Northwestern University	2	1	1
University of North Carolina School of Medicine	1	1	0

EoC, eosinophilic colitis

Supplementary Table 2. Inclusion/exclusion criteria, thresholds of eosinophilia, and definition of disease activity for EoC

<table>
<tr><th colspan="4">Inclusion/Exclusion criteria</th></tr>
<tr><th colspan="2">Inclusion</th><th colspan="2">Exclusion</th></tr>
<tr><td colspan="2">• Presence of symptoms; symptoms include (but are not limited to) hematochezia, bloody/non-bloody diarrhea, tenesmus, and abdominal pain

• A history of one of the following at the time of biopsy
1) anemia
2) peripheral eosinophilia
3) hemooccult positive stool
4) EGID
5) allergic diseases (allergic rhinitis, asthma, food allergy, eczema or other allergic features suggestive of atopic disease)

• Mucosal eosinophilia (see below)</td><td colspan="2">• History of intestinal surgery other than G tube placement
• Planned or recent enrollment in blinded investigational studies
• Other identifiable potential causes for eosinophilia except for IBD (CD and UC). In the case of IBD, investigators will review the clinical history, serology, and accompanying biopsies to determine if the diagnosis captures IBD diagnosis in the context of the histologic finding of mucosal eosinophilia. If the assessment suggests that the subject clearly has IBD, the subject will not be enrolled. If the assessment suggests that the patient may have EoC, then the potential participant could enroll if all other inclusion/exclusion criteria are met.
• Any physical, mental, or social condition, history or concurrent illness or laboratory abnormality that, in the investigator's judgement, might interfere with study procedures or the ability of the subject to adhere to and complete the study
• Potential participants will be excluded if the investigator determines that the potential participant has diminished capacity and is not cognitively able to participate fully in the consenting process</td></tr>
<tr><th colspan="4">Thresholds of mucosal eosinophilia in the GI tract</th></tr>
<tr><th>Location</th><th>Sites of biopsy</th><th>Thresholds</th><th>Diagnosis</th></tr>
<tr><td>Esophagus</td><td>Distal, proximal</td><td>≥15 eosinophils/HPF</td><td>Eosinophilic esophagitis (EoE)</td></tr>
<tr><td>Stomach</td><td>Antrum, body, fundus</td><td>≥30 eosinophils/HPF in 5 HPF</td><td>Eosinophilic gastritis (EoG)</td></tr>
<tr><td rowspan="3">Colon</td><td>Ascending</td><td>≥100 eosinophils/HPF</td><td rowspan="3">Eosinophilic colitis (EoC)</td></tr>
<tr><td>Descending</td><td>≥85 eosinophils/HPF</td></tr>
<tr><td>Sigmoid</td><td>≥65 eosinophils/HPF</td></tr>
<tr><th colspan="4">Definition of disease activity in EoC</th></tr>
<tr><th>Location</th><th>Sites of biopsy</th><th>Active state</th><th>Inactive state</th></tr>
<tr><td rowspan="3">Colon</td><td>Ascending</td><td>≥100 eosinophils/HPF</td><td><100 eosinophils/HPF</td></tr>
<tr><td>Descending</td><td>≥85 eosinophils/HPF</td><td><85 eosinophils/HPF</td></tr>
<tr><td>Sigmoid</td><td>≥65 eosinophils/HPF</td><td><65 eosinophils/HPF</td></tr>
</table>

CD, Crohn disease; EoC, eosinophilic colitis; EoG, eosinophilic gatritis; EGID, eosinophilic gastrointestinal disorder; EoE, eosinophilic esophagitis; GI, gastrointestinal; HPF, high-power microscopic field; IBD, inflammatory bowel disease; UC, ulcerative colitis.

Supplementary Table 3. Definitions of EoC histologic features

Features	Definition	Mild/moderate	Marked
Overall eosinophilic inflammation	Estimate overall eosinophilic inflammation	≤ 50% of HPF contain 65 or more eosinophils	> 50% of HPF contain 65 or more eosinophils
Lamina propria eosinophil sheets	Contiguous eosinophils that form masses in the lamina propria and may increase intercryptal distance	Contiguous eosinophil masses without increased intercryptal distance	Contiguous eosinophil masses with increased intercryptal distance
Pericryptal circumferential collars	At least one layer of eosinophils that surround ≥3/4 of circumference of crypt cut in cross section or entire base of a crypt cut lengthwise	Single layer of eosinophils forms collar	More than 1 layer of eosinophils forms collar
Eosinophils in surface epithelium	Eosinophils in surface epithelium	3-5 eosinophils/100 surface colonocytes	> 5 eosinophils/100 surface colonocytes or any size of group of eosinophils
Lymphocytes in surface epithelium	Lymphocytes in surface epithelium	< 10 IEL/100 surface colonocytes	> 10 IEL/100 surface colonocytes
Surface epithelial injury	Surface colonocytes that do not appear homogeneous or intact	Vacuolization, flattening or mucin depletion in epithelial cells that are attached to underlying lamina propria	Detached injured epithelial cells
Eosinophil cryptitis	Eosinophils in crypt epithelium ± eosinophils in lumen	< 20 eosinophils/crypt	≥ 20 eosinophils/crypt or any size of group of eosinophils
Eosinophil crypt abscess	Dilated crypt lined by attenuated epithelium with eosinophils in pericryptal lamina propria, crypt epithelium, and crypt lumen	≤ 10% of crypts	> 10% of crypts
Acute cryptitis	Intraepithelial acute inflammatory cells in any quantity of crypts	Focal infiltration by acute inflammatory cells	Circumferential infiltration by acute inflammatory cells
Acute crypt abscess	Dilated crypt lined by attenuated epithelium with acute inflammatory cells in pericryptal	≤ 10% of crypts	> 10% of crypts

	lamina propria, crypt epithelium, and crypt lumen		
Subcryptal eosinophil aggregates	Groups of 5 or more contiguous eosinophils in lamina propria between crypt base and muscularis mucosa	≤ 10% of crypts	> 10% of crypts
Subcryptal lymphoplasmacytosis	Groups or aggregates of plasma cells or lymphocytes situated between the crypt base and the muscularis mucosa	Affects ≤ 5 crypts	Affects > 5 crypts
Eosinophils in muscularis mucosa/submucosa	Eosinophils in muscularis mucosa/submucosa	Found in ≤ 5 HPF	Found in > 5 HPF
Crypt architectural abnormalities	Elongated crypts, branched crypts, tortuous crypts, atrophic/missing crypts, etc.	≤ 10% of crypts	> 10% of crypts
Crypt dropout/loss	Intercryptal distance is at least doubled	≤ 5 foci	> 5 foci
Crypts partly destroyed by eosinophilic inflammation	Any loss of crypt integrity associated with eosinophils, usually part of a crypt wall is missing and eosinophils are in/near the breach	≤ 10% of crypts	> 10% of crypts
Crypt epithelial injury	Vacuolization, flattening or mucin depletion in crypt epithelial cells	Found in ≤ 5 HPF	Found in > 5 HPF
Acute inflammation	Acute inflammatory cells in lamina propria	Found in ≤ 5 HPF	Found in > 5 HPF
Granulomas	Epithelioid non-necrotizing granulomas in any part of biopsy	Found in ≤ 5 HPF	Found in > 5 HPF

EoC, eosinophilic colitis; HPF, high-power microscopic field; IEL, intraepithelial lymphocytes.

Supplementary Table 4. Demographic and clinical characteristics of study subjects

		NL	Inactive EoC	Active EoC	Inflamed CD	CD with high eosinophils
No. of subjects		8	16	11	6	5
Demographics						
Age at biopsy (years)		15.1 (10.4–17.2)	16.0 (12.4–23.6)	11.2 (7.6–14.2)	17.7 (12.8–19.9)	17.5 (14.1–20.5)
Gender	Male	1 (12.5%)	8 (50.0%)	6 (54.5%)	4 (66.7%)	2 (40.0%)
Race	White	7 (87.5%)	15 (93.8%)	10 (90.9%)	6 (100%)	5 (100%)
Colonic eosinophil counts	Peak (eos/HPF)	28.5 (23.8–37.5)	22 (10.5–40)	100 (80–136)	40.5 (23.3–59.8)	101 (73–106.5)
	Range	2–43	9–42	69 – 187	15–62	66–110
History of EGID						
	EoE	-	6 (37.5%)	9 (81.8%)	-	-
	EoG	-	3 (18.8%)	2 (18.2%)	-	-
	EoC	-	16 (100%)	11 (100%)	-	-
Atopic status						
	Atopy (any)	4 (50.0%)	7 (43.8%)	8 (72.7%)	3 (50.0%)	4 (80.0%)
	Asthma	2 (25.0%)	0 (0%)	6 (54.5%)	1 (16.7%)	1 (20.0%)
	Allergic rhinitis	3 (37.5%)	4 (25.0%)	7 (63.6%)	2 (33.3%)	4 (80.0%)
	Eczema	2 (25.0%)	3 (18.8%)	6 (54.5%)	0 (0%)	1 (20.0%)
	Food allergy	0 (0%)	4 (25.0%)	3 (27.3%)	0 (0%)	0 (0%)
Treatment at biopsy						
	Ongoing diet therapy	1 (12.5%)	9 (56.3%)	3 (27.3%)	1 (16.7%)	1 (20.0%)
	Proton pump inhibitor	4 (50.0%)	2 (12.5%)	7 (63.6%)	0 (0%)	0 (0%)
	Topical steroids	0 (0%)	4 (25.0%)	4 (36.4%)	0 (0%)	0 (0%)
	Systemic steroids	0 (0%)	1 (6.3%)	1 (9.1%)	2 (33.3%)	0 (0%)
	Immune modulator	0 (0%)	0 (0%)	0 (0%)	3 (50.0%)	1 (20.0%)
	Biologics	0 (0%)	0 (0%)	0 (0%)	4 (66.7%)	4 (80.0%)

*Data are n (%) or median (interquartile range [IQR]) unless otherwise stated.
CD, Crohn disease; EoC, eosinophilic colitis; EoG, eosinophilic gastritis; EGID, eosinophilic gastrointestinal disorder; EoE, eosinophilic esophagitis; eos/HPF, eosinophils per high-power microscopic field; NL, normal.

Supplementary Table 5. List of genes in EoC and CD transcriptomes in colon biopsies

EoC transcriptome (Active EoC vs NL)			Correlation with peak colonic eosinophil counts		CD transcriptome (Inflamed CD vs NL)			Correlation with peak colonic eosinophil counts	
Gene Symbol	**FC**	**FDR *P* value**	**Spearman r**	**FDR *P* value**	**Gene Symbol**	**FC**	**FDR *P* value**	**Spearman r**	**FDR *P* value**
CLC	10.2	4.2E-03	0.77	4.5E-05	*SAA1*	19.3	1.3E-03	0.35	2.3E-01
GPA33	8.8	7.0E-03	0.47	2.9E-02	*DMBT1*	14.8	1.5E-02	-0.06	8.7E-01
IFITM1	8.3	1.3E-02	0.61	3.0E-03	*DUOX2*	14.3	1.3E-02	0.01	9.8E-01
MRNIP	7.6	3.7E-03	0.24	2.4E-01	*TNFRSF6B*	11.0	3.8E-04	0.18	5.7E-01
MT1H	7.3	2.8E-02	0.18	3.7E-01	*NOS2*	10.4	1.4E-03	-0.05	8.9E-01
ESRRA	6.6	4.2E-03	0.40	6.0E-02	*DUOXA2*	9.9	2.9E-02	0.09	8.0E-01
MT1X	6.2	1.1E-02	0.06	7.9E-01	*REG1B*	8.9	4.6E-02	0.11	7.5E-01
CDK2AP1	6.1	3.9E-02	-0.06	7.7E-01	*CXCL3*	8.6	4.6E-04	0.36	2.0E-01
CDC26	6.0	2.6E-03	0.35	9.7E-02	*CXCL9*	7.7	1.4E-02	0.02	9.7E-01
SLC35B2	5.4	8.1E-04	0.30	1.5E-01	*MMP3*	7.0	3.0E-02	-0.25	4.1E-01
TMEM251	5.2	9.2E-03	0.34	1.1E-01	*CHI3L1*	6.9	1.2E-02	0.04	9.1E-01
PPP1R35	5.1	3.8E-02	0.16	4.4E-01	*CXCL1*	6.6	2.7E-02	0.40	1.3E-01
PIM1	5.0	1.5E-02	0.60	3.7E-03	*TNIP3*	6.6	6.5E-03	-0.25	4.1E-01
PPP4C	4.9	3.8E-03	0.47	2.5E-02	*SAA2*	6.3	1.3E-02	0.34	2.4E-01
NDUFB3	4.9	3.2E-03	0.41	5.4E-02	*SOCS3*	6.2	8.6E-04	-0.04	9.2E-01
RAB43	4.8	1.8E-02	0.41	5.5E-02	*SAA4*	5.2	1.4E-02	-0.07	8.6E-01
F13A1	4.7	1.1E-02	0.43	4.2E-02	*BATF*	5.2	1.2E-04	-0.02	9.6E-01
IFNGR1	4.6	3.5E-02	0.36	9.0E-02	*G0S2*	5.1	2.2E-02	-0.12	7.4E-01
AC068547.1	4.5	6.7E-03	0.26	2.0E-01	*CXCL10*	5.0	4.1E-02	-0.09	8.1E-01
GNB2	4.5	2.6E-02	0.51	1.6E-02	*IDO1*	4.9	1.6E-02	-0.05	9.0E-01
CLDN23	4.4	1.6E-02	0.31	1.4E-01	*BCL2A1*	4.8	1.5E-02	0.31	2.9E-01
ZFAND3	4.4	4.3E-03	0.42	4.8E-02	*UBD*	4.6	3.1E-03	0.00	9.9E-01
NCSTN	4.4	3.8E-03	0.19	3.5E-01	*C4BPB*	4.6	4.6E-02	-0.26	3.8E-01
PRIMPOL	4.3	3.3E-03	0.26	2.1E-01	*CALHM6*	4.3	1.2E-03	0.34	2.3E-01
PTS	4.2	2.4E-03	0.22	2.7E-01	*GBP5*	4.3	1.4E-03	0.13	7.1E-01
BCL2L10	4.2	4.9E-03	0.39	6.8E-02	*MNDA*	4.1	4.8E-03	0.50	4.5E-02
CTSL	4.2	6.1E-03	0.38	7.4E-02	*TGM2*	4.0	1.0E-02	0.18	5.7E-01
LINC00116	4.1	3.9E-03	0.31	1.4E-01	*IL1B*	4.0	3.9E-02	0.14	6.8E-01
RPIA	4.1	4.2E-03	0.26	2.0E-01	*POU2AF1*	3.9	5.2E-05	0.05	8.9E-01
C5orf15	4.1	4.9E-03	0.46	3.2E-02	*IFITM1*	3.8	1.1E-02	0.61	9.7E-03
JKAMP	4.1	9.1E-03	0.23	2.6E-01	*CDK2AP1*	3.8	2.2E-02	-0.06	8.7E-01
CLEC10A	4.0	4.9E-03	0.60	3.6E-03	*GBP1*	3.7	1.1E-02	0.42	1.2E-01
TXN	3.9	9.1E-03	0.19	3.5E-01	*CFI*	3.7	1.6E-02	0.37	1.9E-01
MAD2L1BP	3.9	3.7E-03	0.48	2.3E-02	*GBP4*	3.7	1.9E-03	0.27	3.7E-01
GAPT	3.9	4.7E-03	0.33	1.2E-01	*CFB*	3.6	2.4E-02	0.06	8.8E-01
SEC61G	3.9	4.7E-03	0.35	1.0E-01	*FCGR1A*	3.5	1.5E-02	0.04	9.1E-01
GAS6	3.9	1.9E-02	0.45	3.4E-02	*CXCL11*	3.5	2.8E-02	0.02	9.7E-01
UNC50	3.8	8.5E-03	0.38	7.7E-02	*SAMD9L*	3.4	1.8E-02	-0.02	9.7E-01
ARL2BP	3.8	3.2E-02	0.37	8.3E-02	*CCL4*	3.4	1.3E-02	0.32	2.7E-01
EEF1A1	3.8	4.6E-03	0.34	1.0E-01	*MDK*	3.4	1.5E-02	-0.19	5.4E-01

CD9	3.8	3.3E-03	0.38	7.0E-02	*APOL1*	3.3	3.9E-02	0.09	8.0E-01
TRPT1	3.8	3.3E-03	0.52	1.4E-02	*NNMT*	3.3	1.2E-03	0.17	5.9E-01
MAP2K1	3.8	8.5E-03	0.45	3.5E-02	*SNX10*	3.3	7.6E-04	-0.07	8.4E-01
IRF8	3.7	1.9E-02	0.18	3.8E-01	*C2*	3.2	1.2E-03	0.56	1.8E-02
CFAP20	3.7	4.1E-03	0.33	1.1E-01	*CD40*	3.2	8.0E-04	0.15	6.4E-01
FCER1A	3.7	4.9E-03	0.27	1.8E-01	*TRIB2*	3.1	2.9E-02	-0.29	3.3E-01
CXCL1	3.6	5.0E-02	0.40	6.0E-02	*OAS2*	3.1	6.5E-04	0.07	8.4E-01
TRIM21	3.6	1.7E-02	0.50	1.8E-02	*KLF2*	3.1	1.3E-02	0.06	8.8E-01
RGCC	3.6	2.7E-02	0.34	1.0E-01	*LYSMD2*	3.1	6.4E-04	0.16	6.1E-01
IFNLR1	3.6	6.5E-03	0.54	1.1E-02	*FGR*	3.1	5.6E-05	0.05	9.0E-01
AKT1	3.5	2.4E-03	0.31	1.5E-01	*HLA-F*	3.1	1.1E-02	0.22	4.7E-01
SLC51B	3.5	3.2E-02	0.49	2.0E-02	*PLA2G16*	3.1	3.2E-03	0.29	3.2E-01
AC138894.1	3.5	3.5E-02	0.34	1.0E-01	*MMP9*	3.0	1.6E-03	0.23	4.4E-01
PIGF	3.5	1.9E-06	0.37	8.3E-02	*PDPN*	3.0	9.4E-03	0.20	5.2E-01
CEBPB	3.4	3.7E-03	0.47	2.5E-02	*KCND3*	3.0	2.6E-02	0.45	8.2E-02
PDE6D	3.4	9.2E-03	0.14	5.0E-01	*RPL22L1*	3.0	5.8E-04	0.10	7.7E-01
TMEM126A	3.4	2.7E-02	0.19	3.6E-01	*TNFAIP2*	3.0	8.5E-05	0.22	4.7E-01
CD300A	3.4	4.2E-03	0.40	5.7E-02	*SOCS1*	3.0	9.3E-03	0.29	3.1E-01
KCTD14	3.4	3.3E-02	0.27	1.9E-01	*TRIM69*	3.0	1.9E-03	0.13	7.1E-01
MYD88	3.4	3.3E-03	0.27	1.9E-01	*GZMB*	3.0	2.5E-02	0.19	5.4E-01
TMEM171	3.4	1.1E-02	0.55	1.1E-02	*DOK3*	3.0	3.7E-04	0.31	3.0E-01
CLIC6	3.4	2.6E-02	0.44	4.0E-02	*IFIT3*	3.0	4.8E-02	0.12	7.4E-01
LRFN4	3.3	4.3E-02	0.24	2.4E-01	*DAPP1*	3.0	8.6E-03	-0.04	9.1E-01
TWF2	3.3	2.9E-02	0.26	2.0E-01	*RAMP3*	2.9	2.5E-02	-0.09	8.1E-01
PRR14	3.2	2.6E-02	0.20	3.3E-01	*CCL11*	2.9	3.1E-02	0.78	1.0E-04
CHPT1	3.2	4.2E-03	0.28	1.7E-01	*TMEM158*	2.9	1.6E-02	-0.21	4.9E-01
NAXD	3.2	1.3E-02	0.40	5.7E-02	*PIM2*	2.9	1.6E-03	-0.05	9.0E-01
MUS81	3.2	8.1E-03	0.19	3.6E-01	*C10orf10*	2.9	2.4E-03	-0.01	9.7E-01
RAB1B	3.2	1.4E-02	0.18	3.7E-01	*RARRES3*	2.9	9.3E-03	0.15	6.5E-01
ACKR3	3.2	9.2E-03	0.28	1.8E-01	*DUSP2*	2.9	1.7E-03	0.24	4.2E-01
MRPL32	3.2	1.9E-02	0.36	9.1E-02	*CD38*	2.8	5.2E-05	0.29	3.2E-01
PTGER2	3.2	4.9E-03	0.64	2.2E-03	*PTP4A3*	2.8	2.8E-02	0.28	3.5E-01
MARCKSL1	3.2	1.9E-03	0.25	2.2E-01	*PLEK*	2.8	9.4E-04	0.42	1.2E-01
FBXL12	3.2	3.9E-03	0.21	3.0E-01	*TIMP1*	2.8	2.2E-02	-0.39	1.5E-01
TTYH3	3.2	1.0E-02	0.44	4.0E-02	*REC8*	2.8	3.9E-03	-0.12	7.3E-01
BMF	3.2	1.2E-04	0.65	1.5E-03	*STAT1*	2.8	6.2E-03	0.06	8.8E-01
MMP12	3.2	2.4E-02	0.44	3.7E-02	*CD53*	2.8	8.9E-03	0.27	3.6E-01
CYSTM1	3.2	9.9E-05	0.54	1.1E-02	*IFNGR1*	2.8	3.3E-02	0.36	2.0E-01
NCF2	3.1	1.2E-02	0.44	4.1E-02	*NMB*	2.7	4.3E-02	-0.11	7.4E-01
TMSB4X	3.1	2.7E-02	0.33	1.1E-01	*IFIT2*	2.7	5.5E-03	0.13	7.1E-01
LY96	3.1	9.4E-03	0.18	3.7E-01	*ARFGAP3*	2.7	1.8E-03	-0.23	4.5E-01
CD53	3.1	9.5E-03	0.27	1.8E-01	*CIITA*	2.7	6.0E-04	0.15	6.6E-01
C16orf91	3.1	2.9E-02	0.31	1.4E-01	*PARP9*	2.7	1.1E-03	0.36	2.1E-01
KTI12	3.1	9.1E-03	0.35	9.7E-02	*PIK3AP1*	2.7	2.0E-03	0.16	6.2E-01

NOP10	3.1	3.1E-04	0.37	8.2E-02	*SMOC2*	2.7	1.8E-02	0.22	4.7E-01
PNP	3.1	1.0E-02	0.35	1.0E-01	*BACE2*	2.7	6.5E-03	0.08	8.3E-01
MGST1	3.1	3.8E-03	0.48	2.4E-02	*SEC14L1*	2.6	3.2E-04	0.39	1.4E-01
NRAS	3.1	8.4E-04	0.45	3.4E-02	*TRIM21*	2.6	7.6E-03	0.50	4.1E-02
DERA	3.0	1.2E-02	0.44	4.0E-02	*PLAUR*	2.6	5.2E-03	0.14	6.7E-01
SEC14L1	3.0	4.2E-03	0.39	6.5E-02	*PNOC*	2.6	2.4E-02	0.21	4.9E-01
CEBPE	3.0	2.7E-02	0.53	1.3E-02	*FCRL5*	2.6	1.4E-02	0.05	8.9E-01
CREG1	3.0	1.4E-02	0.33	1.2E-01	*HLA-DMA*	2.6	6.8E-03	0.20	5.2E-01
DTD1	3.0	1.0E-02	0.25	2.2E-01	*CASP1*	2.6	9.4E-03	0.54	2.5E-02
MNDA	3.0	2.5E-02	0.50	2.0E-02	*ARHGAP25*	2.5	4.6E-03	-0.27	3.7E-01
ZNRF2	3.0	3.7E-02	0.46	3.3E-02	*RASGRP1*	2.5	3.4E-02	0.30	3.0E-01
SDHB	3.0	4.2E-03	0.35	9.3E-02	*LST1*	2.5	6.3E-04	0.52	3.3E-02
ITGAE	3.0	5.4E-03	0.26	2.1E-01	*LAX1*	2.5	4.2E-02	0.04	9.2E-01
C1orf174	2.9	1.2E-02	0.34	1.0E-01	*LINC00116*	2.5	4.1E-03	0.31	2.9E-01
P2RY14	2.9	9.4E-03	0.63	2.3E-03	*BIRC3*	2.5	4.3E-03	0.01	9.7E-01
MGST3	2.9	2.5E-03	0.41	5.5E-02	*CARD6*	2.5	3.2E-02	-0.01	9.7E-01
ELK1	2.9	1.0E-02	0.22	2.7E-01	*WARS*	2.5	7.7E-03	-0.05	8.9E-01
CLDND1	2.9	1.1E-02	0.44	3.9E-02	*TTYH3*	2.5	4.5E-02	0.44	9.1E-02
SLC35A5	2.9	7.4E-03	0.13	5.3E-01	*ARID5A*	2.5	3.8E-03	-0.10	7.8E-01
TMEM150A	2.9	3.3E-03	0.30	1.6E-01	*SRGN*	2.5	3.5E-03	0.31	2.8E-01
CHCHD3	2.8	4.8E-03	0.16	4.2E-01	*MAP3K8*	2.5	1.9E-03	-0.32	2.8E-01
HLA-DMA	2.8	1.6E-02	0.20	3.3E-01	*ST8SIA4*	2.4	6.9E-05	0.33	2.6E-01
RNF146	2.8	1.0E-02	0.25	2.1E-01	*C5orf15*	2.4	4.1E-03	0.46	6.9E-02
CSTB	2.8	1.6E-03	0.63	2.3E-03	*SERPINB9*	2.4	2.0E-02	0.07	8.4E-01
HDHD5	2.8	2.7E-02	0.27	1.9E-01	*ACSL4*	2.4	5.3E-03	0.27	3.6E-01
BCL7B	2.8	1.2E-02	0.32	1.3E-01	*CLEC2B*	2.4	1.3E-02	-0.05	8.9E-01
TDRD7	2.8	8.5E-03	0.48	2.5E-02	*CSF2RB*	2.4	1.8E-04	0.28	3.4E-01
CXCL3	2.8	4.6E-02	0.36	8.7E-02	*RASSF5*	2.4	8.3E-03	0.34	2.4E-01
HS6ST1	2.8	2.2E-02	0.30	1.6E-01	*IRF4*	2.4	1.1E-02	-0.04	9.1E-01
MIPEP	2.8	2.1E-02	0.33	1.2E-01	*LYN*	2.4	3.4E-03	0.26	3.8E-01
LPCAT3	2.8	4.7E-02	0.38	6.9E-02	*MGP*	2.4	3.6E-02	-0.26	3.8E-01
PNRC1	2.8	1.8E-02	0.45	3.7E-02	*TRIM59*	2.4	6.0E-04	0.09	8.0E-01
SMOC2	2.8	4.8E-02	0.22	2.8E-01	*JAK2*	2.4	3.1E-03	-0.13	7.1E-01
NT5C3B	2.7	3.4E-02	0.51	1.6E-02	*TAP2*	2.4	3.7E-03	0.12	7.4E-01
CD4	2.7	1.2E-02	0.35	1.0E-01	*HLA-DOB*	2.4	4.4E-02	-0.08	8.3E-01
COMMD6	2.7	2.0E-02	0.24	2.4E-01	*PRDM1*	2.4	2.3E-02	0.40	1.3E-01
WRNIP1	2.7	3.2E-02	0.31	1.4E-01	*PHLDA1*	2.4	3.2E-02	-0.19	5.3E-01
ALKBH5	2.7	8.5E-03	0.34	1.1E-01	*HLA-B*	2.4	2.9E-03	0.35	2.1E-01
SMIM26	2.7	1.7E-02	0.10	6.2E-01	*LCP1*	2.4	2.9E-04	0.29	3.2E-01
CCL4L2	2.7	2.2E-02	0.35	9.8E-02	*SCPEP1*	2.3	6.1E-03	0.40	1.4E-01
TPBG	2.7	6.4E-04	0.45	3.5E-02	*KLHL6*	2.3	6.6E-03	0.16	6.2E-01
SERPINF1	2.7	4.3E-02	0.37	8.2E-02	*CLEC4E*	2.3	2.3E-03	0.14	6.9E-01
FOXF2	2.7	1.5E-02	0.22	2.8E-01	*LRFN4*	2.3	1.1E-02	0.24	4.2E-01
TMEM230	2.7	3.7E-03	0.35	1.0E-01	*ANXA3*	2.3	1.9E-02	-0.21	5.0E-01

PLD3	2.7	3.3E-03	0.37	8.3E-02	*RAB8B*	2.3	1.8E-03	0.37	1.9E-01
FOXA1	2.7	2.7E-02	0.51	1.7E-02	*LY6E*	2.3	4.2E-02	-0.32	2.8E-01
SF3B4	2.7	2.5E-02	0.27	1.8E-01	*TSPAN5*	2.3	2.2E-02	-0.10	7.7E-01
TIPARP	2.7	1.6E-02	0.67	1.1E-03	*CYTIP*	2.3	1.5E-02	-0.09	8.1E-01
HLA-DQB2	2.7	8.5E-03	0.30	1.5E-01	*NDUFB3*	2.3	2.9E-03	0.41	1.2E-01
RNF128	2.7	3.1E-02	0.55	1.1E-02	*APOBEC3D*	2.3	3.7E-02	-0.31	2.9E-01
CTDSP2	2.6	4.9E-03	0.35	1.0E-01	*CLEC4A*	2.3	4.1E-02	-0.25	4.1E-01
MED20	2.6	1.8E-02	0.40	6.2E-02	*UBE2L6*	2.3	6.9E-03	0.61	9.7E-03
CEBPD	2.6	1.3E-02	0.56	8.6E-03	*SLC35B2*	2.3	1.9E-02	0.30	3.0E-01
GCH1	2.6	8.1E-03	0.43	4.2E-02	*PNO1*	2.3	1.1E-03	0.01	9.8E-01
ZNF706	2.6	4.2E-03	0.14	5.0E-01	*ITGAX*	2.3	1.0E-02	0.30	3.0E-01
NDUFC1	2.6	1.2E-02	0.09	6.7E-01	*NLRC5*	2.3	4.0E-03	-0.48	5.6E-02
YAP1	2.6	4.0E-03	0.56	9.5E-03	*KLHL5*	2.3	5.7E-03	0.20	5.2E-01
ITM2C	2.6	3.1E-02	0.11	5.9E-01	*MZB1*	2.3	1.8E-02	0.20	5.2E-01
BRPF3	2.6	1.6E-02	0.07	7.3E-01	*PDP1*	2.2	3.1E-03	-0.14	6.7E-01
ACVR1B	2.6	1.9E-02	0.36	8.7E-02	*LILRB3*	2.2	4.9E-02	0.19	5.4E-01
OST4	2.6	4.1E-03	0.20	3.2E-01	*COL1A2*	2.2	3.7E-02	0.64	6.2E-03
SDHAF3	2.6	1.1E-02	0.05	8.3E-01	*FAM129A*	2.2	7.6E-03	0.13	6.9E-01
ZNF513	2.6	1.1E-02	0.35	9.7E-02	*IRF8*	2.2	4.7E-02	0.18	5.7E-01
RPL30	2.6	3.9E-03	0.29	1.6E-01	*GPX2*	2.2	8.3E-03	-0.43	9.7E-02
DNAJB9	2.6	3.1E-02	0.33	1.2E-01	*CCL4L2*	2.2	2.0E-02	0.35	2.2E-01
TCEAL7	2.6	2.6E-02	0.40	6.0E-02	*CYSLTR1*	2.2	2.8E-02	0.29	3.2E-01
FAM214B	2.6	4.1E-02	0.55	1.1E-02	*ITGB2*	2.2	1.9E-03	0.10	7.8E-01
CDK8	2.6	4.4E-02	0.48	2.3E-02	*SKAP1*	2.2	3.2E-02	0.08	8.3E-01
CYP2C9	2.6	2.0E-02	0.66	1.4E-03	*PPP1R18*	2.2	3.8E-02	0.26	3.8E-01
WDR6	2.6	1.8E-02	0.34	1.1E-01	*CTSK*	2.2	3.5E-02	0.19	5.2E-01
LHFPL6	2.6	3.1E-02	0.25	2.3E-01	*PFKFB3*	2.2	4.2E-02	-0.20	5.2E-01
CTGF	2.5	6.8E-03	0.34	1.1E-01	*PLEKHO1*	2.2	1.1E-03	0.10	7.9E-01
EIF2D	2.5	1.3E-02	0.35	9.8E-02	*SLAMF7*	2.2	1.8E-02	0.44	9.4E-02
EIF1AD	2.5	1.2E-03	0.48	2.5E-02	*IFI27L2*	2.2	2.4E-02	-0.26	3.8E-01
DCTN6	2.5	1.8E-02	0.15	4.6E-01	*TMEM126A*	2.2	4.1E-03	0.19	5.4E-01
KLF4	2.5	2.9E-02	0.55	9.8E-03	*CD300A*	2.2	3.6E-03	0.40	1.3E-01
MRPL34	2.5	3.0E-03	0.35	9.6E-02	*MCUB*	2.2	1.4E-03	0.06	8.8E-01
MFSD1	2.5	5.7E-03	0.35	9.9E-02	*LPGAT1*	2.2	1.9E-02	0.49	4.6E-02
GLRX	2.5	2.1E-02	0.54	1.1E-02	*PTPRC*	2.2	2.8E-02	0.03	9.4E-01
ACAT1	2.5	3.1E-02	0.44	3.8E-02	*LYZ*	2.2	1.4E-02	-0.11	7.4E-01
DDHD2	2.5	3.3E-03	0.29	1.6E-01	*SLFN5*	2.2	3.7E-02	0.12	7.4E-01
ELOC	2.5	1.4E-02	0.28	1.8E-01	*SCRN1*	2.2	1.2E-02	0.08	8.2E-01
B4GALT4	2.5	1.7E-02	0.19	3.5E-01	*MSN*	2.2	3.5E-04	0.13	7.1E-01
TMEM14C	2.5	1.4E-02	0.37	7.9E-02	*SERPING1*	2.2	2.2E-02	-0.21	5.0E-01
SH3BP4	2.5	4.9E-03	0.08	7.2E-01	*SAMSN1*	2.2	1.8E-02	0.29	3.3E-01
EMC7	2.5	2.5E-02	0.10	6.4E-01	*DNAJB9*	2.2	2.0E-02	0.33	2.6E-01
TAF5L	2.5	7.6E-03	0.14	5.0E-01	*CD274*	2.2	1.8E-02	0.03	9.5E-01
C2orf76	2.5	5.7E-03	0.42	5.0E-02	*PLEKHA4*	2.2	4.7E-02	-0.16	6.2E-01

TMEM35B	2.5	1.5E-02	0.43	4.2E-02	*HLA-DRA*	2.1	3.0E-03	0.33	2.4E-01
PHLPP2	2.5	1.8E-02	0.68	1.0E-03	*PCDH7*	2.1	4.7E-02	0.34	2.3E-01
RPL22L1	2.5	1.4E-02	0.10	6.1E-01	*TMEM251*	2.1	1.8E-02	0.34	2.4E-01
ABCB10	2.5	3.7E-03	0.47	2.6E-02	*IGFBP7*	2.1	3.4E-02	0.42	1.2E-01
HOXB2	2.5	4.4E-02	0.41	5.2E-02	*DRAM1*	2.1	3.2E-02	0.23	4.6E-01
GLIPR1	2.5	4.0E-02	0.18	3.7E-01	*JKAMP*	2.1	5.5E-03	0.23	4.5E-01
HLA-F	2.5	1.7E-02	0.22	2.7E-01	*TEAD3*	2.1	1.9E-03	0.03	9.5E-01
IGIP	2.5	1.3E-02	0.25	2.1E-01	*EVI2B*	2.1	6.5E-03	0.18	5.6E-01
GRAMD4	2.5	1.9E-02	0.58	5.6E-03	*SLA*	2.1	4.7E-02	0.31	2.9E-01
RAP2A	2.5	4.5E-02	0.11	5.9E-01	*CHST11*	2.1	3.6E-03	0.26	3.9E-01
RPS25	2.5	3.7E-03	0.24	2.3E-01	*GIMAP5*	2.1	3.6E-02	-0.02	9.6E-01
SPHK2	2.5	4.3E-02	0.56	8.7E-03	*BCL6*	2.1	2.7E-02	-0.02	9.7E-01
LIPA	2.4	5.0E-03	0.45	3.7E-02	*LPIN1*	2.1	2.3E-03	-0.19	5.4E-01
RNF5	2.4	3.8E-03	0.47	2.6E-02	*GIMAP1*	2.1	1.1E-02	0.12	7.3E-01
PHC2	2.4	1.3E-02	0.37	8.3E-02	*PDE6D*	2.1	1.9E-02	0.14	6.7E-01
SDHC	2.4	3.7E-03	0.34	1.1E-01	*CLEC7A*	2.1	9.6E-03	0.13	7.1E-01
PCDH18	2.4	1.8E-02	0.49	2.2E-02	*TRIM22*	2.1	2.3E-02	0.26	3.9E-01
SEC61B	2.4	3.5E-02	0.30	1.5E-01	*ASPHD2*	2.1	1.6E-02	0.15	6.6E-01
LYSMD3	2.4	1.8E-03	0.43	4.5E-02	*FBXO5*	2.1	3.9E-02	-0.14	6.6E-01
TMEM242	2.4	3.8E-03	0.24	2.4E-01	*RIOX2*	2.1	8.3E-04	0.20	5.2E-01
LGMN	2.4	1.7E-02	0.53	1.2E-02	*CD82*	2.1	2.9E-02	0.12	7.3E-01
CKLF	2.4	2.4E-02	0.40	5.7E-02	*PSMB9*	2.1	1.8E-02	0.31	2.9E-01
LSM6	2.4	3.0E-02	0.41	5.4E-02	*TAP1*	2.1	1.4E-02	0.15	6.6E-01
MAGEF1	2.4	6.3E-03	0.01	9.5E-01	*LAP3*	2.1	5.2E-03	0.35	2.2E-01
PRIM2	2.4	1.3E-02	0.20	3.3E-01	*CEBPB*	2.1	2.3E-02	0.47	5.7E-02
ZNF319	2.4	4.3E-02	0.18	3.7E-01	*PLCG2*	2.1	1.7E-02	0.13	7.1E-01
TMTC2	2.4	1.1E-02	0.28	1.7E-01	*ISG20*	2.1	3.7E-02	0.17	5.8E-01
SF3B6	2.4	9.1E-03	0.45	3.7E-02	*RNF24*	2.1	3.4E-04	0.63	7.2E-03
TCF21	2.4	2.8E-02	0.52	1.5E-02	*SIRPA*	2.1	7.6E-03	0.43	9.7E-02
KLRB1	2.4	4.0E-02	0.20	3.4E-01	*ANGPT2*	2.1	8.2E-03	-0.20	5.1E-01
TFB2M	2.4	1.2E-02	0.45	3.4E-02	*TCEAL3*	2.1	2.8E-02	-0.06	8.8E-01
WRAP73	2.4	1.0E-02	0.32	1.3E-01	*IFI16*	2.0	3.9E-03	-0.07	8.5E-01
GATM	2.4	2.2E-02	0.38	7.4E-02	*FAM117A*	2.0	1.4E-02	0.04	9.1E-01
HSPA1A	2.4	4.9E-02	0.62	2.5E-03	*XBP1*	2.0	2.9E-02	-0.01	9.7E-01
YRDC	2.4	2.4E-02	0.16	4.3E-01	*CCDC71L*	2.0	7.6E-03	0.31	3.0E-01
IGFBP7	2.4	4.3E-02	0.42	5.1E-02	*IFITM3*	2.0	7.8E-03	0.25	4.0E-01
ZC3H7B	2.4	4.7E-02	0.26	2.0E-01	*CDC26*	2.0	1.6E-02	0.35	2.2E-01
CYBRD1	2.4	9.1E-03	0.45	3.4E-02	*VAMP5*	2.0	1.9E-02	0.23	4.4E-01
SGSH	2.4	3.7E-03	0.32	1.3E-01	*PMEPA1*	2.0	2.0E-02	0.11	7.6E-01
MAPK7	2.3	9.9E-05	0.37	8.1E-02	*PTAFR*	2.0	1.1E-02	0.49	4.9E-02
MYC	2.3	3.0E-02	0.34	1.1E-01	*SOD2*	2.0	9.6E-04	0.35	2.2E-01
HIKESHI	2.3	2.8E-02	0.25	2.2E-01	*STX2*	2.0	1.3E-02	0.12	7.1E-01
SRP9	2.3	4.2E-02	0.34	1.1E-01	*PTS*	2.0	7.6E-03	0.22	4.6E-01
OXER1	2.3	2.7E-02	0.17	4.0E-01	*MRPL32*	2.0	1.3E-02	0.36	2.1E-01

B3GALT1	2.3	4.0E-02	0.03	8.7E-01	*IL3RA*	2.0	3.2E-02	-0.24	4.2E-01
TBC1D22B	2.3	2.3E-02	0.15	4.6E-01	*BASP1*	2.0	3.1E-02	0.32	2.7E-01
SLBP	2.3	1.8E-02	0.33	1.1E-01	*TBXAS1*	2.0	4.7E-02	0.21	4.9E-01
LUM	2.3	1.0E-02	0.49	2.2E-02	*IRF9*	2.0	3.5E-02	0.22	4.7E-01
OGT	2.3	1.9E-02	0.36	9.1E-02	*VCAM1*	2.0	3.2E-02	0.30	3.0E-01
POLR2K	2.3	1.9E-02	0.02	9.4E-01	*CTSL*	2.0	4.4E-02	0.38	1.7E-01
B2M	2.3	1.0E-02	0.34	1.1E-01	*CASP8*	2.0	2.8E-02	-0.05	9.0E-01
DUSP2	2.3	8.5E-03	0.24	2.4E-01	*MAP2K1*	2.0	2.5E-02	0.45	8.0E-02
CPSF7	2.3	5.7E-03	0.41	5.2E-02	*PECAM1*	2.0	2.7E-02	-0.21	5.0E-01
NBPF11	2.3	1.9E-02	0.17	3.9E-01	*DCK*	2.0	1.3E-02	-0.34	2.3E-01
RHPN2	2.3	3.5E-02	0.25	2.2E-01	*MUS81*	2.0	7.7E-03	0.19	5.4E-01
SPINT2	2.3	4.7E-03	0.22	2.8E-01	*CD74*	2.0	8.3E-03	0.11	7.4E-01
TM9SF2	2.3	6.2E-03	0.42	4.7E-02	*IRF1*	1.9	3.8E-02	0.26	3.8E-01
HLA-B	2.3	6.8E-03	0.35	9.3E-02	*HLA-DMB*	1.9	6.2E-03	0.25	4.0E-01
SNX27	2.3	7.6E-03	0.44	3.7E-02	*DPYD*	1.9	3.0E-02	0.23	4.6E-01
PFN2	2.3	1.5E-02	0.54	1.1E-02	*IFITM2*	1.9	7.4E-03	0.12	7.3E-01
COL4A1	2.3	3.1E-02	0.53	1.2E-02	*ASRGL1*	1.9	3.1E-02	-0.60	9.9E-03
PPP1R14B	2.3	8.5E-03	0.48	2.5E-02	*CHST15*	1.9	1.2E-02	0.37	1.8E-01
SLC16A5	2.3	4.3E-02	0.59	4.7E-03	*ARHGDIB*	1.9	4.6E-02	0.01	9.8E-01
IL15RA	2.3	1.8E-02	0.55	9.7E-03	*RAB31*	1.9	1.2E-02	0.17	5.8E-01
RGP1	2.3	3.1E-02	0.48	2.5E-02	*ZYX*	1.9	4.4E-02	0.30	3.0E-01
DYNLT1	2.3	2.4E-03	0.32	1.2E-01	*BLVRA*	1.9	3.4E-02	0.05	9.0E-01
C19orf38	2.3	1.6E-02	0.25	2.2E-01	*USP18*	1.9	3.7E-02	0.02	9.7E-01
SRSF2	2.3	1.9E-02	0.07	7.5E-01	*TAF5L*	1.9	8.3E-04	0.14	6.8E-01
RB1	2.3	4.9E-03	0.25	2.2E-01	*TMEM165*	1.9	2.6E-03	0.20	5.2E-01
SIAH2	2.3	1.4E-02	0.27	1.9E-01	*ADGRE2*	1.9	2.1E-02	0.36	1.9E-01
PCNP	2.3	6.3E-03	0.23	2.5E-01	*TXN*	1.9	2.8E-02	0.19	5.4E-01
NUP37	2.3	2.8E-02	0.42	4.8E-02	*B2M*	1.9	1.4E-02	0.34	2.4E-01
PIK3AP1	2.3	2.7E-02	0.16	4.3E-01	*PARP14*	1.9	1.6E-02	0.07	8.4E-01
CSF2RB	2.3	2.6E-02	0.28	1.7E-01	*ST6GAL1*	1.9	2.0E-02	-0.05	8.9E-01
REPIN1	2.2	3.7E-03	0.28	1.8E-01	*IFI30*	1.9	1.6E-02	-0.07	8.4E-01
OCRL	2.2	3.7E-03	0.43	4.2E-02	*MTHFD2*	1.9	2.5E-04	-0.16	6.2E-01
RPS15A	2.2	3.4E-03	0.12	5.5E-01	*HERPUD1*	1.9	1.1E-02	0.23	4.5E-01
NECTIN1	2.2	3.9E-03	0.21	3.0E-01	*SGMS1*	1.9	3.9E-02	0.28	3.5E-01
BCL2L11	2.2	2.9E-02	0.39	6.3E-02	*COL6A3*	1.9	4.4E-02	0.49	4.9E-02
SDF2	2.2	1.5E-02	0.49	2.2E-02	*TDRD7*	1.9	3.2E-02	0.48	5.4E-02
SDCCAG3	2.2	1.4E-02	0.28	1.7E-01	*PDE4B*	1.9	1.6E-02	0.07	8.6E-01
RDH10	2.2	3.1E-02	0.48	2.3E-02	*ANXA5*	1.9	2.1E-02	0.40	1.4E-01
WLS	2.2	1.7E-02	0.39	6.3E-02	*SETD7*	1.9	1.3E-02	-0.33	2.6E-01
MCM2	2.2	4.4E-02	0.03	9.0E-01	*HIKESHI*	1.9	1.3E-02	0.25	4.1E-01
OAT	2.2	2.7E-02	0.50	1.9E-02	*TNFAIP8*	1.9	1.3E-02	-0.03	9.3E-01
GTF2A1	2.2	3.7E-03	0.39	6.5E-02	*ADA2*	1.9	6.5E-03	0.46	6.5E-02
AMY2B	2.2	2.0E-02	0.25	2.2E-01	*ORC6*	1.9	2.6E-02	-0.35	2.2E-01
DUS3L	2.2	1.9E-02	0.02	9.4E-01	*GLRX*	1.9	3.3E-02	0.54	2.6E-02

TMEM206	2.2	2.4E-02	0.29	1.6E-01	*CARD8*	1.9	7.0E-03	0.18	5.7E-01
ZBTB5	2.2	2.5E-02	0.31	1.4E-01	*ORAI2*	1.9	3.4E-02	0.12	7.4E-01
PAN2	2.2	2.5E-02	0.46	3.1E-02	*RAP2A*	1.9	2.5E-02	0.11	7.6E-01
SIRPA	2.2	1.8E-02	0.43	4.2E-02	*GIMAP8*	1.9	4.0E-02	0.21	5.1E-01
CLDN7	2.2	9.1E-03	0.60	3.7E-03	*LRP8*	1.9	2.0E-02	-0.53	2.8E-02
SGCE	2.2	4.2E-02	0.27	1.9E-01	*HAPLN3*	1.9	2.4E-02	0.03	9.3E-01
TMIGD3	2.2	3.7E-02	0.35	9.3E-02	*ICAM1*	1.9	2.6E-02	-0.18	5.7E-01
DTX3	2.2	2.7E-02	0.24	2.4E-01	*PI4K2B*	1.9	4.3E-02	0.12	7.3E-01
C15orf48	2.2	1.1E-02	0.30	1.5E-01	*TIFA*	1.8	4.5E-02	0.46	6.5E-02
TNS3	2.2	2.2E-02	0.62	2.5E-03	*FSTL1*	1.8	2.9E-02	0.19	5.3E-01
CD276	2.2	1.0E-02	0.29	1.7E-01	*ARHGAP15*	1.8	4.3E-02	0.09	8.0E-01
ISCA2	2.2	6.2E-03	0.36	9.1E-02	*GCH1*	1.8	3.5E-03	0.43	9.7E-02
GADD45B	2.2	4.0E-02	0.62	2.5E-03	*SYT11*	1.8	2.7E-02	0.14	6.7E-01
TICAM1	2.2	3.3E-02	0.30	1.5E-01	*FKBP5*	1.8	1.3E-02	-0.02	9.6E-01
ZBED6CL	2.2	4.7E-02	0.14	5.0E-01	*DBF4*	1.8	3.9E-02	-0.07	8.4E-01
TEAD3	2.2	2.1E-02	0.03	9.0E-01	*FAM46C*	1.8	4.3E-02	-0.02	9.7E-01
MS4A4A	2.2	3.8E-02	0.41	5.5E-02	*LILRB4*	1.8	3.3E-02	0.05	8.9E-01
LST1	2.2	4.5E-02	0.52	1.5E-02	*CKLF*	1.8	1.9E-02	0.40	1.3E-01
F2RL1	2.1	2.2E-02	0.51	1.6E-02	*TVP23B*	1.8	2.7E-02	0.00	1.0E+00
ZFAND1	2.1	1.9E-02	0.20	3.2E-01	*MALT1*	1.8	2.5E-03	-0.25	4.0E-01
FAM117A	2.1	8.8E-03	0.04	8.4E-01	*MANF*	1.8	7.7E-03	0.27	3.6E-01
VIM	2.1	2.2E-02	0.50	1.9E-02	*PELO*	1.8	1.4E-02	-0.20	5.2E-01
PATL1	2.1	2.2E-02	0.28	1.7E-01	*MYD88*	1.8	6.3E-03	0.27	3.6E-01
CCL11	2.1	5.0E-02	0.78	4.5E-05	*ELOVL5*	1.8	1.4E-02	0.18	5.7E-01
CNKSR1	2.1	3.7E-02	0.30	1.5E-01	*RBPMS*	1.8	3.2E-02	0.19	5.4E-01
MXD3	2.1	4.3E-02	0.19	3.5E-01	*CCDC102B*	1.8	3.2E-02	-0.02	9.7E-01
RNPEP	2.1	5.7E-03	0.34	1.1E-01	*SYVN1*	1.8	2.1E-02	0.21	5.0E-01
DNAJA3	2.1	3.2E-02	0.26	2.1E-01	*TRAM1*	1.8	3.8E-02	0.47	5.9E-02
PODXL	2.1	1.1E-02	0.25	2.1E-01	*QKI*	1.8	6.9E-03	0.42	1.1E-01
ZDHHC5	2.1	6.7E-03	0.55	1.1E-02	*MYC*	1.8	1.6E-02	0.34	2.4E-01
NR1I2	2.1	1.6E-02	0.44	4.0E-02	*HPS5*	1.8	3.4E-02	0.06	8.7E-01
ADAMDEC1	2.1	1.6E-03	0.51	1.6E-02	*C1R*	1.8	1.2E-02	0.24	4.2E-01
MDH1	2.1	4.6E-03	0.33	1.2E-01	*WRAP73*	1.8	1.3E-03	0.32	2.7E-01
NUDT21	2.1	2.0E-02	0.29	1.6E-01	*PIM3*	1.8	2.1E-03	-0.41	1.2E-01
UBL5	2.1	3.0E-02	0.05	8.2E-01	*MCFD2*	1.8	1.9E-02	-0.27	3.7E-01
NECAP2	2.1	1.8E-03	0.45	3.4E-02	*IRF7*	1.8	1.4E-03	0.25	4.0E-01
PLCG2	2.1	2.1E-02	0.13	5.3E-01	*GLCCI1*	1.8	2.8E-02	0.04	9.1E-01
COL3A1	2.1	4.4E-02	0.60	3.7E-03	*NCOA7*	1.8	1.5E-02	0.18	5.5E-01
QSOX2	2.1	2.8E-02	0.45	3.4E-02	*C1orf174*	1.8	1.4E-02	0.34	2.3E-01
PLAU	2.1	4.8E-02	0.42	5.0E-02	*MCM2*	1.8	4.3E-02	0.03	9.5E-01
CHEK2	2.1	1.9E-02	0.25	2.2E-01	*CTSC*	1.8	1.8E-04	0.61	9.9E-03
ADD1	2.1	5.7E-03	0.53	1.1E-02	*RBMS1*	1.8	3.8E-02	0.30	3.0E-01
JOSD1	2.1	3.3E-03	0.70	5.5E-04	*ABCB10*	1.8	1.0E-02	0.47	5.8E-02
ZFP36L2	2.1	1.3E-02	0.33	1.1E-01	*AKAP2*	1.8	1.4E-02	0.00	1.0E+00

ETNK1	2.1	1.4E-02	0.70	5.5E-04	*MTMR6*	1.8	2.8E-04	0.08	8.4E-01
LZTS2	2.1	2.3E-02	0.48	2.5E-02	*PIP4K2A*	1.8	1.1E-02	0.38	1.6E-01
C2	2.1	3.8E-02	0.56	8.5E-03	*FAM49A*	1.7	3.4E-03	0.23	4.6E-01
ZNF816	2.1	4.6E-02	0.52	1.5E-02	*ZC3H7B*	1.7	2.0E-02	0.26	3.8E-01
MRPS14	2.1	2.8E-02	0.24	2.3E-01	*LMO4*	1.7	2.3E-02	0.22	4.7E-01
DYRK4	2.1	4.9E-02	0.26	2.0E-01	*TRAFD1*	1.7	4.0E-02	0.29	3.3E-01
ADA2	2.1	1.3E-02	0.46	3.0E-02	*SLC25A28*	1.7	7.3E-03	-0.09	8.0E-01
HBP1	2.1	1.9E-02	0.41	5.5E-02	*H2AFX*	1.7	1.1E-02	0.12	7.1E-01
RCC1	2.1	5.1E-03	0.40	6.0E-02	*AMPD2*	1.7	2.4E-02	0.20	5.2E-01
MAT2B	2.1	7.4E-03	0.36	8.7E-02	*CYTH4*	1.7	5.5E-03	-0.15	6.6E-01
WDR11	2.1	2.1E-02	0.19	3.5E-01	*TFEC*	1.7	1.2E-02	0.28	3.4E-01
CCNG1	2.0	4.6E-03	0.25	2.1E-01	*ALKBH5*	1.7	1.2E-02	0.34	2.4E-01
SLC38A9	2.0	3.4E-02	0.32	1.3E-01	*CHPT1*	1.7	1.5E-02	0.28	3.3E-01
GTF3C2	2.0	3.8E-02	0.23	2.7E-01	*ST3GAL1*	1.7	3.6E-02	-0.04	9.2E-01
ANXA5	2.0	4.1E-02	0.40	6.2E-02	*SP110*	1.7	5.3E-03	-0.05	8.9E-01
KBTBD3	2.0	9.5E-03	0.12	5.7E-01	*PSMB8*	1.7	3.3E-02	0.31	2.8E-01
SNRPF	2.0	3.5E-02	-0.06	7.7E-01	*RNF145*	1.7	2.8E-03	0.18	5.7E-01
LTA4H	2.0	3.1E-03	0.54	1.1E-02	*LINS1*	1.7	2.6E-02	0.20	5.2E-01
TRAM1	2.0	4.4E-02	0.47	2.6E-02	*ARID3A*	1.7	2.8E-02	0.48	5.1E-02
ZNF598	2.0	4.1E-02	0.22	2.7E-01	*TCIRG1*	1.7	2.7E-02	-0.16	6.1E-01
XYLT1	2.0	1.8E-02	0.54	1.1E-02	*CREB3L2*	1.7	4.7E-03	0.41	1.2E-01
AMPD2	2.0	5.0E-02	0.20	3.3E-01	*PPT1*	1.7	3.6E-03	0.25	4.1E-01
ARMC8	2.0	1.8E-02	0.21	3.0E-01	*IL15RA*	1.7	4.2E-02	0.55	2.1E-02
FERMT2	2.0	2.7E-02	0.51	1.6E-02	*FAM241B*	1.7	1.6E-02	0.13	7.1E-01
PHF1	2.0	4.3E-03	0.10	6.2E-01	*MAFB*	1.7	2.9E-03	0.42	1.1E-01
LYPLA1	2.0	4.2E-02	0.45	3.6E-02	*HIF1A*	1.7	7.3E-03	0.21	4.9E-01
TADA2B	2.0	9.2E-03	0.33	1.2E-01	*CDK17*	1.7	5.1E-03	0.33	2.6E-01
WDR48	2.0	1.3E-02	0.52	1.4E-02	*FAM3C*	1.7	4.9E-03	-0.20	5.2E-01
TSEN54	2.0	2.6E-02	0.36	8.7E-02	*RNF213*	1.7	1.3E-02	0.32	2.8E-01
C1QBP	2.0	3.1E-02	0.06	7.9E-01	*ELOC*	1.7	1.0E-02	0.28	3.5E-01
CTSC	2.0	8.5E-03	0.61	3.5E-03	*COTL1*	1.7	4.2E-02	0.12	7.1E-01
WASHC5	2.0	4.3E-02	0.19	3.4E-01	*KLHL2*	1.7	4.0E-02	-0.01	9.7E-01
SIK3	2.0	3.1E-02	0.41	5.5E-02	*ZBTB17*	1.7	3.1E-02	0.23	4.5E-01
GON7	2.0	8.1E-03	0.32	1.3E-01	*WDR11*	1.7	5.7E-03	0.19	5.3E-01
RBM27	2.0	2.0E-02	0.19	3.6E-01	*PIEZO1*	1.7	3.5E-02	0.25	4.0E-01
LEFTY1	2.0	4.6E-02	0.05	8.1E-01	*MAGEF1*	1.7	1.0E-02	0.01	9.7E-01
PYCARD	2.0	1.3E-02	0.28	1.7E-01	*MMP25*	1.7	1.8E-02	0.43	9.7E-02
LSM14B	2.0	1.6E-02	0.28	1.7E-01	*ODC1*	1.7	3.6E-02	-0.16	6.1E-01
RPS18	2.0	1.2E-02	0.07	7.3E-01	*DCTN6*	1.7	4.2E-02	0.15	6.4E-01
KCTD5	2.0	3.8E-02	0.51	1.6E-02	*ASAP1*	1.7	1.2E-02	-0.03	9.5E-01
PYURF	2.0	3.5E-02	0.45	3.4E-02	*HRH2*	1.7	1.3E-02	0.38	1.6E-01
GCHFR	2.0	3.1E-02	0.16	4.2E-01	*RHOQ*	1.7	6.7E-03	0.10	7.8E-01
MANSC1	2.0	3.2E-02	0.41	5.5E-02	*RRP15*	1.7	8.1E-04	-0.43	9.7E-02
EFNB1	2.0	3.8E-02	0.40	6.2E-02	*DSE*	1.7	2.5E-02	0.19	5.3E-01

DENND6A	2.0	5.0E-02	0.57	6.9E-03	*ELK1*	1.6	4.2E-02	0.22	4.6E-01
SLC44A3	2.0	2.5E-02	0.37	8.0E-02	*BTN3A1*	1.6	1.5E-02	-0.13	7.1E-01
KDM6B	2.0	2.5E-02	0.44	4.0E-02	*PAPSS1*	1.6	3.7E-02	0.24	4.2E-01
PIP4P1	2.0	4.0E-02	0.13	5.4E-01	*SH3BP4*	1.6	4.6E-02	0.08	8.4E-01
KDM4C	2.0	1.2E-02	0.57	7.6E-03	*SNRPF*	1.6	7.6E-03	-0.06	8.7E-01
RPS27	2.0	3.7E-02	0.06	7.7E-01	*HELZ2*	1.6	4.5E-02	0.36	2.1E-01
FAM122A	1.9	3.7E-02	0.18	3.7E-01	*C1GALT1*	1.6	4.1E-03	0.39	1.4E-01
GPR82	1.9	5.0E-02	0.55	9.7E-03	*IGIP*	1.6	4.5E-02	0.25	4.0E-01
MINOS1	1.9	4.0E-02	0.30	1.5E-01	*MTMR14*	1.6	1.5E-02	0.20	5.2E-01
AP3M1	1.9	4.3E-03	0.31	1.4E-01	*CASP4*	1.6	3.6E-02	-0.19	5.4E-01
RFT1	1.9	4.4E-02	0.21	3.0E-01	*HLA-DPA1*	1.6	1.2E-02	0.17	5.9E-01
HSPA8	1.9	4.7E-02	0.08	7.2E-01	*RASGEF1B*	1.6	4.8E-02	0.01	9.7E-01
FASTKD3	1.9	4.4E-02	0.55	1.1E-02	*FBXW11*	1.6	1.3E-02	0.46	6.8E-02
LIX1L	1.9	4.8E-02	0.26	2.0E-01	*SESTD1*	1.6	1.5E-02	-0.54	2.5E-02
UMAD1	1.9	3.2E-02	0.23	2.5E-01	*CARD16*	1.6	3.7E-02	0.31	3.0E-01
NCAPG2	1.9	1.1E-02	-0.01	9.6E-01	*TRAF1*	1.6	2.6E-02	-0.09	8.1E-01
ATP6V0D2	1.9	4.4E-02	0.32	1.3E-01	*NUCB2*	1.6	2.3E-02	-0.57	1.4E-02
DENND3	1.9	2.1E-02	0.38	7.4E-02	*TGFBR2*	1.6	1.7E-02	0.27	3.7E-01
SPATA33	1.9	4.7E-02	-0.06	7.7E-01	*STAT5A*	1.6	3.5E-02	0.22	4.6E-01
HIGD2A	1.9	1.7E-02	-0.01	9.6E-01	*MARCKSL1*	1.6	4.7E-02	0.25	4.1E-01
PCMTD2	1.9	3.5E-02	0.48	2.5E-02	*TC2N*	1.6	9.2E-03	-0.24	4.2E-01
PNMA1	1.9	1.3E-02	0.27	1.9E-01	*PPA1*	1.6	9.4E-03	0.22	4.8E-01
QPCT	1.9	4.3E-02	0.63	2.3E-03	*CCDC69*	1.6	2.0E-02	0.11	7.6E-01
PPP1R14C	1.9	9.1E-03	0.49	2.2E-02	*RB1*	1.6	4.9E-03	0.25	4.0E-01
USP32	1.9	2.8E-02	0.48	2.4E-02	*PEA15*	1.6	1.9E-02	-0.29	3.3E-01
ANXA4	1.9	4.2E-03	0.41	5.5E-02	*PRKAR2B*	1.6	3.8E-02	-0.33	2.4E-01
SMIM20	1.9	4.2E-02	0.34	1.0E-01	*PHC2*	1.6	3.9E-02	0.37	1.9E-01
NUS1	1.9	8.5E-03	0.45	3.7E-02	*PPP1R2*	1.6	3.9E-03	0.16	6.2E-01
ARPC1A	1.9	1.5E-02	0.08	7.0E-01	*RGL1*	1.6	1.4E-02	0.49	4.9E-02
RASSF5	1.9	1.2E-02	0.34	1.1E-01	*M6PR*	1.6	4.9E-03	0.30	3.0E-01
PEX5	1.9	2.1E-02	0.22	2.8E-01	*C19orf66*	1.6	4.0E-02	0.38	1.6E-01
COG3	1.9	4.3E-02	0.22	2.8E-01	*AIF1*	1.6	1.4E-02	-0.01	9.7E-01
DERL1	1.9	1.6E-02	0.49	2.2E-02	*CD44*	1.6	1.2E-02	0.21	4.9E-01
PLK2	1.9	5.0E-02	0.02	9.4E-01	*CREM*	1.6	2.7E-02	0.09	8.0E-01
NDUFC2	1.9	4.7E-02	0.06	7.8E-01	*SEMA4A*	1.6	1.4E-02	0.08	8.4E-01
DACH1	1.9	2.5E-02	0.40	5.9E-02	*ZNF618*	1.6	4.6E-02	-0.14	6.8E-01
WDR26	1.9	1.9E-03	0.41	5.2E-02	*MARS*	1.6	2.3E-02	-0.49	4.8E-02
THAP11	1.9	8.5E-03	0.36	9.0E-02	*LMAN1*	1.6	4.3E-03	-0.23	4.5E-01
CDAN1	1.9	3.0E-02	0.21	3.0E-01	*TNFRSF1B*	1.6	1.9E-02	0.09	8.1E-01
ABHD17B	1.9	2.3E-02	0.00	9.9E-01	*BICDL1*	1.6	1.6E-02	0.04	9.2E-01
KLF7	1.9	1.9E-02	0.33	1.2E-01	*SLC1A4*	1.6	2.6E-03	-0.14	6.7E-01
ERLIN1	1.9	1.8E-02	0.15	4.6E-01	*STAT2*	1.6	1.9E-02	0.24	4.2E-01
INTS4	1.9	2.7E-02	0.33	1.2E-01	*JADE1*	1.6	2.5E-02	-0.10	8.0E-01
PRDX3	1.9	1.3E-02	0.02	9.4E-01	*MLKL*	1.6	1.3E-02	-0.20	5.2E-01

AIDA	1.9	4.1E-02	0.37	7.7E-02	*GART*	1.6	1.9E-03	0.39	1.4E-01
MYL12B	1.9	1.8E-02	0.48	2.3E-02	*GTF2A1*	1.6	4.7E-03	0.39	1.4E-01
SLC35B3	1.9	2.2E-02	0.42	4.7E-02	*MX1*	1.5	1.2E-02	-0.04	9.2E-01
FPR1	1.9	4.9E-02	0.48	2.5E-02	*IL6ST*	1.5	1.5E-02	0.40	1.3E-01
MT-CO2	1.9	5.7E-03	0.36	8.9E-02	*MYO1F*	1.5	2.1E-02	0.33	2.4E-01
ERBB2	1.9	2.5E-02	0.62	2.9E-03	*IL1R1*	1.5	4.7E-02	0.40	1.3E-01
CAMTA1	1.9	4.2E-02	0.44	3.9E-02	*CXXC5*	1.5	3.3E-02	-0.09	8.1E-01
GATA2	1.9	2.1E-02	0.27	1.9E-01	*FCER1G*	1.5	3.3E-02	0.08	8.4E-01
MAFG	1.9	1.9E-02	0.35	1.0E-01	*NUS1*	1.5	4.3E-03	0.45	8.2E-02
CASP9	1.9	5.0E-02	0.12	5.6E-01	*LIPA*	1.5	4.4E-02	0.45	8.2E-02
SERTAD3	1.9	3.4E-02	0.25	2.2E-01	*GLS*	1.5	9.3E-03	0.38	1.7E-01
HTT	1.9	7.6E-03	0.53	1.2E-02	*OST4*	1.5	3.9E-02	0.20	5.2E-01
PSMB8	1.9	3.5E-02	0.31	1.3E-01	*MYCBP2*	1.5	2.7E-02	0.30	3.0E-01
FUCA2	1.9	1.9E-02	0.24	2.4E-01	*UBE2J1*	1.5	1.2E-02	0.19	5.4E-01
TAF4	1.9	4.0E-03	0.47	2.7E-02	*ZNF267*	1.5	4.0E-02	-0.09	8.1E-01
RPL17	1.9	9.3E-03	0.20	3.3E-01	*PATL1*	1.5	3.8E-02	0.28	3.4E-01
S100A6	1.9	8.4E-03	0.28	1.7E-01	*IRAK4*	1.5	2.6E-02	0.24	4.2E-01
TMEM70	1.9	9.2E-03	0.13	5.4E-01	*PHACTR4*	-1.5	1.1E-02	-0.25	4.1E-01
CCT4	1.9	8.2E-03	0.16	4.2E-01	*SLC25A39*	-1.5	2.2E-02	0.13	7.1E-01
HLA-DPA1	1.9	1.1E-02	0.17	4.1E-01	*COX10*	-1.5	1.1E-02	-0.17	5.9E-01
HERC5	1.9	4.8E-02	0.25	2.2E-01	*PFKL*	-1.5	1.5E-02	-0.06	8.7E-01
COMT	1.9	1.2E-02	0.22	2.8E-01	*ZNF20*	-1.5	2.8E-02	-0.07	8.4E-01
EIF3H	1.9	1.1E-02	0.11	5.9E-01	*GATB*	-1.5	4.6E-02	-0.02	9.7E-01
SOX13	1.8	2.4E-02	0.29	1.6E-01	*SPRY1*	-1.5	1.2E-02	0.32	2.7E-01
ATP6V1H	1.8	3.3E-03	0.41	5.4E-02	*HCRT*	-1.5	4.8E-02	-0.04	9.2E-01
SLC25A5	1.8	1.8E-02	0.53	1.2E-02	*ISCA1*	-1.5	6.1E-03	0.29	3.2E-01
WIPI1	1.8	3.3E-02	0.32	1.2E-01	*HADHA*	-1.5	1.4E-02	0.21	5.0E-01
POLR1D	1.8	3.8E-03	0.30	1.5E-01	*ITPR3*	-1.5	4.1E-02	0.35	2.2E-01
LPGAT1	1.8	4.8E-02	0.49	2.0E-02	*PWWP2B*	-1.5	2.4E-02	-0.01	9.8E-01
KIAA1147	1.8	1.6E-02	0.26	2.0E-01	*ADCK2*	-1.5	1.6E-02	-0.20	5.2E-01
PLXND1	1.8	1.6E-02	0.42	4.6E-02	*LEXM*	-1.5	2.7E-02	-0.11	7.6E-01
PEF1	1.8	1.6E-02	0.26	2.0E-01	*NBPF1*	-1.5	3.9E-02	-0.08	8.2E-01
COX7A2L	1.8	4.2E-03	0.37	7.7E-02	*EXOC3*	-1.5	3.1E-02	0.67	3.4E-03
PGLS	1.8	2.6E-02	0.41	5.3E-02	*URGCP*	-1.5	2.8E-02	-0.29	3.3E-01
DYNLT3	1.8	1.9E-03	0.28	1.8E-01	*MRPS18B*	-1.5	2.0E-02	-0.32	2.7E-01
RPL27	1.8	1.1E-02	0.27	1.9E-01	*PEBP1*	-1.5	2.7E-02	0.30	3.0E-01
LAMP2	1.8	5.7E-03	0.61	3.5E-03	*TSTD1*	-1.5	3.3E-03	-0.30	3.0E-01
SOD2	1.8	6.5E-03	0.35	9.6E-02	*IL10RB*	-1.5	1.0E-02	-0.19	5.4E-01
ARF4	1.8	4.3E-02	0.06	7.7E-01	*DDO*	-1.5	4.0E-03	-0.26	3.8E-01
HERPUD1	1.8	4.1E-02	0.23	2.6E-01	*SPR*	-1.5	4.5E-02	-0.16	6.0E-01
ARHGAP27	1.8	2.9E-02	0.14	4.8E-01	*C11orf71*	-1.5	3.2E-02	-0.15	6.4E-01
LAMTOR3	1.8	5.4E-03	0.36	8.5E-02	*MBOAT7*	-1.5	4.7E-03	-0.03	9.4E-01
TOR1A	1.8	2.5E-02	0.09	6.6E-01	*SLC25A2*	-1.5	3.6E-02	0.01	9.8E-01
COTL1	1.8	1.1E-02	0.12	5.4E-01	*ZDHHC19*	-1.5	3.1E-02	0.12	7.1E-01

LLGL2	1.8	1.5E-02	0.51	1.6E-02	*PCDH1*	-1.5	4.2E-02	-0.31	3.0E-01
PIGP	1.8	4.4E-02	0.12	5.6E-01	*MAL2*	-1.5	4.3E-02	-0.16	6.2E-01
SARAF	1.8	1.4E-02	0.31	1.4E-01	*SCG3*	-1.5	2.7E-02	-0.26	3.8E-01
MPZL1	1.8	1.0E-02	0.36	9.0E-02	*APLP2*	-1.5	2.8E-03	0.10	7.8E-01
PRKAA1	1.8	4.6E-02	0.33	1.2E-01	*PGRMC2*	-1.5	2.6E-04	-0.28	3.4E-01
DSCR3	1.8	2.5E-02	0.30	1.5E-01	*ABHD14B*	-1.5	2.0E-02	-0.07	8.4E-01
CCNY	1.8	7.2E-03	0.37	8.2E-02	*MRPL41*	-1.5	3.5E-02	-0.49	4.6E-02
ZSWIM8	1.8	1.9E-02	0.16	4.3E-01	*OTUD7B*	-1.5	2.3E-02	0.02	9.7E-01
CAPN12	1.8	1.5E-02	0.33	1.2E-01	*KDM4A*	-1.5	4.1E-03	0.14	6.8E-01
GTF2H1	1.8	1.0E-02	0.32	1.3E-01	*IL17C*	-1.5	3.9E-02	0.17	5.9E-01
SELENOM	1.8	4.0E-02	0.02	9.3E-01	*NDUFS1*	-1.5	1.9E-02	0.07	8.4E-01
CGGBP1	1.8	2.2E-02	0.31	1.5E-01	*ANKDD1B*	-1.5	4.2E-02	0.20	5.2E-01
SLC35A2	1.8	9.9E-03	0.15	4.6E-01	*PUF60*	-1.5	2.5E-02	-0.17	5.9E-01
CLPTM1L	1.8	9.7E-03	0.24	2.4E-01	*DLST*	-1.5	1.0E-02	0.02	9.7E-01
BDH2	1.8	3.2E-02	0.43	4.6E-02	*TCEAL5*	-1.5	3.5E-02	0.01	9.7E-01
DPY30	1.8	2.6E-02	0.27	1.8E-01	*GPRASP2*	-1.5	2.5E-02	-0.19	5.3E-01
SRPRA	1.8	3.0E-02	0.32	1.3E-01	*FBXW5*	-1.5	9.2E-03	-0.29	3.3E-01
CHKA	1.8	1.9E-02	0.62	2.9E-03	*STAB1*	-1.5	3.1E-02	-0.15	6.6E-01
ABCG1	1.8	3.1E-02	0.32	1.3E-01	*SCAF1*	-1.5	1.8E-03	0.08	8.2E-01
LASP1	1.8	1.0E-02	0.61	3.0E-03	*AFG3L2*	-1.5	5.9E-03	0.14	6.8E-01
EIF4E3	1.8	3.0E-02	0.67	1.1E-03	*IQCC*	-1.5	2.5E-02	-0.18	5.7E-01
SEC16B	1.8	2.7E-02	0.22	2.7E-01	*HSDL2*	-1.5	1.0E-02	0.06	8.8E-01
RBPMS	1.8	3.1E-02	0.19	3.6E-01	*MFSD4B*	-1.5	3.5E-02	-0.07	8.4E-01
NAIP	1.8	1.8E-02	0.31	1.3E-01	*SNX7*	-1.5	1.2E-02	-0.31	2.8E-01
RIN3	1.8	5.1E-03	0.39	6.8E-02	*GAREM1*	-1.5	3.6E-02	0.49	4.9E-02
HNRNPH3	1.8	4.7E-02	0.28	1.8E-01	*CLDN8*	-1.5	3.0E-02	-0.64	6.6E-03
NOTCH1	1.8	2.3E-02	0.38	7.4E-02	*LIAS*	-1.5	1.6E-02	0.01	9.7E-01
RNPS1	1.8	3.2E-02	0.28	1.7E-01	*GSTO2*	-1.5	1.6E-02	-0.30	3.0E-01
C9orf152	1.8	2.3E-02	0.04	8.7E-01	*NFKBIL1*	-1.5	5.0E-04	0.20	5.2E-01
EIF4A3	1.8	8.3E-03	0.29	1.6E-01	*AC002310.4*	-1.5	3.8E-02	0.06	8.8E-01
SLC35D2	1.8	1.7E-02	0.42	4.9E-02	*IMMT*	-1.5	1.1E-03	0.14	6.6E-01
CD164	1.8	2.2E-02	0.27	1.9E-01	*TIMM22*	-1.5	3.2E-02	-0.01	9.8E-01
MS4A6A	1.8	3.7E-03	0.39	6.8E-02	*CDS1*	-1.5	3.4E-02	0.15	6.4E-01
PSMA2	1.8	1.9E-02	0.19	3.6E-01	*PGPEP1*	-1.5	1.5E-02	-0.09	8.1E-01
ABAT	1.8	4.6E-02	0.72	4.3E-04	*BRF1*	-1.5	1.7E-03	-0.11	7.5E-01
TWSG1	1.8	4.3E-02	0.07	7.4E-01	*COX4I1*	-1.5	3.7E-03	-0.54	2.5E-02
MGST2	1.7	2.3E-02	0.03	9.0E-01	*RXRA*	-1.5	1.5E-03	0.24	4.2E-01
CEACAM1	1.7	9.8E-03	0.65	1.5E-03	*DNASE1L2*	-1.5	1.2E-02	0.17	5.9E-01
MTX3	1.7	1.2E-02	0.28	1.8E-01	*AL591806.3*	-1.5	4.7E-02	0.17	5.9E-01
SOCS1	1.7	3.4E-02	0.29	1.6E-01	*HSD11B1L*	-1.5	1.6E-02	0.09	8.1E-01
COMMD2	1.7	5.0E-02	0.30	1.5E-01	*NPIPB12*	-1.5	2.9E-02	0.09	8.0E-01
B3GALNT2	1.7	4.1E-02	0.18	3.6E-01	*GPR37L1*	-1.5	3.7E-02	0.25	4.1E-01
GABARAPL2	1.7	2.8E-02	0.29	1.6E-01	*CNPPD1*	-1.5	1.1E-02	0.01	9.8E-01
PSMD9	1.7	3.8E-02	0.28	1.8E-01	*AMELX*	-1.5	4.8E-02	-0.04	9.1E-01

PDZRN3	1.7	3.3E-02	0.06	7.7E-01	*PYGO2*	-1.5	2.7E-02	-0.15	6.5E-01
CNOT8	1.7	3.5E-02	0.33	1.2E-01	*UQCRC2*	-1.5	7.0E-03	-0.36	2.0E-01
M6PR	1.7	2.4E-02	0.30	1.5E-01	*PDE5A*	-1.5	3.9E-02	0.46	6.9E-02
USMG5	1.7	4.2E-02	0.14	5.0E-01	*TJP3*	-1.5	3.8E-02	0.08	8.4E-01
GOLM1	1.7	1.3E-02	0.49	2.2E-02	*MINPP1*	-1.5	2.0E-02	0.32	2.8E-01
HLA-DPB1	1.7	1.7E-02	0.20	3.2E-01	*TMEM8B*	-1.5	2.5E-03	-0.04	9.3E-01
ALOX5AP	1.7	3.4E-02	0.49	2.0E-02	*UEVLD*	-1.5	4.4E-02	0.17	5.8E-01
PHF10	1.7	1.5E-02	0.39	6.4E-02	*PHLDB1*	-1.5	7.9E-03	0.30	3.0E-01
ATP5C1	1.7	4.4E-02	0.22	2.7E-01	*DLL4*	-1.5	1.6E-02	0.00	9.9E-01
RPS29	1.7	1.9E-02	0.03	8.7E-01	*MEGF8*	-1.5	1.6E-03	0.46	6.6E-02
MCL1	1.7	3.8E-03	0.42	4.8E-02	*PLEKHA6*	-1.5	4.0E-02	0.06	8.7E-01
EXOC3L2	1.7	2.8E-02	0.54	1.1E-02	*RILP*	-1.5	4.0E-02	-0.07	8.4E-01
SMAD4	1.7	4.1E-02	0.27	1.8E-01	*OR6F1*	-1.6	1.3E-02	-0.03	9.5E-01
TMEM59	1.7	3.2E-02	0.26	2.0E-01	*GFER*	-1.6	1.7E-02	-0.22	4.9E-01
RRNAD1	1.7	1.9E-02	0.42	4.8E-02	*ANKRD40*	-1.6	4.1E-02	0.21	4.9E-01
CCNG2	1.7	4.3E-02	0.32	1.3E-01	*FGF9*	-1.6	3.1E-02	0.00	1.0E+00
IL1R1	1.7	3.1E-02	0.40	5.7E-02	*PDLIM1*	-1.6	4.0E-03	-0.01	9.7E-01
NOA1	1.7	3.8E-02	0.43	4.3E-02	*ECH1*	-1.6	1.0E-03	-0.28	3.5E-01
PIGG	1.7	4.1E-02	0.44	4.1E-02	*SLC22A23*	-1.6	3.4E-02	-0.26	3.8E-01
MEF2D	1.7	3.5E-02	0.20	3.3E-01	*ECI1*	-1.6	5.3E-03	-0.04	9.1E-01
RPS7	1.7	2.3E-02	0.03	8.8E-01	*NOL4L*	-1.6	5.5E-04	0.17	5.9E-01
ATRAID	1.7	2.7E-02	0.28	1.7E-01	*CMTM4*	-1.6	1.9E-02	-0.22	4.7E-01
ATP2C1	1.7	2.4E-02	0.06	7.7E-01	*RETREG2*	-1.6	8.9E-04	-0.05	9.0E-01
PTPN9	1.7	2.7E-02	0.46	3.1E-02	*MOB2*	-1.6	2.2E-02	-0.07	8.5E-01
CRLS1	1.7	1.5E-02	0.24	2.3E-01	*C10orf143*	-1.6	3.8E-02	0.19	5.3E-01
SAR1B	1.7	1.7E-02	0.36	9.1E-02	*TMEM9B*	-1.6	3.0E-02	-0.61	9.9E-03
AXIN1	1.7	4.6E-02	0.24	2.4E-01	*ZNF354B*	-1.6	4.9E-02	0.26	3.8E-01
RPL19	1.7	8.5E-03	0.03	9.0E-01	*HECTD3*	-1.6	9.8E-03	-0.29	3.2E-01
PGM5	1.7	4.7E-02	0.47	2.7E-02	*43526*	-1.6	3.3E-02	-0.04	9.2E-01
MYL12A	1.7	2.7E-02	0.36	9.1E-02	*UNC5B*	-1.6	3.4E-02	0.21	4.9E-01
SLCO2B1	1.7	2.2E-02	0.45	3.5E-02	*GNG12*	-1.6	1.3E-02	0.52	3.2E-02
CMC2	1.7	3.3E-02	0.51	1.5E-02	*C19orf33*	-1.6	3.3E-02	-0.33	2.4E-01
MRPL11	1.7	3.1E-02	0.06	7.8E-01	*COX5B*	-1.6	1.9E-02	0.01	9.8E-01
ARRDC2	1.7	3.1E-02	0.31	1.5E-01	*SLC35F2*	-1.6	1.9E-02	-0.08	8.3E-01
RPL7	1.7	1.0E-02	0.15	4.7E-01	*ACBD4*	-1.6	2.7E-02	0.21	4.9E-01
HLA-DRA	1.7	7.1E-03	0.33	1.2E-01	*ZNF850*	-1.6	5.5E-04	0.12	7.3E-01
EFTUD2	1.7	1.9E-02	0.31	1.4E-01	*FBXO48*	-1.6	3.9E-02	0.09	8.0E-01
NSMF	1.6	2.7E-02	0.32	1.3E-01	*SPSB3*	-1.6	3.3E-03	-0.13	6.9E-01
NCKAP1	1.6	2.7E-02	0.32	1.3E-01	*GBA2*	-1.6	2.9E-02	-0.41	1.2E-01
PPP6R2	1.6	1.7E-02	-0.17	3.9E-01	*FAM218A*	-1.6	3.5E-02	0.08	8.3E-01
SLC44A1	1.6	2.2E-02	0.28	1.8E-01	*SYNPO*	-1.6	3.0E-03	0.34	2.4E-01
HDAC5	1.6	3.3E-02	0.22	2.7E-01	*MAPK13*	-1.6	4.7E-02	-0.43	9.7E-02
ZNF227	1.6	3.7E-02	0.28	1.8E-01	*IMPA2*	-1.6	1.7E-02	0.16	6.2E-01
UBE2Q1	1.6	2.0E-02	0.35	9.6E-02	*ETFB*	-1.6	3.1E-02	-0.27	3.6E-01

RNF138	1.6	3.8E-02	-0.12	5.7E-01	*RTL8A*	-1.6	1.7E-02	-0.14	6.7E-01
CD209	1.6	3.3E-02	0.77	4.5E-05	*FAM71E1*	-1.6	2.6E-02	-0.08	8.3E-01
SCARB2	1.6	2.7E-02	0.52	1.5E-02	*TPRG1L*	-1.6	4.5E-04	-0.16	6.2E-01
UBE2L6	1.6	2.3E-02	0.61	3.1E-03	*DHRS1*	-1.6	6.8E-03	-0.22	4.9E-01
TRIOBP	1.6	3.3E-02	0.38	7.7E-02	*ZKSCAN1*	-1.6	1.1E-02	-0.20	5.2E-01
43710	1.6	2.8E-02	0.42	4.8E-02	*VSIG10*	-1.6	3.4E-02	0.20	5.2E-01
APPBP2	1.6	3.8E-02	0.29	1.6E-01	*LUZP2*	-1.6	7.8E-04	0.02	9.6E-01
ASH2L	1.6	4.6E-02	0.45	3.4E-02	*PMPCA*	-1.6	5.6E-03	0.30	3.0E-01
BICRA	1.6	2.8E-02	0.55	1.1E-02	*FBXL15*	-1.6	2.7E-02	0.10	7.8E-01
FYTTD1	1.6	2.7E-02	0.38	7.0E-02	*PSKH1*	-1.6	2.8E-02	-0.40	1.3E-01
TMEM41B	1.6	1.9E-02	0.39	6.5E-02	*LRRC57*	-1.6	2.6E-02	-0.04	9.2E-01
CDC42EP4	1.6	4.7E-02	0.41	5.4E-02	*ZNF768*	-1.6	1.9E-02	0.00	9.9E-01
SPARC	1.6	3.2E-02	0.49	2.2E-02	*SLC10A5*	-1.6	2.1E-02	-0.26	3.9E-01
LARP4B	1.6	2.5E-02	0.28	1.8E-01	*LANCL3*	-1.6	5.2E-03	0.09	8.1E-01
THBD	1.6	2.2E-02	0.43	4.2E-02	*USH1C*	-1.6	3.3E-02	-0.03	9.3E-01
LRRC41	1.6	2.8E-02	0.40	6.2E-02	*SPON1*	-1.6	4.6E-02	-0.43	1.0E-01
C1GALT1	1.6	2.4E-02	0.39	6.3E-02	*TRIM45*	-1.6	3.8E-02	-0.16	6.2E-01
FGGY	1.6	2.7E-02	0.24	2.3E-01	*SCAP*	-1.6	1.1E-02	-0.14	6.8E-01
ESS2	1.6	3.8E-02	0.22	2.8E-01	*ABHD17C*	-1.6	2.1E-02	0.06	8.7E-01
BAHD1	1.6	3.7E-02	0.54	1.1E-02	*KCNE2*	-1.6	6.6E-03	-0.08	8.4E-01
AP3S1	1.6	4.6E-02	0.59	4.1E-03	*CAT*	-1.6	3.9E-04	0.48	5.3E-02
KHDC4	1.6	3.8E-02	0.49	2.1E-02	*KIAA1671*	-1.6	3.3E-03	0.27	3.6E-01
PPP1R2	1.6	5.0E-02	0.16	4.3E-01	*SRGAP1*	-1.6	9.2E-03	-0.40	1.4E-01
ARRDC1	1.6	3.1E-02	0.31	1.4E-01	*HSD17B11*	-1.6	4.2E-03	-0.08	8.3E-01
MAPRE1	1.6	3.6E-02	0.16	4.2E-01	*PGM1*	-1.6	1.3E-02	0.19	5.4E-01
EIF4A2	1.6	2.7E-02	0.15	4.7E-01	*PANK3*	-1.6	3.3E-02	0.54	2.5E-02
FTL	1.6	3.1E-02	0.50	2.0E-02	*NR1H3*	-1.6	3.5E-02	0.20	5.2E-01
INF2	1.6	1.0E-02	0.48	2.3E-02	*TFRC*	-1.6	4.6E-02	0.29	3.2E-01
ADGRE5	1.6	4.0E-02	0.14	5.1E-01	*ZBED1*	-1.6	2.6E-03	0.26	3.9E-01
KDM1A	1.6	4.9E-02	0.35	9.6E-02	*PET117*	-1.6	1.1E-02	0.09	8.1E-01
AZIN1	1.6	4.4E-02	0.39	6.6E-02	*NME7*	-1.6	2.2E-02	-0.27	3.6E-01
UQCRH	1.6	4.8E-02	-0.01	9.7E-01	*FOXN3*	-1.6	9.5E-03	0.11	7.4E-01
ARNT	1.6	5.0E-02	0.34	1.1E-01	*NDUFA10*	-1.6	2.1E-02	0.16	6.1E-01
ABR	1.5	2.9E-02	0.25	2.1E-01	*MUL1*	-1.6	2.7E-02	-0.10	7.8E-01
BCAR1	1.5	4.3E-02	-0.04	8.6E-01	*TRAK2*	-1.6	2.1E-03	-0.01	9.8E-01
GHITM	1.5	3.7E-02	0.43	4.4E-02	*MAPK3*	-1.6	3.5E-03	0.09	8.1E-01
NAGA	1.5	3.1E-02	0.06	7.9E-01	*SSUH2*	-1.6	4.7E-02	-0.24	4.2E-01
TM7SF3	1.5	1.5E-02	0.14	5.0E-01	*MT-CYB*	-1.6	2.4E-02	-0.41	1.2E-01
HNRNPA3	1.5	4.2E-02	0.30	1.6E-01	*PLPP1*	-1.6	3.3E-02	0.53	2.7E-02
RPL38	1.5	4.3E-03	0.23	2.6E-01	*DAB2IP*	-1.6	2.1E-02	0.41	1.2E-01
HMGN1	1.5	1.6E-02	0.05	8.0E-01	*RAD52*	-1.6	4.0E-02	-0.07	8.4E-01
PSMA1	1.5	7.0E-03	0.29	1.6E-01	*TDRD10*	-1.6	2.2E-02	-0.10	7.9E-01
RNF13	1.5	1.9E-02	0.23	2.6E-01	*THRA*	-1.6	9.0E-04	0.31	3.0E-01
VCPIP1	1.5	1.4E-02	0.21	3.1E-01	*PRSS36*	-1.6	1.3E-02	-0.13	6.9E-01

MYRF	1.5	8.0E-03	0.41	5.2E-02	*DNAJC27*	-1.6	1.8E-02	-0.17	5.9E-01
YTHDF1	1.5	4.9E-02	0.05	8.2E-01	*GP2*	-1.6	1.8E-03	-0.28	3.3E-01
SPINT1	1.5	2.3E-02	0.26	2.0E-01	*GALNT12*	-1.6	6.5E-03	0.05	9.0E-01
SPTSSA	1.5	4.0E-02	0.18	3.8E-01	*GNMT*	-1.6	3.8E-02	0.01	9.8E-01
SRSF7	1.5	5.0E-02	0.00	9.8E-01	*RAD9A*	-1.6	4.8E-03	-0.05	9.0E-01
PFDN2	1.5	4.4E-02	0.17	4.1E-01	*GRB7*	-1.6	2.9E-02	0.26	3.8E-01
GLS	1.5	3.2E-02	0.38	7.4E-02	*AAMDC*	-1.6	4.6E-02	-0.22	4.6E-01
ERGIC1	1.5	3.9E-02	0.32	1.3E-01	*LNPK*	-1.6	8.8E-03	0.18	5.7E-01
SLC35A1	1.5	3.1E-02	0.09	6.5E-01	*SLC25A20*	-1.6	3.5E-02	0.22	4.8E-01
KRT18	-1.5	3.2E-02	-0.51	1.7E-02	*SCNN1A*	-1.6	3.8E-02	-0.06	8.8E-01
NAP1L4	-1.5	4.9E-03	-0.49	2.1E-02	*IQSEC2*	-1.6	1.2E-02	-0.15	6.4E-01
NEDD4L	-1.5	3.8E-02	-0.67	1.0E-03	*CLCN2*	-1.6	3.8E-02	-0.01	9.8E-01
AFDN	-1.5	1.9E-02	-0.25	2.2E-01	*RITA1*	-1.6	3.4E-02	0.03	9.4E-01
MARVELD2	-1.5	3.0E-02	0.12	5.6E-01	*ABCD3*	-1.6	3.7E-02	0.53	2.8E-02
DCAF8	-1.5	8.4E-03	-0.26	2.0E-01	*SDCBP2*	-1.6	3.3E-02	-0.10	7.8E-01
DENND4C	-1.5	4.3E-02	-0.05	8.0E-01	*NUBPL*	-1.6	1.6E-02	-0.36	2.1E-01
SRP68	-1.5	4.1E-02	-0.22	2.8E-01	*ATP5I*	-1.7	3.8E-02	-0.32	2.8E-01
FUBP3	-1.5	3.1E-02	-0.36	9.1E-02	*DDR1*	-1.7	9.5E-03	-0.07	8.4E-01
STT3B	-1.5	2.8E-02	-0.05	8.3E-01	*MLYCD*	-1.7	4.0E-04	-0.08	8.3E-01
USP42	-1.5	2.6E-02	-0.09	6.6E-01	*TBC1D3*	-1.7	3.9E-02	0.00	9.9E-01
CHMP3	-1.5	5.4E-03	-0.41	5.5E-02	*CHP1*	-1.7	3.2E-03	0.53	2.8E-02
SCO1	-1.5	2.1E-02	0.28	1.7E-01	*TIMM13*	-1.7	2.6E-02	-0.29	3.2E-01
PPHLN1	-1.5	1.2E-02	-0.08	6.9E-01	*SLC1A7*	-1.7	1.6E-04	0.41	1.2E-01
BRD9	-1.5	2.2E-02	-0.46	3.2E-02	*AUTS2*	-1.7	5.1E-03	-0.09	8.1E-01
DYNC1LI2	-1.5	2.7E-02	-0.16	4.4E-01	*MSI1*	-1.7	7.4E-03	0.18	5.7E-01
ZNF318	-1.5	4.3E-02	-0.29	1.7E-01	*ANKRD62*	-1.7	1.6E-02	-0.26	3.9E-01
SLTM	-1.5	3.8E-02	-0.40	5.7E-02	*GLYCTK*	-1.7	4.1E-02	0.25	4.1E-01
PEAK1	-1.5	2.1E-02	-0.15	4.7E-01	*AC058822.1*	-1.7	3.2E-02	-0.02	9.7E-01
BTBD7	-1.5	2.9E-02	-0.31	1.4E-01	*MAEL*	-1.7	2.8E-02	0.25	4.0E-01
RAB8A	-1.5	2.3E-02	-0.28	1.8E-01	*COLEC11*	-1.7	1.7E-02	-0.06	8.8E-01
OLA1	-1.5	3.3E-02	-0.37	8.3E-02	*UQCRC1*	-1.7	5.0E-02	-0.19	5.3E-01
SUGT1	-1.5	3.3E-02	-0.27	1.8E-01	*IQGAP2*	-1.7	1.7E-02	0.34	2.4E-01
SAP30BP	-1.5	1.2E-02	-0.40	5.8E-02	*MYRIP*	-1.7	2.4E-02	-0.19	5.4E-01
UBN1	-1.5	8.8E-03	-0.33	1.2E-01	*IDH3G*	-1.7	2.1E-02	-0.25	4.0E-01
TLK2	-1.5	8.5E-03	-0.23	2.7E-01	*TMCC3*	-1.7	2.2E-02	0.26	3.9E-01
SRSF11	-1.5	1.3E-02	-0.55	1.1E-02	*HMGCL*	-1.7	2.4E-02	0.41	1.2E-01
PSMC1	-1.5	4.0E-02	-0.54	1.1E-02	*AP3S2*	-1.7	1.2E-02	-0.08	8.3E-01
BRCC3	-1.5	3.2E-02	-0.28	1.8E-01	*KCNQ1*	-1.7	8.8E-03	-0.30	3.0E-01
ETFB	-1.5	4.7E-02	-0.27	1.9E-01	*TMEM120A*	-1.7	4.2E-03	-0.31	2.8E-01
STK39	-1.5	3.9E-02	0.18	3.8E-01	*RNF223*	-1.7	1.9E-02	0.03	9.3E-01
CALM1	-1.5	1.3E-02	-0.26	2.1E-01	*MAGI1*	-1.7	5.2E-05	0.39	1.4E-01
POLR2J3	-1.5	2.2E-02	-0.10	6.1E-01	*NRGN*	-1.7	1.9E-02	0.27	3.7E-01
ZC3H18	-1.5	3.5E-02	-0.18	3.7E-01	*HIGD1A*	-1.7	3.1E-02	0.00	9.9E-01
ZNF326	-1.6	2.6E-02	-0.29	1.6E-01	*CRYBB2*	-1.7	2.9E-02	-0.05	8.9E-01

GOLGA2	-1.6	4.1E-02	-0.32	1.3E-01	*C1orf115*	-1.7	1.5E-02	0.62	8.9E-03
CHCHD10	-1.6	2.4E-02	-0.37	8.3E-02	*TMEM82*	-1.7	4.1E-02	-0.13	7.1E-01
EIF4E2	-1.6	2.3E-02	-0.39	6.3E-02	*AP1M2*	-1.7	4.3E-02	0.18	5.6E-01
TLN1	-1.6	3.2E-02	-0.14	4.8E-01	*ACKR2*	-1.7	2.6E-03	0.05	9.0E-01
TAF15	-1.6	2.6E-02	-0.50	1.8E-02	*ERBB3*	-1.7	2.6E-02	0.25	3.9E-01
BRD2	-1.6	2.8E-02	-0.65	1.7E-03	*RAB40C*	-1.7	2.9E-02	0.07	8.4E-01
KRIT1	-1.6	5.7E-03	-0.35	1.0E-01	*TMEM63C*	-1.7	9.5E-03	-0.17	5.9E-01
TFCP2L1	-1.6	1.5E-02	-0.67	1.0E-03	*DENND4C*	-1.7	1.5E-03	-0.05	8.9E-01
ACOT11	-1.6	3.9E-02	-0.32	1.3E-01	*DDT*	-1.7	2.5E-04	-0.20	5.2E-01
CHCHD2	-1.6	2.3E-02	-0.49	2.0E-02	*ZDHHC23*	-1.7	3.7E-02	-0.14	6.6E-01
ABCF1	-1.6	1.4E-02	-0.28	1.8E-01	*FAM229A*	-1.7	2.1E-02	0.17	5.8E-01
SH3GLB2	-1.6	3.8E-02	-0.38	7.4E-02	*C4orf19*	-1.7	3.2E-02	-0.05	9.0E-01
KIAA0141	-1.6	4.2E-02	-0.54	1.1E-02	*GKN2*	-1.7	4.9E-03	-0.35	2.1E-01
EPM2AIP1	-1.6	3.9E-02	-0.26	2.0E-01	*EIF4EBP2*	-1.7	2.4E-04	0.55	2.1E-02
SRRM1	-1.6	5.0E-02	-0.26	2.1E-01	*VDR*	-1.7	1.5E-02	-0.69	2.9E-03
RNF168	-1.6	4.6E-02	-0.06	7.8E-01	*ENDOD1*	-1.7	4.1E-02	-0.62	8.4E-03
CPSF2	-1.6	3.2E-02	-0.13	5.2E-01	*LAMTOR4*	-1.7	1.9E-02	-0.60	1.1E-02
SARS	-1.6	3.5E-02	-0.46	3.2E-02	*SERF1B*	-1.7	5.6E-03	-0.02	9.7E-01
NOP56	-1.6	2.3E-02	-0.41	5.2E-02	*PRADC1*	-1.7	3.3E-02	-0.19	5.3E-01
FBXW7	-1.6	1.2E-02	-0.30	1.6E-01	*ZNF677*	-1.7	4.7E-02	-0.23	4.4E-01
NCOR1	-1.6	3.7E-03	-0.19	3.5E-01	*GDE1*	-1.7	3.9E-03	0.28	3.4E-01
ENAH	-1.6	2.0E-02	-0.48	2.3E-02	*FITM1*	-1.7	3.3E-02	-0.29	3.2E-01
OS9	-1.6	2.4E-02	-0.27	1.8E-01	*CCDC15*	-1.7	3.7E-02	0.06	8.8E-01
ZCRB1	-1.6	8.1E-03	-0.05	8.0E-01	*COMMD9*	-1.7	1.0E-03	-0.17	5.9E-01
TTC1	-1.6	2.2E-02	-0.35	1.0E-01	*SFXN5*	-1.7	3.2E-02	-0.15	6.4E-01
CMTM6	-1.6	3.5E-02	-0.27	1.8E-01	*CXorf56*	-1.7	2.4E-02	0.11	7.6E-01
PPIG	-1.6	2.2E-02	-0.54	1.1E-02	*ZNF525*	-1.7	1.0E-02	-0.22	4.7E-01
NEMF	-1.6	2.4E-02	-0.27	1.9E-01	*SLC19A1*	-1.7	2.5E-03	-0.21	5.0E-01
GGNBP2	-1.6	1.9E-02	-0.47	2.6E-02	*ECHS1*	-1.7	6.9E-03	0.24	4.2E-01
CTR9	-1.6	1.2E-02	-0.31	1.3E-01	*EXD3*	-1.7	4.1E-02	-0.21	5.0E-01
FIP1L1	-1.6	2.4E-02	-0.55	9.7E-03	*BMP1*	-1.7	2.8E-02	-0.13	7.1E-01
SPOP	-1.6	1.7E-02	-0.39	6.6E-02	*MXI1*	-1.7	4.3E-02	0.12	7.2E-01
BAZ2A	-1.6	1.0E-02	-0.05	8.2E-01	*HDHD3*	-1.7	4.0E-02	0.47	5.8E-02
MCU	-1.6	4.3E-02	-0.60	3.7E-03	*ACO2*	-1.7	2.5E-03	0.14	6.8E-01
TPRKB	-1.6	4.2E-02	-0.29	1.6E-01	*DDAH1*	-1.7	6.4E-03	-0.49	5.1E-02
COMMD1	-1.6	2.7E-02	-0.21	2.9E-01	*THG1L*	-1.7	8.1E-03	0.04	9.1E-01
SLU7	-1.6	1.0E-02	-0.40	6.0E-02	*ARL6IP6*	-1.7	1.5E-02	0.20	5.2E-01
SSRP1	-1.6	7.2E-03	-0.40	6.0E-02	*ATP9A*	-1.7	5.2E-05	0.20	5.2E-01
EZR	-1.6	1.9E-02	-0.20	3.3E-01	*PCK2*	-1.7	2.0E-02	0.11	7.6E-01
UBE2E1	-1.6	2.3E-02	-0.51	1.6E-02	*CBSL*	-1.7	2.9E-02	0.09	8.0E-01
CLIP1	-1.6	4.2E-02	-0.31	1.4E-01	*PSMD3*	-1.7	2.9E-02	-0.21	5.0E-01
CALCOCO2	-1.6	2.4E-02	-0.32	1.2E-01	*NOMO3*	-1.7	3.6E-02	-0.11	7.5E-01
NUPR1	-1.6	2.1E-02	-0.62	2.9E-03	*CACFD1*	-1.7	1.7E-02	-0.17	5.9E-01
ABHD15	-1.6	9.5E-03	0.21	3.0E-01	*SUCLG1*	-1.7	1.5E-02	-0.22	4.7E-01

RPN2	-1.6	3.5E-02	-0.38	7.6E-02	*SORBS3*	-1.7	4.4E-02	0.15	6.4E-01
FRG1	-1.6	2.0E-02	-0.30	1.5E-01	*PLXNA2*	-1.7	2.3E-02	0.12	7.3E-01
ZC3H13	-1.6	4.0E-02	-0.28	1.7E-01	*GTPBP6*	-1.7	3.6E-02	-0.09	8.1E-01
YKT6	-1.6	2.2E-02	-0.50	1.9E-02	*AVPI1*	-1.7	9.7E-03	0.16	6.1E-01
ESF1	-1.6	9.4E-03	-0.53	1.2E-02	*AK3*	-1.7	5.5E-04	0.24	4.2E-01
SRPK2	-1.6	2.4E-02	-0.15	4.5E-01	*CYTL1*	-1.7	1.1E-02	0.04	9.2E-01
CHD3	-1.6	8.5E-03	-0.29	1.6E-01	*PEX26*	-1.7	1.1E-02	-0.22	4.7E-01
ANKS4B	-1.6	3.0E-02	-0.30	1.5E-01	*PIGB*	-1.7	3.0E-02	0.12	7.1E-01
TRPM7	-1.6	1.4E-02	-0.02	9.4E-01	*SFXN1*	-1.7	8.2E-03	0.51	3.8E-02
CTBP2	-1.6	1.2E-02	-0.32	1.3E-01	*NDUFV1*	-1.7	2.8E-02	-0.33	2.5E-01
DYNC1I2	-1.6	1.5E-02	-0.53	1.2E-02	*HNF1B*	-1.7	3.2E-02	-0.11	7.6E-01
RWDD2B	-1.6	2.8E-02	-0.12	5.7E-01	*LRRN2*	-1.7	4.3E-03	0.07	8.5E-01
RPS12	-1.6	4.2E-02	-0.69	7.3E-04	*METTL7A*	-1.7	1.9E-02	0.22	4.7E-01
NMT1	-1.6	1.9E-02	-0.44	3.8E-02	*RAP1GAP*	-1.7	4.7E-02	-0.17	5.9E-01
SLC12A2	-1.6	2.7E-02	-0.23	2.6E-01	*AMN*	-1.7	4.7E-02	0.02	9.6E-01
BRD4	-1.6	1.0E-02	-0.12	5.5E-01	*BDH1*	-1.7	4.9E-03	0.08	8.3E-01
SFMBT1	-1.6	3.1E-02	-0.29	1.6E-01	*MT-CO1*	-1.7	5.2E-05	0.36	2.0E-01
SRRT	-1.6	3.8E-02	-0.71	5.0E-04	*EPB41L1*	-1.7	1.6E-02	-0.07	8.6E-01
CEBPZOS	-1.6	8.5E-03	-0.56	8.3E-03	*MICAL3*	-1.7	2.5E-02	0.23	4.4E-01
RETSAT	-1.6	2.2E-02	-0.39	6.5E-02	*MRPS33*	-1.8	1.3E-04	-0.07	8.4E-01
DDX46	-1.6	1.1E-02	-0.56	8.5E-03	*GNG4*	-1.8	2.6E-02	-0.28	3.5E-01
WDR3	-1.6	7.0E-03	-0.29	1.6E-01	*SLC25A10*	-1.8	4.3E-02	0.01	9.7E-01
ROCK2	-1.6	1.9E-02	-0.13	5.3E-01	*ZNF91*	-1.8	1.5E-02	-0.20	5.2E-01
DENND5B	-1.6	3.1E-02	-0.02	9.4E-01	*TMEM125*	-1.8	2.0E-02	-0.43	1.0E-01
CTNNBL1	-1.6	1.4E-02	-0.29	1.6E-01	*PRDX6*	-1.8	4.6E-02	-0.57	1.6E-02
HCFC2	-1.6	2.1E-02	-0.33	1.2E-01	*ADGRA3*	-1.8	2.9E-02	-0.06	8.7E-01
UQCRB	-1.6	8.5E-03	-0.64	2.2E-03	*ANKMY2*	-1.8	9.8E-03	0.02	9.7E-01
NUBPL	-1.6	3.7E-03	-0.36	9.1E-02	*SPATA18*	-1.8	2.5E-03	-0.05	8.9E-01
ZRSR2	-1.6	3.3E-02	-0.48	2.3E-02	*GPX3*	-1.8	2.8E-02	0.16	6.1E-01
PUS7L	-1.6	2.9E-02	-0.27	1.8E-01	*LGALS4*	-1.8	1.1E-02	-0.40	1.3E-01
DDX21	-1.6	1.1E-02	-0.43	4.4E-02	*FAM13A*	-1.8	5.8E-04	0.58	1.2E-02
SMARCA4	-1.6	4.2E-02	-0.42	4.7E-02	*ANO9*	-1.8	4.4E-02	-0.06	8.6E-01
DDAH1	-1.7	3.6E-02	-0.49	2.3E-02	*KDF1*	-1.8	8.3E-03	-0.05	8.9E-01
PARD3	-1.7	1.3E-02	-0.11	6.0E-01	*SRI*	-1.8	5.7E-03	0.48	5.3E-02
NDUFA5	-1.7	9.2E-03	-0.67	1.1E-03	*ABHD11*	-1.8	1.1E-02	-0.33	2.4E-01
SETBP1	-1.7	4.3E-02	-0.05	8.1E-01	*LIPC*	-1.8	1.1E-03	-0.14	6.8E-01
IGF2BP2	-1.7	1.5E-02	-0.09	6.7E-01	*TMC4*	-1.8	1.1E-02	0.25	4.1E-01
DCAF7	-1.7	3.9E-03	-0.21	3.0E-01	*NMT2*	-1.8	2.0E-02	-0.06	8.7E-01
C1orf131	-1.7	2.3E-02	-0.38	7.7E-02	*PYGB*	-1.8	1.9E-02	0.05	9.0E-01
ZMAT2	-1.7	1.8E-02	-0.20	3.1E-01	*SPIRE2*	-1.8	2.3E-02	0.13	7.1E-01
URGCP	-1.7	1.2E-02	-0.29	1.7E-01	*TMEM98*	-1.8	2.6E-03	-0.53	2.8E-02
PSMD1	-1.7	4.0E-02	-0.21	3.0E-01	*SLC22A18*	-1.8	2.2E-02	-0.24	4.2E-01
MON1B	-1.7	4.9E-03	-0.24	2.3E-01	*LRP12*	-1.8	3.2E-02	0.48	5.1E-02
NDUFB9	-1.7	6.2E-03	-0.63	2.3E-03	*DTX4*	-1.8	1.2E-02	0.03	9.5E-01

TFG	-1.7	2.1E-03	-0.37	8.3E-02	*MYOT*	-1.8	1.3E-02	-0.35	2.2E-01
TPM4	-1.7	1.9E-02	-0.24	2.4E-01	*CPNE2*	-1.8	4.0E-03	0.41	1.2E-01
CHD2	-1.7	3.7E-02	-0.18	3.8E-01	*CHCHD10*	-1.8	1.3E-03	-0.37	1.9E-01
TAF11	-1.7	9.0E-03	-0.51	1.7E-02	*GAL3ST4*	-1.8	4.0E-02	-0.53	2.9E-02
DR1	-1.7	4.9E-03	-0.54	1.1E-02	*NR2F6*	-1.8	3.4E-03	-0.29	3.2E-01
FAM114A1	-1.7	1.9E-02	-0.16	4.2E-01	*PTGR2*	-1.8	2.2E-02	-0.27	3.6E-01
PNISR	-1.7	2.9E-02	-0.46	3.2E-02	*GIPC2*	-1.8	3.9E-02	0.24	4.2E-01
DDX24	-1.7	4.2E-03	-0.15	4.6E-01	*ACSS2*	-1.8	3.1E-02	-0.02	9.7E-01
CEP41	-1.7	4.9E-02	-0.31	1.4E-01	*PGAP3*	-1.8	1.2E-02	-0.09	8.1E-01
ZCCHC6	-1.7	2.4E-02	-0.18	3.9E-01	*EVI5L*	-1.8	4.7E-02	0.08	8.3E-01
RRM1	-1.7	4.2E-02	-0.39	6.5E-02	*SREBF2*	-1.8	3.4E-03	-0.19	5.4E-01
HSP90AB1	-1.7	1.4E-02	-0.26	2.0E-01	*RRAS2*	-1.8	7.2E-03	0.33	2.4E-01
TSC22D2	-1.7	1.8E-02	-0.37	7.9E-02	*SUCLG2*	-1.8	4.5E-02	0.38	1.6E-01
PRPF6	-1.7	1.8E-02	-0.53	1.2E-02	*SFN*	-1.8	4.1E-02	-0.11	7.6E-01
YLPM1	-1.7	1.2E-02	-0.35	9.8E-02	*CLYBL*	-1.8	6.2E-03	0.04	9.2E-01
PHACTR4	-1.7	1.0E-02	-0.25	2.2E-01	*BAX*	-1.8	1.8E-03	0.02	9.7E-01
VTI1A	-1.7	1.6E-02	-0.39	6.5E-02	*CPE*	-1.8	1.9E-02	-0.20	5.2E-01
RTFDC1	-1.7	1.8E-02	-0.53	1.2E-02	*ZNF441*	-1.8	2.8E-03	-0.20	5.2E-01
LRRFIP1	-1.7	1.6E-02	-0.29	1.6E-01	*GTF2H2C*	-1.8	2.5E-02	-0.03	9.4E-01
SMARCA2	-1.7	2.4E-02	-0.23	2.7E-01	*AGPAT2*	-1.8	3.5E-02	0.32	2.7E-01
LYRM2	-1.7	1.7E-02	-0.40	6.2E-02	*SMPDL3B*	-1.8	3.5E-04	-0.53	2.9E-02
HYI	-1.7	3.0E-02	-0.26	2.0E-01	*PTK6*	-1.8	3.2E-02	-0.02	9.7E-01
DNASE1	-1.7	4.5E-02	-0.48	2.5E-02	*LMBR1L*	-1.8	3.2E-02	0.23	4.5E-01
PARD3B	-1.7	4.1E-02	-0.15	4.6E-01	*MT-ND1*	-1.8	2.5E-03	-0.13	7.1E-01
CHD6	-1.7	4.2E-02	-0.25	2.1E-01	*MIGA2*	-1.8	5.0E-04	0.26	3.8E-01
CNOT11	-1.7	1.7E-02	-0.59	4.5E-03	*MT-ATP6*	-1.8	6.9E-03	-0.50	4.5E-02
C5orf63	-1.7	1.9E-02	-0.10	6.1E-01	*EHHADH*	-1.8	5.3E-03	0.67	3.4E-03
DNAJC5	-1.7	8.5E-03	-0.62	2.7E-03	*ARF5*	-1.8	4.0E-02	0.35	2.2E-01
CCDC43	-1.7	4.1E-02	-0.39	6.5E-02	*TRAF3IP2*	-1.8	9.0E-03	0.13	7.1E-01
RPL26	-1.7	1.6E-02	-0.70	5.5E-04	*EVPL*	-1.8	7.3E-03	-0.16	6.2E-01
POF1B	-1.7	4.2E-02	-0.43	4.3E-02	*SLC25A35*	-1.8	4.5E-03	-0.15	6.6E-01
PA2G4	-1.7	1.8E-02	-0.39	6.4E-02	*ZNF219*	-1.8	3.8E-04	-0.41	1.2E-01
RBM33	-1.7	3.1E-03	-0.36	9.1E-02	*SERINC2*	-1.8	7.3E-03	-0.10	7.7E-01
INO80	-1.7	4.2E-03	-0.30	1.5E-01	*C4orf48*	-1.8	9.7E-03	0.04	9.1E-01
MAN1A2	-1.7	3.0E-02	-0.44	3.9E-02	*PLCE1*	-1.8	1.9E-02	-0.07	8.5E-01
CEP63	-1.7	3.6E-02	-0.29	1.6E-01	*ANKRD9*	-1.8	1.8E-02	-0.11	7.7E-01
STT3A	-1.7	3.4E-02	-0.29	1.7E-01	*ADGRL3*	-1.8	7.9E-05	0.16	6.2E-01
ARHGAP11A	-1.7	3.2E-02	-0.29	1.6E-01	*ANO10*	-1.8	2.2E-03	0.08	8.4E-01
KIAA0368	-1.7	4.3E-02	-0.25	2.1E-01	*RAPGEFL1*	-1.8	1.3E-02	0.23	4.5E-01
TMEM253	-1.7	2.0E-02	-0.35	9.6E-02	*XK*	-1.8	4.0E-02	0.52	3.3E-02
PSMD7	-1.7	9.8E-03	-0.46	3.0E-02	*FAM234A*	-1.8	1.4E-03	0.44	8.4E-02
LARP7	-1.7	2.7E-02	-0.44	4.1E-02	*MGAT4B*	-1.8	1.6E-03	-0.45	8.1E-02
ZNFX1	-1.7	3.2E-02	-0.43	4.2E-02	*CES1*	-1.8	4.3E-02	0.37	1.9E-01
RBBP6	-1.7	1.4E-02	-0.55	9.7E-03	*CYP27A1*	-1.8	1.8E-02	-0.09	8.1E-01

HNRNPH1	-1.7	3.3E-02	-0.33	1.2E-01	*TLN2*	-1.8	6.8E-04	-0.32	2.8E-01
SCAPER	-1.7	3.4E-02	-0.53	1.3E-02	*SLC10A1*	-1.8	5.1E-03	-0.01	9.8E-01
DSP	-1.7	4.1E-02	-0.30	1.5E-01	*BBIP1*	-1.8	2.9E-02	-0.03	9.4E-01
SLC30A9	-1.7	1.4E-02	-0.52	1.5E-02	*MT-ND3*	-1.9	2.5E-04	-0.20	5.2E-01
PPCS	-1.7	8.6E-03	-0.27	1.8E-01	*ABCA8*	-1.9	1.4E-02	0.17	5.9E-01
SUPT16H	-1.7	6.2E-03	-0.37	8.4E-02	*SF3A2*	-1.9	3.8E-02	-0.10	8.0E-01
NIPBL	-1.7	3.3E-03	-0.27	1.9E-01	*MT-CO3*	-1.9	7.6E-03	0.02	9.6E-01
SLC37A4	-1.7	6.5E-03	-0.46	3.2E-02	*POU5F1B*	-1.9	1.2E-02	0.10	7.9E-01
POLE3	-1.7	3.2E-02	-0.70	5.5E-04	*MLXIP*	-1.9	7.3E-04	0.25	4.1E-01
C22orf46	-1.7	1.6E-02	-0.25	2.1E-01	*ABHD5*	-1.9	2.0E-02	0.32	2.8E-01
CEP78	-1.7	3.9E-02	-0.34	1.1E-01	*TFCP2L1*	-1.9	8.8E-03	-0.67	3.4E-03
NASP	-1.7	7.6E-03	-0.48	2.5E-02	*RAVER2*	-1.9	1.3E-02	0.16	6.2E-01
EIF5B	-1.7	4.9E-03	-0.49	2.1E-02	*GSTZ1*	-1.9	4.0E-02	-0.14	6.6E-01
KMT2B	-1.7	4.2E-02	-0.32	1.3E-01	*EMILIN3*	-1.9	2.0E-02	-0.20	5.2E-01
CCDC82	-1.7	2.9E-02	-0.32	1.3E-01	*PHYH*	-1.9	4.3E-03	0.24	4.2E-01
ARL11	-1.7	3.2E-02	-0.13	5.3E-01	*TMEM100*	-1.9	1.2E-02	0.38	1.7E-01
ARHGEF3	-1.7	1.1E-02	-0.51	1.5E-02	*FAM183A*	-1.9	4.0E-02	-0.06	8.7E-01
ACADS	-1.8	3.9E-03	-0.12	5.5E-01	*THAP3*	-1.9	2.5E-02	-0.09	8.0E-01
PPP2R2A	-1.8	5.0E-03	-0.32	1.3E-01	*SH2D6*	-1.9	4.1E-02	-0.18	5.7E-01
RSRC1	-1.8	9.3E-03	-0.59	4.6E-03	*ACOT11*	-1.9	4.7E-04	-0.32	2.7E-01
MYLK	-1.8	2.1E-02	-0.65	1.7E-03	*BSG*	-1.9	4.9E-02	-0.14	6.7E-01
MFHAS1	-1.8	1.1E-02	-0.48	2.3E-02	*HOXB5*	-1.9	3.9E-02	0.56	1.9E-02
NRP1	-1.8	4.3E-02	-0.10	6.3E-01	*MT-ND4L*	-1.9	1.7E-02	-0.31	2.8E-01
MRE11	-1.8	2.5E-02	-0.31	1.4E-01	*FMO5*	-1.9	3.4E-02	-0.04	9.2E-01
METAP2	-1.8	4.8E-03	-0.32	1.3E-01	*GNA11*	-1.9	1.5E-02	0.34	2.4E-01
PDE9A	-1.8	4.9E-02	-0.10	6.4E-01	*HSPB1*	-1.9	3.6E-02	0.59	1.2E-02
CTCF	-1.8	1.5E-02	-0.31	1.4E-01	*BCAS1*	-1.9	1.9E-02	-0.55	2.3E-02
CDC37	-1.8	1.6E-02	-0.50	2.0E-02	*ODF3L1*	-1.9	1.1E-02	0.06	8.8E-01
AUP1	-1.8	3.5E-02	-0.73	2.8E-04	*ETHE1*	-1.9	8.3E-03	-0.41	1.2E-01
PSMD4	-1.8	2.5E-02	-0.53	1.1E-02	*MAST2*	-1.9	8.4E-05	0.28	3.3E-01
DSN1	-1.8	1.8E-02	-0.26	2.0E-01	*PLIN2*	-1.9	2.6E-02	0.30	3.0E-01
CHD7	-1.8	1.6E-02	-0.22	2.9E-01	*NR5A2*	-1.9	3.7E-02	0.03	9.5E-01
LTV1	-1.8	2.7E-02	-0.33	1.2E-01	*CRNN*	-1.9	4.2E-02	0.29	3.2E-01
DGKA	-1.8	4.4E-02	-0.39	6.4E-02	*TTR*	-1.9	2.5E-03	-0.32	2.7E-01
PRRC2C	-1.8	2.4E-02	-0.26	2.0E-01	*ABHD15*	-1.9	6.2E-04	0.21	5.0E-01
PNPO	-1.8	1.5E-02	-0.44	4.1E-02	*RAB17*	-1.9	2.0E-03	-0.17	5.8E-01
CCNA2	-1.8	1.7E-02	-0.42	4.8E-02	*CAMK2N1*	-1.9	3.0E-02	-0.14	6.7E-01
ZNF219	-1.8	1.8E-02	-0.41	5.5E-02	*ZNF701*	-1.9	1.3E-02	0.00	1.0E+00
FAM49B	-1.8	3.8E-02	-0.28	1.7E-01	*PRR26*	-1.9	3.2E-04	-0.23	4.5E-01
MFAP1	-1.8	3.9E-03	-0.33	1.1E-01	*ANKS4B*	-1.9	2.2E-02	-0.30	3.0E-01
CEP170B	-1.8	3.1E-02	-0.60	3.6E-03	*TTC38*	-1.9	4.0E-02	-0.25	4.0E-01
FAAP20	-1.8	4.0E-02	-0.28	1.8E-01	*ESPN*	-1.9	4.0E-03	0.18	5.5E-01
EIF6	-1.8	3.3E-02	-0.44	4.0E-02	*CPEB3*	-1.9	2.1E-03	-0.07	8.5E-01
PSME2	-1.8	2.2E-02	-0.35	9.3E-02	*FAH*	-1.9	1.8E-03	-0.20	5.2E-01

OPA3	-1.8	3.1E-02	0.01	9.6E-01	*OPLAH*	-1.9	2.0E-02	0.11	7.4E-01
ANKRD36	-1.8	4.0E-02	-0.28	1.8E-01	*SLC9A3R1*	-1.9	7.5E-04	0.24	4.3E-01
PSMC6	-1.8	8.1E-03	-0.14	4.8E-01	*MYO1D*	-1.9	9.8E-03	0.24	4.2E-01
TCF25	-1.8	3.0E-03	-0.32	1.2E-01	*DIO3*	-1.9	1.2E-02	-0.58	1.3E-02
TNPO1	-1.8	3.3E-03	-0.34	1.0E-01	*CLDN3*	-1.9	2.8E-02	-0.15	6.6E-01
MPHOSPH9	-1.8	2.4E-02	-0.42	4.8E-02	*EFNA1*	-1.9	2.4E-02	0.31	2.9E-01
DDX27	-1.8	4.2E-03	-0.40	6.0E-02	*AOC1*	-1.9	1.4E-02	0.01	9.8E-01
RAB11FIP2	-1.8	1.9E-02	-0.26	2.0E-01	*MT-ND4*	-1.9	3.6E-04	-0.52	3.1E-02
CDK16	-1.8	3.8E-02	-0.02	9.4E-01	*CHDH*	-1.9	2.9E-03	-0.30	3.1E-01
DROSHA	-1.8	4.2E-03	-0.55	1.1E-02	*PTGR1*	-1.9	1.2E-03	0.40	1.3E-01
NEU3	-1.8	5.0E-02	-0.03	9.0E-01	*PNPLA2*	-1.9	9.4E-04	-0.08	8.3E-01
PPFIBP2	-1.8	1.3E-02	-0.31	1.4E-01	*GPRC5C*	-1.9	1.9E-03	0.08	8.2E-01
HMGB2	-1.8	3.3E-02	-0.28	1.8E-01	*OSBPL1A*	-2.0	2.5E-03	0.24	4.2E-01
KCNQ1	-1.8	1.5E-02	-0.30	1.5E-01	*TSPAN7*	-2.0	3.4E-03	0.05	8.9E-01
PGRMC2	-1.8	6.4E-04	-0.28	1.7E-01	*MARVELD3*	-2.0	2.4E-03	0.39	1.5E-01
WSB2	-1.8	2.7E-02	-0.19	3.6E-01	*MGLL*	-2.0	2.9E-03	0.49	4.9E-02
NOP14	-1.8	1.4E-02	-0.30	1.6E-01	*HHLA2*	-2.0	2.6E-02	-0.63	7.8E-03
GON4L	-1.8	5.0E-03	-0.29	1.6E-01	*EPHX2*	-2.0	6.1E-03	-0.09	8.1E-01
ZNF141	-1.8	3.4E-02	0.13	5.2E-01	*VIL1*	-2.0	2.5E-02	-0.37	1.8E-01
SORD	-1.8	2.6E-02	-0.32	1.3E-01	*CXorf40A*	-2.0	1.7E-02	-0.27	3.6E-01
WDR60	-1.8	3.0E-02	-0.42	4.8E-02	*TGFA*	-2.0	1.5E-03	0.06	8.7E-01
WDR92	-1.8	2.7E-02	-0.36	8.7E-02	*PDCD4*	-2.0	1.4E-02	-0.05	8.9E-01
MEA1	-1.8	2.1E-02	-0.57	6.8E-03	*CPT1A*	-2.0	1.3E-03	0.36	2.1E-01
SPTLC2	-1.8	2.3E-03	-0.12	5.5E-01	*ZNF341*	-2.0	7.4E-03	0.15	6.4E-01
MYO1A	-1.8	4.5E-02	-0.42	4.9E-02	*ARHGAP44*	-2.0	3.7E-02	0.43	9.7E-02
RBM25	-1.8	1.7E-02	-0.43	4.4E-02	*ASAP3*	-2.0	4.0E-02	0.65	5.6E-03
PRPF38B	-1.8	1.9E-02	-0.54	1.1E-02	*TSEN2*	-2.0	9.1E-05	-0.01	9.8E-01
DDX10	-1.8	4.1E-02	-0.37	8.2E-02	*CDIP1*	-2.0	2.6E-02	0.24	4.2E-01
RPS27A	-1.8	1.7E-02	-0.72	4.3E-04	*ETNK1*	-2.0	4.0E-02	0.70	2.9E-03
LRRC47	-1.8	2.7E-02	-0.64	2.0E-03	*HES5*	-2.0	4.5E-02	-0.18	5.7E-01
MMS19	-1.8	4.6E-02	-0.58	5.7E-03	*PXMP2*	-2.0	7.4E-03	0.19	5.3E-01
WWP2	-1.8	4.9E-03	-0.43	4.3E-02	*USP30*	-2.0	6.0E-03	0.38	1.6E-01
SREK1	-1.8	9.2E-03	-0.45	3.6E-02	*UGDH*	-2.0	1.9E-02	0.10	7.7E-01
HSPA5	-1.8	2.7E-02	-0.28	1.7E-01	*PLCD3*	-2.0	3.5E-02	-0.40	1.3E-01
DEK	-1.8	8.5E-03	-0.36	8.5E-02	*GRAMD2A*	-2.0	4.0E-02	0.24	4.2E-01
HYPK	-1.8	2.7E-02	-0.27	1.9E-01	*LETM1*	-2.0	3.4E-03	0.07	8.4E-01
43719	-1.8	7.2E-03	-0.16	4.4E-01	*SLC25A42*	-2.0	4.8E-03	0.27	3.6E-01
DNASE2	-1.8	3.9E-02	-0.10	6.4E-01	*RNASE1*	-2.0	3.2E-02	-0.29	3.2E-01
SNRPD1	-1.8	1.9E-02	-0.66	1.3E-03	*CPT2*	-2.0	9.8E-03	0.46	6.8E-02
JAGN1	-1.8	3.7E-03	-0.35	1.0E-01	*RNF152*	-2.0	4.1E-02	-0.53	2.9E-02
CKMT1A	-1.9	1.2E-02	-0.40	5.7E-02	*CDX2*	-2.0	3.2E-02	0.30	3.0E-01
B3GNT2	-1.9	5.0E-02	-0.39	6.4E-02	*SLC22A5*	-2.0	3.8E-02	0.26	3.9E-01
RPS24	-1.9	2.4E-02	-0.66	1.3E-03	*LONRF3*	-2.0	2.9E-03	0.08	8.2E-01
BCAS1	-1.9	1.3E-02	-0.55	1.0E-02	*MPST*	-2.0	1.4E-02	0.42	1.2E-01

USP48	-1.9	3.7E-03	-0.37	8.2E-02	*RCN3*	-2.1	4.3E-02	0.15	6.6E-01
TOP2A	-1.9	2.8E-02	-0.29	1.6E-01	*NCKAP5*	-2.1	1.5E-02	0.46	7.0E-02
SDAD1	-1.9	9.9E-03	-0.43	4.4E-02	*SH3BGRL2*	-2.1	8.4E-03	0.14	6.7E-01
TLCD2	-1.9	1.6E-02	-0.33	1.2E-01	*SERPINA6*	-2.1	3.5E-02	-0.23	4.5E-01
RPP21	-1.9	4.4E-02	-0.59	4.1E-03	*EFCAB5*	-2.1	2.0E-03	-0.09	8.1E-01
NUCKS1	-1.9	5.7E-03	-0.43	4.2E-02	*OAF*	-2.1	5.2E-05	-0.30	3.1E-01
RBM34	-1.9	4.7E-02	-0.37	7.7E-02	*IL37*	-2.1	8.6E-03	-0.10	7.9E-01
DDAH2	-1.9	4.4E-02	-0.12	5.7E-01	*ADIRF*	-2.1	4.9E-02	0.27	3.6E-01
PUM3	-1.9	3.5E-02	-0.46	3.0E-02	*TPRN*	-2.1	1.5E-02	-0.09	8.1E-01
BDP1	-1.9	3.1E-02	-0.45	3.4E-02	*MYZAP*	-2.1	1.4E-04	0.26	3.9E-01
PRR11	-1.9	4.4E-02	-0.10	6.4E-01	*PLA2R1*	-2.1	3.8E-02	0.26	3.8E-01
MYADM	-1.9	2.4E-02	-0.43	4.4E-02	*GJB1*	-2.1	3.1E-03	-0.39	1.4E-01
IL32	-1.9	2.2E-02	-0.22	2.7E-01	*TCTA*	-2.1	1.5E-02	-0.26	3.9E-01
CKAP4	-1.9	7.0E-03	-0.69	7.3E-04	*CLDN15*	-2.1	1.1E-03	-0.03	9.3E-01
ATF6B	-1.9	3.8E-02	-0.41	5.5E-02	*LCE2A*	-2.1	1.8E-02	-0.11	7.6E-01
MEPCE	-1.9	1.8E-02	-0.49	2.3E-02	*PRR15*	-2.1	4.9E-03	-0.11	7.6E-01
C6orf132	-1.9	3.1E-02	-0.39	6.4E-02	*CYP4F12*	-2.1	6.5E-03	0.00	1.0E+00
ZNF69	-1.9	4.5E-02	-0.24	2.3E-01	*P2RY1*	-2.1	4.4E-02	-0.58	1.3E-02
CCDC112	-1.9	1.6E-02	-0.32	1.3E-01	*MOGAT2*	-2.1	1.5E-03	-0.34	2.3E-01
CWC15	-1.9	3.3E-03	-0.60	3.8E-03	*PCOTH*	-2.1	4.8E-02	-0.32	2.8E-01
MRPL21	-1.9	3.5E-02	-0.43	4.2E-02	*GLOD5*	-2.1	3.1E-02	-0.19	5.3E-01
NDUFV3	-1.9	3.0E-02	-0.45	3.4E-02	*GLB1L2*	-2.1	2.1E-02	-0.21	4.9E-01
WDR43	-1.9	7.3E-03	-0.48	2.4E-02	*TM4SF5*	-2.1	4.0E-02	-0.10	7.8E-01
LGALS9	-1.9	3.2E-02	-0.14	4.8E-01	*TMEM177*	-2.1	1.5E-02	-0.40	1.3E-01
TNPO2	-1.9	2.7E-02	-0.22	2.7E-01	*KLF8*	-2.1	1.4E-02	0.30	3.0E-01
EIF3CL	-1.9	3.8E-02	-0.37	7.7E-02	*FLVCR1*	-2.1	4.4E-03	0.46	6.8E-02
NDRG2	-1.9	3.4E-02	-0.57	6.7E-03	*TMEM37*	-2.1	3.1E-02	0.14	6.7E-01
COX16	-1.9	1.8E-02	-0.35	9.3E-02	*NETO2*	-2.1	7.5E-03	0.42	1.2E-01
CWF19L2	-1.9	1.6E-02	-0.54	1.1E-02	*A1CF*	-2.1	2.5E-02	0.11	7.7E-01
TAPBPL	-1.9	2.6E-02	-0.36	8.7E-02	*TMEM253*	-2.2	2.0E-02	-0.35	2.2E-01
EPB41L1	-1.9	3.8E-02	-0.07	7.6E-01	*EPB41L4B*	-2.2	8.8E-03	0.35	2.2E-01
BRCA1	-1.9	2.6E-02	-0.27	1.8E-01	*SLITRK6*	-2.2	4.7E-02	-0.08	8.3E-01
ANP32B	-1.9	4.0E-03	-0.27	1.9E-01	*ZBTB7C*	-2.2	3.3E-02	-0.20	5.2E-01
ZC3H15	-1.9	3.3E-03	-0.43	4.3E-02	*TRPM4*	-2.2	5.0E-03	-0.23	4.5E-01
PIK3R3	-1.9	2.1E-02	-0.28	1.7E-01	*CES2*	-2.2	3.7E-03	0.02	9.6E-01
WDR76	-1.9	2.7E-02	-0.20	3.3E-01	*NDRG2*	-2.2	2.8E-02	-0.57	1.4E-02
SPAG7	-2.0	2.7E-02	-0.71	5.0E-04	*ACAA1*	-2.2	6.2E-05	-0.30	3.0E-01
AP2B1	-2.0	3.1E-02	-0.64	2.2E-03	*MAOA*	-2.2	1.6E-02	-0.24	4.2E-01
ATAD2	-2.0	1.7E-02	-0.51	1.7E-02	*FXYD3*	-2.2	5.3E-05	-0.16	6.0E-01
EBP	-2.0	2.6E-02	-0.49	2.0E-02	*SEMA5A*	-2.2	2.3E-02	0.10	7.9E-01
MRPS18B	-2.0	3.7E-03	-0.32	1.3E-01	*CDKN2B*	-2.2	6.6E-03	0.06	8.8E-01
FAM193A	-2.0	3.0E-02	-0.16	4.3E-01	*PDK4*	-2.2	2.3E-02	0.20	5.2E-01
FAM208B	-2.0	4.0E-02	-0.24	2.4E-01	*NICN1*	-2.2	1.7E-03	0.13	7.1E-01
THOC5	-2.0	2.7E-02	-0.30	1.5E-01	*CMBL*	-2.2	2.7E-03	0.59	1.1E-02

PKP4	-2.0	1.2E-03	-0.39	6.8E-02	*UFSP1*	-2.3	3.2E-03	0.04	9.0E-01
CEP104	-2.0	9.2E-03	-0.46	3.3E-02	*PDSS1*	-2.3	4.4E-02	0.12	7.3E-01
APOBEC3C	-2.0	1.7E-02	-0.63	2.3E-03	*HOXB8*	-2.3	2.6E-02	0.34	2.4E-01
GNL2	-2.0	4.2E-02	-0.57	7.0E-03	*AGFG2*	-2.3	1.9E-03	0.34	2.4E-01
PPP1R10	-2.0	1.5E-02	-0.26	2.0E-01	*DDAH2*	-2.3	5.2E-05	-0.12	7.4E-01
CEP152	-2.0	1.1E-02	-0.11	5.7E-01	*TMEM56*	-2.3	1.1E-02	0.46	6.7E-02
NOMO1	-2.0	1.7E-02	-0.29	1.7E-01	*ALKAL2*	-2.3	5.5E-04	0.07	8.4E-01
PSMG3	-2.0	3.3E-02	-0.56	8.5E-03	*ARSE*	-2.3	6.2E-03	-0.24	4.3E-01
ENDOD1	-2.0	1.2E-02	-0.62	2.5E-03	*AHCYL2*	-2.3	1.5E-03	-0.13	7.1E-01
TRA2A	-2.0	1.1E-02	-0.36	9.1E-02	*RHOU*	-2.3	1.7E-03	0.04	9.2E-01
KMT5A	-2.0	1.4E-02	-0.25	2.2E-01	*FAM213A*	-2.3	1.2E-03	0.18	5.7E-01
LYAR	-2.0	4.2E-02	-0.42	4.8E-02	*TINAG*	-2.3	3.8E-02	-0.47	6.2E-02
ZFP62	-2.0	2.1E-02	-0.46	3.2E-02	*MAP7D2*	-2.3	2.9E-02	-0.58	1.3E-02
TRAPPC6A	-2.0	2.4E-02	-0.24	2.4E-01	*SLC19A3*	-2.3	1.0E-02	0.21	4.9E-01
MYH14	-2.0	4.5E-02	-0.01	9.4E-01	*TBX10*	-2.3	3.5E-02	-0.23	4.4E-01
TMEM125	-2.0	1.3E-02	-0.43	4.5E-02	*BMP5*	-2.3	6.9E-03	0.60	1.1E-02
HAUS6	-2.0	7.0E-03	-0.31	1.4E-01	*FOXO4*	-2.3	2.9E-02	0.06	8.8E-01
DHRS7B	-2.0	1.9E-02	-0.44	4.1E-02	*SLC4A10*	-2.3	1.5E-02	0.22	4.6E-01
CCDC47	-2.1	4.2E-03	-0.18	3.9E-01	*MACROD1*	-2.3	2.3E-02	0.17	5.8E-01
HSF2	-2.1	3.5E-02	-0.32	1.3E-01	*CA12*	-2.4	2.4E-03	0.33	2.4E-01
CDT1	-2.1	3.9E-02	-0.30	1.5E-01	*AC092587.1*	-2.4	5.0E-02	-0.10	7.8E-01
CPSF3	-2.1	3.7E-03	-0.42	4.8E-02	*SLC27A4*	-2.4	2.5E-02	0.28	3.5E-01
FAM32A	-2.1	7.6E-03	-0.61	3.1E-03	*NUDT4P1*	-2.4	8.6E-03	0.05	8.9E-01
SYTL4	-2.1	3.1E-02	-0.60	3.8E-03	*TST*	-2.4	1.5E-03	-0.02	9.6E-01
SRFBP1	-2.1	4.8E-02	-0.29	1.6E-01	*CCDC153*	-2.4	1.0E-02	-0.36	2.1E-01
DTX3L	-2.1	3.4E-02	-0.05	8.2E-01	*PMM1*	-2.4	1.3E-03	0.10	7.8E-01
GRIPAP1	-2.1	6.2E-03	-0.21	3.0E-01	*TMUB1*	-2.4	8.5E-03	0.18	5.7E-01
GTSE1	-2.1	2.4E-02	-0.32	1.3E-01	*SLC13A2*	-2.4	2.6E-02	-0.60	1.1E-02
AURKA	-2.1	3.7E-03	-0.45	3.6E-02	*PPP2R5D*	-2.4	2.5E-02	0.01	9.8E-01
TANGO2	-2.1	3.5E-02	-0.28	1.8E-01	*NAT8*	-2.4	1.7E-02	-0.08	8.3E-01
GPI	-2.1	1.0E-02	-0.47	2.9E-02	*AMACR*	-2.4	1.5E-02	-0.34	2.3E-01
HDAC7	-2.1	2.3E-03	-0.42	4.7E-02	*DHRS11*	-2.4	3.2E-03	0.53	2.7E-02
ADRM1	-2.1	4.8E-02	-0.54	1.1E-02	*METTL7B*	-2.4	4.2E-02	0.44	9.0E-02
NDST1	-2.1	4.3E-02	-0.38	7.7E-02	*PLA2G12B*	-2.4	2.2E-02	-0.34	2.4E-01
UPF3B	-2.1	9.0E-03	-0.46	3.2E-02	*ACOT4*	-2.4	1.3E-02	0.15	6.6E-01
STAU2	-2.1	6.2E-03	-0.24	2.3E-01	*INPP5J*	-2.5	5.8E-03	0.07	8.4E-01
CENPL	-2.1	1.4E-02	-0.48	2.4E-02	*MEP1A*	-2.5	2.2E-02	0.40	1.3E-01
PPDPF	-2.1	4.2E-03	-0.19	3.5E-01	*AC007906.2*	-2.5	1.8E-02	-0.07	8.4E-01
EEF1D	-2.1	1.5E-02	-0.61	3.1E-03	*ACADS*	-2.5	1.7E-03	-0.12	7.2E-01
GJB1	-2.1	2.5E-02	-0.39	6.5E-02	*ADH1C*	-2.5	3.9E-02	0.40	1.3E-01
SLC39A11	-2.1	2.1E-02	-0.59	4.3E-03	*HR*	-2.5	1.7E-03	-0.48	5.2E-02
USP28	-2.1	2.4E-02	-0.20	3.3E-01	*PDXP*	-2.5	4.2E-02	-0.22	4.7E-01
GPR89B	-2.1	3.5E-02	-0.44	4.1E-02	*PDK2*	-2.5	2.3E-03	-0.02	9.7E-01
RNF214	-2.1	3.7E-02	-0.40	5.7E-02	*IQCM*	-2.5	3.6E-02	-0.19	5.4E-01

KIF15	-2.1	4.6E-02	-0.42	4.8E-02	*MUC20*	-2.5	1.3E-02	-0.09	8.1E-01
PES1	-2.1	3.1E-02	-0.14	4.8E-01	*SYCP3*	-2.5	3.4E-04	-0.35	2.3E-01
SAAL1	-2.1	6.2E-03	-0.28	1.8E-01	*MTRNR2L12*	-2.5	3.2E-02	-0.15	6.5E-01
MKI67	-2.1	1.7E-02	-0.37	8.2E-02	*FCGRT*	-2.5	2.4E-04	0.10	7.8E-01
TNFAIP8L1	-2.2	3.7E-03	-0.23	2.7E-01	*LTK*	-2.5	4.2E-03	0.21	5.0E-01
CMIP	-2.2	1.3E-02	-0.26	2.0E-01	*SGK2*	-2.5	3.7E-03	0.07	8.4E-01
SYCP3	-2.2	8.5E-03	-0.35	1.0E-01	*SLC16A1*	-2.5	1.7E-03	0.31	2.9E-01
KHSRP	-2.2	1.8E-02	-0.17	4.0E-01	*CDK3*	-2.5	1.5E-03	-0.11	7.6E-01
DYNC1H1	-2.2	3.2E-03	-0.44	3.7E-02	*NDRG1*	-2.6	6.7E-05	0.41	1.3E-01
TRIAP1	-2.2	1.3E-02	-0.52	1.5E-02	*NUDT14*	-2.6	5.9E-03	0.11	7.6E-01
RAD9A	-2.2	8.5E-03	-0.05	8.3E-01	*ANK3*	-2.6	9.1E-04	0.11	7.5E-01
SIRT6	-2.2	8.4E-03	-0.39	6.3E-02	*WSCD1*	-2.6	2.8E-02	-0.02	9.7E-01
TTK	-2.2	2.2E-02	-0.37	7.7E-02	*PDE6A*	-2.6	2.8E-02	0.20	5.2E-01
SLC39A7	-2.2	1.2E-02	-0.49	2.0E-02	*RETSAT*	-2.6	1.5E-04	-0.39	1.4E-01
AQP1	-2.2	3.3E-02	-0.54	1.1E-02	*SCIN*	-2.6	2.5E-02	0.19	5.4E-01
SDHAF2	-2.2	1.0E-02	-0.46	3.2E-02	*RAB6B*	-2.6	5.2E-03	0.47	6.0E-02
NCL	-2.3	4.9E-03	-0.51	1.6E-02	*FABP1*	-2.6	6.8E-03	0.19	5.4E-01
PCDH1	-2.3	3.2E-02	-0.31	1.5E-01	*NEURL1B*	-2.6	3.1E-03	-0.21	5.1E-01
STRN3	-2.3	1.1E-02	-0.39	6.6E-02	*SAMD13*	-2.6	8.7E-04	-0.13	7.1E-01
MPHOSPH6	-2.3	3.3E-03	-0.45	3.4E-02	*HSD17B2*	-2.6	9.2E-03	0.66	4.8E-03
ZFC3H1	-2.3	1.5E-02	-0.26	2.0E-01	*SLC22A18AS*	-2.6	1.2E-03	-0.20	5.2E-01
SMC1A	-2.3	3.3E-03	-0.42	4.8E-02	*LDHD*	-2.7	1.8E-02	-0.07	8.5E-01
FUBP1	-2.3	6.3E-03	-0.38	7.7E-02	*WDR78*	-2.7	1.8E-02	0.30	3.1E-01
PPP3R1	-2.3	6.2E-03	-0.39	6.5E-02	*ACSF2*	-2.7	3.1E-02	0.29	3.3E-01
CKAP2L	-2.3	3.3E-02	-0.51	1.6E-02	*ACOX1*	-2.7	4.2E-04	0.27	3.6E-01
MUC3A	-2.3	3.1E-02	-0.19	3.5E-01	*SELENBP1*	-2.7	4.4E-02	-0.41	1.2E-01
TTI1	-2.3	1.1E-02	-0.44	3.7E-02	*MYLPF*	-2.7	5.0E-03	-0.14	6.7E-01
DCAKD	-2.3	4.0E-02	-0.42	4.6E-02	*NEURL3*	-2.7	2.0E-02	-0.04	9.1E-01
GPT2	-2.4	2.0E-02	-0.05	8.0E-01	*KRT12*	-2.7	3.0E-02	0.30	3.0E-01
THOP1	-2.4	1.8E-02	-0.54	1.1E-02	*SOWAHA*	-2.7	6.9E-03	0.43	9.7E-02
CNTLN	-2.4	4.5E-02	-0.30	1.5E-01	*C2orf54*	-2.8	3.7E-03	-0.08	8.3E-01
PTMA	-2.4	4.3E-03	-0.39	6.4E-02	*SLC38A4*	-2.8	2.0E-02	0.58	1.3E-02
TUBA1C	-2.4	2.2E-02	-0.54	1.1E-02	*NHEJ1*	-2.8	6.1E-03	-0.50	4.0E-02
HYOU1	-2.4	1.1E-02	0.00	9.9E-01	*PHGR1*	-2.8	4.1E-03	-0.30	3.0E-01
ARHGEF11	-2.4	3.1E-02	-0.09	6.5E-01	*IGSF9*	-2.8	2.3E-02	-0.35	2.2E-01
NCAPG	-2.4	3.8E-02	-0.48	2.3E-02	*GXYLT2*	-2.9	3.5E-02	0.48	5.2E-02
NDUFS2	-2.4	1.5E-02	-0.53	1.3E-02	*ENTPD5*	-2.9	1.0E-03	0.29	3.2E-01
ATP5EP2	-2.4	8.1E-03	-0.44	4.0E-02	*VIPR1*	-2.9	9.5E-05	-0.24	4.2E-01
FER1L6	-2.5	4.1E-02	-0.27	1.8E-01	*BMP3*	-2.9	2.0E-02	-0.06	8.8E-01
HHLA2	-2.5	2.6E-02	-0.63	2.4E-03	*SLC20A1*	-3.0	3.3E-03	0.59	1.2E-02
HMGN5	-2.5	1.2E-02	-0.39	6.5E-02	*PLCD1*	-3.0	4.0E-03	0.42	1.1E-01
PADI2	-2.5	9.2E-03	-0.22	2.7E-01	*PIGZ*	-3.0	1.1E-02	-0.38	1.7E-01
PSMC3	-2.5	4.1E-03	-0.50	1.9E-02	*SLC39A5*	-3.0	4.2E-02	0.13	6.9E-01
IL2RA	-2.5	2.2E-02	-0.17	4.1E-01	*CCNJL*	-3.1	4.1E-03	0.31	3.0E-01

SMARCB1	-2.5	1.1E-02	-0.60	3.8E-03	*CYP2B6*	-3.1	1.3E-02	0.50	4.3E-02
S100A13	-2.6	1.3E-02	-0.52	1.5E-02	*TIGD6*	-3.1	8.8E-04	0.04	9.2E-01
TRMT11	-2.6	1.1E-02	-0.19	3.5E-01	*CHP2*	-3.2	1.6E-02	-0.52	3.0E-02
MND1	-2.6	4.4E-02	-0.35	1.0E-01	*SLC23A3*	-3.2	4.2E-03	0.61	9.9E-03
SWI5	-2.6	4.2E-02	-0.35	9.4E-02	*DISP2*	-3.3	9.2E-05	-0.02	9.7E-01
ZNF625	-2.6	4.2E-02	-0.30	1.6E-01	*SULT1A2*	-3.4	1.1E-02	0.02	9.7E-01
B3GNT7	-2.6	9.0E-03	-0.66	1.3E-03	*BEST2*	-3.4	4.2E-02	-0.50	4.5E-02
DONSON	-2.7	2.4E-02	-0.32	1.3E-01	*PRKG2*	-3.4	3.3E-03	-0.33	2.5E-01
NCDN	-2.7	2.7E-02	-0.45	3.5E-02	*ABCG2*	-3.5	3.4E-02	0.25	4.0E-01
CETN3	-2.8	3.7E-03	-0.41	5.4E-02	*SLC17A4*	-3.5	3.0E-03	0.29	3.3E-01
VNN2	-2.8	2.9E-02	-0.40	6.2E-02	*SLC16A9*	-3.5	4.3E-02	-0.12	7.4E-01
IL11RA	-2.8	9.9E-03	-0.40	5.7E-02	*OTOP2*	-3.6	2.7E-02	-0.32	2.7E-01
PYCR1	-2.9	4.6E-02	-0.29	1.6E-01	*TMIGD1*	-3.6	4.6E-02	-0.58	1.2E-02
POC1A	-2.9	3.7E-03	-0.29	1.6E-01	*CKB*	-3.7	1.2E-02	-0.54	2.6E-02
SFN	-2.9	9.2E-03	-0.11	5.9E-01	*DEFB1*	-3.7	9.8E-05	0.49	4.6E-02
PAK1IP1	-3.8	2.0E-02	-0.52	1.5E-02	*LYPD8*	-3.7	4.2E-02	0.27	3.7E-01
PLTP	-3.9	3.1E-02	-0.35	9.8E-02	*MEP1B*	-3.9	8.5E-03	0.46	6.8E-02
NOX1	-4.3	2.3E-02	-0.63	2.3E-03	*PITX2*	-3.9	4.2E-02	0.60	1.0E-02
EME1	-6.2	1.1E-02	-0.28	1.7E-01	*AQP7*	-4.0	1.2E-04	-0.02	9.7E-01
AC073610.2	-8.4	1.1E-02	-0.07	7.4E-01	*FRMD1*	-4.1	2.0E-03	-0.19	5.4E-01
NME7	-9.5	1.8E-03	-0.27	1.8E-01	*SLC51A*	-4.1	2.4E-04	0.54	2.5E-02
DND1	-13.6	3.2E-03	-0.36	8.7E-02	*B4GALNT2*	-4.3	3.5E-02	0.54	2.5E-02
SULT1A4	-13.9	3.1E-04	-0.51	1.6E-02	*PADI2*	-4.3	9.3E-04	-0.22	4.7E-01
					ZG16	-4.4	4.9E-02	-0.24	4.3E-01
					PCK1	-4.6	1.9E-02	0.03	9.5E-01
					GSTA1	-4.7	2.6E-02	-0.20	5.2E-01
					TNNC2	-4.8	2.7E-03	-0.04	9.2E-01
					SLC26A2	-4.8	3.3E-02	-0.05	8.9E-01
					SULT1A4	-4.8	1.3E-02	-0.51	3.7E-02
					GUCA2B	-5.5	3.8E-02	-0.52	3.1E-02
					HMGCS2	-7.5	9.1E-03	0.52	3.0E-02
					AQP8	-13.8	2.2E-02	0.26	3.9E-01

CD, Crohn disease; EoC, eosinophilic colitis; FC, fold change; NL, normal.

Supplementary Table 6. Summary of UC transcriptomic datasets

No	Study	Year	Accession	Tissue	Sites of biopsies	Age group	No. of UC cases	No. of controls	References (PMID)
1	Olsen *et al.*	2007	GSE9452	Colon	Descending or sigmoid	Adults	8	5	19177426
2	Wu *et al.*	2007	GSE6731	Colon	Affected area or sigmoid	Adults	5	4	17262812
3	Galamb *et al.*	2008	GSE10714	Colon	Affected area	Adults	3	3	18843029
4	Ahrens *et al.*	2008	GSE10191	Colon	Affected area	Children	8	11	18981162
5	Bjerrum *et al.*	2009	GSE13367	Colon	Descending	Adults	8	10	19834973
6	Kugathasan *et al.*	2009	GSE10616	Colon	Ascending	Children	10	11	18758464
7	Arijs *et al.*	2010	GSE14580	Colon	Rectum	Adults	24	6	19700435
8	Planell *et al.*	2012	GSE38713	Colon	Sigmoid or rectum	Adults	15	13	23135761
9	Montero-Meléndez *et al.*	2013	GSE36807	Colon	Ascending	Adults	15	7	24155895
10	Bjerrum *et al.*	2014	GSE47908	Colon	Descending	Adults	20	15	25358065
11	Vanhove *et al.*	2015	GSE59071	Colon	Sigmoid or rectum	Adults	74	11	26313692
12	Li *et al.*	2018	GSE87473	Colon	Sigmoid	Adults	27	21	29401083
13	Li *et al.*	2018	GSE87473	Colon	Ascending	Children	13	21	29401083
14	Haberman *et al.*	2019	GSE109142	Colon	Rectum	Children	206	20	30604764

UC, ulcerative colitis; GSE, genomic spatial event.

Supplementary Table 7. List of genes in the EoC transcriptome overlapped with EoE and EoG transcriptomes

Upregulated genes in the EoC transcriptome				Downregulated genes in the EoC transcriptome			
Overlapped with EoE upregulated genes		Overlapped with EoG upregulated genes		Overlapped with EoE downregulated genes		Overlapped with EoG downregulated genes	
Gene Symbol	FC (Active EoC vs NL)	Gene Symbol	FC (Active EoC vs NL)	Gene Symbol	FC (Active EoC vs NL)	Gene Symbol	FC (Active EoC vs NL)
CLC	10.2	*CLC*	10.2	*PPDPF*	-2.1	*NUPR1*	-1.6
IFITM1	8.3	*GAPT*	3.9	*C6orf132*	-1.9		
F13A1	4.7	*CD9*	3.8	*TSC22D2*	-1.7		
IFNGR1	4.6	*CXCL1*	3.6	*DDAH1*	-1.7		
CLDN23	4.4	*MMP12*	3.2	*ACOT11*	-1.6		
GAPT	3.9	*NCF2*	3.1				
CD9	3.8	*CEBPE*	3.0				
CXCL1	3.6	*CSF2RB*	2.3				
TRIM21	3.6	*CLDN7*	2.2				
CD300A	3.4	*TMIGD3*	2.2				
MMP12	3.2	*C15orf48*	2.2				
NCF2	3.1	*LST1*	2.2				
LY96	3.1	*CCL11*	2.1				
CD53	3.1	*ADAMDEC1*	2.1				
SERPINF1	2.7	*PLCG2*	2.1				
GCH1	2.6	*FPR1*	1.9				
ITM2C	2.6	*SOCS1*	1.7				
GLRX	2.5	*ALOX5AP*	1.7				
HLA-F	2.5	*CD209*	1.6				
LIPA	2.4						
PRIM2	2.4						
KLRB1	2.4						
LUM	2.3						
B2M	2.3						
HLA-B	2.3						
IL15RA	2.3						
CSF2RB	2.3						
RDH10	2.2						
AMY2B	2.2						
SIRPA	2.2						
VIM	2.1						
COL3A1	2.1						
PLAU	2.1						
CHEK2	2.1						
C2	2.1						
SLC38A9	2.0						
LTA4H	2.0						
CTSC	2.0						
HIGD2A	1.9						
ANXA4	1.9						
GATA2	1.9						
PSMB8	1.9						
COTL1	1.8						
LASP1	1.8						
SOCS1	1.7						
ALOX5AP	1.7						
PTPN9	1.7						
UBE2L6	1.6						
THBD	1.6						

EoC, eosinophilic colitis; EoE, eosinophilic esophagitis; EoG, eosinophilic gastritis; FC, fold change; NL, normal.

Supplementary Table 8. Functional annotation enrichment of the EoC transcriptome

	ID	Name	Source	*P* value	FDR B&H	Genes from Input	Genes in Annotation
327 Upregulated genes							
GO: Molecular Function							
1	GO:0015932	nucleobase-containing compound transmembrane transporter activity	GO: Molecular Function	4.3E-05	3.4E-02	8	45
2	GO:0008234	cysteine-type peptidase activity	GO: Molecular Function	6.6E-05	3.4E-02	40	711
3	GO:0004464	leukotriene-C4 synthase activity	GO: Molecular Function	9.8E-05	3.4E-02	3	4
4	GO:0003735	structural constituent of ribosome	GO: Molecular Function	1.2E-04	3.4E-02	17	205
5	GO:0003723	RNA binding	GO: Molecular Function	1.8E-04	4.1E-02	85	1973
6	GO:0015165	pyrimidine nucleotide-sugar transmembrane transporter activity	GO: Molecular Function	3.0E-04	4.9E-02	4	12
7	GO:0004865	protein serine/threonine phosphatase inhibitor activity	GO: Molecular Function	3.0E-04	4.9E-02	4	12
GO: Biological Process							
1	GO:0044265	cellular macromolecule catabolic process	GO: Biological Process	2.0E-09	1.2E-05	71	1201
2	GO:0043299	leukocyte degranulation	GO: Biological Process	3.8E-09	1.2E-05	42	546
3	GO:0002275	myeloid cell activation involved in immune response	GO: Biological Process	6.8E-09	1.4E-05	42	557
4	GO:0009057	macromolecule catabolic process	GO: Biological Process	9.8E-09	1.5E-05	79	1453
5	GO:0002444	myeloid leukocyte mediated immunity	GO: Biological Process	1.2E-08	1.5E-05	42	568
6	GO:0042119	neutrophil activation	GO: Biological Process	3.3E-08	2.7E-05	38	502
7	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	GO: Biological Process	3.7E-08	2.7E-05	16	105
8	GO:0002446	neutrophil mediated immunity	GO: Biological Process	4.1E-08	2.7E-05	38	506
9	GO:0045047	protein targeting to ER	GO: Biological Process	4.2E-08	2.7E-05	17	120
10	GO:0036230	granulocyte activation	GO: Biological Process	4.5E-08	2.7E-05	38	508

11	GO:0043312	neutrophil degranulation	GO: Biological Process	4.8E-08	2.7E-05	37	488
12	GO:0002283	neutrophil activation involved in immune response	GO: Biological Process	5.6E-08	2.9E-05	37	491
13	GO:0006613	cotranslational protein targeting to membrane	GO: Biological Process	6.3E-08	3.0E-05	16	109
14	GO:0072599	establishment of protein localization to endoplasmic reticulum	GO: Biological Process	6.9E-08	3.0E-05	17	124
15	GO:0006402	mRNA catabolic process	GO: Biological Process	1.0E-07	4.1E-05	31	377
16	GO:0016032	viral process	GO: Biological Process	1.3E-07	5.1E-05	52	853
17	GO:0045055	regulated exocytosis	GO: Biological Process	1.8E-07	6.3E-05	51	837
18	GO:0044403	symbiotic process	GO: Biological Process	1.8E-07	6.3E-05	54	911
19	GO:0070972	protein localization to endoplasmic reticulum	GO: Biological Process	2.0E-07	6.4E-05	18	149
20	GO:0080134	regulation of response to stress	GO: Biological Process	2.1E-07	6.4E-05	83	1671
21	GO:0016071	mRNA metabolic process	GO: Biological Process	7.1E-07	1.7E-04	52	901
22	GO:0002274	myeloid leukocyte activation	GO: Biological Process	7.3E-07	1.7E-04	43	683
23	GO:0002237	response to molecule of bacterial origin	GO: Biological Process	7.5E-07	1.7E-04	29	371
24	GO:0001775	cell activation	GO: Biological Process	7.5E-07	1.7E-04	77	1558
25	GO:0006887	exocytosis	GO: Biological Process	7.6E-07	1.7E-04	54	953
GO: Cellular Component							
1	GO:0005764	lysosome	GO: Cellular Component	1.3E-09	5.2E-07	51	735
2	GO:0000323	lytic vacuole	GO: Cellular Component	1.4E-09	5.2E-07	51	736
3	GO:0005774	vacuolar membrane	GO: Cellular Component	5.2E-09	9.1E-07	35	417
4	GO:0005765	lysosomal membrane	GO: Cellular Component	5.6E-09	9.1E-07	32	359
5	GO:0098852	lytic vacuole membrane	GO: Cellular Component	6.0E-09	9.1E-07	32	360
6	GO:0005739	mitochondrion	GO: Cellular Component	8.5E-08	1.1E-05	90	1866
7	GO:0005789	endoplasmic reticulum membrane	GO: Cellular Component	1.1E-07	1.2E-05	61	1093
8	GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	GO: Cellular Component	2.3E-07	2.2E-05	61	1116

9	GO:0042611	MHC protein complex	GO: Cellular Component	3.1E-07	2.6E-05	8	26
10	GO:0005925	focal adhesion	GO: Cellular Component	4.3E-07	3.2E-05	31	411
11	GO:0030055	cell-substrate junction	GO: Cellular Component	7.2E-07	4.9E-05	31	421
12	GO:0022626	cytosolic ribosome	GO: Cellular Component	8.6E-07	5.4E-05	16	134
13	GO:0005768	endosome	GO: Cellular Component	9.9E-07	5.7E-05	53	956
14	GO:0031967	organelle envelope	GO: Cellular Component	1.2E-06	6.0E-05	65	1279
15	GO:0031975	envelope	GO: Cellular Component	1.2E-06	6.0E-05	65	1280
16	GO:0005794	Golgi apparatus	GO: Cellular Component	1.3E-06	6.2E-05	78	1643
17	GO:0000139	Golgi membrane	GO: Cellular Component	1.7E-06	7.3E-05	45	770
18	GO:1990234	transferase complex	GO: Cellular Component	1.8E-06	7.3E-05	47	821
19	GO:1902494	catalytic complex	GO: Cellular Component	2.9E-06	1.1E-04	73	1536
20	GO:0012506	vesicle membrane	GO: Cellular Component	4.1E-06	1.6E-04	46	822
21	GO:0005740	mitochondrial envelope	GO: Cellular Component	4.6E-06	1.6E-04	45	800
22	GO:0030659	cytoplasmic vesicle membrane	GO: Cellular Component	4.6E-06	1.6E-04	45	800
23	GO:0030141	secretory granule	GO: Cellular Component	5.7E-06	1.9E-04	48	884
24	GO:0005912	adherens junction	GO: Cellular Component	5.9E-06	1.9E-04	35	560
25	GO:0012507	ER to Golgi transport vesicle membrane	GO: Cellular Component	6.7E-06	2.0E-04	10	62
Pathway							
1	1268689	SRP-dependent cotranslational protein targeting to membrane	BioSystems: REACTOME	2.4E-08	2.4E-05	18	116
2	1268678	Translation	BioSystems: REACTOME	5.8E-08	2.9E-05	21	165
3	1269203	Innate Immune System	BioSystems: REACTOME	2.5E-07	8.6E-05	75	1312
4	1457780	Neutrophil degranulation	BioSystems: REACTOME	9.7E-07	2.1E-04	37	492
5	1268854	Disease	BioSystems: REACTOME	1.3E-06	2.1E-04	54	867
6	1268691	Peptide chain elongation	BioSystems: REACTOME	1.3E-06	2.1E-04	14	93
7	1268690	Eukaryotic Translation Elongation	BioSystems: REACTOME	2.4E-06	3.5E-04	14	98

8	1269056	Infectious disease	BioSystems: REACTOME	2.9E-06	3.7E-04	31	393
9	1268686	GTP hydrolysis and joining of the 60S ribosomal subunit	BioSystems: REACTOME	5.2E-06	4.8E-04	15	119
10	1268688	L13a-mediated translational silencing of Ceruloplasmin expression	BioSystems: REACTOME	5.2E-06	4.8E-04	15	119
11	1269716	Nonsense-Mediated Decay (NMD)	BioSystems: REACTOME	6.4E-06	4.8E-04	15	121
12	1269717	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	BioSystems: REACTOME	6.4E-06	4.8E-04	15	121
13	1268681	Formation of a pool of free 40S subunits	BioSystems: REACTOME	6.9E-06	4.8E-04	14	107
14	1269941	Transport of nucleotide sugars	BioSystems: REACTOME	6.9E-06	4.8E-04	5	10
15	1269120	Viral mRNA Translation	BioSystems: REACTOME	7.1E-06	4.8E-04	13	93
16	1339156	Selenocysteine synthesis	BioSystems: REACTOME	1.0E-05	6.3E-04	13	96
17	1268692	Eukaryotic Translation Termination	BioSystems: REACTOME	1.1E-05	6.3E-04	13	97
18	1268680	Cap-dependent Translation Initiation	BioSystems: REACTOME	1.2E-05	6.3E-04	15	127
19	1268679	Eukaryotic Translation Initiation	BioSystems: REACTOME	1.2E-05	6.3E-04	15	127
20	1269718	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	BioSystems: REACTOME	1.6E-05	8.0E-04	13	100
21	1269109	Influenza Life Cycle	BioSystems: REACTOME	1.7E-05	8.3E-04	16	147
22	1269195	Antigen processing-Cross presentation	BioSystems: REACTOME	2.2E-05	1.0E-03	13	103
23	1269311	Interferon Signaling	BioSystems: REACTOME	2.3E-05	1.0E-03	19	202
24	1269115	Influenza Viral RNA Transcription and Replication	BioSystems: REACTOME	3.2E-05	1.3E-03	15	138
25	1269310	Cytokine Signaling in Immune system	BioSystems: REACTOME	4.1E-05	1.6E-03	45	763

310 Downregulated genes

GO: Molecular Function							
1	GO:0003723	RNA binding	GO: Molecular Function	3.40E-26	2.99E-23	117	1973
2	GO:0042393	histone binding	GO: Molecular Function	6.28E-08	2.76E-05	19	203
3	GO:0008301	DNA binding, bending	GO: Molecular Function	1.13E-05	3.32E-03	17	236
4	GO:0070577	lysine-acetylated histone binding	GO: Molecular Function	3.67E-05	6.45E-03	5	19
5	GO:0140033	acetylation-dependent protein binding	GO: Molecular Function	3.67E-05	6.45E-03	5	19
6	GO:0016887	ATPase activity	GO: Molecular Function	6.91E-05	1.01E-02	28	596

7	GO:0004386	helicase activity	GO: Molecular Function	9.93E-05	1.25E-02	13	177
8	GO:0003682	chromatin binding	GO: Molecular Function	1.71E-04	1.88E-02	28	629
9	GO:0004843	thiol-dependent ubiquitin-specific protease activity	GO: Molecular Function	4.08E-04	2.81E-02	16	287
10	GO:0043022	ribosome binding	GO: Molecular Function	4.22E-04	2.81E-02	7	65
11	GO:0101005	ubiquitinyl hydrolase activity	GO: Molecular Function	4.40E-04	2.81E-02	16	289
12	GO:0016403	dimethylargininase activity	GO: Molecular Function	4.51E-04	2.81E-02	2	2
13	GO:0043021	ribonucleoprotein complex binding	GO: Molecular Function	4.76E-04	2.81E-02	11	156
14	GO:0001164	RNA polymerase I core promoter sequence-specific DNA binding	GO: Molecular Function	4.79E-04	2.81E-02	3	8
15	GO:0001163	RNA polymerase I transcription regulatory region sequence-specific DNA binding	GO: Molecular Function	4.79E-04	2.81E-02	3	8
16	GO:0045296	cadherin binding	GO: Molecular Function	8.71E-04	4.79E-02	17	338
GO: Biological Process							
1	GO:0007049	cell cycle	GO: Biological Process	1.04E-12	4.98E-09	87	1971
2	GO:0016071	mRNA metabolic process	GO: Biological Process	6.78E-12	1.63E-08	52	901
3	GO:0006325	chromatin organization	GO: Biological Process	6.96E-11	5.67E-08	48	841
4	GO:0000278	mitotic cell cycle	GO: Biological Process	7.08E-11	5.67E-08	56	1083
5	GO:0140014	mitotic nuclear division	GO: Biological Process	7.08E-11	5.67E-08	56	1083
6	GO:1903047	mitotic cell cycle process	GO: Biological Process	7.08E-11	5.67E-08	56	1083
7	GO:0051276	chromosome organization	GO: Biological Process	1.09E-10	7.50E-08	62	1287
8	GO:0031570	DNA integrity checkpoint	GO: Biological Process	8.50E-10	5.03E-07	19	164
9	GO:0022402	cell cycle process	GO: Biological Process	9.43E-10	5.03E-07	70	1632
10	GO:0010564	regulation of cell cycle process	GO: Biological Process	2.05E-09	9.36E-07	45	839
11	GO:0000280	nuclear division	GO: Biological Process	2.31E-09	9.36E-07	58	1256
12	GO:0044839	cell cycle G2/M phase transition	GO: Biological Process	2.43E-09	9.36E-07	24	279
13	GO:0042254	ribosome biogenesis	GO: Biological Process	2.65E-09	9.36E-07	25	303
14	GO:0051726	regulation of cell cycle	GO: Biological Process	2.73E-09	9.36E-07	59	1295
15	GO:1901987	regulation of cell cycle phase transition	GO: Biological Process	3.47E-09	1.11E-06	33	508
16	GO:0022613	ribonucleoprotein complex biogenesis	GO: Biological Process	4.21E-09	1.26E-06	33	512
17	GO:1902749	regulation of cell cycle G2/M phase transition	GO: Biological Process	4.96E-09	1.40E-06	21	223
18	GO:0071824	protein-DNA complex subunit organization	GO: Biological Process	7.27E-09	1.87E-06	27	367
19	GO:1901990	regulation of mitotic cell cycle phase transition	GO: Biological Process	7.38E-09	1.87E-06	31	470

20	GO:0048285	organelle fission	GO: Biological Process	8.32E-09	1.93E-06	58	1301
21	GO:0044770	cell cycle phase transition	GO: Biological Process	8.42E-09	1.93E-06	38	668
22	GO:0008380	RNA splicing	GO: Biological Process	9.93E-09	2.17E-06	31	476
23	GO:0000077	DNA damage checkpoint	GO: Biological Process	1.14E-08	2.37E-06	17	152
24	GO:0044772	mitotic cell cycle phase transition	GO: Biological Process	1.37E-08	2.73E-06	36	622
25	GO:0000086	G2/M transition of mitotic cell cycle	GO: Biological Process	1.53E-08	2.86E-06	22	260
GO: Cellular Component							
1	GO:1902494	catalytic complex	GO: Cellular Component	1.80E-14	1.29E-11	77	1536
2	GO:0005730	nucleolus	GO: Cellular Component	1.17E-09	4.17E-07	65	1495
3	GO:0022624	proteasome accessory complex	GO: Cellular Component	1.69E-08	4.04E-06	8	25
4	GO:0005838	proteasome regulatory particle	GO: Cellular Component	1.43E-07	2.56E-05	7	22
5	GO:0016604	nuclear body	GO: Cellular Component	5.26E-07	7.53E-05	38	799
6	GO:0008540	proteasome regulatory particle, base subcomplex	GO: Cellular Component	2.03E-06	2.43E-04	5	12
7	GO:0005681	spliceosomal complex	GO: Cellular Component	4.40E-06	4.50E-04	15	186
8	GO:0005814	centriole	GO: Cellular Component	5.23E-06	4.68E-04	29	583
9	GO:0000502	proteasome complex	GO: Cellular Component	6.31E-06	5.02E-04	9	67
10	GO:1905369	endopeptidase complex	GO: Cellular Component	7.15E-06	5.12E-04	9	68
11	GO:0005815	microtubule organizing center	GO: Cellular Component	1.80E-05	1.17E-03	33	756
12	GO:0016607	nuclear speck	GO: Cellular Component	2.01E-05	1.20E-03	22	406
13	GO:0005813	centrosome	GO: Cellular Component	2.19E-05	1.21E-03	26	532
14	GO:0000922	spindle pole	GO: Cellular Component	2.95E-05	1.51E-03	13	168
15	GO:0005819	spindle	GO: Cellular Component	3.24E-05	1.55E-03	20	359
16	GO:0015630	microtubule cytoskeleton	GO: Cellular Component	3.57E-05	1.60E-03	49	1368
17	GO:0000775	chromosome, centromeric region	GO: Cellular Component	4.98E-05	2.10E-03	14	202
18	GO:0000793	condensed chromosome	GO: Cellular Component	7.29E-05	2.90E-03	15	236
19	GO:1905368	peptidase complex	GO: Cellular Component	9.05E-05	3.41E-03	9	93
20	GO:1990234	transferase complex	GO: Cellular Component	2.00E-04	7.15E-03	32	821
21	GO:0098687	chromosomal region	GO: Cellular Component	3.25E-04	1.11E-02	18	362
22	GO:0005682	U5 snRNP	GO: Cellular Component	3.88E-04	1.23E-02	10	137
23	GO:1990565	HSP90-CDC37 chaperone complex	GO: Cellular Component	3.94E-04	1.23E-02	2	2
24	GO:0016514	SWI/SNF complex	GO: Cellular Component	4.53E-04	1.35E-02	4	19
25	GO:0000974	Prp19 complex	GO: Cellular Component	5.34E-04	1.53E-02	8	94

Pathway							
1	1269741	Cell Cycle	BioSystems: REACTOME	1.44E-10	1.21E-07	41	624
2	1269799	G2/M Transition	BioSystems: REACTOME	4.47E-10	1.53E-07	21	184
3	1269797	Mitotic G2-G2/M phases	BioSystems: REACTOME	5.47E-10	1.53E-07	21	186
4	1269649	Gene Expression	BioSystems: REACTOME	2.99E-09	6.26E-07	77	1844
5	1269763	Cell Cycle, Mitotic	BioSystems: REACTOME	2.21E-08	3.69E-06	33	517
6	1383017	The role of GTSE1 in G2/M progression after G2 checkpoint	BioSystems: REACTOME	8.66E-07	1.21E-04	10	63
7	1269742	Cell Cycle Checkpoints	BioSystems: REACTOME	2.03E-06	2.34E-04	17	204
8	1269837	Regulation of mitotic cell cycle	BioSystems: REACTOME	3.18E-06	2.34E-04	11	89
9	1269838	APC/C-mediated degradation of cell cycle proteins	BioSystems: REACTOME	3.18E-06	2.34E-04	11	89
10	1457807	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	BioSystems: REACTOME	3.75E-06	2.34E-04	9	58
11	1269781	Switching of origins to a post-replicative state	BioSystems: REACTOME	3.95E-06	2.34E-04	10	74
12	1269782	Orc1 removal from chromatin	BioSystems: REACTOME	3.95E-06	2.34E-04	10	74
13	1269851	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	BioSystems: REACTOME	4.47E-06	2.34E-04	10	75
14	1269846	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	BioSystems: REACTOME	4.47E-06	2.34E-04	10	75
15	1269753	G2/M Checkpoints	BioSystems: REACTOME	4.68E-06	2.34E-04	15	172
16	1268928	Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	BioSystems: REACTOME	5.02E-06	2.34E-04	9	60
17	1269796	Removal of licensing factors from origins	BioSystems: REACTOME	5.05E-06	2.34E-04	10	76
18	1269845	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	BioSystems: REACTOME	5.05E-06	2.34E-04	10	76
19	1269689	mRNA Splicing	BioSystems: REACTOME	5.31E-06	2.34E-04	16	196
20	1269844	APC/C:Cdc20 mediated degradation of mitotic proteins	BioSystems: REACTOME	6.41E-06	2.51E-04	10	78
21	1268927	Hh mutants abrogate ligand secretion	BioSystems: REACTOME	6.63E-06	2.51E-04	9	62
22	1269836	CDT1 association with the CDC6:ORC:origin complex	BioSystems: REACTOME	6.63E-06	2.51E-04	9	62
23	1269794	Regulation of DNA replication	BioSystems: REACTOME	7.20E-06	2.51E-04	10	79
24	1269842	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	BioSystems: REACTOME	7.20E-06	2.51E-04	10	79
25	1269770	SCF(Skp2)-mediated degradation of p27/p21	BioSystems: REACTOME	7.59E-06	2.54E-04	9	63

B&H, Benjamini and Hochberg; EoC, eosinophilic colitis; FDR, false discovery rate; GO, gene ontology.

Supplementary Table 9. Biological processes enriched in histo-molecular correlation for EoC

	ID	Name	*P* value	FDR B&H	Genes from Input	Genes in Annotation
Overall eosinophilic inflammation						
1	GO:0009206	purine ribonucleoside triphosphate biosynthetic process	2.8E-07	5.3E-04	13	204
2	GO:0009145	purine nucleoside triphosphate biosynthetic process	3.0E-07	5.3E-04	13	205
3	GO:0009201	ribonucleoside triphosphate biosynthetic process	4.0E-07	5.3E-04	13	210
4	GO:0009205	purine ribonucleoside triphosphate metabolic process	6.1E-07	5.3E-04	13	218
5	GO:0009142	nucleoside triphosphate biosynthetic process	6.7E-07	5.3E-04	13	220
6	GO:0009199	ribonucleoside triphosphate metabolic process	8.7E-07	5.3E-04	13	225
7	GO:0009144	purine nucleoside triphosphate metabolic process	9.6E-07	5.3E-04	13	227
8	GO:0006754	ATP biosynthetic process	1.0E-06	5.3E-04	12	192
9	GO:0009152	purine ribonucleotide biosynthetic process	1.4E-06	5.7E-04	15	314
10	GO:0042775	mitochondrial ATP synthesis coupled electron transport	1.4E-06	5.7E-04	9	102
Pericryptal circumferential eosinophil collars						
1	GO:0007005	mitochondrion organization	3.2E-07	9.7E-04	15	599
Lamina propria eosinophil sheets						
1	GO:0045047	protein targeting to ER	8.6E-06	3.0E-03	5	123
2	GO:0043604	amide biosynthetic process	6.4E-06	3.0E-03	11	943
3	GO:0006518	peptide metabolic process	8.8E-06	3.0E-03	11	975
4	GO:0043043	peptide biosynthetic process	9.9E-06	3.0E-03	10	799
5	GO:0072599	establishment of protein localization to endoplasmic reticulum	1.0E-05	3.0E-03	5	127
6	GO:0043603	cellular amide metabolic process	2.0E-05	4.9E-03	12	1276
7	GO:0070972	protein localization to endoplasmic reticulum	2.6E-05	5.6E-03	5	155
8	GO:0006414	translational elongation	5.0E-05	8.2E-03	9	770
9	GO:0006412	translation	5.0E-05	8.2E-03	9	770
10	GO:0006413	translational initiation	8.7E-05	1.3E-02	5	199

B&H, Benjamini and Hochberg; EoC, eosinophilic colitis; FDR, false discovery rate; GO, gene ontology.

Supplementary Table 10. Gene list for EoC-IBD differential score

Gene symbol	*P* value Active EoC vs UC (High eos)	Fold Change	Regulation	*P* value Active EoC vs CD (High eos)	Fold Change	Regulation
CAPN12	1.0E-20	46.6	up	8.6E-04	1.9	up
CD9	9.8E-11	2.1	up	2.0E-07	5.0	up
COMMD6	3.2E-07	2.9	up	1.8E-04	5.5	up
F13A1	2.1E-04	2.4	up	1.5E-04	5.5	up
IFITM1	4.5E-02	1.4	up	1.9E-03	5.3	up
MGST3	8.6E-05	1.6	up	8.1E-06	5.1	up
MT1H	2.3E-14	59.3	up	2.7E-04	15.8	up
MT1X	3.6E-03	2.1	up	1.4E-04	10.9	up
PHLPP2	3.6E-12	3.9	up	2.9E-06	6.9	up
SLC51B	7.5E-06	2.3	up	1.1E-04	7.2	up
TMEM171	1.2E-12	4.4	up	1.0E-04	8.3	up
TMEM251	4.4E-04	1.5	up	1.2E-05	5.2	up
ZFAND3	2.7E-05	1.9	up	9.8E-06	5.0	up
EEF1D	3.9E-21	-10.6	down	1.6E-04	-2.6	down
HYOU1	2.0E-28	-20.5	down	3.0E-04	-2.5	down
STT3A	2.8E-27	-12.6	down	4.3E-04	-2.4	down
VNN2	5.8E-07	-3.5	down	7.2E-05	-5.3	down

EoC, eosinophilic colitis; IBD, inflammatory bowel disease; UC, ulcerative colitis; CD, Crohn disease.

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Dominique	Bailey
Alexis	Berry
Bridget	Besl
Scott	Bolton
Peter	Bonis
Wendy	Book
Kimberly	Bray
Teresa	Brown
Cassandra	Burger
Deirdre	Burke
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Kelley	Capocelli
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