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Gain-of-function CEBPE mutation causes non-canonical autoinflammatory inflammasomopathy

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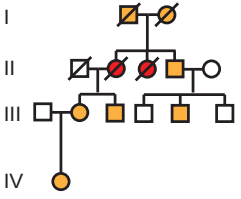


**C/EBPε: CCAAT/enhancer-binding protein epsilon*

**NLRP3: NACHT, LRR and PYD domains-containing protein 3*

**ASC: the adaptor protein ASC*

Affected family



WT

GTG CGC AAG

V R K

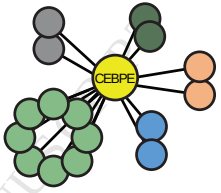
CAIN patient

GTG CAC AAG

V H K

219

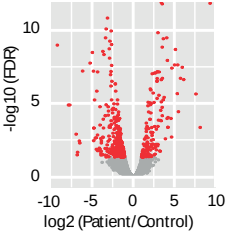
Proteomics

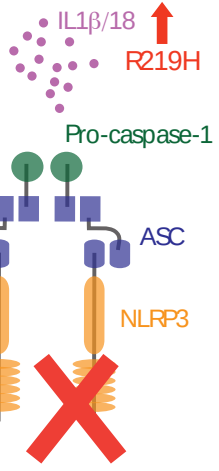


DNA binding



Transcriptional profiling





Dysregulated non-canonival NLRP3 inflammasome activation

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Gain-of-function *CEBPE* mutation causes non-canonical autoinflammatory inflammasomopathy

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Competing interests

Authors report no competing interests.

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Abstract

Background: C/EBPε is a transcription factor involved in late myeloid lineage differentiation and cellular function. The only previously known disorder linked to C/EBPε is the autosomal recessive neutrophil-specific granule deficiency leading to severely impaired neutrophil function and early mortality.

Objective: The aim was to molecularly characterize the effects of C/EBPε transcription factor's Arg219His mutation, identified in Finnish family with previously genetically uncharacterized autoinflammatory and immunodeficiency syndrome.

Methods: Genetic analysis, proteomics, genome-wide transcriptional profiling by RNA-sequencing, ChIP-sequencing and assessment of the inflammasome function of primary macrophages were performed.

Results: Studies revealed a novel mechanism of genome-wide gain-of-function that dysregulated transcription of 464 genes. Mechanisms involved dysregulated non-canonical inflammasome activation due to decreased association with transcriptional repressors leading to increased chromatin occupancy and considerable changes in transcriptional activity including increased expression of *NLRP3* and constitutively expressed caspase-5 in macrophages.

Conclusion: We describe a novel autoinflammatory disease with defective neutrophil function caused by homozygous Arg219His mutation in transcription factor C/EBPε. Mutated C/EBPε acts as a regulator of both the inflammasome and interferome, and the Arg219His mutation causes the first human monogenic neomorphic and non-canonical inflammasomopathy/immunodeficiency. The mechanism, including widely dysregulated transcription, is likely not unique for C/EBPε. Similar multiomics approaches should as well be utilized in studying other transcription factor-associated diseases.

Key messages

- Patients with biallelic *CEBPE* (14:23586886 C>T; p.Arg219His) missense mutation displayed a non-canonical inflammasome-mediated autoinflammatory and immunodeficiency disease, leading to aberrantly activated non-canonical inflammasome.
- C/EBPε acts as a regulator of both the inflammasome and interferome.
- We describe a novel gain-of-function mechanism due to a missense transcription factor mutation, which leads to widely dysregulated transcription. This mechanism is most likely not unique for the transcription factor C/EBPε, and similar multiomics approaches should be applied in other diseases associated with transcription factors.

Capsule Summary

Biallelic *CEBPE* (p.Arg219His) mutation causes a non-canonical inflammasome-mediated autoinflammatory and immunodeficiency disease. The mechanism, including considerable changes in C/EBPε transcriptional activity, is likely unspecific for C/EBPε and might be observed in other transcription factor-related diseases.

Keywords: Immunologic Deficiency Syndromes; Autoinflammatory Diseases, Hereditary; Chemotaxis; Interferons; Inflammasomes; NLR Family, Pyrin Domain-Containing 3 Protein; Gain of Function Mutation, Neomorphic mutation

Abbreviations: AD (autosomal dominant), AID (autoinflammatory disease), BioID-MS (proximity-dependent biotin identification coupled to mass spectrometry), CAIN (C/EBPε-associated autoinflammation and immune impairment of neutrophils), DNA_Pa (DNA extracted from Pseudomonas aeruginosa), GOF (gain-of-function), IL (interleukin), LOF (loss-of-function), LPS (lipopolysaccharide), LPS_Ec (LPS from E. coli), LPS_Pa (LPS extracted from Pseudomonas aeruginosa), PBMC (peripheral blood mononuclear cell), PH (Pelger-Huët anomaly), PID (primary

immunodeficiency), PPI (protein-protein interactions), SGD (neutrophil-specific granule deficiency)

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Introduction

Primary immunodeficiencies (PIDs) are caused by inherent defects in the immune system and offer a unique glimpse into the regulation of the human immune system. Findings in PIDs can help to develop treatments for immune dysregulation, known to lead to various common diseases including atherosclerosis, asthma and diabetes[1]. Of the over 350 currently known PIDs, approximately 20 are caused by germline autosomal dominant (AD) gain-of-function (GOF) mutations[2-4]. In general, GOF mutations may be caused by hyperactivating or neomorphic mechanisms. To date, all known GOF PIDs have been hypermorphic, i.e. resulting in increased protein activity[4]. No neomorphic mutations, resulting in completely novel molecular functions, have been described in PIDs.

Many autoinflammatory diseases (AIDs), such as cryopyrinopathies, are driven by activation of canonical NLRP3 inflammasome, via production of highly proinflammatory interleukins (IL)-1β and IL-18. The non-canonical caspase-4/5 (murine ortholog, caspase-11) inflammasome is a recently discovered inflammasome activated by intracellular bacterial lipopolysaccharide (LPS) and involved in first line defense against gram-negative bacteria. Similar to canonical activation, non-canonical inflammasome activation results in increased IL-1β and IL-18 production[5]. In mice, induction of caspase-11 expression by type I interferon signaling is required for the activation of non-canonical inflammasome[6-9]. In humans, local activation of non-canonical inflammasome has been shown to contribute to the pathogenesis of age-related macular degeneration[10]. However, the potential role of non-canonical inflammasome in systemic human diseases remains to be explored.

The C/EBPε proteins, encoded by *CEBPE*, are transcription factors expressed in myeloid and lymphoid lineage cells and known to be involved in the cellular differentiation and function of late myeloid lineages[11]. The only previously known *CEBPE*-associated disorder, autosomal recessive neutrophil-specific granule deficiency (SGD), is caused by frameshift mutations resulting in the abrogation of at least two of the four known C/EBPε isoforms. This leads to a complete loss of

specific neutrophilic granules and consequently in severely impaired neutrophil function with pronounced susceptibility to bacterial infections and early mortality[12, 13]. A milder autosomal dominant *CEBPE* (Val218Ala) variant leads to total SGD with recurrent deep-seated abscesses[14]. Early studies in *Cebpe* knockout mice showed *Cebpe* to be integral for the maintenance of constitutive levels of several cytokines, including interferon gamma (IFNγ)[15].

We report an autosomal recessive, GOF PID, C/EBPε-associated autoinflammation and immune impairment of neutrophils (CAIN), in a family with a genetically uncharacterized autoinflammatory syndrome[16-18]. According our results, C/EBPε acts as a regulator of both the inflammasome and interferome. Homozygous missense mutations in *CEBPE* (14:23586886 C->T;p.Arg219His) resulted in markedly decreased C/EBPε association with transcriptional repressors and increased occupancy on chromatin leading to dysregulated C/EBPε-mediated transcription of IL and IFN response genes in neutrophils. Patient macrophages displayed aberrant caspase-5-mediated activation of the non-canonical inflammasome pathway. CAIN displays a loss-of-function (LOF) mechanism in protein-protein interactions and a novel gain-of-function mechanism in DNA binding and transcriptional regulation. Furthermore, CAIN is the first PID and systemic AID involving non-canonical inflammasome.

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Methods

Written informed consent was obtained from study participants and the study was approved by the institutional ethical review board (138/13/03/00/2013).

DNA from three affected family members (Fig 1, *A*) were analyzed by whole exome sequencing and sanger sequencing was further used to confirm the mutation status of the other family members. Before whole exome sequencing was available, patients were tested against *LBR*, *MVK* and *NLRP3* mutations; no rare cosegregated variants in known autoinflammatory disease genes were noted. Further details of the genetic analysis are available in the Supplementary Appendix

Functional Studies of CEBPE mutation

Flp-In™ T-REx™ 293 cell lines stably expressing mutant or wild type (WT) C/EBPε were generated and used to investigate protein-protein interactions (PPIs) by proximity-dependent biotin identification coupled to mass spectrometry (BioID-MS) as described in [19] and in Supplementary Appendix.

Functional studies of patients' primary cells

Granulocytes were isolated from two homozygous patients, two heterozygous carriers and three sex- and age-matched controls, and chromatin immunoprecipitation followed by sequencing (ChIP-seq) was used to assess C/EBPε binding to chromatin in freshly isolated and LPS stimulated cells.

RNA sequencing (RNA-seq) was used for genome-wide transcriptional profiling of freshly isolated untreated granulocytes from patients and controls. Given the clinical phenotype of increased bacterial infections, we also used 5′-end RNA-seq to identify the genes differentially expressed after three different stimulation: 1. DNA (DNA_Pa) or 2. LPS (LPS_Pa) extracted from *Pseudomonas aeruginosa* or 3. LPS from *E. coli* (LPS_Ec). Moreover, granulocytes were stimulated with IFNα2 and IFNγ followed by transcriptional profile analysis by 5′-end RNA-seq.

Nanostring[20] analysis was used for direct digital detection of the mRNA levels of selected genes from peripheral blood mononuclear cells (PBMC).

To access the inflammasome activation and inflammasome-mediated cytokine secretion more deeply, levels of caspase-5 were analyzed by quantitative PCR and western blot, Caspase-1 activity was measured by flow cytometry from blood immune cells, and IL-1β/IL-18 secretion by ELISA from cultured macrophages.

We also assessed granule exocytosis, granulocyte responsiveness, neutrophilic and monocytic NFκB phosphorylation by flow cytometry. Subcellular morphology of granulocytes and granule abundance of platelets were assessed using transmission electron microscopy as well as Wright staining of granulocytes.

Further details of the methods are available in the Supplementary Appendix.

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Results

Case Reports

In the 1970s, the affected members of the index family were thought to have atypical Pelger-Huët anomaly (PH) as they presented with neutrophil hyposegmentation, aberrant neutrophil responsiveness and impaired chemotaxis[16-18]. Patients suffered from recurrent attacks of abdominal pain, aseptic fever and systemic inflammation lasting four to five days. These were accompanied by an acute phase response and occasionally by nailbed, tongue, submandibular and gluteal abscesses, intra-abdominal granulomas, pyoderma gangrenosum and buccal ulcerations. Furthermore, they suffered from frequent episodes of purulent paronychia complicated by lymphangitis, superficial skin, mucosal and purulent upper respiratory tract infections. Their autoinflammatory symptoms manifested more clearly during puberty and subsided after menopause (Table 1). All affected members further displayed a mild bleeding diathesis with frequent nosebleeds and tendency towards hematomas after needlesticks and procedures. Extended case reports are available in Supplementary Appendix.

Genetic analysis found novel homozygous CEBPE mutation

To identify causative mutation, we analyzed the DNA from three surviving members (II.2, II.7 and II.13) of an index family by performing whole exome sequencing. In the exome data, we identified between 20,638 and 21,313 single nucleotide variants and small insertions/deletions in each patient. A total of 149 variants were very rare, i.e. those not seen in the 6,500 NHLBI Exomes, 1000 Genomes database (April 2012 data release) and 2,500 exomes analyzed internally using the same bioinformatics pipeline. Of these, 22 variants were shared between all three patients. Only one of these variants was homozygous in all three patients (ENSG00000092067:ENST00000206513: exon2:c.G656A;p.Arg219His), in the *CEPBE* gene. The novel homozygous *CEBPE* 14:23586886 C>T mutation co-segregated perfectly with the disease phenotype (Fig 1, *A* and Fig E1)[16-18].

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Arg219His was predicted to be detrimental and not listed in major public or in-house databases. It resided in the highly conserved basic zipper (bZIP) region's carboxyl terminal DNA binding domain (DBD), shared by all four C/EBPε isoforms (Fig 1, *B* and *C*)[11, 21, 22]. Identified homozygous or heterozygous novel germline mutations were validated by Sanger sequencing (Fig 1, *A*).

Widely altered C/EBPε *protein-protein interactions*

To understand the functional effects of p.Arg219His mutation, we assayed protein-protein interactions (PPIs) of WT and mutant C/EBPε by BioID-MS (Fig E2, *A*). This identified 144 C/EBPε interaction partners, of which 141 were previously not reported (Fig 1, *D* and Table E1). Based on quantitative interaction analysis, 108 PPIs were significantly ($p<0.05$) altered; 106 showed decreased and two increased interaction with mutant C/EBPε compared to WT (Fig 1, *E* and Table E1). Importantly, many of the diminished interactors were transcriptional repressors suggesting widely dysregulated C/EBPε-driven transcription (Fig 1, *E* and Table E1). 24 of the novel interactions were also seen in Jurkat T-cells (Table E1). We observed similar loss of transcriptional repressors when analyzing mouse Arg219His c/ebpε mutant, suggesting a high degree of conservation of C/EBPε functions and effects of the mutation (Fig E2, *B*)[15]. One of the known interactions was C/EBPε interaction to SWI/SNF complex subunit SMARCC2 (SMRC2) that is an important regulator of myeloid differentiation[23]. This affinity was reduced in mutant compared to wt (Log2 Mut/WT =-0.41). Besides SMRC2, we found C/EBPε to interact with four other SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily members (SNF5, SMRD1 and 2, SMCE1) all of which were downregulated in patients compared to controls (Table E1).

To see how specific changes in protein-protein interactions were for the Arg219His mutated C/EBPε, we generated a cell line expressing Val218Ala C/EBPε which is known to cause SGD[14, 24] and compared the interactions changes between these two mutants (Table E1, Fig E2, *C*). Most of the studied interactions did not differ between Val218Ala and wild type C/EBPε.

Increased chromatin occupancy of Arg219His C/EBPε

Mapping of p.Arg219His mutation to DBD of C/EBPε prompted us to profile the chromatin occupancy of C/EBPε. We performed ChIP-seq from granulocytes without and with LPS stimulation (Fig 2, Table E2). Peak calling and overlap analysis from biological replicates revealed 3391 C/EBPε binding sites in controls, 4686 in Arg219His heterozygotes carriers and 10322 in homozygous patients (Fig 2, *A*). Similar results were observed upon LPS stimulation (Fig 2, *B*). Increased occupancy was also evident in the average ChIP-seq signal intensities (Fig 2, *C*). Interestingly, *de novo* motif analyses identified highly similar consensus DNA binding sequences in WT and mutant C/EBPε (Fig 2, *D*). This suggests that the increased C/EBPε chromatin occupancy was caused by mechanisms other than the altered DNA binding motifs usually seen in neomorphism[25].

Pronounced transcriptional changes in mutated unstimulated granulocytes

Increased mutant C/EBPε binding to DNA and decreased association with transcription repressors may lead to dysregulated transcriptome. Thus, we compared CAIN patients' and controls' transcriptomes in unstimulated granulocytes by RNA-seq (Fig 3, *A*). This identified 464 significantly differentially transcribed (Fold Change (FC) ≥2 or ≤0.5; FDR ≤0.05) genes of which 198, including *NLRP3* (FC 8.25), were IFN-related (Fig 3, *B* and Table E3). Furthermore, Gene Ontology analysis revealed upregulation of genes involved in inflammatory responses, transcription, chemotaxis and LPS response (Table E4). One of the upregulated genes was PRTN3 that encodes serine protease PR3, which is ubiquitous especially in neutrophils[26]. Activated neutrophils secrete PR3 that, among its other functions, cleaves structural proteins and activates inflammasome-regulated cytokines, IL-1β and IL-18[26, 27]. Upregulation of *PRTN3* was verified by RT-PCR (Fig E3, *A*). *CEBPE* expression was not among the differentially expressed genes in granulocytes, even slightly elevated expression was detected by RT-PCR (Fig E3, *B*).

To investigate whether these differentially transcribed genes were under C/EBPε control, we mapped ChIP-seq peaks to nearby genes within ±50 kb range and performed overlap analysis. Of the 464 differentially expressed genes, 271 had C/EBPε binding sites and, importantly, 80 genes had patient-specific binding (Fig 3, *C* and Table E3). We noted increased occupancy and novel C/EBPε binding sites in patients for overexpressed inflammasome-IL-related genes (e.g. *NLRP3* (Fig E4, *A*), *NFKBIA* and *IL1R2*) suggesting aberrant inflammasome activation.

Comparison of differentially expressed genes to other studies

Recently, Serwas et al. performed a proteomics analysis of SGD neutrophils (C/EBPε mutation p.Val218Ala)[24]. They detected decreased expression of several granule proteins and an increased expression of proteins linked to nucleoskeleton and cytoskeleton, such as nesprin, vimentin and laminB2. As our proteomic analysis was performed to identify the changes on protein-protein interactions, not the changes in proteome, we compared the differentially expressed proteins from Serwas et al. to our differentially expressed genes in RNA-seq experiments. In our data, opposite to proteins of SGD patients, nesprin-2 (SYNE2) was detected with decreased expression in CAIN patients' neutrophils (Table E3). Vimentin was detected with 2.2-fold increase in CAIN patients, but because of FDR 0.09 it was filtered out from the differentially expressed genes (FDR cut-off 0.05). LaminB2 was not differentially expressed in RNA-seq analysis, but we found Lamin G1 (LAMC1) to be upregulated in patients (LogFC 5.0, Table E3).

Serwas et al. also identified lactotransferrin (LTF) and Neutrophil gelatinase-associated lipocalin (NGAL/LCN2) to be downregulated in patients both with proteomics method and qPCR[24]. In CAIN patients' RNA-seq experiments, LTF was also decreased (fold change 0.34), but with high FDR-value 0.84. Similarly, LCN2 was slightly decreased but with high FDR value.

Khanna-Kupta et al. detected increased expression of PU.1 and decreased expression of Gfi-1 in patients neutrophils with SGD (C/EBPε mutation Val218Ala)[14]. We did not find Gfi-1 (GFI) and

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PU.1 (SPI1) to interact with C/EBPε in protein-protein interaction analysis. However, PU.1 expression was detected in RNA-seq, but it did not show changes between CAIN patients and healthy controls (data not shown). Gfi-1 expression was not found in RNA-seq analysis.

The clinical characters of patients with different C/EBPε mutations or SGD are compared in Table E5.

Transcriptional changes after LPS and bacterial DNA stimulation

Given the clinical phenotype of frequent bacterial infections and neutrophilic skin symptoms (Table 1), we stimulated patients' granulocytes with bacterial LPS and DNA. A total of 470 genes were found significantly differentially transcribed between patients and controls (FC ≥2 or ≤0.5; FDR ≤0.05) (Fig 3, *D* and Table E6). Of these, 183 were involved in IFN signaling (Fig 3, *E* and Table E6). Particularly, gene transcription of the IFIT family (*IFIT1*, *IFIT3* and *IFIT5)* was decreased and *NLRP3* increased in patient cells.

Overlap analysis between ChIP-seq mapped genes and RNA-seq results identified 289 of 470 differentially transcribed genes having C/EBPε binding sites, 81 of them showing patient-specific binding (Fig 3, *F* and Table E6). Analogous to differentially transcribed genes in unstimulated granulocytes, various inflammasome-related genes such as *IL18* and *NLRP3* showed increased C/EBPε occupancy on chromatin in patients. Results again highlight dysregulated IL and inflammasome signaling in CAIN.

Transcriptional changes after IFN stimulation

Dysregulated IFN signaling led us to test the direct effects of type I (IFNα2b) and type II (IFNγ) IFN stimulation on granulocytes. In response to IFNα2b stimulation 534 genes were differentially transcribed (FC ≥2 or ≤0.5; FDR ≤0.05) between patients and controls (Fig 4, *A* and Table E7, *A*), with significant alterations in immune response and inflammasome-related genes. These included significant 13.6-fold increase in *NLRP12* expression in patients. NLRP12, a known suppressor of

neutrophil migration and chemotaxis[28], had also increased C/EBPε occupancy on chromatin in patients (Fig E4, *B*). Overall, 266 of 534 differentially transcribed genes had C/EBPε binding sites; 83 genes displayed patient-specific binding (Fig 4, *B* and Table E7, *A*).

In response to IFNγ stimulation, 427 genes were differentially expressed (FC ≥2 or ≤0.5; FDR ≤0.05) between the patients and controls (Fig 4, *C* and Table E7, *B*), with significant alterations in immune response and inflammasome-related genes. These included a modest 1.7-fold increase in NLRP3 expression under both conditions and significant 3.8-fold increases in NLRP12 expression following IFNγ stimulation. Comparison with ChIP-seq mapped genes showed that 49% (208/427) of differentially expressed genes after IFNγ treatment had C/EBPε binding sites. Of these, 54 showed patient-specific binding, respectively (Fig 4, *D*).

Importantly, IFN-related genes such as *NLRP3, TLR4, NLRP12, IL1RAP* and *IL1R2* showed increased transcription and C/EBPε chromatin binding in patients after IFNα2b and IFNγ stimulations. Similar effect was observed with *IL18, IL13RA1, IL17RA* and *MEFV* after IFNα2b stimulation.

mRNA levels in PBMCs

Next, we performed direct digital detection of mRNA molecules by Nanostring. This does not require conversion of mRNA to cDNA by reverse transcription nor amplification of the resulting cDNA by PCR. Nanostring showed increased mRNA levels of both JAK/STAT pathway genes and inflammasome components (such as *CASP5, NLRP3, CASP8),* as well as dysregulation of the NFκB-pathway (Fig 5, *A*). Interestingly, the changes in mRNA levels were not concordant with autoinflammation due to type I interferonopathy (Table E8). Importantly, inflammasome and inflammation-related genes such as *CASP8* (Fig E5, *A*), *NLRP3* (Fig E4, *A*), *NLRP12* (Fig E4, *B*), *IL18, NFKB1* and *STAT6* were found to be significantly overexpressed with aberrantly higher C/EBPε chromatin binding in patients. Moreover, Arg219His mutated C/EBPε functions as an

NFκB2 regulator, with NFκB2 binding only observed in patient cells (Fig E5, *B*) resulting in 3-4-fold increase in *NFKB2* transcription (Fig 5, *A*) in patients. Further studies are required to elucidate which role C/EBPe plays in *NFKB2* regulation. Our results suggest neomorphism through enhanced chromatin occupancy of mutant C/EBPε, leading to increased transcription, aberrant inflammasome activation and dysregulated IL, NFκB2 and IFN signaling.

NLRP3 inflammasome activation in monocytes and macrophages by non-canonical inflammasome

The differences in transcription of inflammasome components led us to investigate functional changes in canonical and non-canonical inflammasomes. We detected no differences between patients and controls in whole blood canonical NLRP3 activation nor in inflammasome-triggered caspase-1 activity in monocytes (Fig 5, *B*). In cultured macrophages, secretion of both IL-1β and of constitutively expressed IL-18 was similar after canonical activation (Fig 5, *C*), but markedly enhanced after non-canonical caspase-4/5-mediated NLRP3 activation in patients compared to controls (Fig 5, *D* and *E*). This was caused by aberrantly induced caspase-5 expression in resting macrophages of patients (Fig 5, *F*). In agreement with macrophage results, the increased protein expression of procaspase-5 was also detected from non-stimulated patient PBMCs (Fig 5, *G*). Moreover, considerably more caspase-5 was processed in the patient's PBMCs, as shown by a clear intermediate band of caspase-5 ~30 kDa (Fig 5, *G*). Aberrant activation of patients' macrophages required no priming by interferon response, as priming with IFNα2b instead of a TLR agonist abolished any differences in IL-18 expression (Fig 5, *E*) and CASP5 mRNA levels (Fig E6, *A*). Results further suggested elevated expression of other IFN-regulated genes (Fig E6, *B*).

Neutrophils displayed impaired CD66b expression

Patients were known to have impaired granulocyte function and chemotaxis, suggesting hypomorphic loss-of-function in these[16, 18]. We used flow cytometry to assay the expression of CD66a, CD66b and CD11b involved in cellular adhesion and migration, found within neutrophil

granules and with subsequent increase in their surface expression following exocytosis [29]. CD66a and CD11b are found in secondary and tertiary granules, respectively. In flow cytometry, CD66a and CD11b expression was unaffected, consistent with a non-SGD disease (Fig E7). Additionally, patients' granulocytes displayed side-scattered light within the normal range, unlike in SGD[12, 13].

CD66b is involved in neutrophil localization and activation and has been implicated in the interaction of granulocytes with each other. Patients' granulocytes displayed impaired expression of CD66b compared with age- and gender-matched controls (Fig E7). The aberrantly low CD66b likely contributes, with elevated transcription of NLRP12, to the impaired chemotaxis previously reported[16]. Taken together, the data suggest a deficiency in specific granule function.

NFκB plays a key role in inflammation and immune response[30-32]. We therefore assessed the NFκB activity in patients' whole blood. No differences were seen in NFκB phosphorylation at baseline or in response to stimulation with bacterial LPS and DNA, suggesting that their periodic inflammation was not caused by dysregulated NFκB activity.

Normal neutrophil and platelet morphology

To determine the possible structural changes in neutrophils, we analyzed endoplasmic reticulum size and shape, and mitochondrial size by using transmission electron microscopy. No clear differences were seen between patients and controls. In addition, electron microscopy analysis showed that both patients′ neutrophils contained normal-sized azurophilic, specific and tertiary granules, in normal numbers (data not shown).

This was also seen with the staining with Wright method[33]. From the Wright stained smears of both patient and control subject 200 consecutive leukocytes were studied for granules and morphology. The patient's neutrophils presented both primary and secondary granules and no difference was observed in comparison to the healthy control subject (Fig E8, *A*). However, as seen earlier[16], 20 %

of the patient's neutrophils were hyposegmented (Fig E8, *B*). Eosinophils and basophils showed also normal granules as compared to the healthy control subject.

C/EBPε is known to control platelet granule formation[15, 21]. Patients displayed mild bleeding diathesis; we thus investigated platelet morphology and platelet granule abundance in CAIN patients. No morphological aberrancies were found in alpha granule and overall platelets structure. Dilated open canalicular systems were detected in both patients. Patient II.7 displayed some multivesicular bodies, more common in megakaryocytes. Platelets were slightly activated based on the detected pseudopodia, but mainly displayed normal discoid form (data not shown).

Post-transcriptional compensatory mechanisms

Compared to their RNA-seq and ChIP-seq results, patients are bafflingly mildly symptomatic but with mixed neo- and hypomorphisms. Analysis of heterozygous relatives without reported clinical manifestations of the disease showed intermediate cellular level changes. Results thus suggest a novel autosomal recessive inheritance pattern, where the disease in heterozygote state lacks expressivity due to unknown post-transcriptional compensatory mechanisms and needs homozygous state to become clinically manifest. The reduced heritability of disease phenotype even in the presence of the severely altered DNA binding seen in the asymptomatic carriers likely reflects the complex nature of compensatory mechanisms and underscores the astonishing extent to which the human body can maintain homeostasis even in the presence of an otherwise pathogenic mutation.

To address this, we analyzed DNA methylation of the patients (n=2) compared to controls and found no changes that would explain the patients' symptoms or the relative mildness of them compared with RNA-seq and ChIP-seq (data not shown).

The results from RNA-seq and ChIP-seq raise the possibility that histone methylation could be one compensatory posttranscriptional mechanism. This and open chromatin binding will need to be explored in knock-in animal models allowing for larger numbers of mutation carriers.

Discussion

We report a novel gain-of-function mechanism due to a transcription factor mutation. Homozygous Arg219His *CEBPE* mutation lead to CAIN, that was clinically characterized by a combination of autoinflammation, immunodeficiency and neutrophil dysfunction. To our knowledge, this is the first mutation to cause such widely dysregulated transcription in PIDs. It is also the first AID that involves aberrant expression and activation of non-canonical caspase-4/5 inflammasome. After the Li-Fraumeni syndrome, CAIN seems to be only the second germline neomorphic human disease caused by transcription factor mutations[25]. Our results highlight the potential for germline mutations in transcription factors to cause widespread and complex genome-wide mechanism, with only limited concomitant morbidity. Such changes will not readily be evident by targeted functional assessment and typical non-genomic types of analyses, causing probable underdiagnosis. For example, transcription factor mutations with pronounced overlap between known clinical GOF and LOF phenotypes (such as *STAT1*[34]) may need to be studied using similar data-driven systems-level approaches.

Arg219His mutation in the DNA-binding domain of the C/EBPε was predicted to lead to loss of DNA binding and possible LOF. However, the mutation resulted in a pronounced increase in C/EBPε chromatin binding, likely due to a decreased association with multiple transcriptional repressors. This decreased transcriptional repressor association could have been driven by C/EBPε Arg219His induced conformational changes to protein structure, as no difference was seen in the consensus DNA recognition motif between controls and patients. This mechanism has previously been described for a single (not orthologous) transcriptional repressor in AD SGD and in *Drosophila*[35].

Our results reveal the role of C/EBPε in complex interlinked signaling cascades. The reported deficiency in neutrophil chemotaxis[18] is likely caused by multiple factors including differentially transcribed genes (i.e. *CD66B,* Fig E7) affecting cellular maturation and movement and increased expression of NLRP12, a known suppressor of neutrophil migration [28].

Results also show that C/EBPε regulates interferon pathways and non-canonical inflammasome target genes (e.g. *NLRP3, CASP5, IL18*), further highlighting the overlap between inflammasome and IFN signaling. Pathway components associated with non-canonical inflammasome activation were aberrantly transcribed, together with decreased NFκB1 and increased NFBκ2 and JAK/STAT components (Fig 5, *A*)[36]. Whereas caspase-4 is known to be constitutively expressed, the expression of human caspase-5 is IFN-dependent[8, 9, 37]. Notably, we found increased baseline expression of caspase-5 in patient macrophages and elevated IL-1β and IL-18 secretion upon stimulation of the non-canonical caspase-4/5 inflammasome with intracellular LPS. Due to constitutively expressed caspase-5, IFN priming was not required. Consequently, IFNα2b priming before intracellular LPS transfection induced caspase-5 expression also in control cells and thus abolished the difference in cytokine secretion between patients and controls (Fig 5, *E* and Fig E6, *A*). Our data thus implies that the *CEBPE* Arg219His neomorphic mutation was alone sufficient to maintain constitutive caspase-5 expression. This sensitized the patients' macrophages to respond pronouncedly to intracellular LPS –clinically causing hyperinflammation after bacterial stimuli. Investigating both the inflammasome and interferon pathways together in inflammatory conditions may lead to a deeper understanding of their etiology and to targeted treatments[38-40]. In CAIN, anti-IL1β and anti-IL18 seem likely treatment modalities but remain untested.

The index family has been studied since the 1970's[16-18]. A systems level approach combining genomics, transcriptomics and proteomics finally made it possible to unravel the causative pathogenic mechanisms. In conclusion, CAIN reveals GOF mechanisms resulting in autoinflammation and immunodeficiency, potentially relevant for various transcription factor-

related diseases. Also, C/EBPε seems to be involved in the regulation of non-canonical inflammasome and IFN signaling, suggesting a novel target for drug development. The widely dysregulated transcription seen in asymptomatic heterozygous carriers compared with controls suggests extremely effective post-transcriptional regulatory capacity in humans that needs further investigation. Given their apparent roles in idiopathic inflammation, roles of both C/EBPε and the non-canonical inflammasome should be further explored in the context of autoimmune and autoinflammatory diseases.

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Author contributions

H.G., C.L.F., M.V. and M.R.J.S. wrote the manuscript and prepared the figures. A.R. and T.P. collected patient samples and participated together with As.J. and M.R.J.S in clinical patient data collection and clinical care of patients. H.G., X.L., and S.K. performed the interactome and Nanostring analysis. C.L.F. and M.L. executed the flow cytometry analysis and B.H. did the ChIP-seq analysis. V.P., J.C. and S.N. performed the genetic analysis and contributed to RNA-seq analysis. K.R. and K.N aided by K.E. and D.N., did the inflammasome activation analyses and RT-PCR and WB. K.K., E.E., J.K., M.M., O.V. and P.S. participated in RNA-seq of stimulated granulocytes. An.J. and R.F. performed the TEM of platelets and H.V. the TEM of neutrophils. P.E.K did the Wright staining and analyses of granules. D.G. and G.S. contributed in data analysis. H.G., C.L.F., L.D.N., K.E., M.V., J.T. and M.R.J.S. designed and supervised the study. All of the authors reviewed the manuscript critically.

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Figure Legends

Fig 1. Pedigree of the index family and changes in protein-protein interactions. A, The pedigree of the index family with the C/EBPε Arg219His mutation. Homozygous individuals are shown in red, heterozygous carriers in orange and deceased individuals by diagonal bars. **B,** The three-dimensional structure of a C/EBPε dimer (blue and red helixes) bound to a DNA fragment. The top right panel shows the WT Arg219-DNA interaction and the right bottom panel mutated 219His interaction. **C,** Schematic illustration showing the Arg219His mutation within the basic zipper (bZIP) region of DNA binding domain of C/EBPε. **D,** C/EBPε protein-protein interactions detected using BioID-MS analysis. Interacting proteins were classified by CORUM and UniProt databases and the complex and/or functional group membership are depicted by different colors. Novel interactions are shown with red edges and the two previously known C/EBPε interactions in blue. **E,** Arg219His mutation in C/EBPε causes decreased associations with transcriptional repressors. Log2 fold-changes of protein-protein interactions (mean, n=4) between Arg219His and WT C/EBPε are shown. Color-coding highlights the transcription regulation action (Uniprot) of proteins with more than 2-fold decrease in interaction (log2 fold change <-1).

Fig 2. ChIP-seq analysis of C/EBPε DNA binding. Area-proportional Venn diagrams of the C/EBPε ChIP-seq binding sites and the tag density maps of C/EBPε -binding events flanking ± 5 kb in absence (**A**) and presence of LPS treatment (**B**). **C,** Average C/EBPε ChIP-seq signal profiles. **D,** Binding motif as determined by ChIP-seq. No significant changes were seen in the binding site of the Arg219His mutant. All ChIP-seq experiments were carried out in freshly isolated human granulocytes. C: controls, Ca: heterozygous carriers, P: homozygous patients.

Fig 3. Transcriptome analysis of unstimulated (A-C) and bacterial LPS and DNA stimulated (D-F) granulocytes by RNA-sequencing. A, RNA-seq revealed 464 differentially transcribed genes (Fold change >2 and FDR<0.05) between the patients and controls in unstimulated granulocytes. Of these **B,** 198 were identified to be IFN-related by Interferome v.2.01 (www.interferome.org) and **C,** 271 had C/EBPε binding sites (mapping to nearby genes within ±50 kb). Importantly, 80 of these 271 genes were associated with patient-specific C/EBPε binding. **D,** Similarly, 470 genes were differentially transcribed in bacterial LPS and DNA stimulated granulocytes. Of these **E,** 183 were identified to be IFN-related and **F,** 289 had C/EBPε binding sites. 81 genes had patient-specific C/EBPε binding. The volcano plots represent log2 fold change and -log10FDR of transcripts between the patients and controls. Different groups are color-coded. C: controls, Ca: heterozygous carriers, P: homozygous patients.

Fig 4. Transcriptome analysis of IFNα2 stimulated (A-B) and IFNγ stimulated (C-D) granulocytes by RNA-sequencing. A, RNA-seq revealed 534 differentially transcribed genes (Fold change >2 and FDR<0.05) between the patients and controls after IFNα2 stimulation. **B,** Of these 266 had C/EBPε binding sites (mapping to nearby genes within ±50 kb) and, importantly, 83 of these were associated with patient-specific C/EBPε binding. **C,** Similarly, 427 genes were differentially transcribed in IFNγ stimulated granulocytes. Of these 208 had C/EBPε binding sites, **D,** 54 being associated with patient-specific C/EBPε binding. The volcano plots represent log2 fold change and -log10FDR of transcripts between the patients and controls. Different groups are color-coded. C: controls, Ca: heterozygous carriers, P: homozygous patients.

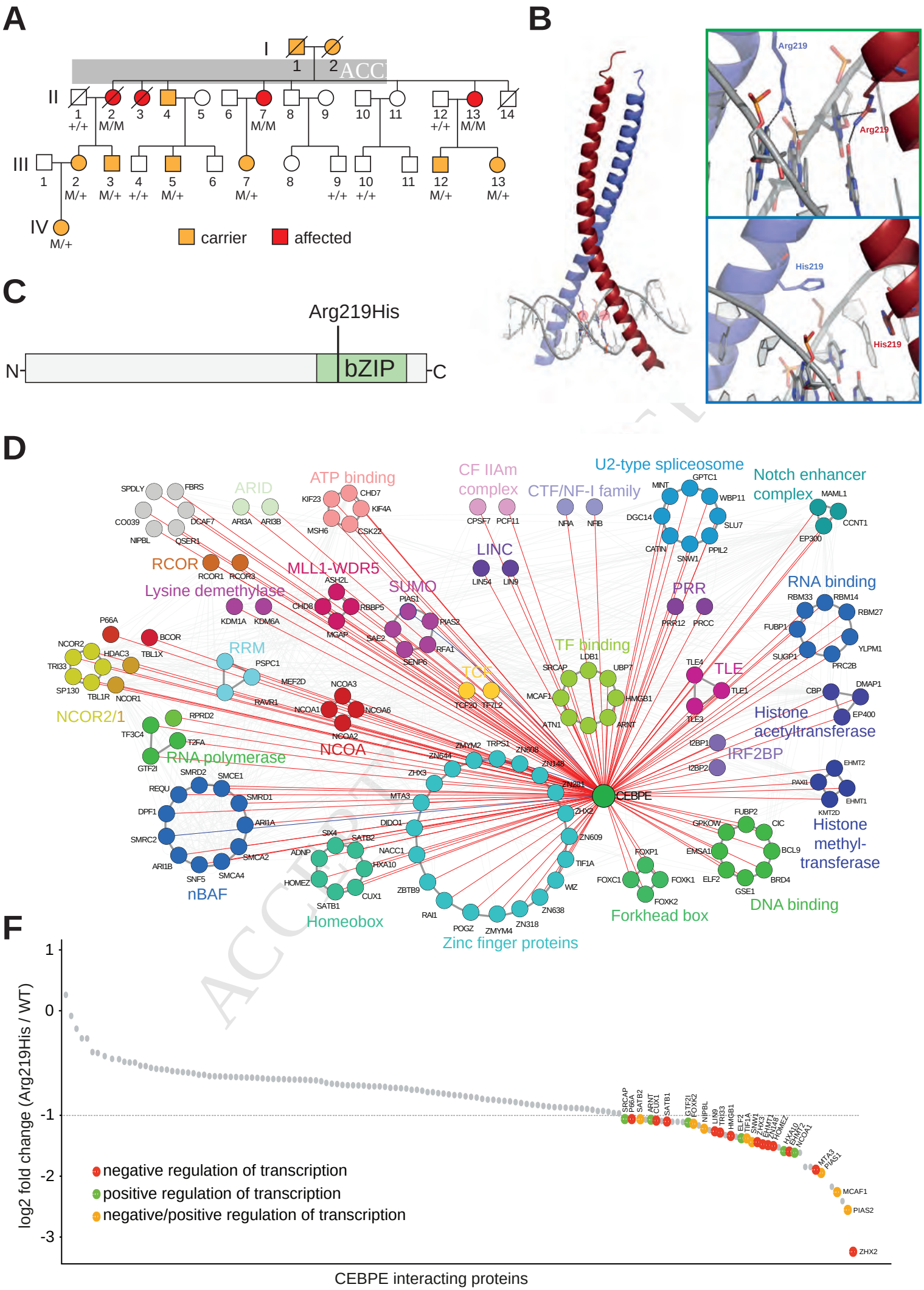
Fig 5. **Transcriptome analysis and characterization of changes in inflammasome activation. A,** mRNA levels of patient and control PBMC-cells analyzed using Nanostring technology. Custom gene panel with selected inflammasome, interleukin, JAK/STAT pathway and NFκB1 pathway related genes were used in analysis and average fold changes of three technical replicates are presented. Statistically significant changes (Student's t-test) of combined patients to controls are highlighted (***p<0.001, **p<0.01, *p<0.05). **B,** Levels of active CASP1 were measured by flow cytometry after canonical activation of the NLRP3 inflammasome with ATP in whole blood. **C-E,** Peripheral blood monocyte-derived macrophages were primed with TLR ligands LPS/P_3C or IFNα2b, followed by canonical (**C**) or noncanonical (**D, E**) activation of the NLRP3 inflammasome with ATP or transfection of LPS to cytoplasm, respectively. IL1β or IL-18 cytokine secretion was measured from culture supernatants by ELISA. **F,** Relative expression of CASP5 mRNA in resting macrophages, as determined by quantitative PCR. **G,** The expression of the procaspase-5 (48 kDa) and the processed intermediate form of caspase-5 (~30 kDa) assessed from non-stimulated PBMC cell lysates by western blot. Quantification of bands as fold changes compared to the control are showed next to the blot. AU, arbitrary units; MFI, median fluorescence intensity; P_3C, Pam_3Cys-SKKKK; TF, transfected.

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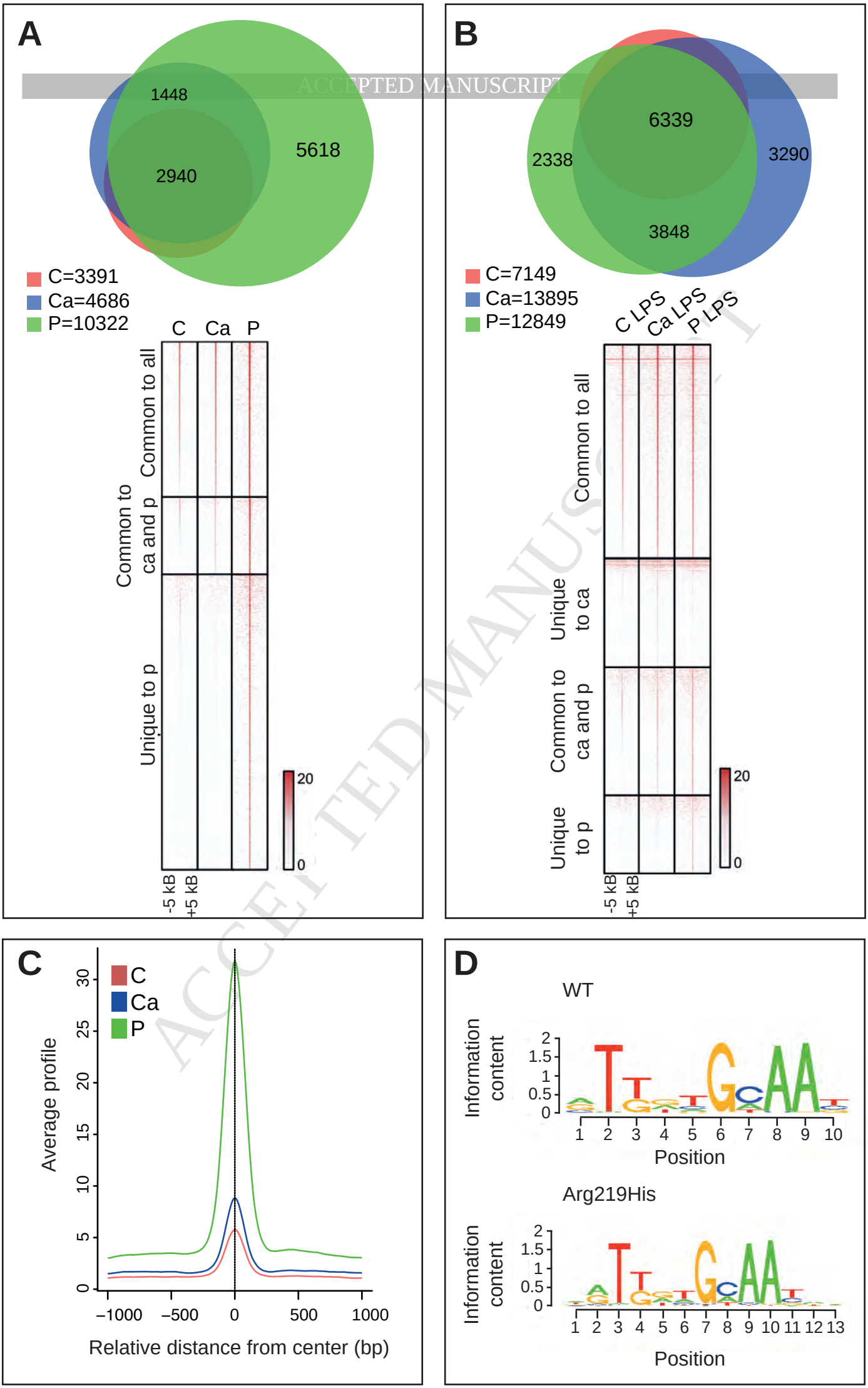
Table 1. Clinical characteristic of patients. ESR= erythrocyte sedimentation rate. In addition, II.3 was likely a carrier with similar systemic symptoms, periodic fever and skin and mucosal sequelae. At age 18 years, she acquired rheumatic fever causing mitral and aortic valve insufficiency, and cardiac arrhythmias. At age 23 years, she suffered from subacute endocarditis by Streptococcus viridans, and died at age 34 years due to ventricular fibrillation. Post-mortem autopsy showed "substantial" numbers of calcified mesenteric lymph nodes, with nonspecific inflammation".

Patient	II.2	II.7	II.13
Age at onset of symptoms	*17 yrs*	*17 yrs*	*Youth*
Current age	*Deceased at age 78*	*74*	*69*
Main symptoms	*Abdominal pain, high fever* *Crater-like ulcers of buccal mucosa occasionally during periodic fever*	*Abdominal pain, high fever*	*Abdominal pain, high fever* *Crater-like ulcers of buccal mucosa occasionally during periodic fever*
Duration of attacks (average)	*4-5 days*	*4-5 days*	*4-5 days*
Frequency of attacks (average)	*Every 2-4 weeks, later on more seldom*	*Every 2-4 weeks, later on more seldom*	*Every 2-4 weeks, later on more seldom*
Other symptoms during attacks	*Lymphangitis* *Vomiting* *Myalgia* *Pleurisy* *Arthralgia* *Ileitis diagnosed by laparotomy*	*Lymphangitis* *Pleurisy* *Episcleritis* *Scleritis* *Aphthous colitis*	*Lymphangitis* *Vomiting* *Myalgia*
ESR (mm/h) at attacks	*70-80*	*>50*	*70-80*
Other major clinical events	*Myocardial infarction at age 46*	*Operated for ileal leiomyosarcoma at age 35* *Pyoderma gangrenosum at age 43*	*Mesenterial lymph node biopsy at laparotomy at age 55 showed granulomatous inflammation* *Recurrent respiratory tract infections since age 42* *Laparotomy at age 55 showed ileitis and mesenterial lymph node biopsy granulomatous inflammation*
Infections	*Severe recurrent tongue abscesses when very young* *Easily acquired purulent wounds with delayed healing* *Paronychia*		
	Gluteal and submandibular abscesses		
Bleeding Diathesis	*Moderately severe nose bleeds as well as need for prolonged compression after needle sticks* *Postoperative hematomas*		

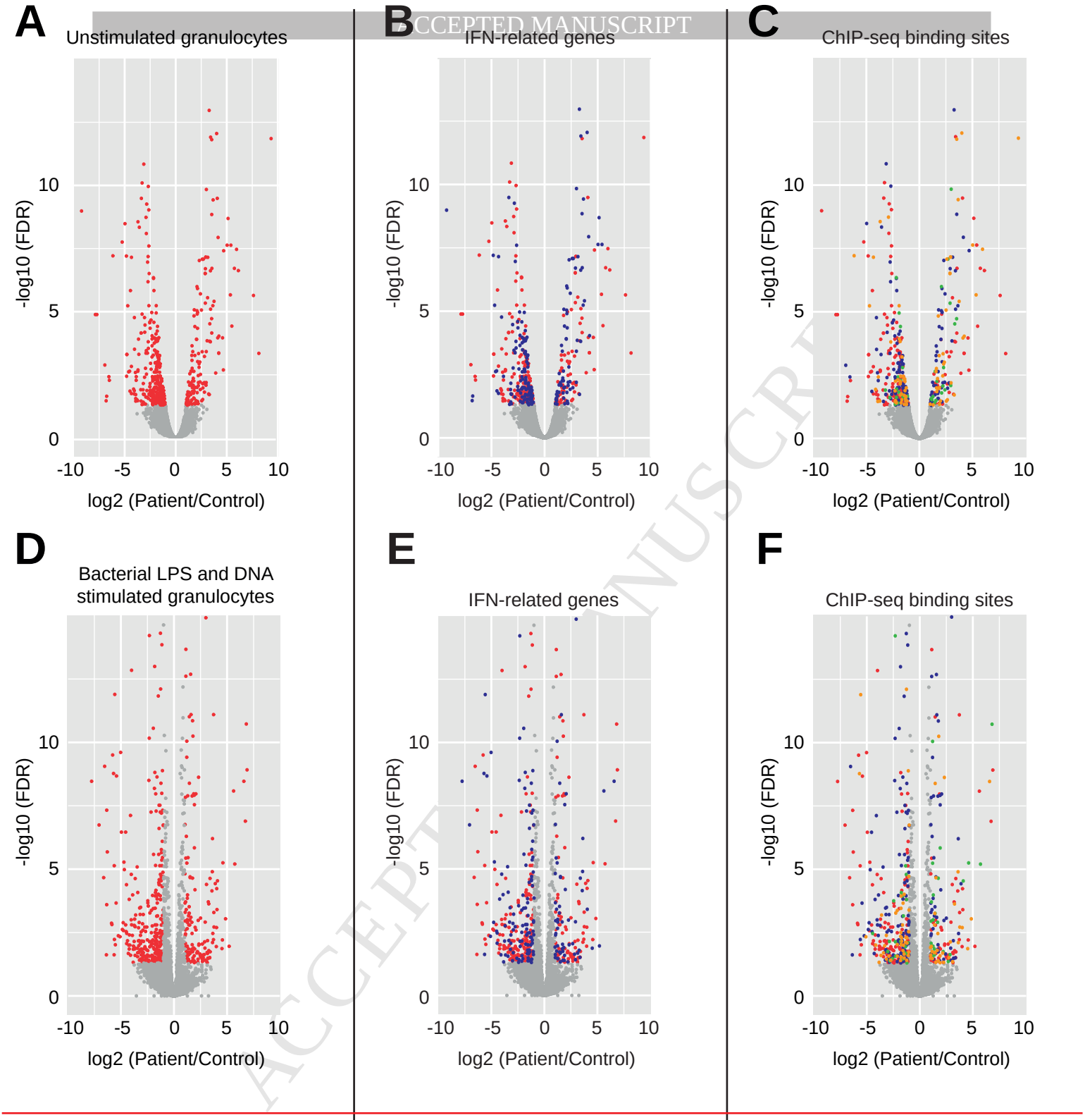
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A
I
1
2
ACC
II
1 +/+
2 M/M
3
4
5
6
7 M/M
8
9
10
11
12 +/+
13 M/M
14
III
1
2 M/+
3 M/+
4 +/+
5 M/+
6
7 M/+
8
9 +/+
10 +/+
11
12 M/+
13 M/+
IV
M/+
carrier
affected
B
Arg219
Arg219
His219
His219
C
Arg219His
N
bZIP
C
D
ATP binding
ARID
CF IIAm complex
CTF/NF-I family
U2-type spliceosome
Notch enhancer complex
LINC
MLL1-WDR5
Lysine demethylase
SUMO
PRR
RNA binding
TF binding
TLE
RRM
TCF
NCOR2/1
NCOA
RNA polymerase
Histone acetyltransferase
IRF2BP
CEBPE
Histone methyl-transferase
nBAF
Homeobox
Zinc finger proteins
Forkhead box
DNA binding
F
log2 fold change (Arg219His / WT)
1
0
-1
-2
-3
negative regulation of transcription
positive regulation of transcription
negative/positive regulation of transcription
MCAF1
PIAS2
ZHX2
CEBPE interacting proteins

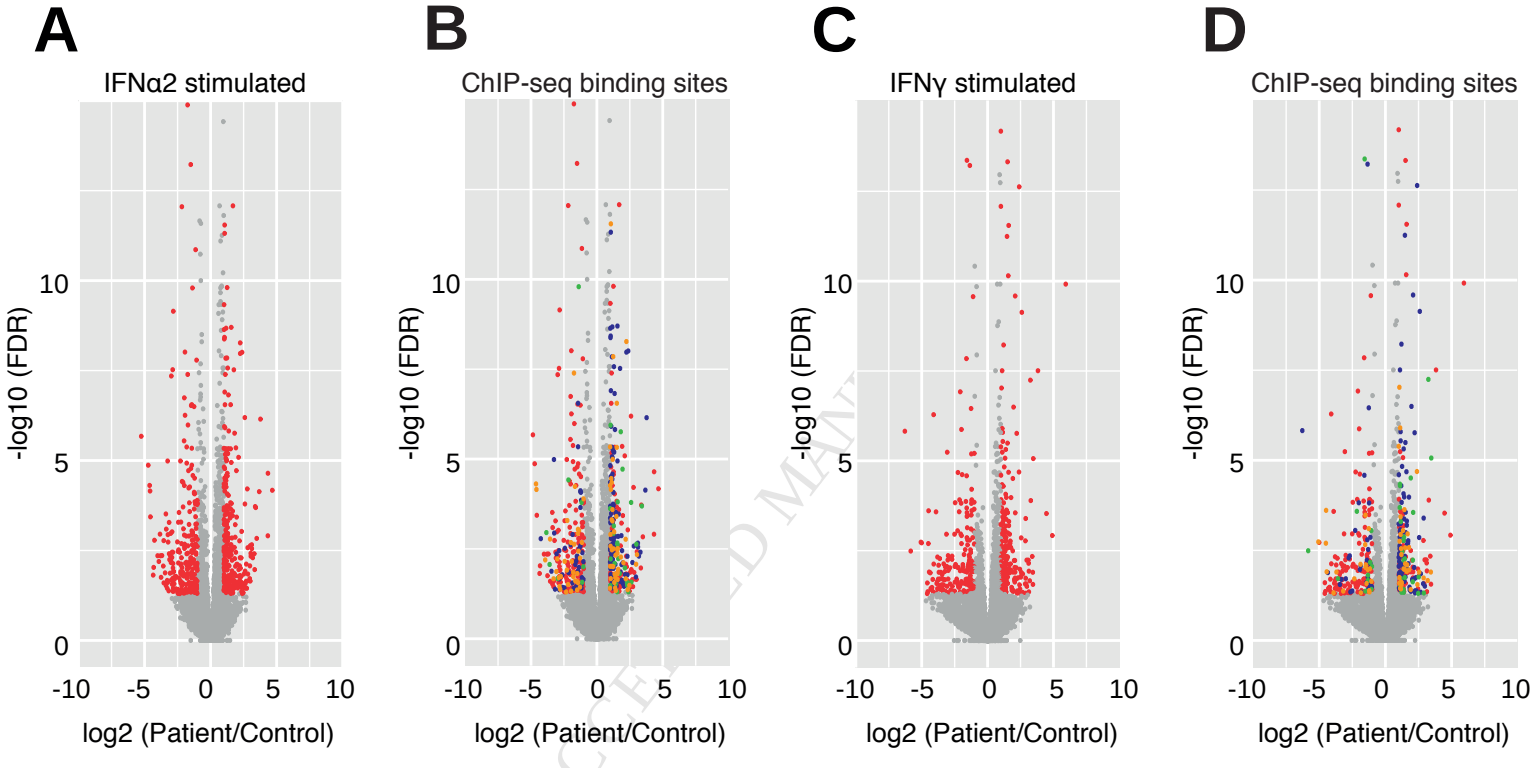
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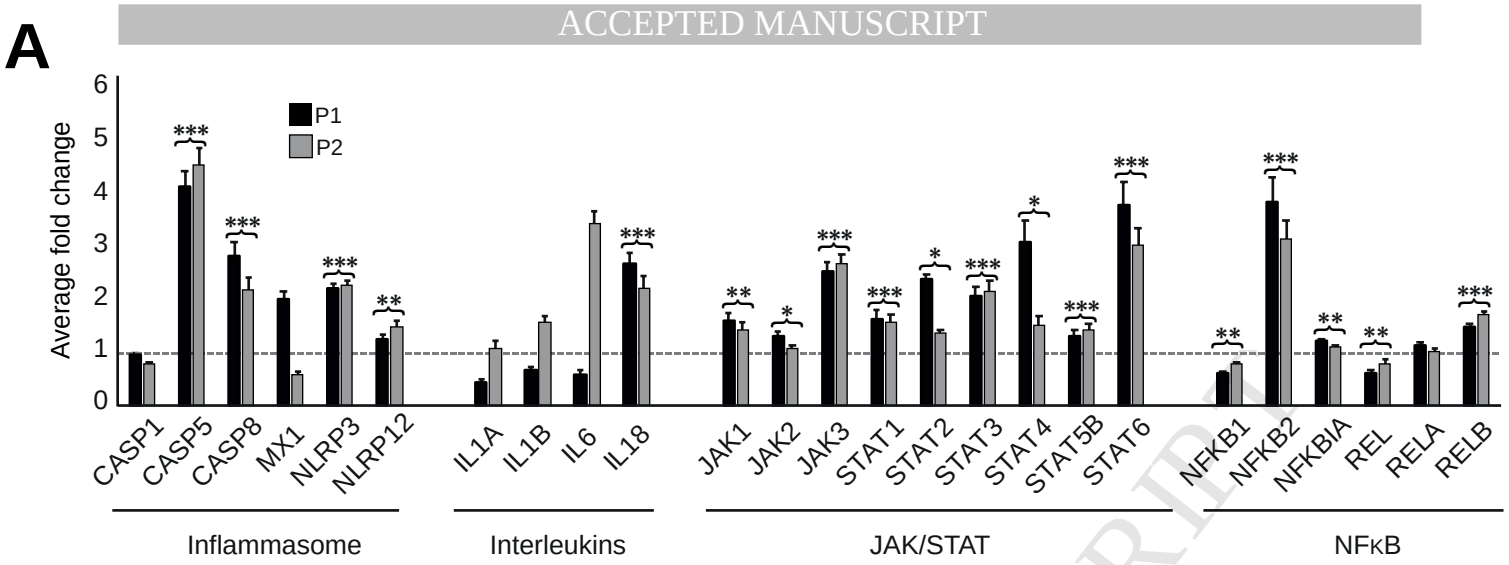
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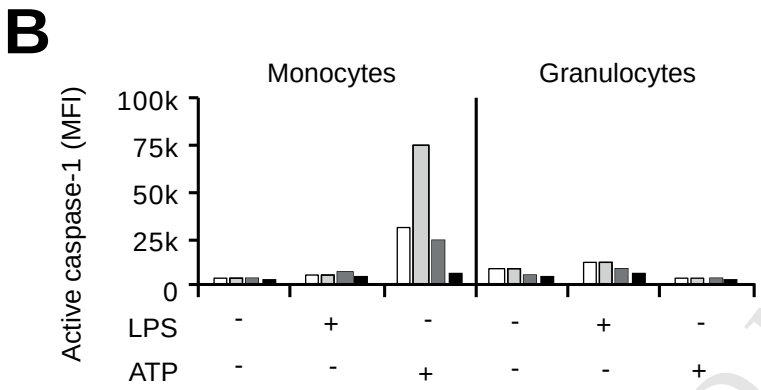


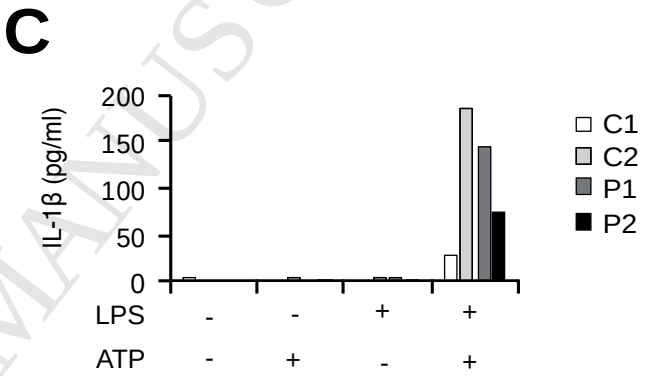
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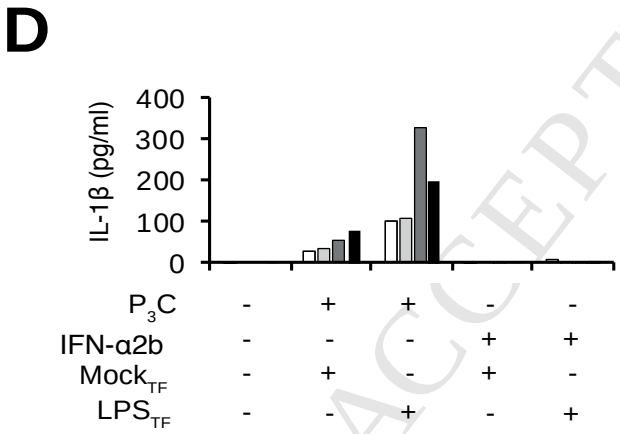


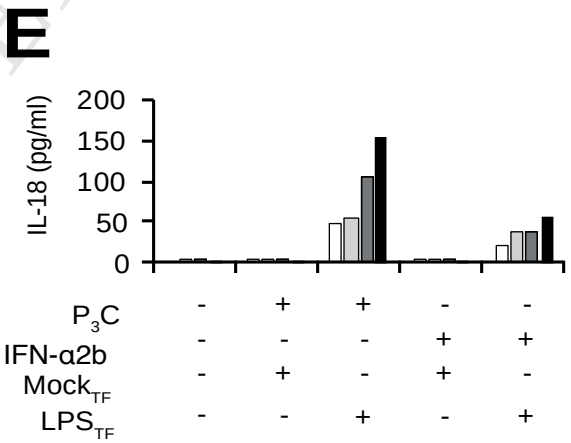
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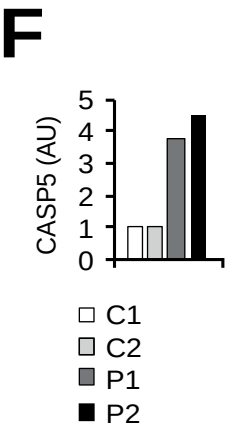


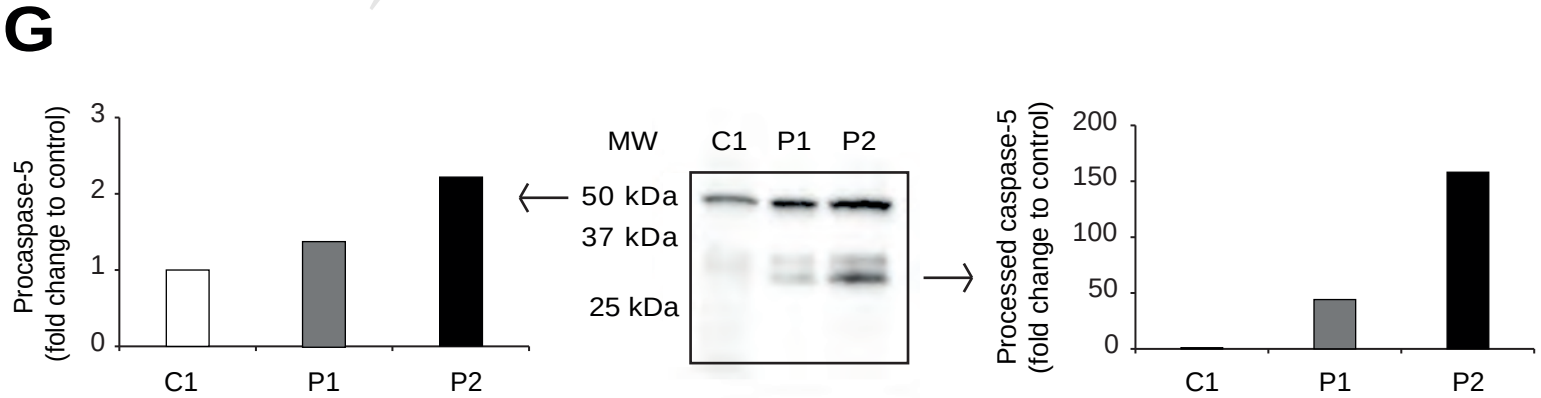












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Table E1.
Average fold changes and p-values between WT and Arg219His C/EBPε interacting proteins as assessed using the BioID assay in Flp-In™ T-REx™ 293 cells stably expressing C/EBPε. Accession represents the UniProt Accession number. Name is the Official gene name. Mut/WT represents the Log2 fold change in the interaction affinity of mutant vs WT C/EBPε. 29 of the interactions were validated with Jurkat cells (x) using similar BioID assay. WT/GFP represent the fold change between wt C/EBPε (n=4) and gfp-controls (n=52). V218A/WT shows the Log2 fold change in the interaction affinity of Val218Ala vs WT.

Accession	Name	Protein name	Log2 Mut/WT	p-value	Transcription regulation	Validated in Jurkat-cells	WT/GFP	Log2 V218A/WT
O00512	BCL9	B-cell CLL/lymphoma 9 protein	-0.63	0.0004	Positive		64.54	0.15
O00712	NFIB	Nuclear factor 1 B-type	-0.4	0.2005	Both		72.43	0.33
O14497	ARI1A	AT-rich interactive domain-containing protein 1A	-0.48	0.0114	Both	x	11.32	0.16
O14686	KMT2D	Histone-lysine N-methyltransferase 2D	-0.3	0.1002	Positive		37.89	0.12
O15014	ZN609	Zinc finger protein 609	-0.5	0.0018	None		26.29	0.22
O15164	TIF1A	Transcription intermediary factor 1-alpha	-1.37	6.30E-05	Both		50.47	0.07
O15379	HDAC3	Histone deacetylase 3	-0.9	0.0057	Both		6.75	0.37
O15550	KDM6A	Lysine-specific demethylase 6A	-0.37	0.1384	Both		43.16	0.21
O60341	KDM1A	Lysine-specific histone demethylase 1A	-0.44	0.013	Both		4.97	0.28
O60563	CCNT1	Cyclin-T1	-0.61	0.003	Positive		2.80	0.04
O60885	BRD4	Bromodomain-containing protein 4	-0.75	0.0033	Positive	x	3.70	0.12
O60907	TBL1X	F-box-like/WD repeat-containing protein TBL1X	-0.84	0.0215	Both		10.16	0.16
O75376	NCOR1	Nuclear receptor corepressor 1	-0.35	0.012	Negative	x	14.51	0.24
O75925	PIAS1	E3 SUMO-protein ligase PIAS1	-1.94	0.0015	Both		#DIV/0!	0.32
O75928	PIAS2	E3 SUMO-protein ligase PIAS2	-2.55	0.0032	Both		106.60	0.13
O94913	PCF11	Pre-mRNA cleavage complex 2 protein Pcf11	-0.27	0.0392	None		6.91	-0.25
O95239	KIF4A	Chromosome-associated kinesin KIF4A	-0.92	0.0397	None		3.77	0.16
O95391	SLU7	Pre-mRNA-splicing factor SLU7	-1.1	0.0042	None		11.94	0.13
O95785	WIZ	Protein Wiz	-0.88	3.90E-05	Negative		28.00	0.38
P09429	HMGB1	High mobility group protein B1	-1.33	8.50E-05	Negative	x	10.69	0.41
P19784	CSK22	Casein kinase II subunit alpha'	-0.5	0.0975	None		8.05	-0.01
P27540	ARNT	Aryl hydrocarbon receptor nuclear translocator	-1.06	0.0087	Positive		86.13	0.11
P27694	RFA1	Replication protein A 70 kDa DNA-binding subunit	-1.1	0.0013	None	x	2.73	0.01
P31260	HXA10	Homeobox protein Hox-A10	-1.58	0.0006	Positive		#DIV/0!	0.30
P35269	T2FA	General transcription factor IIF subunit 1	-0.57	0.0055	Positive		3.68	-0.10
P39880	CUX1	Homeobox protein cut-like 1	-1.08	0.0011	Negative		16.60	-0.04
P46937	YAP1	Transcriptional coactivator YAP1	-0.86	0.0037	Both		988.00	-0.90
P49750	YLPM1	YLP motif-containing protein 1	0.64	0.0007	Negative	x	2.38	-0.20
P51531	SMCA2	Probable global transcription activator SNF2L2	-0.35	0.0429	Both		6.84	0.38
P51532	SMCA4	Transcription activator BRG1	-0.35	0.0555	Both	x	4.13	0.31
P52701	MSH6	DNA mismatch repair protein Msh6	-2.16	0.0073	None		4.66	2.24
P54259	ATN1	Atrophin-1	-0.43	0.2087	Negative		227.50	-1.22
P61962	DCAF7	DDB1- and CUL4-associated factor 7	-1.1	0.0072	None		9.38	-0.03
P78347	GTF2I	General transcription factor II-I	-1.11	0.0001	Positive		3.72	0.18
P85037	FOXK1	Forkhead box protein K1	-0.65	0.0494	Both		99.67	0.17
Q01167	FOXK2	Forkhead box protein K2	-1.13	0.0002	Both		20.28	0.03
Q01826	SATB1	DNA-binding protein SATB1	-1.09	0.0008	Negative	x	16.35	-0.14
Q02241	KIF23	Kinesin-like protein KIF23	-1.52	0.0289	None		5.41	0.34
Q04724	TLE1	Transducin-like enhancer protein 1	-0.51	0.021	Negative		20.66	0.28
Q04726	TLE3	Transducin-like enhancer protein 3	-0.37	0.017	Negative	x	10.58	0.24
Q04727	TLE4	Transducin-like enhancer protein 4	-0.36	0.0267	Negative		#DIV/0!	0.50
Q09472	EP300	Histone acetyltransferase p300	-0.73	0.0043	Both		147.64	0.01
Q12824	SNF5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	-0.23	0.4401	Positive		4.27	0.30
Q12857	NFIA	Nuclear factor 1 A-type	-0.69	0.017	Both		34.67	0.33
Q12948	FOXC1	Forkhead box protein C1	-0.5	0.0156	Positive		62.40	0.41
Q13356	PPIL2	Peptidyl-prolyl cis-trans isomerase-like 2	-1.34	0.0031	None		45.50	-0.65
Q13573	SNW1	SNW domain-containing protein 1	-1.43	0.001	Both		18.74	-0.36
Q14686	NCOA6	Nuclear receptor coactivator 6	-0.7	0.0156	Positive		7.23	0.10
Q14687	GSE1	Genetic suppressor element 1	-0.55	4.70E-05	None		8.19	0.45
Q14814	MEF2D	Myocyte-specific enhancer factor 2D	-0.51	0.0025	Positive		13.00	0.49
Q14966	ZN638	Zinc finger protein 638	0.27	0.1194	Both		3.39	-0.32
Q15291	RBBP5	Retinoblastoma-binding protein 5	-0.43	0.024	Both		5.96	0.34
Q15596	NCOA2	Nuclear receptor coactivator 2	-0.86	5.30E-05	Positive		17.91	0.29
Q15723	ELF2	ETS-related transcription factor Elf-2	-1.37	0.0004	Both		9.12	0.11
Q15788	NCOA1	Nuclear receptor coactivator 1	-1.61	0.0002	Positive		70.57	-0.15
Q2KHR3	QSER1	Glutamine and serine-rich protein 1	-1.06	0.0011	None		52.00	-0.11
Q5JSZ5	PRC2B	Protein PRRC2B	-0.36	0.0281	None		59.68	-0.84
Q5TKA1	LIN9	Protein lin-9 homolog	-1.25	0.0116	Negative		28.29	0.21
Q5VT52	RPRD2	Regulation of nuclear pre-mRNA domain-containing protein 2	0.43	0.0006	None	x	2.66	-0.60
Q5VUA4	ZN318	Zinc finger protein 318	-0.11	0.3529	Negative	x	3.96	0.02
Q5VZL5	ZMYM4	Zinc finger MYM-type protein 4	-0.8	0.0089	None		4.85	0.09
Q6KC79	NIPBL	Nipped-B-like protein	-1.21	0.0121	Both	x	50.47	-0.27
Q6MZP7	LIN54	Protein lin-54 homolog	-0.87	2.90E-05	Both		16.40	0.08

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Q6PJG2	EMSA1	ELM2 and SANT domain-containing protein 1	0.03	0.8967	Both		24.47	0.18
Q6VMQ6	MCAF1	Activating transcription factor 7-interacting protein 1	-2.25	0.0042	Both		6.22	-0.24
Q6W2J9	BCOR	BCL-6 corepressor	-0.07	0.3789	Negative		6.44	0.13
Q6ZRI6	CO039	Uncharacterized protein C15orf39	-0.96	0.0073	None		137.80	-0.53
Q6ZRS2	SRCAP	Helicase SRCAP	-1.05	0.0052	Positive		4.55	0.03
Q6ZW49	PAXI1	PAX-interacting protein 1	-0.54	0.1407	Both		17.53	0.11
Q7Z3K3	POGZ	Pogo transposable element with ZNF domain	-0.73	0.0126	None		19.12	-0.05
Q7Z5J4	RAI1	Retinoic acid-induced protein 1	-0.41	0.0702	Positive		182.00	-0.18
Q7Z5L9	I2BP2	Interferon regulatory factor 2-binding protein 2	-0.4	0.0058	Both		11.30	0.34
Q86U70	LDB1	LIM domain-binding protein 1	-0.78	0.0027	Both		611.00	0.05
Q86YP4	P66A	Transcriptional repressor p66-alpha	-1.05	0.0003	Negative	x	3.86	0.10
Q8IU81	I2BP1	Interferon regulatory factor 2-binding protein 1	-0.93	0.0098	Negative		32.07	0.48
Q8IVW6	ARI3B	AT-rich interactive domain-containing protein 3B	-0.28	0.0965	Positive		8.26	0.13
Q8IWI9	MGAP	MAX gene-associated protein	-0.54	0.0767	Both		9.19	-0.46
Q8IWZ8	SUGP1	SURP and G-patch domain-containing protein 1	-0.77	0.0089	None		5.21	0.00
Q8IX15	HOMEZ	Homeobox and leucine zipper protein Homez	-1.5	0.0002	Negative		156.00	0.11
Q8IY67	RAVR1	Ribonucleoprotein PTB-binding 1	-1.08	0.0034	None		34.67	-0.26
Q8N684	CPSF7	Cleavage and polyadenylation specificity factor subunit 7	-0.12	0.4529	None	x	3.66	-0.07
Q8NFD5	ARI1B	AT-rich interactive domain-containing protein 1B	-0.17	0.5042	Both		11.39	0.34
Q8TAQ2	SMRC2	SWI/SNF complex subunit SMARCC2	-0.41	0.0349	Both	x	4.61	0.17
Q8WUQ7	CATIN	Cactin	-0.88	0.0158	None		6.77	0.06
Q8WXF1	PSPC1	Paraspeckle component 1	-0.32	0.0196	Negative	x	3.58	-0.01
Q92585	MAML1	Mastermind-like protein 1	-0.39	0.033	Positive		47.53	0.40
Q92733	PRCC	Proline-rich protein PRCC	-0.57	0.037	None		7.13	0.37
Q92782	DPF1	Zinc finger protein neuro-d4	-0.66	0.0237	Both		195.00	0.06
Q92785	REQU	Zinc finger protein ubi-d4	-0.26	0.2571	Both		7.32	0.13
Q92793	CBP	CREB-binding protein	-0.72	0.0063	Both		105.73	0.06
Q92917	GPKOW	G patch domain and KOW motifs-containing protein	-0.47	0.0779	None	x	2.29	0.04
Q92925	SMRD2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	-0.4	0.0795	Both		7.05	0.21
Q92945	FUBP2	Far upstream element-binding protein 2	-0.06	0.3962	Both	x	2.26	0.03
Q93009	UBP7	Ubiquitin carboxyl-terminal hydrolase 7	-0.54	0.1252	Negative		3.54	0.08
Q969G3	SMCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	-0.18	0.2519	Both	x	4.56	0.35
Q96AE4	FUBP1	Far upstream element-binding protein 1	-0.32	0.0961	Both	x	5.64	0.02
Q96C00	ZBTB9	Zinc finger and BTB domain-containing protein 9	-0.38	0.0499	Both		5.47	0.41
Q96DF8	DGC14	Protein DGCR14	-1.16	0.0003	None		43.79	-0.49
Q96EA4	SPDLY	Protein Spindly	-1.23	0.0289	None		2.15	0.00
Q96EV2	RBM33	RNA-binding protein 33	-0.29	0.0199	None		8.17	0.25
Q96GM5	SMRD1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	-0.52	0.0694	Positive		5.67	0.11
Q96KQ7	EHMT2	Histone-lysine N-methyltransferase EHMT2	-1.59	0.0027	Negative		23.14	0.53
Q96L91	EP400	E1A-binding protein p400	-0.82	0.0002	Positive		6.33	-0.16
Q96PK6	RBM14	RNA-binding protein 14	-0.39	0.0038	Negative	x	173.33	-0.18
Q96RE7	NACC1	Nucleus accumbens-associated protein 1	-0.59	0.0206	Negative	x	6.50	0.11
Q96RK0	CIC	Protein capicua homolog	-0.49	0.0032	Negative		13.76	0.31
Q96T58	MINT	Msx2-interacting protein	-0.85	0.0016	Negative		4.71	0.07
Q99856	ARI3A	AT-rich interactive domain-containing protein 3A	-0.24	0.2654	Positive		12.45	0.20
Q9BRR8	GPTC1	G patch domain-containing protein 1	-0.02	0.9256	None		2.32	0.43
Q9BTC0	DIDO1	Death-inducer obliterator 1	-0.63	0.0019	Both		2.74	0.19
Q9BTC8	MTA3	Metastasis-associated protein MTA3	-1.88	0.0117	Negative		4.43	0.16
Q9BZK7	TBL1R	F-box-like/WD repeat-containing protein TBL1XR1	-0.52	0.0247	Both	x	4.81	0.21
Q9GZR1	SENP6	Sentrin-specific protease 6	-1.84	0.0086	None		5.24	-0.16
Q9H0E3	SP130	Histone deacetylase complex subunit SAP130	-0.5	0.1245	Negative		5.31	0.31
Q9H2P0	ADNP	Activity-dependent neuroprotector homeobox protein	-0.82	0.0006	None		4.11	-0.03
Q9H334	FOXP1	Forkhead box protein P1	-0.95	0.0008	Negative		53.18	-0.06
Q9H4I2	ZHX3	Zinc fingers and homeoboxes protein 3	-1.43	0.0017	Negative		6.00	0.37
Q9H582	ZN644	Zinc finger protein 644	-1.61	0.0013	None		59.09	0.58
Q9H9B1	EHMT1	Histone-lysine N-methyltransferase EHMT1	-1.47	0.0002	Negative		23.31	0.26
Q9HAH7	FBRS	Probable fibrosin-1	-0.21	0.4892	None		72.43	-0.22
Q9HCK8	CHD8	Chromodomain-helicase-DNA-binding protein 8	-0.39	0.0278	Negative		2.85	0.19
Q9NPF5	DMAP1	DNA methyltransferase 1-associated protein 1	-0.92	0.0443	Negative		3.27	0.12
Q9NQB0	TF7L2	Transcription factor 7-like 2	-0.12	0.2157	Both		88.40	0.07
Q9P2D1	CHD7	Chromodomain-helicase-DNA-binding protein 7	0.05	0.8111	Both		5.84	0.01
Q9P2K3	RCOR3	REST corepressor 3	-0.86	0.0032	Negative		8.33	0.27
Q9P2N5	RBM27	RNA-binding protein 27	-0.4	0.0199	None		7.56	-0.05
Q9UBL3	ASH2L	Set1/Ash2 histone methyltransferase complex subunit ASH2	-0.35	0.1313	Both		4.33	0.06
Q9UBT2	SAE2	SUMO-activating enzyme subunit 2	-2.4	0.0144	None	x	4.26	-0.31
Q9UBW7	ZMYM2	Zinc finger MYM-type protein 2	-1.84	0.0012	None		3.80	-0.09
Q9UGU0	TCF20	Transcription factor 20	-0.61	0.0163	Positive		112.41	-0.44
Q9UHF7	TRPS1	Zinc finger transcription factor Trps1	-0.87	0.0292	Negative		31.11	0.13
Q9UIU6	SIX4	Homeobox protein SIX4	-0.76	0.0276	Both		43.73	-0.23
Q9UKL0	RCOR1	REST corepressor 1	-0.75	0.0011	Negative		4.69	0.22
Q9UKN8	TF3C4	General transcription factor 3C polypeptide 4	-1.32	0.0006	None		2.90	-0.20
Q9ULD9	ZN608	Zinc finger protein 608	-0.66	0.0275	None		30.11	0.10

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Q9ULL5	PRR12	Proline-rich protein 12	-0.38	0.4891	None		93.60	0.18
Q9UPN9	TRI33	E3 ubiquitin-protein ligase TRIM33	-1.27	0.0019	Negative		14.48	0.12
Q9UPW6	SATB2	DNA-binding protein SATB2	-1.05	0.0061	Both		13.57	-0.10
Q9UQR1	ZN148	Zinc finger protein 148	-1.48	0.0035	Negative		28.17	0.07
Q9Y2W2	WBP11	WW domain-binding protein 11	0.27	0.2473	None		2.56	-0.20
Q9Y2X9	ZN281	Zinc finger protein 281	-0.23	0.2256	Negative		10.60	0.08
Q9Y618	NCOR2	Nuclear receptor corepressor 2	-0.37	0.0171	Negative		40.31	0.35
Q9Y6Q9	NCOA3	Nuclear receptor coactivator 3	-0.82	0.0098	Positive		124.22	-0.08
Q9Y6X8	ZHX2	Zinc fingers and homeoboxes protein 2	-3.23	0.0002	Negative		25.32	-0.18

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Table E2: The number of C/EBPε binding sites obtained from PBMCs of all the individuals and their high confidence overlaps. Peak calling was performed with MACS at q-value 0.05 using rabbit IgG as control.

Sample	CEBPE sites	Replicate overlap	CEBPE sites	Replicate overlap	CEBPB sites
	w/o LPS		**w/ LPS**		**w/o LPS**
Control1 (C1)	5,603		8,731		65,060
Control2 (C2)	6,577	3,391	11,305	7,149	76,484
Control3 (C3)	4,940		28,497		80,233
Carrier 1 (Ca1)	8,848	4,686	25,941	13,895	72,202
Carrier 2 (Ca2)	5,900		17,116		103,638
Patient1 (P1)	16,331	10,322	14,895	12,849	71,618
Patient2 (P2)	11,259		19,484		91,866

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Table E3.
464 differentially transcribed (Fold change >2 (absLog2FC>1) and FDR<0.05) genes between patients and controls in unstimulated granulocytes. Of these, 198 were identified to be IFN-related (Interferome v.2.01). Overap with ChIP-seq peaks mapped to nearby genes within ±50 kb range is shown as following: p= patients spesific binding; p, ca= binding in patient and carrier cells; p, ca, and c= binding in patient, carrier and control cells.

	logFC	ABSFC	logCPM	LR	PValue	FDR	fold change	IFN-related	Overlap with ChiP-seq peaks
CYP26B1	9.3421409	9.3421409	2.26587499	63.834552	1.35E-15	1.40E-12	649.029797		p
DAAM2	-9.2238596	9.2238596	2.48654345	49.3952074	2.09E-12	1.03E-09	0.00167241	yes	
COCH	8.33875732	8.33875732	4.16346053	119.896072	6.67E-28	3.46E-24	323.754698	yes	p
GPC4	8.14425512	8.14425512	4.90428084	133.591383	6.71E-31	6.97E-27	282.920935	yes	
BTNL3	8.13882777	8.13882777	1.19978147	20.4641414	6.08E-06	0.00044733	281.858599		
CRISP3	-7.8716512	7.87165116	1.29899089	28.3299294	1.02E-07	1.30E-05	0.0042697		
RIPK4	-7.7230141	7.72301413	1.18227999	28.328358	1.02E-07	1.30E-05	0.00473305		
SCN8A	7.61692893	7.61692893	0.56384501	32.1788432	1.41E-08	2.28E-06	196.301709		
PCOLCE2	7.51588259	7.51588259	3.34400602	93.2642413	4.58E-22	9.50E-19	183.023183	yes	p
ORM2	-6.9412392	6.94123922	0.52908564	18.0431994	2.16E-05	0.00129582	0.00813727		p, ca, c
CLEC4C	-6.8151414	6.81514136	0.39727353	10.2804659	0.00134446	0.03387582	0.00888051	yes	
LGALS9C	-6.7645408	6.76454084	0.36172991	11.3013566	0.0007745	0.02237539	0.00919751	yes	
ZDHHC19	-6.5471171	6.54711709	0.23090743	15.6403254	7.66E-05	0.00375104	0.01069354		p, ca, c
SLC5A9	-6.5023967	6.50239673	0.21434352	14.8956988	0.00011362	0.00521906	0.0110302		
EFHC2	-6.1531485	6.15314851	2.24822894	40.3456318	2.13E-10	6.14E-08	0.01405134		p
PRICKLE1	6.13294505	6.13294505	1.114878	37.0764135	1.14E-09	2.36E-07	70.1779087		
DAB2IP	5.95944494	5.95944494	2.31344014	41.6027088	1.12E-10	3.41E-08	62.2259712		p
NEGR1	5.74624419	5.74624419	1.49964358	37.5623849	8.85E-10	1.93E-07	53.6774483		
SAPCD2	5.53979468	5.53979468	4.82319435	107.45011	3.55E-25	1.23E-21	46.5204993		
PRTN3	5.49518171	5.49518171	0.50712853	26.0421191	3.34E-07	3.73E-05	45.1039447		
ST5	5.40523435	5.40523435	1.72767334	42.4920967	7.10E-11	2.33E-08	42.3777284	yes	
STON2	5.35411752	5.35411752	1.74796582	32.3186273	1.31E-08	2.16E-06	40.9025114		p
PRDM5	-5.2459806	5.24598058	2.76872913	43.1572816	5.05E-11	1.75E-08	0.02635133		
FZD1	5.12956086	5.12956086	3.67024474	47.7978966	4.72E-12	2.04E-09	35.0067413	yes	
LAMC1	5.03059759	5.03059759	2.05916655	42.4725206	7.17E-11	2.33E-08	32.6859242	yes	p
TGM3	-4.9707937	4.97079375	3.60352585	46.714626	8.21E-12	3.28E-09	0.03188908		p, ca, c
PDK4	-4.8325444	4.83254441	4.76948087	40.2514651	2.23E-10	6.26E-08	0.03509613	yes	
SLC16A14	-4.809983	4.80998304	1.09161692	15.7389099	7.27E-05	0.00361164	0.03564929		
LOC1019282	-4.7854096	4.78540963	1.05667717	20.1929925	7.00E-06	0.0004944	0.0362617		
VSIG10	-4.7854048	4.7854048	1.05667717	20.196843	6.99E-06	0.0004944	0.03626182		
CLEC12A	-4.7011651	4.7011651	5.74639036	30.1527814	3.99E-08	5.84E-06	0.03844221	yes	p
SNAI1	4.69326751	4.69326751	2.99174636	41.3061393	1.30E-10	3.86E-08	25.8710644		p, ca, c
XCL1	4.66581372	4.66581372	0.64658658	17.0322817	3.67E-05	0.00202925	25.3834053		
SLC6A12	-4.6108968	4.61089685	0.92249003	16.6366192	4.53E-05	0.00240991	0.04092435	yes	
GLIS3	4.58633821	4.58633821	1.39562065	23.6946009	1.13E-06	0.00010855	24.0228965		
NAV3	4.5184561	4.5184561	4.52024062	79.7419264	4.27E-19	7.38E-16	22.9187444	yes	
PAPSS2	-4.5145443	4.51454429	0.8607905	16.7834738	4.19E-05	0.00227711	0.04375088	yes	
APOBEC3B	-4.4818225	4.48182251	2.61908253	12.4992941	0.00040711	0.01399191	0.04475453	yes	p, ca, c
SPATA6	-4.4348895	4.43488948	2.35383323	33.1348855	8.60E-09	1.46E-06	0.0462344		
FBN1	-4.340806	4.340806	1.4133524	17.7552956	2.51E-05	0.00147338	0.04935		
GALNT12	-4.3392696	4.3392696	0.71179207	11.964134	0.00054234	0.0174847	0.04940259	yes	
FRMD4B	-4.3316677	4.33166767	4.35032639	39.7748936	2.85E-10	7.04E-08	0.04966359	yes	p
CDKN2B	4.23182773	4.23182773	1.04048535	24.0504635	9.38E-07	9.28E-05	18.7891478	yes	p
C1orf186	4.21536569	4.21536569	0.67109415	20.5278419	5.88E-06	0.00043809	18.5759707		

RP11-38J22.6	4.21535912	4.21535912	0.67109415	20.5242422	5.89E-06	0.00043809	18.575886		
CXCL3	4.14968675	4.14968675	2.86734514	44.0407771	3.22E-11	1.15E-08	17.7492572	yes	p, ca, c
FUT10	-4.1247569	4.12475691	0.56930539	12.9499991	0.00031992	0.01161226	0.05732241		p
MYOM2	4.11428809	4.11428809	0.90352663	23.6940836	1.13E-06	0.00010855	17.3190524		p
TPPP	-4.0728263	4.07282635	0.536516	11.866136	0.00057164	0.01802651	0.05942335		
MPO	4.06833808	4.06833808	3.30669545	52.1231927	5.21E-13	3.26E-10	16.7761305		
PXDC1	-4.056075	4.05607497	0.46923456	12.59083	0.00038764	0.01341377	0.06011734		
ST14	-4.0480083	4.04800833	3.19623581	27.7266129	1.40E-07	1.71E-05	0.06045442	yes	p, ca, c
RNF222	-4.0362141	4.03621409	1.65104098	21.3833661	3.76E-06	0.00030736	0.06095067		p, ca, c
PCSK5	4.00589764	4.00589764	4.50605726	65.1918878	6.79E-16	8.82E-13	16.0655408	yes	p
ID3	-3.9492809	3.94928093	1.64873077	16.470348	4.94E-05	0.00256499	0.06473632		p, ca, c
PTPRS	-3.9214804	3.92148039	0.38587681	10.7862117	0.00102259	0.02757273	0.06599587		
SPAG4	-3.9164689	3.91646892	0.35072007	10.2195275	0.00138961	0.03484441	0.06622552		p
SPATC1L	-3.914486	3.91448597	0.36852411	11.6764289	0.00063297	0.01922376	0.06631661		
NTRK1	3.91378998	3.91378998	1.91776574	16.3719072	5.21E-05	0.00268827	15.0719062		
DCTPP1	-3.8756233	3.87562326	1.04033321	14.9051954	0.00011305	0.00521593	0.0681273		p, ca, c
LAMP3	-3.868777	3.86877695	1.09842428	15.6642139	7.56E-05	0.00373923	0.06845136	yes	p
SERINC2	-3.79262	3.79261996	0.27253951	10.5355125	0.00117102	0.03062066	0.07216185		
CPAMD8	3.75333268	3.75333268	2.40465744	31.0795002	2.48E-08	3.90E-06	13.4854586	yes	p
PPP1R1B	-3.729782	3.72978202	0.2319289	10.301784	0.00132902	0.03368059	0.07537438		p
TNNT1	-3.7022889	3.70228895	2.21872994	16.7873695	4.18E-05	0.00227711	0.07682454		
PFKFB2	-3.6968103	3.69681028	3.98032475	47.1271892	6.65E-12	2.76E-09	0.07711684		p
HIC1	-3.693581	3.69358097	1.36653864	17.0209726	3.70E-05	0.00203057	0.07728965		
TDRD9	3.66002604	3.66002604	4.10899307	51.6889621	6.50E-13	3.75E-10	12.6408892	yes	p
CFD	3.65834947	3.65834947	8.80600803	96.5580866	8.67E-23	2.25E-19	12.6262075	yes	
PLD4	-3.644512	3.64451201	2.65707703	23.3933622	1.32E-06	0.00012238	0.07996364		
CLEC5A	3.63427357	3.63427357	2.15589007	30.2309745	3.84E-08	5.79E-06	12.4172481	yes	p, ca, c
SULT1A2	-3.6129219	3.61292187	1.68032181	20.2561907	6.77E-06	0.0004883	0.08173389		p, ca, c
SORD	-3.5645117	3.56451166	4.22221849	46.0019684	1.18E-11	4.54E-09	0.08452303		p, ca, c
AOC1	3.5450591	3.5450591	5.4895659	37.5423322	8.95E-10	1.93E-07	11.6726409	yes	
CTSG	3.52824121	3.52824121	1.94417698	24.6784405	6.77E-07	6.99E-05	11.5373598		
CXCL2	3.52646982	3.52646982	4.49083244	48.6840428	3.01E-12	1.42E-09	11.5232025	yes	p, ca, c
CCDC149	3.52521456	3.52521456	4.64409687	63.4716672	1.63E-15	1.54E-12	11.5131808		p
IDNK	3.51451311	3.51451311	2.18729638	27.5114144	1.56E-07	1.89E-05	11.4280957		p, ca
TRIM9	-3.4225215	3.42252149	1.70574069	12.8220921	0.00034255	0.01230456	0.09326493		
BTBD11	3.41694362	3.41694362	5.09358679	64.3110663	1.06E-15	1.23E-12	10.680769	yes	
ATOH8	3.4149563	3.4149563	2.88889305	29.5236596	5.52E-08	7.96E-06	10.6660663		p, ca, c
PTX3	3.40305343	3.40305343	3.51799313	37.0037964	1.18E-09	2.40E-07	10.5784286	yes	p, ca, c
LYPD3	3.39971026	3.39971026	1.98586867	22.7858891	1.81E-06	0.00015536	10.5539435	yes	
GNAT2	-3.3892268	3.3892268	0.65272366	10.229198	0.00138235	0.03474613	0.09544234		p, ca, c
CNTNAP3B	-3.3885136	3.38851363	2.70000552	24.6531171	6.86E-07	6.99E-05	0.09548953		
LOC441402	-3.3884962	3.38849617	2.70000552	24.6614843	6.83E-07	6.99E-05	0.09549069		
MAK	-3.363827	3.36382695	4.56175927	52.077911	5.33E-13	3.26E-10	0.09713756	yes	
TMEM176A	3.33816276	3.33816276	5.04432819	26.4920761	2.65E-07	3.02E-05	10.1131657		p, ca
DEFA4	3.31437623	3.31437623	2.2246405	22.9184076	1.69E-06	0.00014806	9.94779124		
FGF13	-3.2979354	3.29793544	0.64686969	9.46697872	0.00209204	0.04751073	0.10167695	yes	
ZSCAN18	-3.2948956	3.29489556	3.13938198	28.4525972	9.60E-08	1.25E-05	0.10189142		
CD59	-3.2925548	3.29255482	5.96567427	55.3608208	1.00E-13	8.01E-11	0.10205687		
MMP8	3.28987045	3.28987045	1.50416673	11.7023284	0.00062422	0.01917166	9.78024393	yes	p
CYP27A1	3.27714293	3.27714293	8.21049328	69.6057711	7.24E-17	1.07E-13	9.69434168	yes	p, ca, c
GRIK5	3.22522967	3.22522967	0.47733387	11.8382586	0.00058026	0.01814363	9.35170663		
HSD17B7	-3.2027781	3.20277805	1.01851346	12.795054	0.00034754	0.01239787	0.10860948	yes	p, ca
STARD8	-3.1820805	3.1820805	0.53612805	10.0070919	0.00155939	0.03826946	0.11017887	yes	
ASPHD2	-3.1768997	3.17689973	1.59822571	14.1653479	0.00016743	0.00700825	0.11057524	yes	
MYBPH	-3.1669184	3.16691837	1.01975112	11.8057615	0.00059048	0.01840763	0.11134291	yes	p, ca, c

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NLRP3	3.14168958	3.14168958	8.53425102	39.7885409	2.83E-10	7.04E-08	8.82557072	yes	p, ca, c
ZNF85	-3.1351905	3.13519051	0.53350961	9.60836637	0.00193693	0.04518485	0.1138187	yes	
F5	-3.1279901	3.1279901	6.12035291	58.8866157	1.67E-14	1.44E-11	0.11438818		p, ca, c
UAP1L1	3.12064362	3.12064362	3.57302305	31.7493701	1.75E-08	2.80E-06	8.69775832		
TSPAN13	-3.1172506	3.11725059	1.3442984	11.7236576	0.00061711	0.01906599	0.11524287	yes	
SLC2A4	-3.0769299	3.07692985	2.12271477	11.7620405	0.00060451	0.01878865	0.11850913		
RHOB	3.07369413	3.07369413	10.0875737	23.0283428	1.60E-06	0.00014163	8.41926407	yes	p, ca, c
KCNH3	-3.0580689	3.05806889	3.22300138	27.7186378	1.40E-07	1.71E-05	0.12006862		
CLEC12B	-3.0544479	3.05444794	2.23614637	15.5136409	8.19E-05	0.00395502	0.12037036		p, ca, c
LIPN	-3.0352261	3.03522608	3.53134657	24.8473844	6.21E-07	6.51E-05	0.12198485		p, ca, c
DNMBP	-3.0060019	3.00600192	3.00704561	26.250536	3.00E-07	3.38E-05	0.12448105	yes	
EMILIN2	3.00208473	3.00208473	7.01241995	53.9120722	2.10E-13	1.45E-10	8.01156856	yes	p, ca
SEMA4C	2.99462048	2.99462048	2.85775017	20.9006345	4.84E-06	0.00038102	7.97022516	yes	
HS3ST3B1	2.9884604	2.9884604	1.85020762	14.4145406	0.00014667	0.00642419	7.93626609	yes	p
ACOT11	-2.9740742	2.97407424	0.78063682	9.5903576	0.00195602	0.04527201	0.1272666		
TMEM176B	2.96440709	2.96440709	5.85544655	13.8170775	0.0002015	0.00817084	7.80504573		p, ca
KIT	-2.9612807	2.96128065	2.22429984	17.3651834	3.08E-05	0.00174756	0.1284002	yes	
MIR6824	2.94176348	2.94176348	4.54218475	39.9068275	2.66E-10	6.93E-08	7.68349913		p
SLC26A6	2.94176288	2.94176288	4.54218475	39.9017076	2.67E-10	6.93E-08	7.68349596		p
RGPD1	-2.9281067	2.92810672	1.63767162	11.1277099	0.00085048	0.02399126	0.13138689		
WDSUB1	2.92542428	2.92542428	1.56329373	14.1966066	0.00016467	0.00698112	7.5969708		p, ca, c
DOK4	-2.9170617	2.91706173	2.50586782	20.5177228	5.91E-06	0.00043809	0.13239663		
CNTNAP3	-2.9120212	2.91202125	5.40203263	48.0835283	4.08E-12	1.84E-09	0.13286		p
PNKD	2.90583485	2.90583485	5.96827516	37.4435006	9.41E-10	1.99E-07	7.49451359	yes	p, ca, c
CACNB4	2.89548563	2.89548563	5.62183656	30.7337217	2.96E-08	4.59E-06	7.44094385		p, ca
BPI	2.88672731	2.88672731	3.95874887	36.4674906	1.55E-09	3.07E-07	7.39590814		p
LOC149684	2.88672539	2.88672539	3.95874887	36.4456795	1.57E-09	3.07E-07	7.39589834		p
CDK5R1	-2.8827894	2.88278942	2.74733618	21.0935855	4.37E-06	0.00034927	0.13557946	yes	
KATNBL1	-2.8767459	2.87674593	4.91197221	44.8141032	2.17E-11	8.03E-09	0.1361486		
ISL2	-2.8648985	2.86489851	1.91123905	16.1546883	5.84E-05	0.00298512	0.13727126		
TMCC1	-2.8447534	2.84475336	6.56061122	50.8329704	1.01E-12	5.49E-10	0.1392015	yes	
CTSH	-2.823055	2.82305504	4.43106422	20.68314	5.42E-06	0.00041671	0.14131093		
RAB3A	-2.821632	2.82163195	2.1487907	12.6361199	0.00037836	0.01326176	0.14145039		p, ca, c
AZU1	2.81198266	2.81198266	2.26005009	19.7669457	8.75E-06	0.00059357	7.02248998		
ELANE	2.81079272	2.81079272	1.49536343	12.2747609	0.00045913	0.01534754	7.01670021		
NOL3	2.80693493	2.80693493	1.00852088	14.3948774	0.0001482	0.0064373	6.99796249		p, ca, c
DACT1	2.79427509	2.79427509	1.10705879	14.1915448	0.00016511	0.00698112	6.93682308		
MAP7	-2.7902447	2.7902447	2.25172856	11.0720044	0.00087641	0.02445699	0.1445615	yes	p, ca
SH3D21	-2.7713841	2.77138405	2.65992387	20.5657515	5.76E-06	0.00043809	0.14646379	yes	p, ca, c
ZBP1	-2.7559866	2.7559866	4.74712194	38.7459565	4.83E-10	1.09E-07	0.14803533	yes	p, ca, c
SOAT1	-2.71473	2.71472997	4.61927029	34.8374595	3.58E-09	6.53E-07	0.15232979		p, ca, c
CCDC19	-2.7067001	2.70670011	4.87289317	40.1079534	2.40E-10	6.56E-08	0.15318		
ANKRD22	2.69927966	2.69927966	4.64913861	39.3813734	3.49E-10	8.35E-08	6.49477551	yes	p, ca
LRRN1	-2.6954513	2.69545131	1.1850748	10.8248243	0.00100148	0.02714461	0.15437903		p, ca, c
SMCO4	-2.6939581	2.69395813	3.12641765	22.7698015	1.83E-06	0.00015539	0.15453889	yes	p
ARHGEF40	-2.6883648	2.68836478	7.00222544	54.5861119	1.49E-13	1.10E-10	0.1551392		p, ca, c
ALDH2	-2.680768	2.68076803	4.81394271	21.5499715	3.45E-06	0.00028402	0.15595827	yes	
SERPINB2	2.66064857	2.66064857	1.26271202	13.2390252	0.00027418	0.01046422	6.32317248	yes	p, ca, c
OSBPL6	2.64436472	2.64436472	0.44127527	10.5843459	0.00114049	0.02998166	6.25220344		p
COL18A1	-2.6385868	2.63858681	8.11911904	49.6924605	1.80E-12	9.33E-10	0.16058546		
SYNE2	-2.632165	2.63216503	6.46261096	42.265127	7.97E-11	2.51E-08	0.16130186	yes	
HOXA1	2.63155789	2.63155789	1.76422253	14.1281009	0.00017077	0.0070912	6.19694814		
GNG7	-2.6295082	2.62950816	4.45045812	30.1974409	3.90E-08	5.79E-06	0.16159919		
CYP4F12	-2.6078464	2.60784643	1.53222072	11.8588065	0.00057389	0.01802651	0.16404387		p, ca, c
NAAA	-2.6010984	2.60109841	4.91859837	36.4000794	1.61E-09	3.09E-07	0.16481296		

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DUSP6	2.60085784	2.60085784	8.49454432	39.3524156	3.54E-10	8.35E-08	6.06647237	yes	p
BEGAIN	-2.5911403	2.59114025	1.66571877	11.6744431	0.00063365	0.01922376	0.16595451		
DEFA3	2.58956494	2.58956494	3.18040903	20.8596222	4.94E-06	0.00038574	6.01917158		
ASPRV1	-2.5451883	2.54518833	4.50561417	26.6982783	2.38E-07	2.74E-05	0.17132548		p, ca, c
JUN	2.54438575	2.54438575	9.57184646	10.2847836	0.00134132	0.03387582	5.8335971		p
TBC1D8	-2.5316129	2.53161295	1.94547314	13.5028641	0.0002382	0.00947414	0.17294522	yes	
MTMR1	-2.5290001	2.52900009	3.89257606	26.8849553	2.16E-07	2.55E-05	0.17325873	yes	
TSPEAR	-2.5208638	2.52086383	2.04779059	13.5622889	0.00023078	0.00921416	0.1742386		
CDH2	2.52076099	2.52076099	4.47613057	29.3129107	6.16E-08	8.64E-06	5.73884732		p
JUP	-2.5153932	2.51539324	2.68293063	12.6548424	0.00037459	0.01322674	0.17490055	yes	
TTC9	-2.5082298	2.50822984	4.02750642	14.2017664	0.00016422	0.00698112	0.17577114		
ZNF552	-2.5081728	2.5081728	3.90796396	25.6005973	4.20E-07	4.54E-05	0.17577809	yes	
ARHGAP24	-2.4896777	2.48967766	1.9455956	12.0410646	0.00052041	0.0168825	0.17804605		
BCL9	-2.4645177	2.46451765	3.0386681	18.3941789	1.80E-05	0.00110981	0.18117833		
XRCC6BP1	-2.4609722	2.46097219	1.85735016	12.6010201	0.00038554	0.01338546	0.18162413		p, ca, c
ENTPD2	-2.4589912	2.45899117	1.43619228	10.443647	0.00123072	0.03194027	0.1818737		
DFNB31	-2.4476284	2.44762835	2.73903659	12.5452755	0.00039721	0.0136991	0.18331181		
VIPR1	2.42650793	2.42650793	2.50598182	16.1056619	5.99E-05	0.00304838	5.37590607		
PSRC1	-2.4247253	2.42472534	1.81401275	11.38957	0.00073858	0.02158112	0.18624514		
SLC31A1	-2.4244398	2.42443983	4.15095168	27.2426611	1.79E-07	2.14E-05	0.186282		p, ca, c
SEMA3C	-2.4234097	2.42340971	2.14180987	12.6265954	0.0003803	0.01326176	0.18641506	yes	
SMARCD3	2.41915492	2.41915492	6.46368629	32.5259964	1.18E-08	1.97E-06	5.34857628	yes	p, ca, c
MDM1	-2.412771	2.41277105	2.89733824	17.186323	3.39E-05	0.0019015	0.18779479	yes	p, ca, c
NRG1	2.40998509	2.40998509	1.65619728	12.8568894	0.00033624	0.01211978	5.31468833	yes	p, ca
SAP30	2.38837799	2.38837799	3.07054926	14.5527181	0.00013629	0.0060723	5.23568385	yes	p, ca, c
LETM2	2.36636205	2.36636205	3.65932338	18.6641168	1.56E-05	0.00098676	5.15639237		p
SAMD9L	-2.350689	2.35068905	5.74090186	28.7952283	8.04E-08	1.08E-05	0.19605237	yes	
NIPSNAP1	-2.327637	2.32763701	3.3106143	19.6600926	9.25E-06	0.0006196	0.19921014		
SPINT2	-2.3206058	2.32060577	5.05836623	23.4469982	1.28E-06	0.00012009	0.2001834		
HVCN1	-2.3200378	2.32003776	5.15642465	22.0160257	2.70E-06	0.00022455	0.20026223	yes	
NSUN7	-2.3169197	2.31691968	4.04149759	24.1253871	9.03E-07	9.01E-05	0.20069552	yes	p, ca, c
CD68	2.30791028	2.30791028	7.67455968	39.0727083	4.08E-10	9.42E-08	4.9516532	yes	p, ca, c
TIGD3	-2.3014761	2.30147613	2.87788071	12.6246359	0.0003807	0.01326176	0.20285544		p
GSTM4	-2.2987956	2.29879561	2.41249425	10.1465757	0.0014457	0.03590374	0.20323269		p, ca, c
CCDC170	-2.293683	2.29368302	2.73027834	15.651087	7.62E-05	0.00374743	0.20395418		p, ca, c
TRMT6	2.2902401	2.2902401	3.97450594	18.312662	1.87E-05	0.00115147	4.89137509		p
TJP2	-2.2867277	2.28672769	3.58679317	10.1570784	0.00143748	0.03578538	0.20493983	yes	p
GJB6	2.2859302	2.2859302	7.86672881	17.5617708	2.78E-05	0.00159514	4.87678443	yes	p, ca
C3	-2.2797945	2.27979453	1.74019793	9.62592965	0.00191849	0.04495683	0.20592708		p, ca
FAR2	-2.2574721	2.25747207	4.04553585	14.7385882	0.00012349	0.00556543	0.20913812	yes	p
CLTCL1	-2.2513284	2.25132842	2.29327417	10.4074369	0.00125509	0.0324495	0.21003062		p
ORM1	-2.2493302	2.24933016	3.91087773	15.2014294	9.66E-05	0.004539	0.21032173		p, ca, c
CX3CR1	-2.2457865	2.2457865	2.75308904	12.0176488	0.00052699	0.01704267	0.21083898	yes	p, ca, c
TENM1	-2.2430178	2.24301783	1.95615712	10.9728674	0.00092456	0.0255261	0.21124399		
ARG1	2.2361415	2.2361415	6.14322148	20.4043655	6.27E-06	0.00045507	4.71135323		p
KBTBD7	-2.2337876	2.2337876	2.6133416	9.45013734	0.00211133	0.04775108	0.21259984		p, ca, c
ITGA2B	2.22114793	2.22114793	2.93817721	13.7270105	0.00021139	0.00850568	4.66264286	yes	p, ca
GGT5	2.22067266	2.22067266	3.19918643	14.4314796	0.00014535	0.00639365	4.66110708	yes	p, ca, c
PDLIM1	-2.2190384	2.21903844	3.09230565	15.0488149	0.00010477	0.00487702	0.21478447		
SCARB1	2.20368741	2.20368741	3.119284	15.8900928	6.71E-05	0.00339936	4.60655235		p
TSHZ3	-2.2025247	2.20252466	4.18584685	20.0423726	7.57E-06	0.00053129	0.21725712		
ZNF468	-2.197632	2.19763196	2.93518125	15.2138	9.60E-05	0.00453668	0.21799516		
EGR1	2.19410382	2.19410382	8.25457847	9.68810724	0.00185464	0.04375697	4.57605318	yes	
MLLT4	-2.1802988	2.18029875	2.30357641	11.6060412	0.00065738	0.01972328	0.22063006		
CAST	-2.1753094	2.17530941	6.04487355	35.6242552	2.39E-09	4.52E-07	0.22139439		p, ca

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STK24	-2.1706957	2.17069567	6.50061663	35.4608572	2.60E-09	4.82E-07	0.22210355		p, ca, c
EFHC1	-2.1661477	2.16614766	1.79060218	9.94479906	0.00161304	0.03930755	0.22280482		p
SAMD3	2.16026213	2.16026213	1.90723495	9.70617622	0.0018365	0.04342752	4.46996065		
FAM134B	-2.1573812	2.15738116	2.08628803	11.1191195	0.00085442	0.02403732	0.22416281		p, ca
SLC26A8	2.1523491	2.1523491	5.39946904	28.8729579	7.73E-08	1.06E-05	4.44551051		p, ca, c
F12	-2.150295	2.150295	2.0536447	10.9814374	0.00092029	0.02547609	0.22526655		p, ca, c
NFXL1	-2.1497998	2.14979976	5.16217409	12.3999047	0.00042936	0.01451838	0.22534389		
CEP97	2.14615813	2.14615813	3.66587007	18.7767777	1.47E-05	0.00094748	4.42647455		p, ca, c
IDO1	-2.1431251	2.14312514	2.59952338	13.012144	0.00030948	0.01131227	0.22638886	yes	p, ca
DAPK1	-2.1413882	2.14138816	5.24943833	26.7973161	2.26E-07	2.64E-05	0.22666159	yes	
KYNU	-2.1394401	2.13944007	3.45714072	12.9155533	0.00032586	0.01178671	0.22696786	yes	
EDN1	2.1389963	2.1389963	1.73391282	10.1413634	0.00144979	0.03591947	4.40455511	yes	p, ca, c
HEY1	-2.1382379	2.13823791	4.33231708	11.5802887	0.00066655	0.01994067	0.22715707		
P2RY14	-2.1367202	2.1367202	3.88197257	15.5400823	8.08E-05	0.00391831	0.22739616	yes	p, ca, c
CCNJL	-2.1341839	2.13418389	6.41803034	33.1772153	8.41E-09	1.46E-06	0.22779628		p, ca, c
WLS	2.1333707	2.1333707	8.30276351	25.5768028	4.25E-07	4.55E-05	4.38741354	yes	p, ca, c
PI3	2.13020153	2.13020153	7.7473184	33.5731577	6.86E-09	1.21E-06	4.37778629	yes	p, ca, c
ACP5	-2.1239254	2.12392542	2.54371509	9.88435278	0.0016669	0.04014873	0.22942183	yes	
CEACAM21	-2.1201744	2.12017439	2.72786925	13.0295323	0.00030662	0.01128721	0.23001911	yes	p, ca, c
GADD45G	-2.1113033	2.11130334	3.13396254	11.0783439	0.00087342	0.02443922	0.23143784	yes	p, ca, c
CHI3L1	-2.1079177	2.10791768	7.34295377	22.5049978	2.10E-06	0.0001769	0.23198161	yes	p, ca, c
PAM	2.10310423	2.10310423	6.51810321	28.4819446	9.46E-08	1.24E-05	4.29632827	yes	
GJB2	2.10214999	2.10214999	2.97445836	12.1705998	0.00048549	0.01605045	4.29348749	yes	p, ca
PLSCR1	-2.0993085	2.09930849	5.92751893	16.5673805	4.70E-05	0.00247414	0.23337008	yes	p, ca, c
SORT1	-2.098617	2.098617	4.506668	23.6724574	1.14E-06	0.00010877	0.23348196	yes	
HP	2.09163002	2.09163002	3.20418206	13.3694693	0.00025575	0.00997479	4.26229373		p, ca, c
SLPI	2.08319141	2.08319141	7.05198437	33.9298453	5.71E-09	1.02E-06	4.2374355	yes	p, ca
HPSE	2.0810883	2.0810883	6.19300994	29.1727881	6.62E-08	9.16E-06	4.23126283	yes	p, ca, c
MPP7	-2.0779851	2.0779851	4.49546059	21.199674	4.14E-06	0.00033563	0.23684496	yes	
PRDM8	-2.071764	2.07176404	3.30849515	13.363623	0.00025655	0.00997479	0.23786847		p, ca, c
ANKRD28	-2.0486748	2.04867484	3.85906149	15.0575829	0.00010428	0.00487629	0.241706	yes	p
OSBPL1A	-2.0482863	2.04828633	3.48873822	13.2836354	0.00026773	0.01025585	0.24177109	yes	
YEATS2	2.04491168	2.04491168	4.978762	23.2949624	1.39E-06	0.00012544	4.12648009	yes	
CXCL1	2.03716155	2.03716155	8.76070647	23.3651888	1.34E-06	0.00012309	4.10437215	yes	p, ca, c
DNAJB5	-2.02971	2.02970998	2.12552341	9.86954184	0.00168037	0.04037953	0.2449043	yes	p, ca
CABIN1	-2.0253237	2.02532368	6.24231071	21.1466592	4.25E-06	0.00034237	0.24565003		
GPR160	-2.010938	2.01093804	5.73745762	18.4762174	1.72E-05	0.00106942	0.24811175		p, ca, c
FLVCR1	-2.0068051	2.00680515	3.36208677	15.6301319	7.70E-05	0.00375361	0.24882353		p, ca
CCP110	-1.9958763	1.99587631	3.86102747	18.5173383	1.68E-05	0.00105915	0.2507156		p, ca, c
ERCC1	-1.9924754	1.99247537	3.071034	13.2067551	0.00027894	0.01056823	0.25130733		p, ca, c
ZNF91	1.98847877	1.98847877	2.11637133	10.3455602	0.00129786	0.03318506	3.96818358		p
ZNF518B	-1.9884483	1.98844829	3.6331375	14.2083007	0.00016365	0.00698112	0.2520098		
KLHDC8B	-1.9820181	1.98201806	2.90996617	10.4006353	0.00125972	0.0324495	0.25313553		
MARCKS	-1.9619355	1.96193555	7.62362048	23.3279036	1.37E-06	0.00012439	0.25668385	yes	p, ca, c
PCGF5	-1.9597729	1.95977292	4.9921486	22.7936516	1.80E-06	0.00015536	0.25706892	yes	
RPAP3	-1.9563766	1.95637665	4.49045896	16.5460488	4.75E-05	0.00248949	0.2576748		
MFSD7	-1.9509393	1.95093934	2.50668846	9.70958995	0.00183309	0.04342752	0.25864777		p, ca, c
C10orf105	-1.947315	1.947315	4.2672343	18.5060486	1.69E-05	0.00105915	0.25929836		p, ca, c
SIGLEC10	-1.9357147	1.93571468	7.82362239	24.4580026	7.59E-07	7.65E-05	0.26139172		p, ca, c
FKBPL	-1.9313924	1.93139236	2.94189242	12.3131796	0.00044977	0.01511027	0.26217602		p, ca
PRDM1	-1.9227959	1.92279593	4.63614751	17.1357225	3.48E-05	0.00194234	0.26374288	yes	p, ca, c
B3GNT5	-1.9102305	1.91023052	7.93471535	28.7088882	8.41E-08	1.12E-05	0.26605003	yes	p, ca
CXorf65	-1.909998	1.90999801	2.50122027	10.4741576	0.00121056	0.03157493	0.26609291	yes	p, ca, c
PBXIP1	-1.9077471	1.90774712	8.27363197	30.2083989	3.88E-08	5.79E-06	0.26650839		p
ENPP2	1.90549307	1.90549307	2.38343907	9.61757059	0.00192725	0.04506021	3.74636916	yes	p

RPGR	-1.9034555	1.90345548	4.67611246	20.5257992	5.88E-06	0.00043809	0.26730237		p, ca, c
PPBP	1.90329235	1.90329235	3.01799285	13.3868183	0.0002534	0.00992654	3.74065873	yes	p
MBOAT2	-1.8982324	1.89823238	5.33596228	23.4941401	1.25E-06	0.00011824	0.26827186		p
SGMS1	-1.8974767	1.89747674	3.92110771	13.4197937	0.00024898	0.00980716	0.26841241		p, ca, c
TANC2	-1.8844674	1.88446739	4.06138001	13.2107475	0.00027835	0.01056823	0.27084373	yes	
UCP2	-1.8813604	1.8813604	4.89226516	20.4253692	6.20E-06	0.00045327	0.27142765	yes	
ZNF701	-1.8770107	1.87701071	3.0899531	10.8913426	0.00096615	0.02646327	0.27224723		
NFKBIA	1.87352156	1.87352156	11.412863	25.925085	3.55E-07	3.88E-05	3.6642592	yes	p, ca, c
REEP3	1.871709	1.871709	4.77556292	19.9837576	7.81E-06	0.00054052	3.65965841		p
CSF1R	-1.8710563	1.8710563	4.38481868	17.6658742	2.63E-05	0.00152704	0.2733732		
YBX3	-1.8675653	1.86756525	5.46224537	17.0654093	3.61E-05	0.00200482	0.27403551	yes	
OAS1	-1.8632841	1.86328408	2.75705283	11.2308473	0.00080449	0.02294341	0.27484991	yes	
EFCAB4A	1.84723282	1.84723282	3.09827148	9.77812639	0.001766	0.04214452	3.59809385		
LILRA3	-1.8444315	1.84443153	5.59366715	16.6197585	4.57E-05	0.00241902	0.27846511	yes	p, ca, c
TMEM216	-1.843846	1.84384604	2.99141266	10.0430195	0.00152926	0.03761915	0.27857814		p, ca, c
CA4	-1.8420317	1.84203173	6.39043143	17.6505536	2.65E-05	0.00153084	0.2789287		p, ca, c
DHRS12	-1.8377628	1.83776282	4.69114935	17.909619	2.32E-05	0.00138036	0.27975526		p, ca, c
MGME1	-1.8178603	1.81786027	3.11027557	11.8559362	0.00057478	0.01802651	0.28364134		
RILPL1	1.81614902	1.81614902	3.59349375	13.1540696	0.0002869	0.01071317	3.52139977	yes	p
MAPK14	1.81381527	1.81381527	8.48572194	29.3822922	5.94E-08	8.45E-06	3.51570806	yes	p, ca, c
MMP9	-1.8122636	1.8122636	7.47517155	25.067625	5.54E-07	5.86E-05	0.28474381	yes	p, ca, c
RELL1	-1.8037857	1.80378567	5.76811842	19.9648525	7.89E-06	0.00054228	0.28642202		
ZNF766	-1.8037505	1.8037505	3.39243858	11.8938516	0.0005632	0.01782479	0.28642901		p, ca, c
MAT2A	-1.8033407	1.80334067	5.46418103	17.6832742	2.61E-05	0.00152164	0.28651038		
VDR	-1.8032874	1.80328739	5.10070539	14.7379663	0.00012353	0.00556543	0.28652096	yes	p
GSN	-1.8024379	1.80243789	8.08739737	22.9105142	1.70E-06	0.00014806	0.28668973	yes	p
CCL3	1.80169225	1.80169225	5.03354373	10.8072969	0.00101101	0.02733145	3.4862892	yes	p, ca, c
FOSB	1.80022613	1.80022613	9.2017526	12.4933872	0.0004084	0.01399191	3.4827481		p, ca, c
HLA-DRA	-1.7996626	1.79966262	7.36533515	11.6639711	0.00063722	0.01922376	0.28724175	yes	p
SAMD9	-1.7986782	1.79867823	6.16949493	20.8300398	5.02E-06	0.00038882	0.28743781	yes	
LOC1019287	-1.7975119	1.79751194	4.02825458	14.1878806	0.00016543	0.00698112	0.28767027		
SP140	-1.797509	1.79750898	4.02825458	14.1792658	0.00016619	0.00698476	0.28767086	yes	p
CRTC3	-1.7965859	1.79658593	3.97598058	14.5277765	0.00013811	0.00610085	0.28785498		p
MAP1LC3A	-1.7889419	1.78894191	4.55735905	17.9010132	2.33E-05	0.00138036	0.28938421		
ZNF362	-1.7884345	1.78843454	3.63789168	11.0829221	0.00087126	0.02443922	0.28948599		
WHSC1L1	1.78608723	1.78608723	7.64175457	28.0616385	1.18E-07	1.47E-05	3.44878271		p
IL1RAP	-1.7838586	1.78385864	7.46519586	25.9695205	3.47E-07	3.83E-05	0.29040564		p, ca
LGALS9	-1.7759794	1.77597939	6.47284555	20.2262974	6.88E-06	0.00049257	0.29199602	yes	
SLC2A1	1.77317454	1.77317454	5.3181776	16.7323807	4.30E-05	0.00230309	3.41805247	yes	p, ca, c
MAP2K6	1.77172604	1.77172604	3.95332763	14.7332488	0.00012384	0.00556543	3.41462238	yes	
GIMAP4	-1.7672995	1.76729947	6.26462756	15.4024368	8.69E-05	0.00417529	0.2937581	yes	
FUZ	-1.7646273	1.76462735	4.21540309	15.8185107	6.97E-05	0.00351327	0.29430269		p
FAM105A	-1.7592379	1.75923789	4.14057418	14.9307638	0.00011153	0.00516869	0.29540417	yes	p, ca
UPB1	1.75806891	1.75806891	3.12482508	10.9102898	0.00095632	0.02633293	3.3824507		p, ca, c
SLC15A3	-1.7536369	1.75363689	6.99169428	18.8258674	1.43E-05	0.00092917	0.29655325		
IGF1R	-1.7457608	1.74576084	6.40745842	23.2520694	1.42E-06	0.00012716	0.29817664	yes	
PLAC8	1.74229968	1.74229968	3.60907072	12.0515622	0.00051749	0.01684032	3.34568049	yes	p, ca, c
WDFY2	-1.7411875	1.74118752	4.05305508	13.0437072	0.00030431	0.01125062	0.29912336		
STIM2	-1.7388112	1.7388112	5.14547537	19.562488	9.74E-06	0.0006479	0.29961646		
ZNF845	-1.738245	1.73824496	2.78884545	10.0463318	0.00152652	0.03761915	0.29973408		
APOBEC3G	-1.7381386	1.73813859	3.62640598	12.7878366	0.00034888	0.01240317	0.29975618	yes	
ZNF586	-1.7336168	1.7336168	5.00501842	18.1186811	2.08E-05	0.00125269	0.30069717		
GDPD3	-1.7209789	1.72097894	3.21777034	9.93500259	0.00162165	0.03933264	0.30334282		p
KLF4	1.71431065	1.71431065	7.30568831	15.3136212	9.11E-05	0.00435608	3.28139813	yes	p
PLCL1	1.70353976	1.70353976	4.04477594	13.8605088	0.00019689	0.00811088	3.25699105		

KIAA0355	-1.6991636	1.69916357	4.04287996	13.0802193	0.00029843	0.01110397	0.3079646		
TRIM27	-1.6927752	1.69277525	4.97720907	11.941788	0.00054889	0.01758643	0.30933131		p
FKBP5	-1.6817681	1.68176815	7.25307579	10.5838303	0.00114081	0.02998166	0.31170039	yes	
SYTL3	-1.6808703	1.68087027	5.37801095	18.7086389	1.52E-05	0.00097588	0.31189444		p, ca, c
SCLT1	-1.6793442	1.67934415	5.3526623	18.6805589	1.55E-05	0.00098429	0.31222454	yes	p, ca, c
SGPL1	-1.6725989	1.67259893	4.25359548	14.4065206	0.00014729	0.0064245	0.31368774		
CD14	1.67082736	1.67082736	9.51681176	20.8976364	4.84E-06	0.00038102	3.18397136	yes	p, ca, c
PRKDC	-1.668927	1.66892698	6.92090172	19.3804498	1.07E-05	0.00070814	0.31448716	yes	
CTNNA1	-1.6643636	1.66436355	5.67352884	14.0431036	0.00017867	0.00738945	0.3154835		
TPST1	1.65668476	1.65668476	6.13626687	14.7613267	0.00012201	0.00556543	3.15291169	yes	p, ca
MICAL1	-1.6531199	1.65311991	7.13548061	23.7536132	1.09E-06	0.00010723	0.31795182	yes	
LRP3	1.65053697	1.65053697	3.76651049	12.4491584	0.00041818	0.0141867	3.13950469		p
CSTF2T	-1.648521	1.64852102	3.5619545	10.5960702	0.00113328	0.02993539	0.31896698		p
KCNJ15	-1.6358894	1.63588942	7.66856475	19.1837985	1.19E-05	0.00078	0.32177197		p, ca, c
MAN1A1	-1.6334948	1.63349476	6.84494863	19.7062427	9.03E-06	0.00060874	0.32230651	yes	p
FAM188A	1.62548766	1.62548766	3.9115023	13.3242095	0.000262	0.01011091	3.08546443		p
PLXNA2	-1.6201931	1.62019308	3.98269936	9.9993149	0.00156598	0.03834077	0.32529193	yes	
EPHB4	1.60967331	1.60967331	6.41806357	17.3570395	3.10E-05	0.00174756	3.05182727		p
SCYL3	-1.6037262	1.60372615	3.72794609	12.0803964	0.00050955	0.01668648	0.32902608		
CD84	1.5997869	1.5997869	4.71302879	9.57527839	0.00197215	0.04547106	3.0309854		
TRPM6	-1.5991915	1.59919154	5.16207622	11.9438804	0.00054827	0.01758643	0.33006189		
ZNF200	-1.5972271	1.59722713	4.42040651	13.8250508	0.00020064	0.00817084	0.33051161		p, ca, c
KREMEN1	1.5935185	1.5935185	7.20425208	22.031077	2.68E-06	0.00022455	3.01784456	yes	p, ca, c
PROK2	1.58927096	1.58927096	9.50766522	19.0162426	1.30E-05	0.00084622	3.00897258		p, ca, c
MEF2C	-1.5890199	1.58901987	3.7170602	11.4897348	0.00069982	0.02066135	0.3323972	yes	
RFX2	-1.5826581	1.58265808	5.89277043	17.536067	2.82E-05	0.00160797	0.33386619	yes	p, ca
PHF13	-1.5808729	1.58087289	4.7440326	9.92910786	0.00162685	0.03936682	0.33427958		
DOK1	-1.5760637	1.57606373	4.047076	9.75055012	0.00179269	0.04268331	0.33539574	yes	
CPT1A	-1.5760404	1.57604037	4.29437299	11.2100681	0.00081355	0.02313818	0.33540117		
HSPA5	1.5758064	1.5758064	10.1072343	19.999077	7.75E-06	0.00053981	2.9810207		p, ca, c
CERS4	1.57522258	1.57522258	5.9192297	16.7676061	4.22E-05	0.00227777	2.97981461		p
TSPAN2	-1.5733426	1.57334261	5.97757241	16.5176045	4.82E-05	0.00251442	0.33602894		p, ca, c
HEATR5A	-1.5688247	1.56882467	4.54493513	12.2720594	0.00045979	0.01534754	0.3370829		
DGAT2	-1.5686899	1.56868987	8.11220689	19.9462267	7.97E-06	0.00054398	0.33711439	yes	p, ca, c
DDIT4	-1.5679667	1.5679667	7.80652409	18.2367466	1.95E-05	0.00118428	0.33728342	yes	p, ca, c
ZNF281	1.56366779	1.56366779	6.9383263	10.4506534	0.00122606	0.03189909	2.95604409		p, ca
IL1R2	1.56233776	1.56233776	9.37148031	13.7401961	0.00020991	0.00847904	2.95332015	yes	p, ca, c
RALGPS2	-1.557635	1.55763501	4.38097072	13.4426042	0.00024597	0.00974601	0.3397075		
POLM	-1.5537832	1.55378319	4.91708641	11.3267871	0.00076397	0.02215299	0.34061569		p, ca
XBP1	1.54503389	1.54503389	6.04064748	10.4012289	0.00125931	0.0324495	2.91810924		p, ca
LPCAT4	-1.5415804	1.54158036	3.9095411	11.6690831	0.00063547	0.01922376	0.34350896		p, ca
ARHGEF11	-1.5404186	1.54041865	6.02999359	17.8240958	2.42E-05	0.00142913	0.34378568		
DSE	-1.5333635	1.53336355	4.72558758	13.1774644	0.00028334	0.01066013	0.34547099	yes	p, ca, c
LAP3	-1.531049	1.53104895	4.71835201	10.6715994	0.00108793	0.02903291	0.34602569	yes	p, ca, c
IPO8	-1.5281342	1.52813418	4.12023767	11.4907318	0.00069944	0.02066135	0.34672549		
CAMK1D	-1.5215859	1.52158593	5.61506586	14.1343136	0.00017021	0.0070912	0.34830282	yes	p, ca, c
PPTC7	-1.5213249	1.52132491	5.85143207	13.8188354	0.00020131	0.00817084	0.34836585	yes	p, ca, c
APOL2	-1.5152183	1.51521829	6.21108345	14.2412901	0.0001608	0.00692655	0.34984353	yes	
TAGLN2	-1.5148059	1.51480595	10.5039153	18.2792566	1.91E-05	0.00116495	0.34994353		p, ca, c
CUEDC1	-1.5146051	1.51460507	4.25624454	11.259117	0.00079233	0.02265886	0.34999226		p, ca, c
ARHGAP15	-1.5122751	1.51227511	6.60799917	15.7742725	7.14E-05	0.0035618	0.35055796		p
LOC1019283	-1.5122739	1.51227395	6.60799917	15.7832841	7.10E-05	0.0035618	0.35055824		
GRK5	-1.5090645	1.50906445	4.27471243	11.9239887	0.00055416	0.01770063	0.35133898		
IL4R	-1.495562	1.49556202	8.10318479	11.6793454	0.00063198	0.01922376	0.35464266	yes	p, ca, c
CHPT1	1.49152214	1.49152214	5.99884319	16.7631628	4.23E-05	0.00227777	2.81185487		p, ca

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PDXK	1.4910821	1.4910821	5.79083027	14.3254447	0.00015377	0.00665129	2.81099736	yes	
VEGFA	-1.4900702	1.49007023	4.80712853	9.38894782	0.00218297	0.04915718	0.35599522	yes	p, ca, c
SERPINB8	1.48630787	1.48630787	4.61100161	11.74722	0.00060934	0.01888232	2.80171045		p, ca, c
CDC42EP4	-1.4705734	1.47057342	3.5422609	9.48248718	0.00207443	0.04722502	0.36083885		
NQO2	-1.4691767	1.46917671	5.72596076	11.4876886	0.00070059	0.02066135	0.36118836		p, ca, c
NUDT16	-1.4659702	1.46597024	4.94557519	12.9904729	0.00031308	0.0114038	0.36199201	yes	
SESN2	-1.4592305	1.45923046	7.68434912	9.59275923	0.00195346	0.04527201	0.36368707	yes	p, ca, c
HEXDC	-1.45538	1.45538002	4.02795761	10.3744297	0.00127773	0.03283187	0.36465902		
MTMR12	-1.4548067	1.45480668	4.20164838	10.8933315	0.00096511	0.02646327	0.36480397		
CCDC125	-1.4527292	1.45272925	4.87094591	12.4773623	0.00041191	0.01405197	0.36532965		p, ca, c
DYNLT3	1.44523125	1.44523125	3.88887312	9.94014942	0.00161712	0.03931468	2.72306469		p, ca
IRF2BPL	-1.4411461	1.44114614	5.97258986	15.2689545	9.32E-05	0.00443985	0.36827461		p
TAF4	-1.4390965	1.43909649	4.26938926	11.0345362	0.0008943	0.02482282	0.3687982		
FGD4	-1.4328529	1.43285288	5.47834949	9.65961686	0.00188363	0.04434003	0.37039772		p, ca, c
TNNI2	-1.4281579	1.42815792	3.95526596	9.57218135	0.00197548	0.04547106	0.37160507	yes	p
AMPD3	-1.4272737	1.42727373	5.06992004	13.1701233	0.00028445	0.01066013	0.37183288	yes	p, ca, c
CAND1.11	-1.4272733	1.42727333	5.06992004	13.1744071	0.0002838	0.01066013	0.37183299		p, ca, c
MPEG1	-1.4227759	1.42277589	6.8644225	12.0551288	0.0005165	0.01684032	0.37299394	yes	p, ca, c
UBASH3B	-1.4212901	1.42129011	4.96134682	11.7147489	0.00062007	0.01910063	0.37337827	yes	p, ca, c
TMEM165	-1.4207208	1.42072083	4.55382783	11.5712763	0.00066978	0.01997997	0.37352564	yes	p
DAPP1	-1.4099901	1.40999005	5.94371244	13.2993866	0.00026549	0.01020771	0.37631428	yes	p, ca, c
SLK	-1.4023113	1.40231126	6.68361195	14.7567957	0.00012231	0.00556543	0.37832257		
MRVI1	-1.4010337	1.4010337	5.94352436	11.0592705	0.00088245	0.02455951	0.37865773		p, ca
CTRL	-1.3795188	1.37951884	3.83401742	9.36534712	0.00221126	0.04957905	0.38434696		
WDFY4	1.37713417	1.37713417	7.71564621	16.2332451	5.60E-05	0.00287804	2.59751876	yes	
CLEC7A	-1.3771101	1.37711011	8.65505222	12.2592233	0.00046296	0.01540395	0.3849892	yes	p, ca, c
HMGN2	-1.3749196	1.37491955	7.869019	15.2109564	9.61E-05	0.00453668	0.38557421		p
KLF6	1.36250302	1.36250302	10.1837387	13.8387826	0.0019918	0.00817084	2.57130904	yes	p, ca, c
MANBA	-1.3578031	1.3578031	5.88782209	14.7017449	0.00012593	0.00563482	0.39017599		p
NTNG2	-1.3544391	1.35443907	6.30899687	12.8120842	0.00034439	0.01232789	0.39108685	yes	
CAMKK1	-1.3515656	1.35156562	5.45260784	12.692823	0.00036706	0.01300501	0.39186656	yes	p
UBE2E3	1.35146193	1.35146193	5.25044397	12.20099	0.00047764	0.01584153	2.55170567	yes	
THOC5	-1.3350249	1.33502495	6.26725018	13.4166053	0.00024941	0.00980716	0.39638521		
SLC8B1	-1.3281802	1.32818022	5.19044228	11.6628656	0.0006376	0.01922376	0.39827029		
LDHA	-1.3218649	1.3218649	7.46717982	9.37915095	0.00219467	0.04931361	0.40001752		
CEACAM1	-1.3157609	1.3157609	4.83197507	10.8269651	0.00100032	0.02714461	0.40171357	yes	p, ca
ERGIC1	-1.3145175	1.31451751	8.95952236	11.9169468	0.00055626	0.01771316	0.40205994		p, ca, c
ZNF776	-1.3105474	1.31054743	4.99546011	10.8659391	0.00097949	0.02675814	0.40316787		
CD74	-1.3026136	1.30261363	8.48161205	10.7777308	0.00102729	0.02762759	0.40539111	yes	p
JADE1	-1.3001939	1.30019388	5.9815732	10.3603502	0.00128751	0.03300153	0.40607162	yes	p, ca, c
NUCB2	1.29874327	1.29874327	4.40066674	9.46339382	0.00209613	0.04751073	2.46014486		p
FAM107B	-1.2929754	1.29297541	7.395983	13.5937148	0.00022694	0.00909616	0.40810848		p, ca, c
HDAC7	-1.2926604	1.29266042	6.95699725	13.0422655	0.00030454	0.01125062	0.40819759		p, ca, c
GALC	-1.2900859	1.29008589	5.55025455	10.3001102	0.00133022	0.03368059	0.40892668		p
ADAMTSL4	-1.283818	1.28381799	5.90432826	13.0212195	0.00030798	0.01129736	0.41070716	yes	p, ca, c
CDK14	1.28152619	1.28152619	5.52149231	11.2871188	0.00078047	0.02238302	2.43096006		p, ca
TRAFD1	-1.2631931	1.2631931	6.49889923	11.2869756	0.00078053	0.02238302	0.41662084	yes	p
UBA7	-1.2615163	1.26151628	6.19223428	12.1195195	0.00049897	0.01639172	0.41710535	yes	
MIR5193	-1.2615162	1.26151622	6.19223428	12.1198825	0.00049887	0.01639172	0.41710537	yes	
P4HA1	-1.2605974	1.26059742	4.75175392	9.72837371	0.00181445	0.04310252	0.41737109		
DDX58	-1.2583029	1.2583029	6.01263671	12.4730952	0.00041286	0.01405197	0.41803542	yes	p, ca, c
ERO1L	-1.2581207	1.25812071	6.72330672	11.5314435	0.00068429	0.02035415	0.41808822		p, ca, c
PLEC	-1.2507766	1.25077664	6.24166056	11.4440958	0.00071722	0.02103224	0.42022193		p, ca, c
METTL9	1.24848514	1.24848514	7.35283811	14.5325679	0.00013776	0.00610085	2.37591816		p, ca, c
CCNG2	-1.2337979	1.23379792	7.86629457	13.3329913	0.00026078	0.01010122	0.42519663	yes	p

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TRANK1	-1.23369	1.23368998	7.65513369	10.1594408	0.00143564	0.03578538	0.42522845	yes	p, ca, c
MARCKSL1	-1.2313211	1.2313211	5.89373562	11.1869032	0.00082377	0.02336483	0.42592724	yes	
NBN	-1.2295019	1.22950187	6.04923574	11.4591243	0.00071144	0.02092193	0.42646467	yes	p, ca, c
FCAR	1.2274751	1.2274751	8.3630514	11.350899	0.00075411	0.02192847	2.34156826	yes	p, ca, c
FKBP15	-1.22388	1.22388003	5.75952639	10.6911191	0.00107651	0.02880221	0.42812974		p, ca, c
TLK1	1.21967423	1.21967423	6.0459498	10.0997914	0.00148286	0.03665138	2.32894122		p, ca, c
S100P	1.21856764	1.21856764	9.36172066	9.78007144	0.00176413	0.04214452	2.32715554		p, ca, c
C14orf159	-1.2150881	1.21508805	6.69176385	10.6266157	0.00111472	0.02959555	0.43074679	yes	p, ca, c
KDM1B	-1.2029526	1.20295262	5.35850701	9.58839587	0.00195811	0.04527201	0.43438536		p
LYPLA1	-1.2021367	1.20213675	4.85896988	9.39162673	0.00217979	0.04915718	0.43463108		
PSIP1	-1.2006748	1.20067483	5.41277738	9.51343933	0.00203973	0.04653711	0.43507173	yes	
PPIF	1.19182039	1.19182039	7.61802874	12.3344784	0.00044467	0.01498734	2.28440807	yes	p, ca, c
TCP11L2	-1.1826047	1.18260468	5.89884564	11.2978949	0.00077595	0.02237539	0.44055539		p, ca, c
ANKRD13A	-1.1812882	1.18128817	8.66551999	12.6312307	0.00037936	0.01326176	0.44095759	yes	p, ca, c
KRT23	1.18045992	1.18045992	7.34206899	10.6217158	0.00111767	0.02959837	2.2664902		p, ca
IFNAR2	-1.1737003	1.1737003	6.30735929	10.2090983	0.00139749	0.03495758	0.44328293		p, ca, c
HMOX1	1.17292336	1.17292336	5.79319654	9.52750477	0.00202415	0.04635143	2.25468104	yes	p, ca, c
VPS35	-1.1691657	1.16916567	5.71112111	9.60353785	0.00194203	0.04520224	0.44467843		
NUAK2	-1.1619309	1.16193088	7.99535053	11.8988196	0.0005617	0.01782479	0.44691399		p, ca, c
ATHL1	-1.1600821	1.1600821	9.17589643	11.1814316	0.0008262	0.02336998	0.44748707	yes	p, ca, c
IRAK4	-1.1559265	1.1559265	5.76344633	10.3142875	0.00132004	0.03363003	0.44877789		p
NECAP1	1.13330417	1.13330417	6.6299669	9.34660119	0.00223399	0.0499808	2.19360562		p, ca, c
CANX	1.13015026	1.13015026	7.44270155	10.3119062	0.00132175	0.03363003	2.18881536	yes	p, ca, c
TSPO	1.12418521	1.12418521	7.98952977	11.659141	0.00063888	0.01922376	2.17978404	yes	p, ca, c
FAS	-1.1166523	1.1166523	7.03608364	11.3857655	0.00074009	0.02158112	0.46116269	yes	p, ca
MAN2A2	1.11656072	1.11656072	8.65829925	10.8581041	0.00098364	0.02680106	2.1682945	yes	p, ca
CDC42EP3	1.08634434	1.08634434	7.6902044	10.6267005	0.00111466	0.02959555	2.12335316	yes	p, ca, c
PACSIN2	-1.084765	1.08476501	7.82763072	10.7531463	0.00104102	0.02792467	0.47146905		p, ca, c
HMGB2	1.07151086	1.07151086	8.15488309	10.5508029	0.00116138	0.03044507	2.10163314	yes	
ABHD5	1.06858288	1.06858288	8.44312507	9.52481388	0.00202712	0.04635143	2.09737216		p, ca, c
PRKAR1A	-1.0568046	1.05680461	8.7884921	9.55774447	0.00199108	0.04572867	0.48069556		p, ca, c
C4orf3	-1.0541629	1.05416288	7.04599208	9.92262707	0.00163259	0.03941381	0.48157657	yes	
CTSA	1.05326746	1.05326746	7.36444373	9.78752668	0.001757	0.04212328	2.07522456		p, ca, c
STXBP5	1.0511621	1.0511621	8.05474751	9.99125901	0.00157285	0.03841826	2.07219835		p, ca, c
HIST2H2BE	1.02082195	1.02082195	8.52758132	9.64358941	0.00190014	0.04462739	2.02907467	yes	p

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Table E4.
Significantly enriched Gene ontology (GO) biological process -terms of (A) 153 genes with increased transcription (FC ≥2; FDR ≤0.05) and (B) 311 genes with decreased transcription in patient compared to control in unstimulated granulocytes. GO-terms were identified using Gene Ontology analysis in DAVID Bioinformatics Resources 6.8 (https://david.ncifcrf.gov).

A) Increased transcription

Biological Process Gene Ontology Term	Count	P-Value
GO:0032496~response to lipopolysaccharide	12	1.01E-07
GO:0006954~inflammatory response	14	1.37E-05
GO:0071222~cellular response to lipopolysaccharide	8	3.88E-05
GO:0031663~lipopolysaccharide-mediated signaling pathway	5	1.28E-04
GO:0006955~immune response	13	1.74E-04
GO:0042493~response to drug	11	1.97E-04
GO:0035994~response to muscle stretch	4	2.75E-04
GO:0070098~chemokine-mediated signaling pathway	6	2.84E-04
GO:0031670~cellular response to nutrient	3	3.92E-04
GO:0090023~positive regulation of neutrophil chemotaxis	4	7.30E-04
GO:0071353~cellular response to interleukin-4	4	9.48E-04
GO:0042742~defense response to bacterium	7	0.00121718
GO:0050832~defense response to fungus	4	0.00134638
GO:0060326~cell chemotaxis	5	0.00195326
GO:0030593~neutrophil chemotaxis	5	0.00206628
GO:0090090~negative regulation of canonical Wnt signaling pathway	7	0.00220395
GO:0007568~aging	7	0.00234284
GO:0001525~angiogenesis	8	0.00237332
GO:0002931~response to ischemia	4	0.00242338
GO:0045892~negative regulation of transcription, DNA-templated	12	0.00261553
GO:0006935~chemotaxis	6	0.00324875
GO:0007154~cell communication	4	0.00363746
GO:0043066~negative regulation of apoptotic process	11	0.00415548
GO:0001878~response to yeast	3	0.00485937
GO:0019731~antibacterial humoral response	4	0.00551126
GO:0010595~positive regulation of endothelial cell migration	4	0.00624263
GO:0044130~negative regulation of growth of symbiont in host	3	0.00735728
GO:0071277~cellular response to calcium ion	4	0.00831495
GO:0045087~innate immune response	10	0.00875735
GO:0001935~endothelial cell proliferation	3	0.00928116
GO:0050829~defense response to Gram-negative bacterium	4	0.01023097
GO:0070301~cellular response to hydrogen peroxide	4	0.01127708
GO:0071346~cellular response to interferon-gamma	4	0.01127708
GO:0000187~activation of MAPK activity	5	0.01145763
GO:0070373~negative regulation of ERK1 and ERK2 cascade	4	0.01182244
GO:0048661~positive regulation of smooth muscle cell proliferation	4	0.01295806
GO:0000122~negative regulation of transcription from RNA polymerase I	13	0.01481975
GO:0035924~cellular response to vascular endothelial growth factor stim	3	0.01494494
GO:0051602~response to electrical stimulus	3	0.01621735
GO:0050725~positive regulation of interleukin-1 beta biosynthetic proce	2	0.01625121
GO:0010951~negative regulation of endopeptidase activity	5	0.01729579
GO:0006952~defense response	4	0.01740994
GO:0030335~positive regulation of cell migration	6	0.01751633
GO:0051899~membrane depolarization	3	0.01753439
GO:0051090~regulation of sequence-specific DNA binding transcription f	3	0.01753439
GO:0032088~negative regulation of NF-kappaB transcription factor activi	4	0.0202907
GO:0071347~cellular response to interleukin-1	4	0.0202907
GO:0043392~negative regulation of DNA binding	3	0.02174534
GO:0042149~cellular response to glucose starvation	3	0.02323299
GO:0022617~extracellular matrix disassembly	4	0.02423843
GO:0045893~positive regulation of transcription, DNA-templated	10	0.02535663
GO:0045765~regulation of angiogenesis	3	0.0263297
GO:0045944~positive regulation of transcription from RNA polymerase II	15	0.02938143
GO:0015758~glucose transport	3	0.02958333
GO:0051897~positive regulation of protein kinase B signaling	4	0.03135549
GO:0045415~negative regulation of interleukin-8 biosynthetic process	2	0.03224022
GO:0022602~ovulation cycle process	2	0.03224022
GO:0042345~regulation of NF-kappaB import into nucleus	2	0.03224022
GO:0019730~antimicrobial humoral response	2	0.03224022
GO:0050830~defense response to Gram-positive bacterium	4	0.03231406
GO:0071504~cellular response to heparin	2	0.04013771
GO:2001199~negative regulation of dendritic cell differentiation	2	0.04013771
GO:0071332~cellular response to fructose stimulus	2	0.04013771
GO:0032570~response to progesterone	3	0.040228
GO:0006821~chloride transport	3	0.04212369
GO:0042045~epithelial fluid transport	2	0.04797122
GO:2000553~positive regulation of T-helper 2 cell cytokine production	2	0.04797122
GO:0010042~response to manganese ion	2	0.04797122
GO:0043525~positive regulation of neuron apoptotic process	3	0.04800578
GO:0045429~positive regulation of nitric oxide biosynthetic process	3	0.04800578

B) Decreased transcription

Term	Count	PValue
GO:0010628~positive regulation of gene expression	14	0.000290192
GO:0098609~cell-cell adhesion	13	1.33E-03
GO:0030224~monocyte differentiation	4	2.27E-03
GO:0021795~cerebral cortex cell migration	3	0.008362569
GO:0006631~fatty acid metabolic process	5	9.19E-03
GO:0007163~establishment or maintenance of cell polarity	4	0.010595037
GO:0046323~glucose import	3	1.49E-02
GO:0046777~protein autophosphorylation	8	0.019870273
GO:0005975~carbohydrate metabolic process	8	0.021039622
GO:0006006~glucose metabolic process	5	0.021659504
GO:0032720~negative regulation of tumor necrosis factor production	4	2.20E-02
GO:0032793~positive regulation of CREB transcription factor activity	3	0.022914303
GO:0006953~acute-phase response	4	0.023611996
GO:0030335~positive regulation of cell migration	8	0.027475285
GO:0001541~ovarian follicle development	4	0.028656848
GO:0030225~macrophage differentiation	3	3.24E-02
GO:0045087~innate immune response	13	0.041732638
GO:0060672~epithelial cell morphogenesis involved in placental branching	2	0.046776546
GO:0031334~positive regulation of protein complex assembly	3	4.69E-02

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Table E5. Phenotypic comparison of patients with different *CEBPE* mutations and/or SGD. NA= Not available, NR= Not reported. In patients 3-4, 6, 8-9 variably the differentiation of neutrophils, eosinophils and monocytes from each other impaired due to abnormal morphology, aberrant scatter in flow cytometry as well as abnormal surface marker expression. #of the 4 CEBPE isoforms, p14 and p27 are unable to activate transcription, these mutations lead to truncated p30 and p32 which are unable to initiate transcription. **In LPS and IFNγ-treated monocytes IL8 mRNA levels increased. Abnormally large cytoplasmic monocyte granules, enolase 2 activity and cell-surface marker expression of monocytes impaired. #Patient's elder brother had had similar skin abscesses and died of severe enterocolitis at 10 y without genetic diagnosis.

Patient	*CEBPE*	Inheritance	Sex	Age at onset	Age at diagnosis	Infections	Pathogens	Auto-inflammatory features	Neutrophil nuclei	Neutrophil specific granules	Chemotaxis	Eosinophils	Neutrophil/monocyte count	RNA levels in primary cells	Alkaline phosphatase activity/transactivating efficiency by luciferase CSFR transfection assay	Ref
Patients with truncating *CEBPE* mutations																
2.	**Homozygous p.(Gly171Alafs*34)#**	AR	F	Infancy	7 y	Superficial and deep abscesses of trunk, extremities and buccal region, otitis, pneumonia, mastoiditis, eczema	*Staphylococcus aureus* *Pseudomonas aeruginosa*	NR	Mostly bilobed with nuclear clefts, pockets	Very few elongated, less dense secondary granules with reduced lactoferrin and transcobalamin I content	Reduced by 50%	Absent	Mildly reduced/ Increased	MPO normal CAMP↓ LTF↓ DEFA1↓ DEFA3 ↓ BPI absent**	Severely reduced/ Reduced	Komiyama *et al.* 1979 (1) Ambruso *et al.* 1984 (2) Sakura *et al.* 1993 (3) Tamura *et al.* 1994 (4) Gombart *et al.* 2001 (5) Shiohara *et al.* 2004 (6) Wada *et al.* 2015 (7)
3.	Homozygous p.(Asp84Serfs*119)#	AR	M	Infancy	6 y	Skin infections, adenitis, recurrent bronchopneumonia with lung abscess, severe scalp infections, candidiasis	Staphylococci *Proteus mirabilis*	NR	Bilobed	Numerous elongated, small sacs instead of specific granules, with reduced lactoferrin and transcobalamin I content	Reduced	Reduced, lack normal eosinophilic granules and indistinguishable from neutrophils	Normal/ Normal	LTF absent	Absent/ Reduced	Breton-Gorius *et al.* 1980 (8) Gallin *et al.* 1982 (9) Ganz *et al.* 1988 (10) Lomax *et al.* 1989 (11) Rosenberg *et al.* 1993 (12) Lekstrom-Himes *et al.* 1999 (13)
4.	**Homozygous p.(Gly171Alafs*34)#**	AR	F	Infancy	7 y	Recurrent otitis media, skin abscesses, pneumonia and pulmonary abscess	*Staphylococcus aureus*	NR	Mostly bilobed	Severely reduced secondary granule proteins by flow cytometry	NA	NA	Normal/ Normal	NA	NA/ NA	Shigemura *et al.* 2014 (14)
5.	Homozygous p.(Ser248_Arg249del)	AR	F	Infancy	55 y	Recurrent skin infections, ulcerative skin abscesses with delayed healing, otitis media#	NA	NR	Bilobed	Absent, no lactoferrin	NA	Absent	Reduced/ Increased	NA (In transfected cells LCN2, LTF absent)	Absent/ Reduced	Wada *et al.* 2015 (7)
6.	Homozygous p.(Cys180Alafs*5)	AR	M	NA	55 y	NA	NA	NR	NA	NA	NA	NA	NA	NA	NA/NA	Stray-Pedersen *et al.* 2018 (15)
Patients with missense *CEBPE* mutations																
7.	Heterozygous p.(Val218Ala)	AD	M	Infancy	14 y	Recurrent staphylococcal respiratory infections. Indolent, slowly healing superficial skin infections abating by adulthood	Staphylococci	NR	Mostly bilobed	Minute, elongated, and abnormally structured specific granules with severely reduced content ("vesicles"), in normal numbers.	Reduced by 50%	Mononuclear, with normal granules	Normal/ Normal	MMP8↓ MMP2↓ LTF ↓ TCN1 ↓ CRISP3↓ GFI1 ↓ DEFA1↓ DEFA4 ↓ IL8 ↓ PU.1 ↑ CD18 ↑ CD11b ↑ EGR1 ↑ BPI ↑ NCF1 ↑ CYBB ↑ PGLYRP1 ↑ asf/ Table 1	Absent/ Increased	Strauss *et al.* 1974 (16) Boxer *et al.* 1982 (17) Ganz *et al.* 1988 (10) Lomax *et al.* 1989 (11) Parmley *et al* . 1983 (18) Johnston *et al.* 1992 (19) Khanna-Kupta *et al.* 2007 (20)
8.	Heterozygous p.(Val218Ala)	AD	F	Infancy	3 mo	Life-threatening orbitocellulitis and sepsis	NA	NR	Bilobed	Reduction in number	Normal	Eosinophilic granules lack ALOX15, PRG3 and LPPL	NA	LTF absent BPI ↓ LCN2 ↓ ALOX15 absent OLF4 absent / Table 1-2	NA	Serwas *et al* . 2018 (21)
9.	Heterozygous p.(Val218Ala)	AD	F	Childhood	NA	Frequent bacterial infections during childhood										
10.-13.	Heterozygous p.(Arg219His)	AR	F	Infancy	See text	Severe recurrent tongue abscesses Crater-like ulcers in buccal mucosa Easily acquired purulent wounds with delayed wound healing Paronychia Rheumatic fever Subacute bacterial endocarditis Gluteal and submandibular abscesses	Staphylococci Streptococci	Prominent, with periodic fever and abdominal pain	Hyposegmented 45-60% Bilobed 20-50%	Patient neutrophils presented both primary and secondary granules and no difference was observed in comparison to the healthy control subject. Also basophil granularity was normal.	Reduced	Hyposegmented nuclei, normal granules.	Normal/ Normal	Widely dysregulted RNA expression with 464 significantly dysregulated genes (FC ≥2 or ≤0.5; FDR ≤0.05)	NA	Murros *et al.* 1974 (22) Repo *et al.* 1979 (23) Pasanen *et al* . 1987 (24) This report
SGD patients with unknown causes																
1.	NA	NA	M	NA	43 y	Recurrent bacterial infections		NR	Mostly bilobed	Absent	NA	NA	NA/ NA	NA	Normal/NA	Spitznagel *et al.* 1972 (25)
14.	NA	NA	F	Infancy	5	Ear and throat infections with mastoiditis and stomatitis Diarrhea Oral lesions Necrotic lesions of nostrils, fingers and perineal area Lung abscess	*Pseudomonas* *Klebsiella* *Proteus* *Eschericia coli* Pneumococcus	NR	Multiple small nuclear lobes or notched nuclei	Absent	NA	Occasional eosinophilia	Severely reduced/ increased	NA	Severely reduced/NA	Parmley *et al.* 1975 (26)

Table E6.
470 differentially transcribed (Fold change >2 (absLog2FC>1) and FDR<0.05) genes between patients and controls in becterial stimulated granulocytes. 183 of these were identified to be IFN-related (Interferome v.2.01). Overap with ChIP-seq peaks mapped to nearby genes within ±50 kb range is shown as following: p= patients spesific binding; p, ca= binding in patient and carrier cells; p, ca, and c= binding in patient, carrier and control cells.

	logFC	ABSFC	logCPM	LR	PValue	FDR	FC	IFN-related	Overlap with ChiP-seq peaks
ACP5	-7.7583996	7.75839964	3.34994531	43.6612848	3.90E-11	3.42E-09	0.00461837	yes	
ACPP	-2.1310008	2.13100084	3.08740953	7.41062355	0.00648398	0.04427734	0.22829943	yes	p, ca, c
ACSL4	-1.0256292	1.02562922	4.8901037	8.8458186	0.00293761	0.02423076	0.49119602	yes	p, ca, c
ACSL5	2.88243126	2.88243126	3.17328464	11.6363707	0.00064675	0.00736969	7.37391742		p
ADORA3	-1.53164	1.53164004	5.22046306	8.13032496	0.00435309	0.03302421	0.34588395	yes	p, ca, c
AKR1C3	5.61294506	5.61294506	3.88892314	41.8056683	1.01E-10	8.25E-09	48.9400972	yes	
ALDH2	-4.0920874	4.09208739	2.64541665	8.77901139	0.00304716	0.02489046	0.05863527	yes	
ALKBH2	-4.5528382	4.55283819	2.48813816	15.169657	9.83E-05	0.0015788	0.04260486		
ALOX15	-5.8838745	5.88387449	2.35759833	15.5175211	8.17E-05	0.00135769	0.01693469		
ANKRD22	1.6776355	1.6776355	6.43861534	15.7413613	7.26E-05	0.00124382	3.19903217	yes	p, ca
ANXA3	-1.0618508	1.06185079	7.05331076	13.7544869	0.00020832	0.00290538	0.47901715	yes	p
ANXA5	-1.112666	1.11266602	6.4527764	22.8215984	1.78E-06	4.90E-05	0.46243868		
APOBEC3A	-1.2104417	1.21044171	7.27569466	24.0235368	9.52E-07	2.88E-05	0.43213629	yes	p, ca, c
APOBEC3F	-1.2734526	1.27345258	4.49654774	7.68830445	0.00555798	0.03940918	0.41366862	yes	
ARFIP1	-1.1803726	1.18037257	5.72001389	29.6866447	5.08E-08	2.23E-06	0.44123754		
ARG1	2.31444804	2.31444804	7.85004429	44.4946033	2.55E-11	2.37E-09	4.97414318		p
ARHGAP25	-1.0260779	1.02607786	6.42637695	15.9378041	6.55E-05	0.00113179	0.4910433	yes	p, ca, c
ARHGEF40	-1.5774806	1.57748061	4.43689615	10.531686	0.00117345	0.01182295	0.33506651		p, ca, c
ARRDC4	2.33564344	2.33564344	3.91957286	10.952615	0.00093472	0.00996727	5.04776041	yes	
ASPRV1	-4.5528817	4.55288173	3.56865163	33.5884388	6.81E-09	3.46E-07	0.04260357		p, ca, c
ATF6	-1.1796213	1.17962126	5.03921265	16.3133734	5.37E-05	0.00095844	0.44146738		
ATF6B_loc2	-1.9664622	1.9664622	3.13460299	8.06284564	0.00451822	0.03389882	0.25587973		
ATP10D	3.09292871	3.09292871	2.67945665	7.38419366	0.00657996	0.04468989	8.53226459		p
ATP13A3	1.38287429	1.38287429	3.31504466	7.37406981	0.0066171	0.04483106	2.60787422		
ATXN1	-1.2748606	1.27486056	4.35621314	10.897699	0.00096284	0.01014393	0.4132651	yes	p, ca, c
B3GNT5	-2.3188619	2.31886193	5.85455362	71.9338093	2.23E-17	6.10E-15	0.20042551	yes	p, ca
BCL10	-1.2180664	1.21806638	4.66070983	11.3980776	0.0007352	0.008207	0.42985847		p
BEST1	-1.8875701	1.88757006	3.55570561	7.93214992	0.00485641	0.03563315	0.27026188		p, ca, c
BET1	3.0593207	3.0593207	3.81665833	23.3162706	1.37E-06	4.01E-05	8.33580021		
BEX1	4.55939503	4.55939503	2.85669705	12.0492761	0.00051812	0.00619448	23.5784182		
BFAR	-1.4478136	1.44781356	4.96848971	9.33590474	0.00224707	0.01967444	0.36657656		p, ca
BLOC1S2	-1.0149701	1.01497011	7.56491336	34.8334036	3.59E-09	1.89E-07	0.49483858		p, ca, c
BLZF1	-3.4122469	3.41224691	3.59061227	21.6885679	3.21E-06	8.33E-05	0.09393151	yes	
BMS1P20_p1	-4.7655432	4.76554316	3.10559833	13.9714333	0.00018561	0.0026424	0.03676449		
BRAP	-2.763882	2.76388205	2.5827731	8.59706943	0.00336704	0.02690199	0.14722739		
BRD4	-1.782487	1.78248696	3.50201023	8.36633365	0.00382236	0.02967472	0.29068188		p
BSCL2	-2.5308222	2.53082218	2.58965342	7.31845659	0.006825	0.04595976	0.17304004		
BTNL8	-1.606427	1.60642699	6.47838393	21.0303249	4.52E-06	0.00011111	0.32841069		p, ca
C10orf128	-1.6203868	1.62038679	4.73575439	11.2176413	0.00081023	0.00886406	0.32524825		
C12orf10	3.6289345	3.6289345	1.9188031	11.4929657	0.0006986	0.00784637	12.3713797		p
C14orf159	-4.2194129	4.21941294	3.81956542	20.2837332	6.68E-06	0.00015572	0.05368218	yes	p, ca, c
C15orf48	-1.1520524	1.15205245	7.74793367	28.2543602	1.06E-07	4.38E-06	0.44998461	yes	p, ca, c
C19orf10	3.40486107	3.40486107	2.55933046	9.5154438	0.0020375	0.01820177	10.5916913		

C1GALT1C1	-1.2676643	1.26766431	4.69703052	11.3386377	0.00075911	0.00842021	0.41533164		
C1orf85	2.34524388	2.34524388	3.57827246	11.1747023	0.0008292	0.00899972	5.08146286		
C4orf3	-1.2350736	1.2350736	8.26919143	101.353314	7.70E-24	4.01E-21	0.42482083	yes	
CA2	-5.4183836	5.41838363	5.01583961	44.7936574	2.19E-11	2.11E-09	0.0233832	yes	
CACNB4	2.67642008	2.67642008	2.61089048	7.42926187	0.00641717	0.04396684	6.39267646		p, ca
CAMK1D	-3.4679938	3.46799379	4.09494619	26.7901596	2.27E-07	8.18E-06	0.09037116	yes	p, ca, c
CANX	1.2788582	1.2788582	4.39617112	7.96580118	0.00476694	0.03525991	2.42646861	yes	p, ca, c
CASS4	-1.9245544	1.92455443	6.34935763	29.3377956	6.08E-08	2.62E-06	0.2634216	yes	p, ca, c
CAST	-2.4669741	2.46697409	4.53415219	20.0015604	7.74E-06	0.00017671	0.18087011		p, ca
CAT	-1.0932047	1.09320469	7.07336659	17.0759003	3.59E-05	0.00067415	0.46871904		p, ca, c
CATSPER1	2.65734557	2.65734557	2.75743776	7.95411431	0.00479782	0.03539279	6.30871235		
CCDC147-AS1	-1.7228368	1.72283681	6.89619854	41.1901032	1.38E-10	1.07E-08	0.30295243		
CCDC19	-3.4505018	3.45050185	2.64976164	10.2876201	0.00133926	0.01320627	0.09147353		
CCL3L3_loc2	1.20040334	1.20040334	9.09055295	8.52008541	0.00351248	0.02778052	2.29803909		
CCL5	1.11156925	1.11156925	6.35086693	28.6116162	8.84E-08	3.67E-06	2.16080555	yes	
CCNG2	-1.0455701	1.04557006	4.53934995	9.46510682	0.00209417	0.01863337	0.48445345	yes	p
CCNJL	-3.9921519	3.9921519	3.27243764	15.1911137	9.72E-05	0.00156627	0.06284092		p, ca, c
CD300A	-1.2750352	1.27503519	8.17761707	101.266396	8.04E-24	4.01E-21	0.41321508		p, ca, c
CD300LF	-1.2508957	1.25089571	5.47350758	20.2492401	6.80E-06	0.00015722	0.42018725		p, ca
CD3G	2.51410144	2.51410144	2.99768138	8.38719617	0.00377873	0.02941937	5.71241756		
CD59	-3.9946375	3.99463746	5.85470306	65.3480316	6.28E-16	1.43E-13	0.06273275		
CD68	3.00289578	3.00289578	7.23744306	127.454775	1.48E-29	1.35E-26	8.01607376	yes	p, ca, c
CD74	-1.0886619	1.08866189	8.53616017	45.8870151	1.25E-11	1.30E-09	0.47019728	yes	p
CDC26	-1.140723	1.14072303	6.8214609	27.0777448	1.95E-07	7.29E-06	0.45353223		
CDC42EP2	1.44932541	1.44932541	6.36472375	43.2623827	4.79E-11	4.09E-09	2.73080332	yes	p
CDC42EP3	1.04594214	1.04594214	7.3551725	35.1138824	3.11E-09	1.74E-07	2.06471426	yes	p, ca, c
CDKN2C	5.19373824	5.19373824	1.97341195	10.6956414	0.00107388	0.01104306	36.5991501	yes	
CEACAM1	-2.5941331	2.59413313	2.59102591	8.06688683	0.00450815	0.03389461	0.16561059	yes	p, ca
CEACAM3	-1.2293453	1.22934526	6.9991125	43.236108	4.85E-11	4.09E-09	0.42651097	yes	p, ca, c
CERK	-3.1567897	3.15678973	3.21221698	12.9844901	0.00031408	0.00407934	0.11212736	yes	p
CETN2	-1.2975557	1.29755569	5.40306538	13.9545826	0.00018728	0.00265242	0.40681487		p, ca, c
CFD	4.09904547	4.09904547	7.60630961	361.300994	1.47E-80	4.02E-77	17.1370333	yes	
CHI3L1	-2.0463866	2.04638661	7.14073686	14.9277155	0.00011171	0.00173943	0.24208966	yes	p, ca, c
CHPT1	2.20443887	2.20443887	3.25648856	9.55887896	0.00198985	0.01787925	4.60895242		p, ca
CIB1	-1.1263398	1.12633976	5.64210568	11.4453725	0.00071672	0.00801705	0.45807643		p, ca
CLEC12A	-5.6953523	5.6953523	5.01753143	45.3110935	1.68E-11	1.68E-09	0.0192987	yes	p
CLEC5A	2.93369383	2.93369383	2.86027439	7.74173231	0.0053959	0.03873922	7.6406418	yes	p, ca, c
CLU	2.66836012	2.66836012	3.81704932	11.1789439	0.00082731	0.00899698	6.35706182	yes	
CNOT8	-2.6573689	2.65736894	3.08905619	10.1674106	0.00142945	0.01389935	0.15850838		
CORO1C	-1.5766879	1.5766879	4.44453825	9.59689151	0.00194907	0.01759943	0.33525067		p, ca, c
CTSD	1.70553044	1.70553044	6.12077284	40.7000548	1.77E-10	1.30E-08	3.26148826		p, ca, c
CTSG	4.02545303	4.02545303	4.1452061	22.4462175	2.16E-06	5.86E-05	16.284788		
CTSH	-6.6246974	6.62469736	2.28259033	24.6973222	6.71E-07	2.16E-05	0.01013368		
CXCL1	-1.1289611	1.12896114	9.63248738	22.9512087	1.66E-06	4.60E-05	0.45724486	yes	p, ca, c
CXCL6	-1.7823619	1.78236192	3.76193462	9.23166016	0.00237866	0.02059625	0.29070707		p, ca, c
CXCR4	-1.1838116	1.18381159	11.169832	101.774571	6.22E-24	3.79E-21	0.44018699	yes	p, ca, c
CXorf40A	-1.81252	1.81252	3.56563755	7.66909854	0.00561745	0.03972807	0.28469321		p
CYB5R1	1.23797839	1.23797839	4.5127311	8.01214595	0.00464646	0.03460227	2.35867785	yes	p, ca, c
CYP27A1	3.62650691	3.62650691	4.94681875	32.369072	1.27E-08	6.24E-07	12.3505802	yes	p, ca, c
CYSLTR1	-1.3921228	1.39212282	4.84361866	9.39152395	0.00217991	0.01928496	0.38100377	yes	
DCP2	-1.2035785	1.20357849	6.80642342	24.8572467	6.17E-07	2.01E-05	0.43419695	yes	
DDX50	-1.4446998	1.44469979	4.52835877	8.50396418	0.00354374	0.02798734	0.3673686		
DDX58	-2.1268039	2.12680392	3.61926718	11.7427269	0.00061081	0.00706303	0.22896454	yes	p, ca, c
DEFA3	3.31120308	3.31120308	11.3206054	471.573883	1.46E-104	7.98E-101	9.92593548		
DEFA4	3.72698006	3.72698006	6.15667292	56.8603324	4.68E-14	8.01E-12	13.2413661		

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DEFA8P_p1	6.88172019	6.88172019	2.59223045	46.1026101	1.12E-11	1.21E-09	117.924542		
DHRS9	1.42882364	1.42882364	5.21699285	18.8545912	1.41E-05	0.00030322	2.692271	yes	p, ca, c
DLGAP1-AS1	-1.0746088	1.07460879	5.27260742	8.73956306	0.00311379	0.02520929	0.47479979		p
DNAAF1	-2.9366685	2.93666851	3.29144903	9.24955356	0.00235553	0.02043487	0.13060948	yes	
DPYD	-1.1422995	1.14229948	5.33613296	11.9629184	0.0005427	0.00646637	0.45303692	yes	
DSE	-2.8983783	2.89837833	3.47325358	17.2827731	3.22E-05	0.00061512	0.13412236	yes	p, ca, c
DTX3L	-2.431605	2.43160497	3.18717307	7.16786535	0.0074221	0.04901271	0.18535912	yes	
DUSP11	-1.2527826	1.25278261	4.96652553	8.76131482	0.00307687	0.02502127	0.41963805		
DUSP2	-1.6130342	1.61303418	5.23390054	9.05190217	0.00262422	0.0221282	0.32691009	yes	p, ca, c
EGLN2	-1.0247742	1.02477423	5.36889387	18.1988507	1.99E-05	0.00040698	0.49148721		p
EHD4	-4.5039392	4.5039392	2.6061359	13.7585221	0.00020788	0.00290538	0.04407367	yes	p, ca, c
EIF4G1	2.73831725	2.73831725	2.33468914	8.27894791	0.00401074	0.03087478	6.67291556		p
ELOVL5	-1.003129	1.00312897	6.87259322	34.9799236	3.33E-09	1.81E-07	0.49891676	yes	p
ELP4	3.36723264	3.36723264	2.89945935	8.2878891	0.00399104	0.03076634	10.3190099		
EMILIN2	2.84958493	2.84958493	2.71018505	8.92851225	0.00280753	0.02345742	7.20792967	yes	p, ca
EMP3	1.44326122	1.44326122	6.62327804	56.4262442	5.83E-14	9.69E-12	2.71934882		
ERGIC1	-1.2945048	1.29450482	5.86223582	21.0160596	4.55E-06	0.00011144	0.40767607		p, ca, c
ERGIC2	-1.2093447	1.20934467	5.04222394	13.3976368	0.00025194	0.00341805	0.43246501		p, ca, c
ERV3-1	-1.4463058	1.44630585	5.01031904	10.6570173	0.00109654	0.01123391	0.36695986		p, ca, c
ESYT1	3.19383915	3.19383915	1.96226225	8.1674112	0.00426497	0.03242208	9.15042752		p, ca, c
EXOC6	-1.7619733	1.76197329	4.80756644	20.9572009	4.70E-06	0.0001139	0.29484461		p
FAM101B	1.00483064	1.00483064	5.74759684	10.4517216	0.00122535	0.01227816	2.00670792	yes	p
FAM110A	1.90661317	1.90661317	3.71618972	8.6637849	0.00324596	0.0260485	3.74927896	yes	p
FAM177A1	-1.735669	1.73566898	5.71091274	27.1293642	1.90E-07	7.14E-06	0.30026974	yes	p, ca, c
FAM214B	-2.1541858	2.15418577	3.73090567	10.8607148	0.00098226	0.01031371	0.22465985		
FAM3B	-6.3672667	6.3672667	2.6580258	8.87575804	0.00288982	0.02396235	0.01211328		p, ca, c
FAM45A	1.20074345	1.20074345	6.69756569	48.4986206	3.31E-12	3.85E-10	2.2985809		p, ca, c
FAM49A	-1.3141896	1.3141896	5.04883255	12.5489854	0.00039642	0.0049607	0.40215133	yes	p
FAR2	-2.1233806	2.12338056	3.37057901	8.59827407	0.00336482	0.02690199	0.22950849	yes	p
FCER1A	3.39084362	3.39084362	4.14534543	24.5092966	7.40E-07	2.32E-05	10.4892791	yes	
FCF1	-3.2707004	3.27070045	2.19988013	9.53946973	0.002011	0.01803974	0.10361462		p, ca, c
FES	-2.3082012	2.30820122	3.77291775	11.6796048	0.00063189	0.00724558	0.20191203	yes	p, ca
FOSL1	-3.0262427	3.02624272	2.84504906	9.59323503	0.00195296	0.01760551	0.1227468		p, ca
FRMD4B	-5.5773528	5.57735279	4.09280984	60.6679732	6.76E-15	1.28E-12	0.02094351	yes	p
G0S2	-1.0000917	1.00009175	10.8681487	13.0343967	0.00030582	0.0040005	0.4999682	yes	p, ca, c
GAK	3.36245941	3.36245941	2.34066294	8.24899456	0.00407746	0.03130049	10.2849253	yes	p, ca, c
GAPT	-1.1911644	1.19116439	6.88774967	30.322153	3.66E-08	1.69E-06	0.43794925	yes	
GBA	-4.8636984	4.86369839	2.67638414	14.1841455	0.00016576	0.0023972	0.03434637		p, ca, c
GIMAP4	-1.8016261	1.80162609	6.29620273	45.5263046	1.51E-11	1.53E-09	0.28685109	yes	
GJB6	3.38085517	3.38085517	5.79038795	96.7076093	8.04E-23	3.67E-20	10.4169077	yes	p, ca
GNG11	1.93990933	1.93990933	3.57282985	10.127062	0.00146108	0.01402484	3.83681534		
GNL3L	-3.6926499	3.69264992	2.21525017	10.1422465	0.00144909	0.01398325	0.07733954		
GNLY	1.56679543	1.56679543	7.39671949	64.5675571	9.33E-16	2.05E-13	2.9624595		p, ca, c
GPR160	-2.0275457	2.0275457	3.62744929	8.69331524	0.00319379	0.0257429	0.24527197		p, ca, c
GPR65	-1.2526319	1.2526319	9.05343339	83.2109248	7.37E-20	2.89E-17	0.41968188	yes	p
GPR82	-5.844603	5.84460297	1.91222745	15.2530789	9.40E-05	0.0015292	0.017402		
GPX1	1.16044741	1.16044741	7.07408771	32.8028035	1.02E-08	5.08E-07	2.23526738		p, ca, c
GPX4	1.25329377	1.25329377	6.61104457	20.5202394	5.90E-06	0.00014061	2.38385051		p, ca, c
GRHPR	-3.0005947	3.00059474	2.78387514	8.05260911	0.00454382	0.03402276	0.12494848		
GSN	-1.5455769	1.54557693	4.53567731	10.9198981	0.00095137	0.01005488	0.34255869	yes	p
GSTM3	-5.6392768	5.63927682	1.78598721	8.88492836	0.00287534	0.02393683	0.02006358	yes	
GSTM4	-5.2432495	5.24324946	2.68251955	12.8928362	0.00032984	0.00424381	0.02640126		p, ca, c
GTF3C5	3.74959948	3.74959948	3.46793558	17.7227193	2.56E-05	0.00051121	13.450608		
GYG1	1.08958956	1.08958956	5.99862389	10.6767541	0.0010849	0.01113549	2.12813483		p
GZMB	1.02812348	1.02812348	4.98925482	8.20559502	0.00417614	0.03192389	2.03936991	yes	p

HARS	-3.2566736	3.25667359	2.72811369	7.74075095	0.00539883	0.03873922	0.10462695		p, ca, c
HCAR3	-1.4064437	1.40644375	8.86117242	34.2682496	4.80E-09	2.48E-07	0.37724044	yes	p, ca, c
HCG18_loc4	-2.5091454	2.50914535	3.13968431	12.0622576	0.00051453	0.00618571	0.17565964		
HCG27_loc5	-3.0858709	3.08587094	2.54163216	8.87252293	0.00289495	0.02396859	0.11777694		
HDGF	-2.1253818	2.1253818	3.3307578	11.0976359	0.00086438	0.00933163	0.22919035		p
HEATR5A	-2.4629691	2.46296909	4.29580872	19.5987318	9.55E-06	0.00021372	0.18137291		
HERPUD1	1.14920249	1.14920249	5.55381668	18.2753856	1.91E-05	0.00039354	2.21791256	yes	p, ca, c
HIST1H2BD	-1.7755642	1.77556416	5.21002569	18.5318593	1.67E-05	0.00034822	0.29208007	yes	p
HIST1H4C	1.41580967	1.41580967	5.09182893	17.5323593	2.82E-05	0.00055291	2.66809433	yes	p
HIST2H4B_lo	1.07211315	1.07211315	5.51021849	7.72652018	0.00544155	0.0388718	2.10251071		
HK3	1.51157632	1.51157632	4.01902426	7.24702858	0.00710184	0.04729672	2.85121399	yes	p
HLA-DQA2_lo	6.71847617	6.71847617	2.22150967	35.758621	2.23E-09	1.28E-07	105.308361		
HLA-DRA_loc	-1.3275753	1.32757525	7.56978089	38.8583661	4.56E-10	3.01E-08	0.39843734		
HMCES	-2.4812638	2.48126378	3.33362061	8.57919518	0.00340026	0.02708838	0.17908746		p, ca, c
HMGN2	-1.2599032	1.2599032	9.45616913	61.6985282	4.00E-15	7.84E-13	0.41757198		p
HP	3.8873422	3.8873422	4.02363361	23.4771996	1.26E-06	3.72E-05	14.798122		p, ca, c
HPSE	1.74553673	1.74553673	3.53134723	9.53372369	0.0020173	0.01806674	3.35319581	yes	p, ca, c
HSPA13	1.18454644	1.18454644	4.34410174	8.09754677	0.00443252	0.03350986	2.27291926		p
HSPA9	-1.6487123	1.64871229	4.69804255	11.9264759	0.00055342	0.00656555	0.31892469		p, ca, c
HVCN1	-2.390192	2.39019203	3.91153828	7.75334673	0.00536131	0.03866492	0.19075701	yes	
ID2	-1.0707014	1.07070136	9.2955063	37.9185755	7.38E-10	4.76E-08	0.47608749	yes	p, ca, c
IDNK	4.60372337	4.60372337	3.75486805	27.6757755	1.43E-07	5.62E-06	24.3141351		p, ca
IDO1	-4.4509711	4.45097109	3.54351265	13.3996353	0.00025167	0.00341805	0.04572189	yes	p, ca
IFI16	-1.5448313	1.54483133	5.98226827	17.0047698	3.73E-05	0.00069512	0.34273577	yes	p, ca
IFI27L2	1.39013951	1.39013951	4.54037088	15.1943894	9.70E-05	0.00156627	2.62104024		p
IFIT1	-2.4247477	2.42474768	5.85650332	18.9839662	1.32E-05	0.00028445	0.18624225	yes	
IFIT2	-1.4048389	1.40483886	7.97469496	38.860145	4.55E-10	3.01E-08	0.37766033	yes	p, ca, c
IFIT3	-2.3300732	2.33007322	7.96582361	52.22107	4.96E-13	6.80E-11	0.19887403	yes	p, ca, c
IFIT5	-3.7003467	3.70034665	2.78361473	14.8882549	0.00011407	0.00177117	0.07692804	yes	
IFITM1	-1.0834164	1.08341643	11.8048617	28.7585423	8.20E-08	3.46E-06	0.47190998	yes	p, ca, c
IFITM3	-1.220212	1.22021197	10.4279691	7.13554488	0.00755707	0.0495458	0.42921965	yes	p, ca
IFITM4P_p4	-1.426831	1.42683099	3.6814022	9.34683308	0.00223371	0.01958875	0.37194701		
IGF1R	-2.9639295	2.96392946	3.17037642	15.4120858	8.64E-05	0.00142694	0.12816467	yes	
IL10RB-AS1	-1.2992333	1.29923335	4.24914227	8.19491005	0.00420081	0.03206773	0.40634207		p, ca, c
IL18	-3.1955373	3.19553728	2.82829902	9.947481	0.0016107	0.01514276	0.10915595	yes	p, ca, c
IL4I1	-5.0815209	5.08152094	2.327741	12.6983833	0.00036597	0.00462187	0.02953315	yes	p
IL8	-1.6807319	1.68073193	15.3269572	37.723894	8.15E-10	5.13E-08	0.31192435	yes	
IRF2	-1.5579232	1.55792324	5.75613814	13.3699478	0.00025569	0.00343839	0.33963964	yes	p, ca, c
IRS2	1.03041889	1.03041889	6.17927505	25.4876331	4.45E-07	1.52E-05	2.04261725	yes	
ITFG3	-4.3005192	4.30051924	2.3193318	9.16544373	0.00246628	0.0211583	0.05074751		p, ca, c
ITPKB	-3.6624458	3.6624458	2.51560754	8.74235008	0.00310904	0.02520802	0.07897579	yes	p
JKAMP	-1.2909245	1.29092454	5.20660033	20.2675791	6.73E-06	0.00015638	0.40868904		
JMJD6	-1.6004131	1.60041308	6.56880908	44.5870459	2.43E-11	2.30E-09	0.32978254		p, ca, c
KATNBL1	-3.6521509	3.65215088	3.40466689	24.4743513	7.53E-07	2.35E-05	0.07954136		
KATNBL1P6_	-5.7776937	5.77769373	3.46687056	48.9419139	2.64E-12	3.14E-10	0.01822808		
KCMF1	-1.2282079	1.22820786	4.10901899	7.71820402	0.00546668	0.03889846	0.42684735		p
KCNJ15	-1.8219875	1.82198745	7.3224866	66.1244416	4.23E-16	1.01E-13	0.28283108		p, ca, c
KCNMB3	-3.4200102	3.42001024	2.66706644	9.31390571	0.00227421	0.01984865	0.09342741		p
KDELR2	-2.2990632	2.2990632	2.53649908	8.60092618	0.00335992	0.02690199	0.203195		p, ca
KIAA0040	-2.1313184	2.13131839	4.71651972	13.5327057	0.00023444	0.00321244	0.22824918	yes	
KIAA0226L	-1.4339952	1.43399522	5.75306209	23.6617259	1.15E-06	3.40E-05	0.37010455	yes	p, ca, c
KIAA0391	-4.2193691	4.21936915	2.3439137	10.1026167	0.00148059	0.01417322	0.05368381		
KLF2	1.05559783	1.05559783	4.64093848	12.9869156	0.00031368	0.00407934	2.07857936	yes	p, ca, c
KLF4	1.73878308	1.73878308	4.00976613	7.58089854	0.005899	0.04118415	3.33753527	yes	p
KLRB1	1.37278624	1.37278624	4.55002971	8.87834793	0.00288573	0.02396235	2.58970225		p, ca

KLRG1	3.14924474	3.14924474	2.24856591	9.14993739	0.00248727	0.02123474	8.87191006	yes	
KRT23	1.44360341	1.44360341	6.58294372	17.5520867	2.80E-05	0.00054917	2.71999389		p, ca
LAMTOR4	1.07801161	1.07801161	10.252648	40.4239498	2.04E-10	1.47E-08	2.11112442		p, ca, c
LETM2	4.00247154	4.00247154	2.43150458	14.583233	0.0001341	0.00200824	16.0274337		p
LGALS9	-1.9507811	1.95078112	5.30016912	18.4623067	1.73E-05	0.00035843	0.25867614	yes	
LILRA3	-1.7765514	1.7765514	6.27993304	15.1649964	9.85E-05	0.0015788	0.29188027	yes	p, ca, c
LINC00211	1.91090716	1.91090716	5.54265493	40.8866321	1.61E-10	1.21E-08	3.76045482		p, ca, c
LINC00282	-6.5314132	6.53141315	3.60073749	46.8028494	7.85E-12	8.78E-10	0.01081057		p, ca, c
LINC00493	-1.3753542	1.37535425	6.06964808	23.2924122	1.39E-06	4.03E-05	0.38545805		
LINC00623_lo	-1.397932	1.39793198	5.62280761	24.2348125	8.53E-07	2.62E-05	0.3794727		
LINC00877	-1.4423405	1.44234049	5.79503286	29.3269816	6.11E-08	2.62E-06	0.36796986		p, ca, c
LINC01000	-3.3380778	3.33807783	2.84241885	14.5329969	0.00013773	0.00205129	0.09888683		
LMBRD1	-1.4749133	1.47491331	5.12279072	21.3329731	3.86E-06	9.75E-05	0.35975501		p
LOC10012955	1.785707	1.785707	2.99977027	7.45343614	0.00633155	0.04349336	3.44787388		
LOC10013283	5.43154404	5.43154404	4.37816129	79.6731852	4.42E-19	1.51E-16	43.1576391		
LOC257358	-6.2822171	6.28221706	2.76461599	29.8272636	4.72E-08	2.09E-06	0.01284885		
LPAR2	-1.4117305	1.41173046	4.05351398	7.5234031	0.00609025	0.04236126	0.37586059	yes	
LRRC25	-1.3338503	1.33385026	5.18093042	11.5723637	0.00066939	0.00759615	0.39670809		p
LXN	-3.3555676	3.35556757	3.1800049	11.8521706	0.00057594	0.00675961	0.09769526	yes	
LY96	-1.3466396	1.34663961	8.05655121	102.206169	5.00E-24	3.43E-21	0.39320686		p
LYRM5	-1.1976857	1.19768574	4.98437113	15.1274443	0.00010049	0.00159651	0.43597408		
LYZ	1.52625276	1.52625276	12.7803928	131.436968	1.99E-30	2.18E-27	2.88036723		p, ca, c
MAN1A1	-1.5818906	1.58189057	3.40702321	9.75790796	0.00178553	0.01642028	0.33404386	yes	p
MAN2A1	3.76610488	3.76610488	2.0430267	14.707755	0.00012553	0.0019165	13.6053756		p
MANBA	-1.7919454	1.79194542	5.32621997	13.6004166	0.00022614	0.00312203	0.28878237		p
MAP3K7	-2.7385996	2.73859958	2.25004377	7.74374379	0.00538989	0.03873922	0.14983021		p
MAP3K8	-1.0228308	1.02283078	5.72688468	15.6782909	7.51E-05	0.00126621	0.49214973	yes	p, ca, c
MAPK14	1.97566222	1.97566222	4.95191562	22.2196406	2.43E-06	6.50E-05	3.93308732	yes	p, ca, c
MARS	-3.0972225	3.09722247	3.21677954	13.6804088	0.0002167	0.00299937	0.11685388		p, ca, c
MBOAT2	-2.9176525	2.91765247	2.49529674	8.58837464	0.00338316	0.0269914	0.13234243		p
MCTP2	1.83249631	1.83249631	3.50123619	10.3649647	0.00128429	0.01277534	3.56152794	yes	
METRNL	-1.8076899	1.80768991	3.89487333	7.92224929	0.00488305	0.03578076	0.28564795		p, ca, c
METTL23	-2.0804296	2.08042963	3.42104712	8.75673599	0.00308461	0.025047	0.23644399		p, ca, c
METTL9	1.59237222	1.59237222	4.5416671	16.7313032	4.31E-05	0.00079207	3.01544772		p, ca, c
MGME1	-3.7503104	3.75031035	2.79039053	10.4894438	0.00120059	0.01205203	0.07430946		
MGST1	3.6057205	3.6057205	3.54883904	25.8840105	3.63E-07	1.26E-05	12.1739083	yes	p
MIAT	-2.9223304	2.92233043	3.12265715	7.62187456	0.00576645	0.04061622	0.131914		
MIR22HG	1.20476048	1.20476048	7.27373873	51.5791556	6.88E-13	8.97E-11	2.30498999	yes	p, ca
MIR3652	1.9898419	1.9898419	4.45744655	14.625871	0.0001311	0.0019741	3.97193469		
MIR4707	-3.3418969	3.34189689	2.86303059	9.37392247	0.00220094	0.01938621	0.0986254		p, ca, c
MMP9	-1.6717849	1.67178494	5.28465603	12.9768543	0.00031537	0.00408633	0.31386478	yes	p, ca, c
MPZL3	-1.055912	1.05591203	5.59607665	11.3353715	0.00076045	0.00842021	0.48099306		p, ca, c
MRVI1-AS1	-2.6736138	2.67361385	3.78381189	13.7899095	0.00020443	0.00287305	0.15673357		p, ca, c
MS4A3	3.23123444	3.23123444	4.26892548	19.7868876	8.66E-06	0.00019527	9.39071132		
MSC	6.57799367	6.57799367	3.02425133	43.6467879	3.93E-11	3.42E-09	95.5373974	yes	p
MT2A	-1.2227572	1.22275715	6.02839971	24.2247819	8.57E-07	2.62E-05	0.42846309	yes	
MTF1	1.2700752	1.2700752	6.19050904	21.1785318	4.18E-06	0.00010377	2.41174137		p, ca
MTF2	-3.82049	3.82048997	2.51724995	10.7516182	0.00104188	0.010795	0.0707812		
MTHFS	-1.0475339	1.04753386	6.46787095	25.7582388	3.87E-07	1.33E-05	0.48379446	yes	p, ca, c
MX1	-1.6342057	1.63420566	5.65214207	15.1560389	9.90E-05	0.00158168	0.32214773	yes	p
MYO9B	-1.3547069	1.35470695	4.55891983	10.6284197	0.00111363	0.01136648	0.39101424		p, ca
NAAA	-4.9539153	4.95391532	2.89450418	33.6004894	6.77E-09	3.46E-07	0.03226435		
NCL	1.4804894	1.4804894	5.52696857	16.191059	5.73E-05	0.00101246	2.79043377		
NDRG1	1.43916691	1.43916691	4.61169309	9.39777686	0.00217249	0.01926764	2.71164235	yes	p
NDUFA12	1.85381821	1.85381821	5.77428058	41.1952388	1.38E-10	1.07E-08	3.61455542		

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NDUFA3	1.091066	1.091066	6.41648348	19.7765273	8.70E-06	0.00019553	2.13031386		p, ca
NDUFB6	-1.2753114	1.2753114	7.99681075	72.4497714	1.71E-17	4.94E-15	0.41313598		p, ca, c
NDUFS5	1.08217251	1.08217251	5.61153634	14.1180645	0.00017169	0.00247636	2.11722194		
NFRKB	-3.4303764	3.43037642	1.97607608	8.47546491	0.00359968	0.02818552	0.09275852	yes	
NFXL1	-6.3382456	6.33824561	2.22906936	19.2391203	1.15E-05	0.00025183	0.01235942		
NKG7	1.05490697	1.05490697	6.83641526	15.9795917	6.40E-05	0.00111058	2.07758423	yes	p, ca
NLRP3	2.05932077	2.05932077	6.18092224	41.244312	1.34E-10	1.07E-08	4.16790032	yes	p, ca, c
NR1D2	-2.9998221	2.99982214	2.29083813	7.51726381	0.00611104	0.042452	0.12501541	yes	
NT5C3A	-2.0188798	2.0188798	4.42115625	21.0771609	4.41E-06	0.00010892	0.24674969	yes	p, ca, c
NUAK2	-1.7825607	1.78256066	3.85437772	7.13959757	0.00754001	0.04949315	0.29066703		p, ca, c
NUB1	-1.1034627	1.10346272	6.21154207	31.8710709	1.65E-08	7.99E-07	0.46539812	yes	
NUCB1	-2.131976	2.13197595	4.40782103	18.1109347	2.08E-05	0.00042463	0.22814517	yes	p
OAS1	-7.0566236	7.05662361	2.67205992	34.9959539	3.30E-09	1.81E-07	0.00751181	yes	
OBFC1	-3.7068983	3.70689832	3.13182278	16.369307	5.21E-05	0.00093667	0.07657948		
OLIG1	1.88162042	1.88162042	3.2563834	7.58158316	0.00589676	0.04118415	3.6848871	yes	p, ca, c
OLR1	-2.9288577	2.92885766	3.89952922	14.0445583	0.00017853	0.00256157	0.13131852	yes	p, ca, c
ORAI2	-1.4727239	1.47272392	4.68868799	8.83460067	0.00295572	0.0243248	0.36030138		p, ca, c
ORM1	-2.1637334	2.16373342	6.77405569	37.5159735	9.07E-10	5.60E-08	0.22317798		p, ca, c
OSGIN2	1.7848425	1.7848425	5.54990702	52.6346507	4.02E-13	5.65E-11	3.44580845		p
OSM	-1.6296147	1.62961473	5.22056178	16.9378713	3.86E-05	0.00071761	0.3231745		p, ca, c
OSTC	1.24756179	1.24756179	3.81325964	10.7124267	0.00106418	0.01096389	2.37439802	yes	p, ca
P2RY13	-1.7092064	1.70920644	7.24243053	87.2210365	9.70E-21	4.09E-18	0.30582824	yes	p, ca, c
PAM	3.27955349	3.27955349	2.56422623	9.76308138	0.00178051	0.01640166	9.71055319	yes	
PARK7	1.20636865	1.20636865	6.27530332	27.6108471	1.48E-07	5.77E-06	2.30756079	yes	p, ca
PCM1	2.43120962	2.43120962	3.08052607	9.06220637	0.00260947	0.02203775	5.39345452		p, ca, c
PDIA3	1.47221448	1.47221448	4.69563583	15.1133949	0.0010124	0.00160378	2.77447438		
PDLIM2	-1.8708007	1.87080069	4.15829465	10.0744368	0.00150341	0.01430585	0.27342164		
PELO	1.08087342	1.08087342	6.34671199	9.10065477	0.00255518	0.02167948	2.11531633		p, ca, c
PF4	1.64789453	1.64789453	4.81878851	9.84744331	0.00170068	0.01582585	3.13375964		p
PGLYRP1	-1.2794462	1.27944623	6.33784448	25.3522945	4.78E-07	1.61E-05	0.4119536		p, ca
PGS1	-2.3690756	2.36907561	7.83123598	43.8742356	3.50E-11	3.15E-09	0.19356961	yes	p, ca, c
PHB	-1.8572197	1.85721972	3.88730594	7.15408226	0.00747936	0.0492129	0.27600767		
PI3	1.92265615	1.92265615	12.3260625	38.9994159	4.24E-10	2.87E-08	3.79120416	yes	p, ca, c
PLAC8	1.24667722	1.24667722	5.06480704	14.342757	0.00015236	0.00223292	2.37294263	yes	p, ca, c
PLAUR	-1.1106937	1.11069365	11.7148424	107.128655	4.17E-25	3.27E-22	0.46307133	yes	p, ca, c
PLD3	5.72238441	5.72238441	2.4695688	27.3949786	1.66E-07	6.27E-06	52.7970131		p, ca
PLEKHO2	-1.0608695	1.06086948	6.22140935	15.2069096	9.64E-05	0.00156241	0.47934308		p, ca, c
PLK1S1	-3.6561072	3.65610716	3.56601579	14.7766512	0.00012102	0.00185809	0.07932354		
PLSCR1	-1.9460703	1.94607033	6.94075531	54.135399	1.87E-13	2.77E-11	0.25952217	yes	p, ca, c
PMF1-BGLAP	1.36587029	1.36587029	4.53857725	10.1548087	0.00143925	0.01396181	2.57731752		p, ca
POGZ	-2.5686007	2.56860073	2.42877879	9.92122205	0.00163384	0.01533402	0.16856761		
POLR2L	1.25267651	1.25267651	6.11041219	16.2464009	5.56E-05	0.0009897	2.38283079	yes	p, ca
POLR3K	-2.7352135	2.73521352	4.47650176	10.6083748	0.00112577	0.011469	0.15018228		
PPBP	1.51965571	1.51965571	6.69834006	24.7175702	6.64E-07	2.15E-05	2.86722618	yes	p
PPCDC	-1.2957373	1.29573733	6.86856297	37.5117591	9.09E-10	5.60E-08	0.40732794		p, ca, c
PPP1R16B	3.98404982	3.98404982	1.79846112	10.6403553	0.00110646	0.01131442	15.8240811		
PPP4R2	1.74706157	1.74706157	5.37946408	55.5816535	8.97E-14	1.40E-11	3.35674181		p, ca, c
PRDM5	-5.6292936	5.6292936	2.95952786	27.0461849	1.99E-07	7.31E-06	0.0202029		
PRG2	4.51555423	4.51555423	2.24598493	10.2200553	0.00138922	0.01359696	22.8726914	yes	p
PRKDC	-2.7532977	2.75329769	3.8846931	14.6826677	0.00012721	0.00192608	0.14831149	yes	
PRKRA	-4.1587567	4.15875669	2.28730041	10.9686899	0.00092664	0.00990044	0.0559873		p
PTOV1	2.2540537	2.2540537	2.48271793	7.25853109	0.0070565	0.04727671	4.77021305		p
PTPLAD2	-1.2112993	1.21129927	4.25003458	9.62048623	0.00192419	0.01743219	0.4318795		
PTX3	2.27521006	2.27521006	4.59312209	16.1061305	5.99E-05	0.00104874	4.84068114	yes	p, ca, c
QARS	3.11337615	3.11337615	2.23920492	9.3717581	0.00220354	0.01938621	8.65405413		

RAB11FIP4	-3.6111554	3.61115536	3.51068411	17.1701032	3.42E-05	0.00064373	0.08183403		p
RAB20	1.13374803	1.13374803	4.82437786	8.18410729	0.0042259	0.03221438	2.1942806		p, ca, c
RAB9A	1.32319178	1.32319178	5.4781384	28.7097795	8.41E-08	3.52E-06	2.50219076		p, ca, c
RAC1	1.06756044	1.06756044	5.17328133	11.3389432	0.00075899	0.00842021	2.09588628		p, ca
RAPGEF6	-3.1902721	3.19027205	3.88255351	17.3143859	3.17E-05	0.00061136	0.10955505		p, ca, c
RBKS	-2.8150784	2.81507842	2.90579438	7.57876396	0.00590599	0.04118415	0.1420944		p, ca
RFC2	-4.7841551	4.7841551	2.69233129	15.6332647	7.69E-05	0.00129274	0.03629325	yes	p, ca, c
RGS10	1.26354379	1.26354379	5.10058854	15.7008539	7.42E-05	0.00125894	2.40084754	yes	
RHOB	3.00093442	3.00093442	5.79219996	75.8185113	3.11E-18	1.00E-15	8.00518321	yes	p, ca, c
RIC8A	-2.8214686	2.82146864	3.21007847	10.2058978	0.00139992	0.01367732	0.1414664		
RMND5A	1.15327944	1.15327944	3.90600397	9.58819531	0.00195832	0.01762491	2.22418908	yes	p
RMRP	1.27827061	1.27827061	4.15128808	7.501834	0.00616362	0.04276304	2.42548055		
RNASE3	1.70028484	1.70028484	6.33393673	13.3680279	0.00025595	0.00343839	3.24965111		p
RNPEP	-2.438781	2.438781	2.99080023	7.16058326	0.0074523	0.04915287	0.18443943		
ROCK1	-1.8107649	1.81076488	4.4721129	12.7669165	0.0003528	0.00448659	0.28503977		p
ROMO1	1.29247949	1.29247949	6.28247476	40.7513685	1.73E-10	1.28E-08	2.44948676		p, ca, c
RP11-290F20	-1.4172889	1.41728888	4.27422613	7.68035669	0.00558251	0.03953198	0.37441526		
RPAP3	-1.6342232	1.63422316	4.77333797	10.0801679	0.00149874	0.01428832	0.32214382		
RPIA	-5.6122908	5.61229079	1.78473758	12.1663106	0.0004866	0.00592684	0.02044241		p, ca, c
RPL17-C18or	1.37280868	1.37280868	5.61490308	17.018943	3.70E-05	0.0006923	2.58974254		p, ca, c
RPL36	1.00698718	1.00698718	5.19581203	8.56091137	0.00343457	0.02728247	2.00970978		
RPL9	1.36215604	1.36215604	4.15899128	9.35575735	0.00222286	0.01952484	2.5706907		p
RPLP0	1.03330755	1.03330755	5.72273593	8.82109762	0.00297767	0.02443209	2.0467112	yes	p
RPS16P5_p1	-6.3358743	6.33587427	3.18696753	37.955718	7.24E-10	4.72E-08	0.01237975		
RRM2B	-1.7129124	1.71291239	4.25793386	12.5129668	0.00040414	0.00503427	0.30504365		p
RSAD2	-1.7564516	1.75645162	6.00658777	11.0724106	0.0087622	0.00943526	0.29597524	yes	p
RSBN1L	-3.7430255	3.7430255	3.15434658	15.0516988	0.00010461	0.00165229	0.07468563		p, ca, c
RSRC1	-3.2786596	3.27865957	3.2275597	11.9030419	0.00056042	0.00662	0.10304457		
RUNX1	-4.0308681	4.03086811	2.23349278	16.2306973	5.61E-05	0.0009947	0.06117695		p, ca, c
S100A12	1.11802374	1.11802374	12.2652999	64.1353138	1.16E-15	2.45E-13	2.17049446		p, ca, c
SAMD9L	-4.7147114	4.71471139	3.36116722	27.8218696	1.33E-07	5.28E-06	0.03808294	yes	
SCLT1	-1.846118	1.84611804	6.3231518	42.2971487	7.84E-11	6.51E-09	0.27813977	yes	p, ca, c
SCNM1	-1.4704498	1.47044978	4.75242357	8.21438949	0.00415595	0.03181391	0.36086977		p
SEC61B	1.12127807	1.12127807	7.94048307	69.2798552	8.54E-17	2.13E-14	2.17539603		
SERPINB8	2.50216154	2.50216154	4.31676485	16.5780679	4.67E-05	0.00085299	5.66533607		p, ca, c
SERPING1	-2.2850327	2.28503275	3.53896161	10.5878596	0.00113833	0.01157356	0.20518074	yes	
SESN2	-1.4198825	1.41988254	4.61656504	9.82726219	0.00171944	0.01594629	0.37374274	yes	p, ca, c
SH2D1A	3.71787332	3.71787332	2.88128995	12.1266524	0.00049706	0.0060408	13.1580457		
SIGLEC10	-1.7652055	1.76520551	5.17746132	11.7869813	0.00059646	0.00693008	0.29418477		p, ca, c
SIRT7	-2.8701869	2.87018691	3.30278305	11.7321064	0.00061431	0.0070736	0.13676899		p, ca
SKIL	-1.4057998	1.40579975	5.19159112	23.2528149	1.42E-06	4.05E-05	0.37740887		
SLC15A3	-1.7393968	1.73939675	4.75578635	12.6398146	0.00037762	0.00474707	0.29949488		
SLC22A18AS	-2.9435473	2.94354729	2.93483009	9.4300824	0.00213455	0.01896183	0.12998821		p, ca, c
SLC29A1	-3.2813563	3.28135631	3.82204131	15.686644	7.48E-05	0.00126452	0.10285214	yes	
SLC31A1	-2.8674502	2.86745023	2.67532961	7.30896452	0.00686115	0.04614225	0.13702868		p, ca, c
SLC37A3	1.92033629	1.92033629	4.44055562	30.6419481	3.10E-08	1.44E-06	3.78511279		p, ca
SLPI	2.21445288	2.21445288	10.1510198	192.461823	9.23E-44	1.69E-40	4.64105527	yes	p, ca
SMAD4	-2.9877603	2.9877603	2.32046113	7.25083076	0.00708682	0.04727671	0.126065		
SMAP1	-3.832008	3.832008	2.41411285	10.048818	0.00152446	0.01445597	0.07021835		
SMARCE1	-1.6938456	1.69384564	3.20717343	9.71735513	0.00182536	0.0167025	0.30910189		
SMC4	-3.1615472	3.16154716	2.37940692	11.2673587	0.00078882	0.0086578	0.11175822	yes	
SNAI1	3.15883029	3.15883029	3.07389585	11.9156688	0.00055664	0.00658948	8.93105306		p, ca, c
SNHG16	1.04115582	1.04115582	6.11628449	19.5564585	9.77E-06	0.00021673	2.05787567	yes	p, ca, c
SNORD1B	2.91399339	2.91399339	2.99310005	10.3282626	0.00131008	0.01300829	7.53701568		p, ca, c
SNX17	-2.8947292	2.89472918	3.09168142	9.32303507	0.00226291	0.0197815	0.13446204		

SOCS2	4.04843173	4.04843173	3.44471205	18.2699467	1.92E-05	0.00039354	16.5462425	yes	
SORD	-3.1377678	3.13776778	3.52233722	18.732376	1.50E-05	0.00031953	0.11361555		p, ca, c
SORL1	-1.1838383	1.18383828	7.10636789	37.2824887	1.02E-09	6.15E-08	0.44017885	yes	p, ca, c
SP140	-1.579877	1.57987699	6.42376699	19.5478795	9.81E-06	0.00021678	0.33451041	yes	p
SPAST	-2.4663256	2.46632562	2.39060763	9.77280508	0.00177112	0.01634261	0.18095143		
SPATA13_loc	-1.0265263	1.02652629	5.40937277	9.62606731	0.00191835	0.01740807	0.49089069		
SPP1	2.21316572	2.21316572	5.00817387	7.25405543	0.00707411	0.04727671	4.63691642	yes	
SPTSSA	1.50573604	1.50573604	4.59106457	9.16510753	0.00246673	0.0211583	2.83969511	yes	
SSFA2	-1.9255828	1.9255828	3.18603723	7.84322388	0.00510116	0.03713072	0.2632339		
SSNA1	-2.5636883	2.56368831	4.02566165	14.6988798	0.00012612	0.0019202	0.16914257		
ST20	-1.5101507	1.51015066	4.52189213	9.61371778	0.00193129	0.01746768	0.35107455	yes	p, ca, c
STK24	-4.0986715	4.09867148	3.26147372	36.8057112	1.31E-09	7.61E-08	0.05836829		p, ca, c
STK38	-2.2693923	2.26939234	3.81486011	17.6276787	2.69E-05	0.0005335	0.20741723		p
STRA13	2.47304121	2.47304121	3.12844154	8.73172732	0.0031272	0.02528051	5.55212947		
STX6	-3.9193771	3.91937707	2.7278432	12.9633564	0.00031765	0.00410619	0.06609216		p, ca, c
STX7	-1.0726041	1.07260406	6.07026895	16.1351445	5.90E-05	0.00103611	0.47546002		
STX8	2.06755816	2.06755816	4.23649692	14.1000394	0.00017334	0.00249364	4.19176595		
SULF2	1.0812995	1.0812995	5.65333119	13.2919371	0.00026655	0.00356332	2.11594115	yes	p, ca, c
SULT1A2	-3.0402622	3.04026225	2.61569417	8.03969752	0.00457632	0.03421937	0.12155977		p, ca, c
SVIL	-1.1801973	1.18019728	4.3270113	7.84043141	0.00510904	0.0371388	0.44129115	yes	p, ca, c
SVIP	-1.2398204	1.23982038	5.63938636	12.7064603	0.00036439	0.00461258	0.42342537		
SYNE2	-4.0245167	4.02451669	3.87971787	25.3402481	4.81E-07	1.61E-05	0.06144687	yes	
TACC1	-1.8123113	1.81231135	4.10496632	11.7887681	0.00059589	0.00693008	0.28473439		p, ca
TAGLN2	-1.1386552	1.13865519	12.7188507	70.1892695	5.39E-17	1.41E-14	0.45418275		p, ca, c
TANK	1.36373905	1.36373905	9.69925038	153.639437	2.78E-35	3.80E-32	2.57351297	yes	p, ca, c
TAPSAR1_loc	-1.1523295	1.15232946	7.68712603	41.3648664	1.26E-10	1.02E-08	0.44989821		
TARS	3.1249644	3.1249644	2.20701646	7.18303951	0.00735959	0.04865854	8.72384658		
TBC1D1	1.71494408	1.71494408	3.81183432	11.045869	0.00088885	0.00953383	3.28283918	yes	p, ca, c
TBC1D25	-5.4513155	5.45131554	2.40958398	19.5406403	9.85E-06	0.00021678	0.02285549		p, ca, c
TET2	-1.3396687	1.33966865	5.87497926	27.0456938	1.99E-07	7.31E-06	0.39511139		p, ca
TGFB1	2.25898496	2.25898496	2.58157008	7.91957026	0.00489029	0.03578594	4.78654594		p, ca, c
TGM3	-4.6791089	4.67910891	2.72331101	26.2965033	2.93E-07	1.04E-05	0.03903443		p, ca, c
TGOLN2	-1.2200049	1.22000491	5.20811433	12.4825139	0.00041078	0.0051054	0.42928126	yes	p
THBD	1.69350452	1.69350452	4.0312373	10.0698742	0.00150713	0.01431646	3.23441438	yes	p, ca, c
TM2D2	-2.499528	2.499528	2.82616542	8.84441259	0.00293988	0.02423076	0.17683454		p, ca, c
TM2D3	-1.0450183	1.04501831	7.05943339	24.9930982	5.75E-07	1.91E-05	0.48463876		p
TMCC1	-5.0256426	5.02564259	4.20642715	49.4513387	2.03E-12	2.48E-10	0.03069947	yes	
TMED10	1.05437353	1.05437353	5.39761942	17.7743301	2.49E-05	0.00050303	2.07681619		p, ca, c
TMEM176A	6.81084864	6.81084864	3.30946988	54.9490315	1.24E-13	1.88E-11	112.271554		p, ca
TMEM176B	4.09550399	4.09550399	6.21093209	24.0088799	9.59E-07	2.89E-05	17.0950175		p, ca
TMEM43	-1.1368747	1.13687466	4.69880705	11.2879098	0.00078013	0.0086208	0.45474363	yes	p, ca, c
TMLHE	-1.5964009	1.59640085	3.39235867	7.37771903	0.00660369	0.04479556	0.33070096		
TNFAIP8L2	-3.3161898	3.31618976	2.8727346	10.8271834	0.00100021	0.01046209	0.10039854		p
TNFSF8	1.10757846	1.10757846	4.81357132	8.56609179	0.00342482	0.02724443	2.15483658		p, ca, c
TOPORS-AS1	-1.4772828	1.47728283	7.57599438	60.3102757	8.10E-15	1.48E-12	0.35916463		p, ca, c
TPMT	-1.7100993	1.71009927	4.63921384	11.775855	0.00060004	0.0069531	0.30563904		p
TPP2	1.35652967	1.35652967	3.72016037	7.90721301	0.00492381	0.03593527	2.56068478		
TRAFD1	-1.4877076	1.48770761	3.75726096	9.02900492	0.00265729	0.02230415	0.35657869	yes	p
TRANK1	-3.2344262	3.23442624	3.71402751	18.5919013	1.62E-05	0.00034003	0.10625287	yes	p, ca, c
TREML1	3.65378468	3.65378468	2.50502752	13.3707417	0.00025558	0.00343839	12.5863205		p, ca, c
TRIM26_loc3	-3.0285024	3.02850238	2.91620052	11.8203144	0.00058588	0.00686155	0.12255469		
TRIM38	-1.4059649	1.40596488	5.49128646	13.4421608	0.00024603	0.00336285	0.37736568	yes	
TRMT6	4.85451157	4.85451157	2.4014543	16.4454781	5.01E-05	0.00090871	28.9303439		p
TSC22D1	2.93530872	2.93530872	3.25100186	15.773799	7.14E-05	0.00122651	7.64919918	yes	
TSPAN2	-2.038328	2.03832801	3.8510493	11.2650477	0.0007898	0.0086578	0.24344571		p, ca, c

TSPO	1.6020235	1.6020235	7.22530026	56.8993882	4.59E-14	8.01E-12	3.03568794	yes	p, ca, c
TUBB_loc4	-1.7047856	1.70478562	5.30282511	22.116176	2.57E-06	6.83E-05	0.30676682		
TUFT1	-4.4574863	4.4574863	2.14535015	11.2772653	0.00078462	0.00863555	0.04551588	yes	
TWF1	2.15565108	2.15565108	2.35421386	9.27128851	0.00232774	0.02028352	4.45569684		p
UBA3	-1.5833292	1.58332916	3.61407175	8.02918757	0.00460295	0.03437161	0.33371093		p, ca
UBE2E3	1.51792468	1.51792468	4.6033357	9.24895974	0.00235629	0.02043487	2.86378796	yes	
UBE2H	-1.4125097	1.41250965	4.10478793	9.47044633	0.00208809	0.01860943	0.37565764		
UBE3B	-4.2526567	4.25265675	2.41851524	10.9429809	0.00093959	0.00999978	0.05245933		
UCHL3	-3.7532579	3.75325791	2.53728124	11.7203596	0.0006182	0.00710347	0.07415779	yes	
UCP2	-1.6663853	1.66638526	5.03278397	14.1903241	0.00016522	0.00239566	0.31504171	yes	
USP32P1_p1	-3.03008	3.03008005	2.4515643	7.61992913	0.00577268	0.04061622	0.12242074		
USP47	1.78471663	1.78471663	3.43704415	8.22724789	0.00412661	0.03163346	3.44550781		
VDAC3	-1.1706092	1.17060921	5.11280418	7.60885733	0.00580823	0.04074756	0.44423371		
VIPAS39	-5.522603	5.52260296	2.1734856	11.0296612	0.00089666	0.00959877	0.02175359		
VPS35	-1.2559211	1.25592108	5.57853551	16.4382849	5.03E-05	0.00090916	0.41872615		
VPS8	-1.6436246	1.64362463	4.55232132	11.6439826	0.00064411	0.00735488	0.32005137		p, ca, c
VSTM1	-1.7478946	1.74789457	5.43902674	21.6689119	3.24E-06	8.38E-05	0.29773597		p, ca
VTRNA1-3	3.20237852	3.20237852	2.27816751	8.12209702	0.00437289	0.03310475	9.2047499		p, ca, c
WARS	-1.5915513	1.59155126	5.99171429	20.3816738	6.34E-06	0.00014922	0.33181448	yes	p, ca, c
WBP1	-3.1523802	3.15238021	2.61748078	7.96908111	0.00475831	0.03525991	0.1124706		p
WHSC1L1	1.91604526	1.91604526	3.52493699	7.18776467	0.00734024	0.04858917	3.77387138		p
WLS	1.51799675	1.51799675	5.85875665	24.873296	6.12E-07	2.01E-05	2.86393103	yes	p, ca, c
XAF1	-2.0336472	2.03364717	3.8300588	7.96233761	0.00477607	0.03527983	0.24423686	yes	
XBP1	1.74059296	1.74059296	5.29320778	24.58251	7.12E-07	2.26E-05	3.34172488		p, ca
XKR8	-1.5441222	1.54412225	4.63818359	7.49514866	0.00618654	0.04286781	0.34290426	yes	p, ca, c
YEATS2	3.57280009	3.57280009	4.4688212	21.9972911	2.73E-06	7.19E-05	11.8992611	yes	
ZBP1	-3.8951238	3.89512381	3.52221439	21.1877647	4.16E-06	0.00010374	0.06721263	yes	p, ca, c
ZC3H13	-1.9272257	1.92722572	4.7723288	10.4066686	0.00125561	0.01253552	0.2629343		
ZMYM2	-4.4737207	4.4737207	2.74263558	23.2213627	1.44E-06	4.10E-05	0.04500657		
ZNF200	-1.9905079	1.99050789	4.36529798	12.0470313	0.00051875	0.00619448	0.25165028		p, ca, c
ZNF254	-1.6021341	1.60213412	4.843663	12.7746121	0.00035136	0.00447856	0.32938937		p, ca, c
ZNF268	-4.3781774	4.37817743	2.31515554	11.8877062	0.00056506	0.00666038	0.04808806		
ZNF281	1.218061	1.218061	4.31260639	8.5322059	0.00348917	0.02763601	2.32633844		p, ca
ZNF33A	-1.1392365	1.1392365	4.70944126	7.41343917	0.00647385	0.04427734	0.45399978		
ZNF429	-1.2864753	1.28647533	5.87313315	9.14690267	0.00249139	0.02123691	0.40995137		p, ca
ZNF561	-4.202088	4.202088	2.49914978	13.0807206	0.00029835	0.00392149	0.05433072		
ZNF586	-3.0808296	3.08082962	2.95269227	10.1012213	0.00148171	0.01417322	0.11818922		
ZNF592	-2.6714171	2.67141706	2.70438953	8.12901899	0.00435623	0.03302421	0.15697241		p, ca, c
ZNF675	2.71426917	2.71426917	3.41314878	8.82383472	0.00297321	0.02443205	6.56260758		
ZNF684	-3.8420931	3.8420931	2.22661197	7.2587171	0.00705577	0.04727671	0.06972921	yes	p
ZNF91	3.27331194	3.27331194	4.86062011	19.3877798	1.07E-05	0.0002339	9.66863307		p
ZSCAN16-AS1	1.48638549	1.48638549	4.2573853	7.39920534	0.00652527	0.04442858	2.80186121		

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Table E7.
Differentially transcribed (Fold change >2 (absLog2FC>1) and FDR<0.05) genes between patients and controls in A) IFNα2b and B) IFNγ stimulated granulocytes. Overap with ChIP-seq peaks mapped to nearby genes within ±50 kb range is shown as following: p= patients spesific binding; p, ca= binding in patient and carrier cells; p, ca, and c= binding in patient, carrier and control cells.

A

	logFC	ABSFC	logCPM	LR	PValue	FDR	FC	Overlap with ChiP-seq peaks
A4GALT	2.60231977	2.60231977	1.20552019	8.16573468	0.00426892	0.03539819	6.07262284	
ABCA1	1.09245377	1.09245377	5.05677529	16.2403162	5.58E-05	0.00126355	2.13236406	
ABCG1	1.38715713	1.38715713	3.11564341	14.2796222	0.00015756	0.00283047	2.61562756	p, ca, c
ABHD10	-1.7872182	1.78721821	2.14251526	10.4415958	0.00123209	0.01416268	0.28973016	p
ABLIM1	-1.1433821	1.14338212	5.52386483	19.0957413	1.24E-05	0.00036355	0.45269707	
ACAP1	-1.2526036	1.2526036	4.98244341	35.1078583	3.12E-09	3.17E-07	0.41969012	
ACSL5	1.3528111	1.3528111	2.75307352	10.1464897	0.00144576	0.01590602	2.55409308	p
ADAM15	1.26428837	1.26428837	4.32727964	25.1984164	5.17E-07	2.69E-05	2.40208694	
ADIRF	3.33684343	3.33684343	1.22772732	11.0518378	0.00088599	0.01073168	10.1039215	
AGTRAP	1.05355718	1.05355718	5.48610139	24.8872424	6.08E-07	3.09E-05	2.07564134	p, ca, c
AHSP	2.68855725	2.68855725	1.66211414	9.27367232	0.00232471	0.02263587	6.44668393	
AK5	-4.5597199	4.55971993	1.1932392	19.0716871	1.26E-05	0.00036697	0.04240212	
ALCAM	1.47783077	1.47783077	2.97860155	18.9070243	1.37E-05	0.00039495	2.78529622	p
ANAPC1	-1.196483	1.19648296	2.63819007	7.49282986	0.00619451	0.04625919	0.4363377	
ANK1	-2.781739	2.78173896	1.14329551	7.71067974	0.00548951	0.04228746	0.14541631	p
ANKRD22	1.57668908	1.57668908	3.25133491	21.1741763	4.19E-06	0.00015595	2.98284515	p, ca
ANKRD39	-1.3523023	1.35230226	3.06720214	16.5373975	4.77E-05	0.00111662	0.39166653	
ANO9	-2.4467571	2.44675709	1.36787981	7.32457653	0.0068018	0.04941946	0.18342255	
ANXA5	1.08616483	1.08616483	7.92857702	35.4063602	2.68E-09	2.81E-07	2.12308896	
AP1S2	1.29492377	1.29492377	5.06979387	40.439656	2.03E-10	2.69E-08	2.4536403	p, ca, c
AP5B1	2.31752036	2.31752036	3.15001947	10.0277308	0.00154201	0.0166272	4.98474726	p, ca, c
APBB1	-1.6133785	1.61337851	3.73089581	21.2738507	3.98E-06	0.00014973	0.32683208	
APOC1	2.82615469	2.82615469	1.4346519	10.4166062	0.00124887	0.01426651	7.09181394	
ARMT1	1.69252354	1.69252354	2.22532734	7.42717293	0.00642462	0.04740822	3.23221584	
ASAH1	1.04694974	1.04694974	6.45694856	44.7733244	2.21E-11	3.77E-09	2.06615679	p, ca, c
ASCC2	-1.4267965	1.42679652	3.94039013	35.4377947	2.63E-09	2.80E-07	0.3719559	p, ca, c
ATAT1	-2.4654253	2.46542527	1.61614897	7.96455629	0.00477022	0.03821249	0.18106439	p, ca, c
ATP1B2	2.31964034	2.31964034	1.35844507	8.3926929	0.00376732	0.03256781	4.99207753	p, ca
ATXN7L1	-1.1803709	1.18037094	2.6080614	8.10883023	0.00440501	0.03613983	0.44123803	
AURKA	2.14263495	2.14263495	1.52602712	10.0499025	0.00152356	0.01646757	4.41567793	p, ca, c
AZU1	2.3461805	2.3461805	1.97331911	16.9510041	3.84E-05	0.00093422	5.08476288	
B3GNT5	3.41422619	3.41422619	1.96719919	20.5416072	5.83E-06	0.00020279	10.6606699	p, ca
BACH2	-1.0087891	1.00878914	3.85016216	14.6403913	0.0001301	0.00243282	0.49696318	
BAG5	-1.1072114	1.10721137	3.67398477	13.6481975	0.00022045	0.00366179	0.46419041	
BASP1	1.3740822	1.3740822	5.69742931	31.7094362	1.79E-08	1.51E-06	2.59202961	p, ca, c
BATF2	1.17433993	1.17433993	3.19580382	7.47540602	0.00625475	0.04667042	2.25689599	
BCAT1	1.56889417	1.56889417	3.03500782	14.638677	0.00013021	0.00243282	2.96677223	p, ca
BCL11B	-1.0062859	1.00628588	4.09973332	15.7524296	7.22E-05	0.00154954	0.49782622	
BEX1	1.32746572	1.32746572	4.37082724	20.6845955	5.41E-06	0.00019113	2.50961441	
BEX2	-1.5061596	1.50615957	6.17231171	68.6377527	1.18E-16	5.94E-14	0.35204712	
BEX5	-1.4708693	1.47086926	4.41518789	35.2656647	2.88E-09	2.96E-07	0.36076486	
BPI	2.2398008	2.2398008	3.70354992	43.9741265	3.33E-11	5.37E-09	4.72331843	p
BTBD7	1.57175815	1.57175815	3.1304374	9.28941097	0.00230482	0.02256379	2.9726676	p
C10orf11	1.31866433	1.31866433	2.64009224	13.8947554	0.00019334	0.00330245	2.49435073	
C12orf79	1.78117276	1.78117276	2.14862023	9.00737868	0.00268892	0.02538878	3.43705457	p, ca, c
C16orf72	1.9114205	1.9114205	2.81552475	13.734418	0.00021056	0.00353551	3.76179308	p, ca, c
C17orf97	-2.8342958	2.83429577	1.37574701	8.18728212	0.00421851	0.0352622	0.14021419	p

B

	logFC	ABSFC	logCPM	LR	PValue	FDR	FC	Overlap with ChiP-seq peaks
ABCG1	1.56679759	1.56679759	3.11564341	11.859528	0.00057367	0.01141782	2.96246394	p, ca, c
ABLIM1	-1.5888048	1.5888048	5.52386483	21.8742878	2.91E-06	0.00020506	0.33244675	
ACTA2	2.06120426	2.06120426	2.31069874	9.99122433	0.00157288	0.02359939	4.17334521	p, ca
ADAM15	1.21994522	1.21994522	4.32727964	18.6533161	1.57E-05	0.00078701	2.32937872	
ADAP2	1.39863412	1.39863412	3.53715358	14.0064868	0.00018218	0.00495921	2.6365185	p, ca, c
ADD3	-2.0116671	2.01166709	3.38697533	22.6190559	1.98E-06	0.00015125	0.2479864	p, ca, c
ADGRG1	1.28622974	1.28622974	4.20093584	12.9948809	0.00031234	0.00754636	2.43889853	
ADM	1.58779661	1.58779661	4.42767695	27.3577306	1.69E-07	2.08E-05	3.00589916	p, ca, c
AGPAT2	1.20546458	1.20546458	3.43263621	9.40652681	0.00216214	0.02881583	2.3061152	p
AKR1C1	2.920728	2.920728	1.4292661	9.62388992	0.00192063	0.02661774	7.57228126	
ALAS1	1.08455819	1.08455819	5.84022689	17.1971566	3.37E-05	0.00135919	2.12072594	p, ca, c
ALDH6A1	-4.5848598	4.58485976	1.34148663	7.99550659	0.00468936	0.04950121	0.04166963	
ANKRD22	1.46359442	1.46359442	3.25133491	13.8020922	0.00020311	0.00542989	2.7579464	p, ca
ANKRD36	-1.7433823	1.74338233	3.186422	11.7877087	0.00059623	0.01176623	0.29866864	
ANKRD50	2.05657755	2.05657755	2.11510613	12.4225421	0.00042418	0.00925824	4.15998275	
ANP32E	-1.3172534	1.31725342	3.65258531	10.2260576	0.0013847	0.02157272	0.4012982	p, ca
ANXA2	1.05446344	1.05446344	9.16437002	39.467423	3.34E-10	9.42E-08	2.07694561	p
ANXA5	1.02634545	1.02634545	7.92857702	23.3573819	1.35E-06	0.00012035	2.03685806	
ARHGAP15	-1.1779787	1.17797865	3.71518975	12.154024	0.00048982	0.01026919	0.44197031	p
ARL4C	-1.0111699	1.01116989	5.47384027	30.0932733	4.12E-08	6.20E-06	0.49614376	
ARRDC2	-2.4350258	2.4350258	2.14616615	12.9597117	0.00031827	0.00764855	0.18492013	
ASCC2	-1.5918697	1.59186967	3.94039013	26.7086039	2.37E-07	2.61E-05	0.33174125	p, ca, c
ASGR2	1.27796647	1.27796647	3.81048253	12.9043911	0.00032781	0.00780026	2.42496928	
ATF7IP	-1.4217092	1.4217092	3.31003945	9.37491634	0.00219975	0.02914504	0.37326983	
ATP1B2	2.51575625	2.51575625	1.35844507	10.8119821	0.00100845	0.01727569	5.71897361	p, ca
ATP2B4	-1.0053079	1.00530792	3.62200544	8.66890198	0.00323686	0.03838429	0.49816379	
BAG3	-2.9846105	2.98461054	3.66504438	11.8927945	0.00056352	0.01125855	0.12634053	
BASP1	1.00882852	1.00882852	5.69742931	12.582605	0.00038935	0.00875174	2.01227646	p, ca, c
BATF2	1.3661287	1.3661287	3.19580382	8.69935801	0.00318322	0.03815074	2.57777922	
BATF3	2.41720009	2.41720009	2.11967356	9.46566968	0.00209353	0.0281505	5.34133395	p
BCS1L	-3.8149622	3.81496222	1.5164719	10.1442454	0.00144752	0.02232052	0.07105292	
BEND5	-4.5450698	4.54506977	1.51472744	8.3542524	0.00384796	0.04379111	0.04283489	
BET1L	-1.3981056	1.39810559	3.9365965	12.4798062	0.00041137	0.0090663	0.37942704	
BEX1	1.34616377	1.34616377	4.37082724	15.854201	6.84E-05	0.00233281	2.54235196	
BEX2	-1.2327705	1.23277048	6.17231171	29.964577	4.40E-08	6.41E-06	0.42549955	
BEX5	-2.078419	2.07841897	4.41518789	38.9311708	4.39E-10	1.20E-07	0.23677375	
BIN1	1.34940546	1.34940546	3.69549802	9.10923065	0.00254323	0.03259661	2.54807096	
BPI	1.45776267	1.45776267	3.70354992	12.0469619	0.00051877	0.01065362	2.74682057	p
BST2	1.77446543	1.77446543	3.09395416	15.5594361	8.00E-05	0.00264631	3.42111223	p
BTBD19	2.8870823	2.8870823	1.47049898	10.6283697	0.00111366	0.01847197	7.39772821	p
C10orf11	1.748185	1.748185	2.64009224	15.6396267	7.66E-05	0.00254575	3.35935672	
C12orf10	1.6061895	1.6061895	6.54702747	11.6899622	0.00062838	0.01212108	3.04446664	p
C17orf75	-3.6417934	3.64179342	1.72530136	9.32650007	0.00225863	0.02979418	0.08011447	
C19orf52	-3.5542987	3.55429867	1.64678691	9.3886345	0.00218335	0.02901284	0.0851235	
C2orf74	-2.4915887	2.49158869	2.34263552	12.5996991	0.00038581	0.00871542	0.17781036	
C3AR1	1.14619903	1.14619903	4.00100512	14.5871905	0.00013382	0.00397766	2.21330002	p, ca, c
C7orf43	2.85254464	2.85254464	1.3571011	9.61919502	0.00192554	0.02662605	7.22273199	p, ca, c

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C18orf65	3.11313438	3.11313438	1.51014886	14.8952338	0.00011365	0.00218964	8.652604	p, ca, c
C19orf35	2.34253858	2.34253858	1.71936229	7.66253961	0.00563791	0.04316433	5.07194316	p
C1QA	1.09377253	1.09377253	4.17134066	11.127039	0.00085078	0.0104169	2.13431413	
C2orf74	-1.3665956	1.36659564	2.34263552	7.65150852	0.00567249	0.04329104	0.38780528	
C3orf58	1.38983538	1.38983538	2.28411046	7.95215689	0.00480301	0.03835928	2.62048777	p
C4orf27	-2.2102513	2.21025128	2.30483614	12.9073289	0.0003273	0.00502862	0.21609667	
C4orf32	-2.2747656	2.27476562	1.86627044	10.7561395	0.00103934	0.0122925	0.20664615	p
C5AR1	1.25476833	1.25476833	6.48187808	19.9265664	8.05E-06	0.00025604	2.38628826	p, ca, c
C5orf22	-1.7293931	1.72939305	2.37801021	13.6070982	0.00022533	0.00373596	0.30157881	
C9orf64	-2.8562664	2.85626636	1.54735232	9.37902995	0.00219482	0.02176988	0.13809506	p, ca, c
CA13	2.36962439	2.36962439	1.28520296	8.65663421	0.00325873	0.02906797	5.16806561	
CAMK4	-2.1765711	2.17657106	4.81777466	63.0121961	2.05E-15	8.84E-13	0.22120087	
CAPN10	2.9766223	2.9766223	1.38826695	11.6626054	0.00063769	0.00845952	7.87141113	p
CAPNS1	1.11801292	1.11801292	4.29949379	9.56534163	0.00198285	0.02014001	2.17047818	
CBR3	-1.1016637	1.10166369	3.88047055	13.4319111	0.00024738	0.00402761	0.46597883	p, ca, c
CCAR1	-1.1542685	1.15426847	3.16862467	11.6187751	0.00065289	0.00856248	0.44929395	
CCDC66	-1.9818871	1.98188711	2.37167433	14.3397096	0.00015261	0.00278024	0.25315851	
CCDC88C	-2.1305795	2.13057952	1.74495879	10.2528153	0.00136476	0.01527546	0.22836611	
CCL20	2.12232123	2.12232123	2.14062076	11.0652308	0.00087962	0.01071188	4.3539391	p, ca
CCL7	1.02593085	1.02593085	7.04124656	17.947089	2.27E-05	0.00059317	2.03627279	p, ca, c
CCL8	1.61058007	1.61058007	6.04204171	109.810388	1.08E-25	2.44E-22	3.053746	
CCR6	-1.519048	1.51904799	3.10468592	12.8559397	0.00033641	0.00510033	0.34891609	p, ca, c
CCR7	-1.1379166	1.13791662	7.35120223	56.967792	4.43E-14	1.38E-11	0.45441532	
CCRL2	1.03172984	1.03172984	4.05870078	16.2797529	5.46E-05	0.00124689	2.04447418	p
CD180	1.58747176	1.58747176	2.72262598	8.08238168	0.00446977	0.03645434	3.00522241	
CD24	1.73882668	1.73882668	2.68551451	8.52774391	0.00349773	0.03071476	3.33763614	
CD27	-1.4252261	1.42522609	4.1162356	29.3645239	6.00E-08	4.55E-06	0.37236101	p, ca, c
CD28	-1.8115234	1.81152339	3.74388669	27.0286805	2.00E-07	1.18E-05	0.28488994	
CD300E	1.04290723	1.04290723	5.65660748	12.2305731	0.00047013	0.00671102	2.06037541	
CD300LB	1.56804303	1.56804303	2.9198664	10.3833976	0.00127153	0.01445231	2.96502245	p, ca, c
CD300LF	1.25706636	1.25706636	3.86839455	16.4024389	5.12E-05	0.00117855	2.39009235	p, ca
CD302	1.01485819	1.01485819	3.99671867	12.64085	0.00037741	0.00560898	2.02070426	
CD33	1.21133646	1.21133646	4.27116688	19.8815719	8.24E-06	0.00025977	2.31552038	
CD68	1.00624095	1.00624095	9.3952761	18.7089638	1.52E-05	0.0004354	2.00867053	p, ca, c
CD8B	-1.7438643	1.7438643	5.20848781	76.3962222	2.32E-18	1.31E-15	0.29856888	
CDA	1.08870963	1.08870963	5.56202671	19.3579297	1.08E-05	0.0003275	2.12683723	p, ca, c
CDC20B	2.57944746	2.57944746	1.34300738	8.29267929	0.00398052	0.03384375	5.97710739	
CDC42EP3	1.05789955	1.05789955	6.65317054	59.2308934	1.40E-14	4.87E-12	2.08189823	p, ca, c
CDC42EP4	1.16715245	1.16715245	3.87611013	12.4026824	0.00042872	0.00618507	2.24568013	
CDIPT	2.18568733	2.18568733	3.49561211	15.5060837	8.22E-05	0.00170441	4.54943482	p
CDK10	-1.5462477	1.54624769	2.20511801	8.12069332	0.00437628	0.03594917	0.34239945	p, ca, c
CDKN2B	1.39822362	1.39822362	2.75729579	9.59512966	0.00195094	0.01996456	2.63576842	p
CEACAM21	-1.0228402	1.02284024	4.13828178	12.079213	0.00050987	0.00713188	0.49214651	p, ca, c
CEBPA	2.39329333	2.39329333	3.28802347	7.33871827	0.00674849	0.04925638	5.25355257	p, ca
CEBPB	3.12140713	3.12140713	1.66196113	14.2994015	0.00015591	0.00281769	8.70236263	p, ca, c
CENPT	-1.9103086	1.91030856	2.54982552	12.093658	0.00050594	0.00709882	0.26603564	p
CENPW	1.06650154	1.06650154	4.26247593	22.9917737	1.63E-06	7.03E-05	2.09434851	p
CEP164	-2.329866	2.32986601	1.47255853	7.30411095	0.0068797	0.04985164	0.19890259	p
CFD	1.81697501	1.81697501	7.67784999	95.5254346	1.46E-22	1.47E-19	3.52341645	
CFP	1.07564008	1.07564008	6.40615071	26.2494378	3.00E-07	1.67E-05	2.10765697	
CH25H	1.45297076	1.45297076	1.73096909	9.44043998	0.00212253	0.02126291	2.73771213	
CLEC12A	-1.9662497	1.96624966	2.1466291	14.9926181	0.00010793	0.00211099	0.25591743	p
CLEC4A	1.00939108	1.00939108	4.44522716	20.1266848	7.25E-06	0.00023815	2.01306127	p, ca
CLUAP1	-2.3423641	2.34236412	1.78431893	13.7471694	0.00020914	0.00352565	0.19718694	
CMTM8	-2.7392159	2.73921589	1.39825951	9.78984527	0.00175478	0.01839827	0.14976621	p
COG2	-1.2798303	1.27983026	2.05699356	7.59371339	0.00585722	0.04436364	0.41184396	
CREB3L2	1.8006819	1.8006819	2.82128381	14.4930808	0.00014068	0.00259947	3.48384853	
CRISPLD2	1.55164415	1.55164415	3.24392371	14.920741	0.00011212	0.00216948	2.93151034	p, ca
CSF3R	1.15500544	1.15500544	5.74673757	8.99216894	0.00271139	0.02548162	2.22685163	p, ca, c
CSPP1	-1.024411	1.02441099	3.48499675	11.2366587	0.00080197	0.00991332	0.49161097	p, ca
CSRNP2	2.47020696	2.47020696	1.6287116	7.42842561	0.00642015	0.04740822	5.54123272	

CALD1	-2.6768446	2.67684455	2.42010683	9.21576472	0.0023994	0.03110613	0.15638298	
CAMK1	2.51181485	2.51181485	2.65177548	10.923784	0.00094937	0.01656091	5.70337087	
CAMK4	-1.9868127	1.9868127	4.81777466	33.7104821	6.40E-09	1.34E-06	0.25229566	
CAPG	1.0843097	1.0843097	6.83710173	21.907405	2.86E-06	0.00020506	2.12036069	p, ca
CAPNS1	1.22554575	1.22554575	4.29949379	8.79602854	0.00301887	0.036964	2.33843892	
CBR3	-1.3283846	1.32838463	3.88047055	10.7893655	0.00102085	0.01737173	0.39821387	p, ca, c
CCDC58	-2.4859923	2.4859923	2.00215229	9.96598352	0.00159459	0.02377675	0.17850145	
CCL28	-2.2554787	2.25547866	2.26785637	9.48865337	0.00206747	0.02795263	0.20942729	
CCL7	1.36870749	1.36870749	7.04124656	24.1252265	9.03E-07	8.50E-05	2.58239107	p, ca, c
CCL8	1.51424017	1.51424017	6.04204171	71.2332335	3.17E-17	4.78E-14	2.85648346	
CCR4	-2.2535781	2.25357814	3.89492883	27.2921935	1.75E-07	2.11E-05	0.20970336	
CCR6	-1.869682	1.86968197	3.10468592	12.6177776	0.0003821	0.00866614	0.27363374	p, ca, c
CCRL2	1.43324071	1.43324071	4.05870078	21.5604065	3.43E-06	0.0002347	2.7005265	p
CD109	1.12395684	1.12395684	4.27159864	9.02755391	0.0026594	0.03360888	2.17943903	
CD28	-1.9837215	1.98372152	3.74388669	17.4897449	2.89E-05	0.00120284	0.25283682	
CD300C	1.22456026	1.22456026	6.62375821	22.6848471	1.91E-06	0.00014741	2.33684211	p, ca, c
CD300E	1.32818733	1.32818733	5.65660748	15.0627776	0.00010399	0.00324031	2.51086998	
CD302	1.04085253	1.04085253	3.99671867	9.64939687	0.00189414	0.02633143	2.0574431	
CD33	1.37968832	1.37968832	4.27116688	19.0725439	1.26E-05	0.00064978	2.60212149	
CD8B	-1.610142	1.610142	5.20848781	43.4870583	4.27E-11	1.43E-08	0.32756611	
CDC20B	3.44069454	3.44069454	1.34300738	9.53030227	0.00202107	0.02746222	10.8580607	
CDC42EP2	1.16347767	1.16347767	3.40274166	9.97990489	0.00158258	0.02363666	2.2399673	p
CDC42EP4	1.30609048	1.30609048	3.87611013	12.08942	0.00050709	0.01043745	2.4727056	
CEACAM21	-1.2617179	1.26171791	4.13828178	12.1020287	0.00050367	0.01039564	0.41704706	p, ca, c
CEP70	-3.9164195	3.91641955	1.32783569	8.09346222	0.00444252	0.0478458	0.06622779	p
CEP76	-1.3407872	1.34078722	2.74212573	8.41084241	0.0037299	0.04277076	0.39480517	
CEP85	-3.4238041	3.42380405	1.51538062	8.58913781	0.00338174	0.03958214	0.09318205	
CFAP36	-1.2607395	1.26073948	4.11840618	18.6537302	1.57E-05	0.00078701	0.41732999	p
CFD	1.56607217	1.56607217	7.67784999	55.0479428	1.18E-13	7.09E-11	2.96097471	
CHEK2	-3.8494362	3.84943615	1.54745109	8.00628433	0.00466153	0.04943847	0.0693752	
CISH	1.08888662	1.08888662	5.51786639	18.2115155	1.98E-05	0.00091184	2.12709817	
CLEC16A	-3.251521	3.25152104	2.25033049	11.7460289	0.00060973	0.01200335	0.10500129	
CLIC4	1.30936412	1.30936412	3.40591991	12.25758	0.00046337	0.00987507	2.47832281	
CLUAP1	-3.5566399	3.5566399	1.78431893	11.555986	0.00067531	0.01263762	0.08498548	
CMTR1	-3.3332769	3.33327692	2.52765097	13.0867517	0.00029739	0.00736228	0.09921645	
CNOT3	1.45947889	1.45947889	3.76865848	10.7072056	0.00106719	0.01795742	2.75009011	p, ca
CNOT6L	-1.4275193	1.42751933	3.00297717	9.68180926	0.00186101	0.02619332	0.37176959	p
COG2	-3.1002988	3.10029877	2.05699356	12.6149765	0.00038267	0.00866614	0.11660497	
CPEB4	1.0526224	1.0526224	4.70634938	10.7194318	0.00106016	0.01790584	2.07429689	p
CPPED1	1.19807974	1.19807974	3.57801666	10.5487659	0.00116266	0.01909436	2.29434085	p, ca, c
CRISPLD2	2.09602675	2.09602675	3.24392371	21.0558531	4.46E-06	0.00027992	4.27530324	p, ca
CROT	-2.8617358	2.86173578	2.14352064	12.3528687	0.00044031	0.00945044	0.13757252	
CRTAP	1.1253468	1.1253468	4.92178384	17.8595975	2.38E-05	0.00104316	2.18153982	
CSPP1	-1.3165195	1.31651954	3.48499675	11.0780124	0.00087357	0.01544738	0.40150238	p, ca
CSTA	1.47257847	1.47257847	8.552218	60.286862	8.20E-15	5.70E-12	2.77517447	p, ca, c
CXCL1	2.6727029	2.6727029	1.76982407	11.2842185	0.00078169	0.01412665	6.37622659	p, ca, c
CYB5R1	-1.2982243	1.29822432	3.29906075	8.751875	0.00309284	0.03755529	0.40662637	p, ca, c
DCUN1D5	-1.0659503	1.06595033	4.28235361	18.3008358	1.89E-05	0.00089236	0.47765791	p, ca
DDHD2	-1.842447	1.84244703	2.11405163	8.00815745	0.00465671	0.04943847	0.27884841	
DDRGK1	-2.15909	2.15908999	4.49348864	21.3122996	3.90E-06	0.00026119	0.22389745	p, ca
DDX1	-1.2135914	1.21359141	4.36281837	13.4906967	0.00023975	0.00608532	0.43119388	
DDX47	-1.6486273	1.64862734	3.52377577	22.9725649	1.64E-06	0.00013505	0.31894347	
DDX60L	1.24562082	1.24562082	3.91082154	11.4215781	0.00072596	0.01332004	2.37120569	p, ca, c
DEFB1	2.01324504	2.01324504	4.53960466	13.5534221	0.00023187	0.0059353	4.03689214	
DENND3	1.83758464	1.83758464	2.46019956	8.59748988	0.00336627	0.03955473	3.57411149	p, ca, c
DESI2	1.53347846	1.53347846	3.48878545	14.1611657	0.0001678	0.00475128	2.89482967	
DGKA	-1.5320131	1.53201313	4.24420213	16.8157003	4.12E-05	0.00158384	0.34579451	
DHRS3	-3.0670273	3.06702729	2.74743328	30.3032426	3.70E-08	5.76E-06	0.11932537	
DHRS4L1	-4.4989935	4.49899345	1.00333788	16.2228643	5.63E-05	0.00200323	0.04422502	p
DHRS4L2	-5.065296	5.06529598	1.31834891	16.4466096	5.00E-05	0.00183804	0.02986716	p
DHX38	-1.4412264	1.44122638	3.16056956	9.81121985	0.0017345	0.02499424	0.36825413	p, ca, c

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CSTA	1.49539696	1.49539696	8.552218	81.3658838	1.88E-19	1.21E-16	2.81941717	p, ca, c
CTSB	1.06137924	1.06137924	7.16145914	60.3652508	7.88E-15	2.85E-12	2.08692571	p
CXCL1	2.69977679	2.69977679	1.76982407	11.9428768	0.00054857	0.00755618	6.49701387	p, ca, c
CXorf21	1.29844773	1.29844773	2.94301075	15.0485228	0.00010478	0.00206728	2.45964095	p, ca, c
DAB2	1.34975488	1.34975488	4.81079091	22.3262647	2.30E-06	9.32E-05	2.54868819	
DDAH2	1.09134042	1.09134042	6.54812539	32.1669006	1.41E-08	1.23E-06	2.13071911	p, ca, c
DDHD2	-1.7276872	1.72768718	2.11405163	10.4468004	0.00122862	0.01414244	0.30193561	
DDX47	-1.0600738	1.06007376	3.52377577	18.0019732	2.21E-05	0.00057966	0.47960754	
DDX60L	1.255875	1.255875	3.91082154	22.541718	2.06E-06	8.45E-05	2.38811945	p, ca, c
DEFB1	1.86373531	1.86373531	4.53960466	17.8853598	2.35E-05	0.00060572	3.6394875	
DGKA	-1.4916774	1.49167738	4.24420213	26.2716175	2.97E-07	1.66E-05	0.35559886	
DHRS3	-1.9948126	1.99481263	2.74743328	23.8417826	1.05E-06	4.95E-05	0.25090052	
DHRS4L1	-3.551562	3.55156198	1.00333788	15.5434424	8.06E-05	0.00168048	0.08528513	p
DHRS4L2	-4.5859037	4.58590375	1.31834891	22.9831908	1.63E-06	7.03E-05	0.04163949	p
DIEXF	-1.1135379	1.1135379	2.88950689	7.49828083	0.00617579	0.04619574	0.46215929	
DMTN	-2.4720419	2.47204187	1.54396348	7.81541828	0.00518024	0.04045688	0.18023588	
DMXL2	1.76029158	1.76029158	3.20840969	40.1659068	2.33E-10	3.01E-08	3.38766586	p, ca, c
DNAJA3	-1.4348071	1.43480707	2.75295969	8.79796254	0.00301567	0.02749708	0.36989634	p
DNAJB11	1.03909549	1.03909549	5.63212767	32.3300402	1.30E-08	1.14E-06	2.05493889	p, ca
DNAJB5	1.62348686	1.62348686	3.42739335	12.5280865	0.00040088	0.0058996	3.08118833	p, ca
DOCK4	1.58511291	1.58511291	2.67246564	14.0140465	0.00018145	0.00314628	3.00031278	p
DPAGT1	-2.6105913	2.61059125	1.41931925	8.03353841	0.0045919	0.03707994	0.16373206	p, ca, c
DPP4	-3.0016823	3.00168234	1.32432042	12.4947774	0.00040809	0.00599596	0.12485432	p
DROSHA	-3.1400646	3.14006464	2.07267413	13.5027042	0.00023822	0.00389737	0.11343481	
DSC2	1.9695019	1.9695019	2.67705363	19.0304708	1.29E-05	0.00037378	3.91632881	
DUSP28	2.46584396	2.46584396	1.30279462	8.37657815	0.00380087	0.03277166	5.52450025	p
DUSP6	1.51461901	1.51461901	5.48003009	35.4436407	2.63E-09	2.80E-07	2.85723363	p
ECHDC2	-1.4446635	1.44466352	2.66166092	8.92391323	0.00281461	0.02616543	0.36737783	
EML2	-2.1851767	2.18517667	2.0356441	8.51779349	0.00351691	0.03085317	0.21988534	p
EMP1	1.69057562	1.69057562	7.23784392	63.221126	1.85E-15	8.35E-13	3.22785466	
ENG	1.01773891	1.01773891	4.6232439	11.395496	0.00073622	0.00938123	2.02474316	
ENO2	-1.2491004	1.24910041	3.96559573	14.4793729	0.0001417	0.0026095	0.42071046	p, ca, c
EPAS1	2.01525511	2.01525511	2.99206845	11.9094511	0.0005585	0.00765796	4.04252055	p
EPHB6	-2.4463427	2.44634275	2.46610854	18.2619296	1.93E-05	0.00051928	0.18347524	
EPHX2	-2.2710735	2.27107345	1.90784241	10.5005572	0.00119339	0.01377641	0.20717568	
ERCC6L2	-2.0146453	2.01464535	2.5195257	10.248653	0.00136784	0.01527546	0.24747499	
ERO1L	1.79852394	1.79852394	1.92984913	10.4999578	0.00119377	0.01377641	3.47864134	p, ca, c
ETS2	1.0992148	1.0992148	4.07472444	13.17461	0.00028377	0.00443027	2.1423806	p, ca, c
ETV7	1.19658832	1.19658832	4.41824861	12.4030172	0.00042864	0.00618507	2.29197026	p, ca, c
EVL	-1.0002534	1.00025339	5.22595355	21.2044241	4.13E-06	0.00015414	0.49991219	
EXTL3	1.12400838	1.12400838	4.33203305	18.4261184	1.77E-05	0.00048657	2.17951689	p
FAM118A	-1.1032089	1.10320888	4.07571949	17.385997	3.05E-05	0.00076571	0.46548001	
FAM134B	-2.9864634	2.98646342	1.22652817	9.46159886	0.00209818	0.02111265	0.12617837	p, ca
FAM214B	1.46509219	1.46509219	3.7105681	13.4742203	0.00024186	0.00394491	2.76081113	
FAM216A	-3.2578681	3.25786806	1.18001932	9.09889565	0.00255764	0.02456607	0.10454036	
FAM228B	-1.5724127	1.57241271	2.26608556	8.34702312	0.0038632	0.03315086	0.3362456	
FAM3C	-2.1633302	2.16333019	2.98195356	11.3443441	0.00075678	0.00951354	0.22324036	
FANCM	-4.0125258	4.01252585	1.26259541	13.1863655	0.00028199	0.00442112	0.06195971	
FCMR	-1.1360095	1.13600946	4.74255305	17.9638338	2.25E-05	0.00058968	0.45501643	
FES	1.43307515	1.43307515	2.66577003	8.57869135	0.0034012	0.03001291	2.70021661	p, ca
FGR	1.20330911	1.20330911	5.35453079	17.9218653	2.30E-05	0.00059716	2.3026723	p, ca, c
FHL3	1.65680614	1.65680614	3.35837853	19.2657141	1.14E-05	0.00034029	3.15317697	p, ca, c
FKBP5	1.00895628	1.00895628	2.85656349	9.34816017	0.00223209	0.02209113	2.01245465	
FLT3LG	-1.2606698	1.26066985	7.31084369	98.0943792	3.99E-23	5.15E-20	0.41735014	p, ca, c
FMNL1	-2.1406349	2.14063489	1.7851151	10.3986898	0.00126105	0.01438741	0.22677997	p, ca, c
FNDC3B	1.13861015	1.13861015	4.19871421	13.8521594	0.00019777	0.0033591	2.20168816	p
FOLR3	2.59851996	2.59851996	2.92150439	21.0985507	4.36E-06	0.00016134	6.05664963	p, ca
FOSL1	1.81315606	1.81315606	5.23612564	31.4188561	2.08E-08	1.74E-06	3.51410197	p, ca
FXYD2	-2.1583765	2.15837649	2.81563308	24.4285653	7.71E-07	3.81E-05	0.22400821	p, ca
GAB2	1.56327708	1.56327708	3.90351538	27.1477189	1.88E-07	1.13E-05	2.95524365	p, ca, c
GAMT	-1.6762972	1.67629723	2.32507564	11.4310667	0.00072226	0.00923106	0.31288465	
DMXL2	1.61689805	1.61689805	3.20840969	19.7513903	8.82E-06	0.00048595	3.06714857	p, ca, c
DNAJB11	1.09836417	1.09836417	5.63212767	25.4985069	4.43E-07	4.60E-05	2.1411178	p, ca
DOCK7	3.08650915	3.08650915	1.67656214	13.6447231	0.00022086	0.00580146	8.49438295	
DPP4	-4.4363903	4.43639034	1.32432042	11.6342164	0.0006475	0.01242203	0.04618633	p
DRAM1	1.18685462	1.18685462	3.79394918	13.0225979	0.00030775	0.00745542	2.27655863	p, ca, c
DTX3	-3.4493866	3.44938655	1.72800012	11.2287299	0.00080541	0.01449733	0.09154427	
DUSP1	1.07749525	1.07749525	4.24153092	8.68976826	0.00320001	0.03819725	2.11036895	p, ca, c
DUSP18	1.24895855	1.24895855	3.80267488	14.0259691	0.0001803	0.00495204	2.37669792	
DUT	-1.2297363	1.22973633	3.6897857	11.7273683	0.00061588	0.01207171	0.42639537	
ECHDC2	-2.0810309	2.08103088	2.66166092	9.43717192	0.00212631	0.02850645	0.23634547	
ELP5	1.20615181	1.20615181	5.17703104	8.92286711	0.00281622	0.03505147	2.30721397	
EMP1	1.32506903	1.32506903	7.23784392	29.3690979	5.98E-08	8.45E-06	2.50544876	
ENO2	-1.276373	1.27637302	3.96559573	9.92856417	0.00162733	0.02402711	0.41283208	p, ca, c
ENTPD7	2.04616211	2.04616211	1.92889788	10.218819	0.00139015	0.02161136	4.1300582	p, ca, c
EPB41	-1.1364939	1.13649393	4.31456776	17.1589577	3.44E-05	0.00137453	0.45486366	p, ca, c
EPHX2	-2.6756823	2.6756823	1.90784241	8.40679809	0.0037382	0.04277779	0.15650902	
ESCO1	-1.0560195	1.05601955	3.91451421	8.69627986	0.0031886	0.03816186	0.48095721	p, ca
ETS1	-1.1289374	1.12893743	6.11072527	13.0585331	0.00030191	0.0074333	0.45725237	p, ca, c
ETV5	3.19489747	3.19489747	1.37541087	10.2048785	0.0014007	0.02170959	9.15714247	p
EVL	-1.2411507	1.24115073	5.22595355	20.7393298	5.26E-06	0.0003229	0.4230351	
EXTL3	1.20827562	1.20827562	4.33203305	14.4964551	0.00014042	0.00413312	2.31061295	p
FABP5	1.00706495	1.00706495	7.27422883	64.4092717	1.01E-15	8.30E-13	2.00981812	
FAF2	-2.8425259	2.84252588	2.4720148	9.61061694	0.00193456	0.02667977	0.13941659	
FAM110A	1.18666486	1.18666486	4.97276407	15.3923052	8.73E-05	0.0028369	2.27625922	p
FAM69A	-3.7218601	3.72186008	1.92114742	12.8212421	0.00034271	0.00804336	0.0757894	
FAS	1.21686886	1.21686886	3.48003427	8.2135387	0.0041579	0.04613866	2.32441692	p, ca
FBXO38	2.2959291	2.2959291	2.09895702	10.6875932	0.00107856	0.01804798	4.91070141	p, ca, c
FCGR1A	1.53784602	1.53784602	3.0625635	17.9353496	2.29E-05	0.00101727	2.90360664	p, ca, c
FCGR1B	1.33310182	1.33310182	3.24856439	12.3807828	0.00043378	0.00937702	2.51943776	p, ca, c
FCMR	-1.5723766	1.57237657	4.74255305	20.5263093	5.88E-06	0.00035197	0.33625402	
FES	2.07055594	2.07055594	2.66577003	13.5927649	0.00022706	0.00591269	4.20048507	p, ca
FGD3	-1.2145097	1.21450968	3.91320644	9.41775004	0.00214895	0.02872473	0.43091951	p, ca, c
FGR	1.08784043	1.08784043	5.35453079	10.931615	0.00094537	0.01655498	2.12555624	p, ca, c
FILIP1L	1.55197724	1.55197724	2.77617951	11.3648816	0.00074846	0.01355325	2.93218726	
FLT1	2.17687912	2.17687912	2.30974241	12.3551236	0.00043978	0.00945044	4.5217434	p, ca, c
FLT3LG	-1.3484939	1.34849388	7.31084369	70.4648672	4.69E-17	6.05E-14	0.3927018	p, ca, c
FOLR3	3.46501504	3.46501504	2.92150439	29.291349	6.23E-08	8.66E-06	11.042654	p, ca
FOSL1	1.1557746	1.1557746	5.23612564	10.5548062	0.00115886	0.01909436	2.22803918	p, ca
FTO	-3.6065496	3.60654965	1.32630773	8.7386881	0.00311529	0.03773421	0.08209569	
FXYD7	-2.231016	2.23101605	3.17992225	12.4332532	0.00042176	0.00924998	0.21300865	
GAB2	1.52880064	1.52880064	3.90351538	21.1038394	4.35E-06	0.00027684	2.88545862	p, ca, c
GALT	-1.2091997	1.20919967	3.44982225	8.27198929	0.00402614	0.04519276	0.43250848	p
GART	-3.6334852	3.63348519	2.27570876	13.8872701	0.00019411	0.00523647	0.08057716	
GAS7	2.33981173	2.33981173	1.7310226	8.4380774	0.00367445	0.04218842	5.0623657	p, ca, c
GATA3	-1.0207521	1.02075212	5.16759903	16.1500329	5.85E-05	0.00206549	0.49285934	
GCDH	-3.3404134	3.34041338	1.68297478	9.4485624	0.00211315	0.02837206	0.09872687	
GFOD1	2.24474411	2.24474411	1.68546305	8.07410759	0.00449022	0.04813006	4.73953036	p, ca, c
GIMAP6	-1.9450418	1.94504184	2.83996885	9.80236701	0.00174287	0.02500355	0.25970724	
GIMAP7	-1.1035095	1.10350946	7.91587605	51.7573206	6.28E-13	2.70E-10	0.46538304	
GLIPR2	1.00746969	1.00746969	5.99285154	31.0674144	2.49E-08	4.09E-06	2.01038205	p
GLYR1	-1.3961491	1.39614915	3.4052985	13.5722223	0.00022956	0.00592448	0.37994193	p, ca, c
GNA15	1.25945208	1.25945208	5.81628356	28.112662	1.14E-07	1.48E-05	2.394048	p, ca, c
GPATCH1	-4.1638454	4.16384542	1.62068787	10.4203901	0.00124632	0.01993108	0.05579016	
GPATCH2L	1.2801864	1.2801864	3.24351964	14.0061786	0.00018221	0.00495921	2.42870355	
GPR155	-2.9966842	2.9966842	2.19899111	10.4921549	0.00119882	0.01941323	0.12528762	p, ca, c
GPR171	-1.0225602	1.02256016	5.58947685	9.08777234	0.00257324	0.03284153	0.49224206	p, ca, c
GPR84	1.07138657	1.07138657	5.32033301	10.7524981	0.00104139	0.01765473	2.10145209	p, ca, c
GPX3	1.61344196	1.61344196	3.80595377	19.1383093	1.22E-05	0.00063503	3.05980977	p, ca, c
GRAMD3	-2.6357995	2.63579951	2.50255317	8.11003975	0.00440208	0.04764479	0.16089601	
GTF2H5	-1.2111388	1.21113877	3.88933752	23.1669221	1.49E-06	0.00012759	0.43192755	
HAAO	1.81798317	1.81798317	2.52703638	9.06205401	0.00260969	0.03319514	3.5258795	p, ca, c

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GCH1	1.02128029	1.02128029	3.73774954	10.3590555	0.00128841	0.01457082	2.0297194	
GCSH	-1.7687795	1.76877953	1.95748472	7.53505604	0.00605099	0.04541255	0.29345689	
GLT1D1	2.80988528	2.80988528	1.91569598	14.4491555	0.00014399	0.00264458	7.01228813	p, ca, c
GNA15	1.00993517	1.00993517	5.81628356	24.0569448	9.35E-07	4.47E-05	2.01382061	p, ca, c
GOLPH3	-1.5293301	1.52933005	3.23767652	8.62832078	0.00330977	0.02937823	0.34643821	
GPATCH2L	1.04918648	1.04918648	3.24351964	12.3383435	0.00044375	0.00637746	2.06936263	
GPBAR1	1.41901392	1.41901392	2.98669976	13.0420204	0.00030458	0.00472883	2.67402679	p
GPR155	-1.4332595	1.43325955	2.19899111	10.6173789	0.0011203	0.01309574	0.37029333	p, ca, c
GPR84	1.00879392	1.00879392	5.32033301	14.0924884	0.00017404	0.0030568	2.0122282	p, ca, c
GPX3	1.10672829	1.10672829	3.80595377	12.6285337	0.0003799	0.00563679	2.15356713	p, ca, c
GSTM1	-4.3134162	4.31341619	2.98973752	11.4071346	0.00073163	0.00933753	0.05029587	
GTF2E1	-2.8514672	2.85146717	1.27058576	9.76602946	0.00177766	0.01859136	0.13855521	
HACD2	2.47271787	2.47271787	1.45858901	8.61286993	0.00333796	0.02957039	5.55088526	
HAMP	1.50726815	1.50726815	6.10350184	20.3296611	6.52E-06	0.00021814	2.8427124	
HAVCR2	1.07307884	1.07307884	5.60612285	23.679962	1.14E-06	5.33E-05	2.10391853	
HCAR2	1.28333302	1.28333302	3.66192241	13.3274277	0.00026155	0.00420531	2.4340065	p, ca, c
HCK	1.31031757	1.31031757	5.81207118	28.4669915	9.53E-08	6.43E-06	2.47996124	p, ca, c
HEBP1	1.08649803	1.08649803	3.64172123	15.5930767	7.85E-05	0.00165047	2.12357937	
HES1	1.03681237	1.03681237	4.78607492	14.4352956	0.00014506	0.00265871	2.05168944	p
HEXB	1.1267673	1.1267673	3.99706902	24.0757798	9.26E-07	4.45E-05	2.18368884	p
HIRIP3	-1.3988052	1.39880516	2.7539324	14.9004072	0.00011334	0.00218831	0.3792431	
HLA-DQA2	3.24065501	3.24065501	6.047535	137.098927	1.15E-31	1.04E-27	9.45223181	
HMGN5	-1.4927275	1.4927275	2.68282616	11.9777124	0.00053841	0.00745029	0.35534012	
HMOX1	1.03320275	1.03320275	7.21540081	44.5327038	2.50E-11	4.19E-09	2.04656254	p, ca, c
HNRNPAB	-1.3472667	1.34726673	3.11494997	9.86383655	0.00168559	0.01785582	0.39303597	
HOMER3	1.94873073	1.94873073	3.37897267	25.9596319	3.49E-07	1.91E-05	3.86034752	p, ca
HOOK2	-3.5859962	3.58599617	1.49195982	11.6238302	0.00065112	0.00856248	0.08327365	p, ca
HP	1.97214678	1.97214678	2.33919882	11.8925257	0.0005636	0.00769456	3.92351517	p, ca, c
HRH2	1.17143235	1.17143235	4.42259439	24.554796	7.22E-07	3.61E-05	2.25235207	p, ca, c
HSF2	-1.9941049	1.99410495	3.43572888	36.3520875	1.65E-09	1.81E-07	0.25102362	
HSPA1A	1.0535557	1.0535557	5.65110367	9.44682126	0.00211515	0.02123614	2.07563922	p
HSPA6	3.30494108	3.30494108	1.19986913	13.5024565	0.00023825	0.00389737	9.88294549	p, ca, c
HYI	-2.0619294	2.06192936	2.53896552	17.3163024	3.16E-05	0.00078993	0.23949553	
ICOS	-1.1604017	1.16040171	4.49222123	21.0933147	4.37E-06	0.00016134	0.44738795	p, ca
IFI30	1.17217107	1.17217107	11.4282265	46.0734363	1.14E-11	2.10E-09	2.25350565	p, ca, c
IFNG	1.262109	1.262109	5.06617897	19.5602099	9.75E-06	0.00030062	2.39846104	
IGFBP7	-1.9280165	1.92801652	2.42923369	7.95583836	0.00479325	0.03832903	0.26279022	
IL13RA1	2.61968119	2.61968119	1.24994119	8.88141332	0.00288088	0.02659006	6.1461424	p, ca
IL17RA	1.86186164	1.86186164	3.60481557	16.0674459	6.11E-05	0.00135376	3.63476385	p, ca, c
IL18	1.40292223	1.40292223	2.85905521	15.9647755	6.45E-05	0.00142222	2.64436665	p, ca, c
IL1R2	1.56105006	1.56105006	4.57244756	46.2219803	1.06E-11	1.99E-09	2.95068531	p, ca, c
IL1RAP	1.28353254	1.28353254	4.18998851	17.5162259	2.85E-05	0.00072508	2.43434314	p, ca
IL23A	-1.3535309	1.35353094	3.578038	16.8875922	3.97E-05	0.00095928	0.3913331	p
IL27	1.24954685	1.24954685	3.01586743	10.9832141	0.00091941	0.01104757	2.37766728	p, ca, c
IRF5	1.07044177	1.07044177	4.43246395	13.2997468	0.00026544	0.00424519	2.10007633	
ISYNA1	-4.2549628	4.25496279	1.34488033	15.6058432	7.80E-05	0.00164319	0.05237555	p, ca, c
ITFG1	-1.0591521	1.05915213	3.75606568	11.6086207	0.00065647	0.00858444	0.47991402	
KCNE1	3.18988364	3.18988364	1.36089651	12.8950428	0.00032945	0.00502862	9.12537366	p, ca, c
KCTD15	3.00205436	3.00205436	1.13049093	9.3160556	0.00227154	0.02235913	8.01139992	
KDM2B	-3.1119384	3.11193838	1.25285489	12.6145386	0.00038276	0.00566984	0.11566799	
KIAA0226L	1.23359349	1.23359349	4.49763756	20.8155401	5.06E-06	0.00017991	2.35151982	p, ca, c
KIAA0355	-1.0654966	1.06549658	5.81243246	41.5523306	1.15E-10	1.62E-08	0.47780817	
KIAA0391	-1.6809517	1.68095172	2.50787919	11.2297492	0.00080497	0.00992315	0.31187683	
KIR2DL1	-3.2564811	3.25648114	2.22324136	27.3543739	1.69E-07	1.03E-05	0.10464091	p, ca, c
KIR2DL4	-1.8570638	1.85706382	2.24719263	8.74844805	0.00309866	0.02808371	0.2760375	p, ca, c
KIR3DL1	-3.8327281	3.8327281	2.49975596	16.5559494	4.72E-05	0.00111151	0.07018331	p, ca
KIR3DL2	-1.3599491	1.35994906	3.17201808	11.1381213	0.00084572	0.0103689	0.38959605	p, ca, c
KLRC3	-2.925175	2.92517505	1.5937956	12.9542898	0.00031919	0.00492183	0.13165415	
KNOP1	-1.4006447	1.40064472	2.98045772	15.6292987	7.71E-05	0.00163053	0.37875984	
KRT17	2.19781674	2.19781674	3.08486326	11.6747007	0.00063356	0.00843126	4.58784529	
KRT18	-5.2537163	5.25371626	1.69057489	30.9991115	2.58E-08	2.12E-06	0.02621041	
HAGH	-1.6294193	1.62941927	3.0897984	10.3450535	0.00129822	0.02036584	0.32321829	
HAVCR2	1.16766743	1.16766743	5.60612285	21.1484968	4.25E-06	0.00027238	2.24648188	
HBM	4.46322177	4.46322177	1.94007177	20.9558889	4.70E-06	0.00029288	22.0578729	
HEXB	1.14960815	1.14960815	3.99706902	17.6141533	2.71E-05	0.00114245	2.21853629	p
HIST1H1D	-1.5047047	1.5047047	3.4819691	12.3676159	0.00043685	0.00942084	0.35240231	p
HLA-DQA2	3.26304663	3.26304663	6.047535	119.134454	9.79E-28	8.84E-24	9.60008137	
HNMT	1.44489311	1.44489311	2.84658702	9.90089432	0.00165198	0.02430812	2.72242651	
HOMER3	3.24433781	3.24433781	3.37897267	40.5142138	1.95E-10	5.69E-08	9.47639154	p, ca
HP	2.88877311	2.88877311	2.33919882	20.2194237	6.90E-06	0.00040253	7.40640332	p, ca, c
HSF2	-1.5737093	1.57370928	3.43572888	17.1609442	3.43E-05	0.00137453	0.33594355	
HSPA1A	1.67571441	1.67571441	5.65110367	17.7020495	2.58E-05	0.00110115	3.19477517	p
IER3	1.04223184	1.04223184	7.34172108	13.3727867	0.0002553	0.00644387	2.05941109	p, ca, c
IFI30	1.14771151	1.14771151	11.4282265	33.2317384	8.18E-09	1.61E-06	2.2156216	p, ca, c
IFIT5	-1.9876552	1.9876552	4.45728779	16.2104499	5.67E-05	0.00200849	0.25214837	
IFNG	1.26220613	1.26220613	5.06617897	10.5153639	0.00118386	0.01927454	2.39862252	
IL1R2	2.09051506	2.09051506	4.57244756	51.9381627	5.73E-13	2.59E-10	4.25900096	p, ca, c
IL1RAP	1.37566152	1.37566152	4.18998851	13.5724092	0.00022953	0.00592448	2.59486866	p, ca
IL23A	-1.3331024	1.33310245	3.578038	12.0206559	0.00052614	0.01075615	0.39691378	p
IL6R	1.36483022	1.36483022	4.21129912	16.6795391	4.43E-05	0.00167803	2.57546015	p, ca, c
IRF5	1.37411329	1.37411329	4.43246395	16.5927557	4.63E-05	0.0017227	2.59208547	
IRF7	1.04623791	1.04623791	6.47129082	18.8704618	1.40E-05	0.00071421	2.0651376	
ITFG2	-1.2782338	1.27823382	3.55377018	14.8290577	0.00011771	0.00355722	0.41229995	
ITK	-1.1966114	1.19661145	4.17841008	13.1732016	0.00028398	0.00708844	0.43629884	
ITPA	-1.018076	1.018076	4.12527609	12.5510418	0.00039599	0.00885674	0.49377442	p, ca
JAM3	-2.8084401	2.80844012	2.13006726	8.59171136	0.00337697	0.0395775	0.14274973	
KIFAP3	-1.7027768	1.7027768	3.18253837	15.2911966	9.21E-05	0.0029618	0.30719427	
KIR2DL1	-6.2802804	6.28028036	2.22324136	33.4060657	7.48E-09	1.50E-06	0.01286611	p, ca, c
KIR3DL1	-5.8351252	5.83512521	2.49975596	15.0666404	0.00010378	0.00324031	0.0175167	p, ca
KLHL9	-1.075596	1.07559599	3.7804351	11.7416213	0.00061118	0.01200565	0.47447501	
KLRC3	-3.0971542	3.09715418	1.5937956	8.08280552	0.00446872	0.04807067	0.11685941	
KNOP1	-1.2918248	1.29182482	2.98045772	9.65752454	0.00188578	0.02632226	0.40843409	
KRT18	-5.0078331	5.00783313	1.69057489	16.365432	5.22E-05	0.0019107	0.03108079	
KRTCAP3	2.08583034	2.08583034	4.1441439	11.5999153	0.00065955	0.01252033	4.24519357	
LAIR2	-1.6903944	1.69039441	4.5591186	11.8297639	0.00058291	0.0115509	0.30984221	
LAYN	-3.4140053	3.41400527	1.60417784	8.74980122	0.00309636	0.03755529	0.0938171	
LCK	-1.208323	1.20832303	4.88182877	21.4750747	3.58E-06	0.00024354	0.43277137	
LCOR	1.37027091	1.37027091	3.29507844	16.6740703	4.44E-05	0.00167803	2.58519107	p, ca
LDLRAP1	-3.0272405	3.0272405	2.69332242	13.6676424	0.00021818	0.00576459	0.12266193	
LEF1	-2.4660491	2.46604913	3.53248622	22.713824	1.88E-06	0.00014645	0.18098611	
LGALS2	1.21013185	1.21013185	5.61632919	45.3411347	1.66E-11	5.98E-09	2.31358781	p, ca, c
LGALS3BP	-2.0876842	2.08768416	3.1786297	11.8534547	0.00057554	0.01142994	0.23525803	
LILRA5	1.44044432	1.44044432	3.61975879	10.0590624	0.001516	0.0229206	2.7140444	p, ca, c
LILRB2	1.41169039	1.41169039	5.29987936	20.0691625	7.47E-06	0.00042447	2.66048707	p, ca, c
LIMK2	1.77871858	1.77871858	3.6026749	23.6521932	1.15E-06	0.00010534	3.43121274	p, ca, c
LINS	-1.9263118	1.9263118	2.85565535	11.9973533	0.00053276	0.01085205	0.26310092	p, ca, c
LPCAT2	1.12340011	1.12340011	3.94572628	11.5450554	0.0006793	0.01265593	2.17859815	p, ca, c
LPPR2	1.51559293	1.51559293	3.50049613	10.8222401	0.00100288	0.01722819	2.85916312	p, ca, c
LRRN3	-3.2379039	3.23790395	2.10933571	10.3622661	0.00128617	0.02031525	0.10599705	
LTA	-1.1531381	1.15313808	4.72410569	13.2651572	0.00027038	0.00678666	0.44964612	p, ca
LTB	-1.5691725	1.56917255	6.76394805	71.7799382	2.41E-17	4.35E-14	0.33700162	p, ca
LY9	-1.0416832	1.0416832	3.83240812	8.87454024	0.00289175	0.03584343	0.4857604	
LYZ	1.10706918	1.10706918	11.8064872	18.163	2.03E-05	0.00093011	2.15407605	p, ca, c
MAL	-2.4276791	2.42767908	5.2375005	86.6073816	1.32E-20	5.73E-17	0.18586421	
MAML3	1.50879541	1.50879541	4.54903066	31.6806474	1.82E-08	3.22E-06	2.84572333	p, ca, c
MAPRE3	-3.1873022	3.18730225	1.79102438	8.40593504	0.00373998	0.04277779	0.10978081	p
MBD1	1.11328336	1.11328336	3.23179931	9.1895937	0.00243395	0.03146375	2.1633744	p, ca
MDC1	-3.4391001	3.43910013	1.5432388	9.47740983	0.00208017	0.0280126	0.09219932	p, ca, c
METTL18	-3.7482225	3.74822251	1.80718994	10.4657769	0.00121606	0.0195175	0.07441707	
MLLT3	-1.2011564	1.20115636	5.26227606	23.3011927	1.39E-06	0.00012152	0.43492654	
MMP19	1.40699998	1.40699998	4.47485538	8.31804134	0.00392532	0.04433652	2.65185149	
MMS19	-2.3497942	2.34979415	2.53721369	10.4808717	0.00120617	0.01946239	0.19617401	p

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LAIR2	-1.6349799	1.63497988	4.5591186	17.9296509	2.29E-05	0.0005969	0.3219749	
LAMP3	-1.4919184	1.49191843	2.60745049	8.96611422	0.00275033	0.02564703	0.35553945	p
LARS	-1.6620523	1.66205235	3.14010406	23.4422771	1.29E-06	5.79E-05	0.31598931	p
LAYN	-3.2184888	3.21848884	1.60417784	15.308826	9.13E-05	0.00184539	0.10743315	
LDLRAP1	-1.4448051	1.44480506	2.69332242	10.631491	0.00111178	0.01301302	0.36734179	
LDOC1	-1.2208972	1.2208972	2.92847553	10.3611258	0.00128697	0.01457082	0.42901583	
LEF1	-2.8727467	2.87274666	3.53248622	40.2068895	2.28E-10	2.99E-08	0.13652654	
LGALS2	1.53166562	1.53166562	5.61632919	99.8867972	1.61E-23	2.43E-20	2.89119441	p, ca, c
LGALS3BP	-1.5366771	1.53667711	3.1786297	12.4167208	0.00042551	0.00618507	0.34467842	
LHFPL2	1.21754399	1.21754399	4.15760815	16.7378542	4.29E-05	0.0010205	2.32550492	
LIG4	-3.0698463	3.06984625	1.31880597	10.543122	0.00116621	0.01352664	0.11909244	p
LILRA5	1.25636924	1.25636924	3.61975879	11.056951	0.00088355	0.0107298	2.38893772	p, ca, c
LILRB2	1.07264198	1.07264198	5.29987936	15.6631062	7.57E-05	0.0016054	2.10328154	p, ca, c
LIN7A	3.04569175	3.04569175	1.43106466	13.1118237	0.00029344	0.00456369	8.25742377	p
LINS	-1.5655574	1.56555741	2.85565535	12.1849127	0.00048178	0.00684485	0.33784715	p, ca, c
LMF1	-2.7874933	2.78749327	1.25463539	10.7790354	0.00102656	0.01215729	0.14483746	
LONRF3	3.48846566	3.48846566	1.47228811	15.9053464	6.66E-05	0.00145841	11.2236161	
LPAR2	-2.0879488	2.08794884	3.14253525	24.2995552	8.25E-07	4.03E-05	0.23521487	
LPCAT2	1.00258967	1.00258967	3.94572628	11.9975174	0.00053271	0.00738284	2.00359327	p, ca, c
LRPPRC	-1.5850086	1.58500858	3.333338	19.8546622	8.36E-06	0.00026217	0.33332269	
LRRC23	-1.8428593	1.8428593	2.56162688	16.2544558	5.54E-05	0.0012573	0.27876874	p, ca, c
LRRC25	1.51374854	1.51374854	4.02516585	29.153629	6.69E-08	4.72E-06	2.85551019	p
LRRC8C	1.01721985	1.01721985	4.79120393	11.3078324	0.00077181	0.00967114	2.02401482	p
LRRN3	-1.8347515	1.83475147	2.10933571	7.93608921	0.00484584	0.0385789	0.28033981	
LSR	-3.2922896	3.29228962	1.10642066	8.17358554	0.00425048	0.03537665	0.10207563	
LTB	-1.5950419	1.59504186	6.76394805	118.736436	1.20E-27	5.40E-24	0.33101262	p, ca
LTBR	1.27897987	1.27897987	4.77536144	15.4730808	8.37E-05	0.00172163	2.42667325	p, ca, c
LYL1	2.0588997	2.0588997	2.88093215	8.22021156	0.00414264	0.03485369	4.16668402	p, ca, c
LYZ	1.12329117	1.12329117	11.8064872	24.9264944	5.96E-07	3.06E-05	2.17843365	p, ca, c
LZTFL1	-1.7921803	1.79218033	2.24304443	9.75483492	0.00178852	0.01868328	0.28873535	p
MAGEH1	-1.0944086	1.09440858	3.14194667	11.2565763	0.00079341	0.00983442	0.46832807	
MAL	-2.0641817	2.06418165	5.2375005	112.367113	2.97E-26	8.94E-23	0.23912193	
MALT1	1.50221989	1.50221989	2.90504661	21.294441	3.94E-06	0.00014906	2.83278261	
MAML3	1.19248082	1.19248082	4.54903066	28.9042959	7.60E-08	5.25E-06	2.28545407	p, ca, c
MANBA	1.18490661	1.18490661	5.36690421	18.2066245	1.98E-05	0.00052983	2.27348678	p
MANF	1.21358527	1.21358527	4.07960167	15.7457403	7.25E-05	0.00155134	2.31913253	
MAP1S	1.25227529	1.25227529	5.446961	14.0316236	0.00017976	0.00312973	2.38216821	p
MAP4K1	-1.0430645	1.04306452	3.69344513	8.16936746	0.00426038	0.03539819	0.48529553	
MAP4K3	1.72361189	1.72361189	2.36123762	9.53741368	0.00201325	0.02039434	3.30262207	
MAPK6	1.30917396	1.30917396	3.68290154	16.6517867	4.49E-05	0.00106227	2.47799617	p
MAPRE3	-1.9556932	1.95569325	1.79102438	7.43462586	0.00639807	0.04738765	0.25779689	p
MARCH8	-3.7939078	3.79390779	1.24929019	13.1738768	0.00028388	0.00443027	0.07209746	
MEFV	1.38131992	1.38131992	2.33899634	9.27431941	0.00232389	0.02263587	2.60506599	p, ca, c
MEN1	-2.7500675	2.75006751	1.74808409	9.57662487	0.0019707	0.02007585	0.14864393	
MFI2	3.03761265	3.03761265	1.60847231	13.5660584	0.00023031	0.00379763	8.2113114	
MFSD2B	-2.6509648	2.65096483	1.81051062	7.99122851	0.00470045	0.0377713	0.15921357	
MGST1	1.32307119	1.32307119	3.03224372	8.8236418	0.00297353	0.02714307	2.50198161	p
MGST2	1.56079112	1.56079112	2.46570724	13.3301364	0.00026117	0.00420531	2.95015576	p
MIDN	1.57634875	1.57634875	3.30444883	10.4192251	0.0012471	0.01426432	2.98214157	p
MMP19	1.20972781	1.20972781	4.47485538	8.34510649	0.00386727	0.03315436	2.31293996	
MNDA	1.06518283	1.06518283	6.96374397	37.1817316	1.08E-09	1.25E-07	2.09243503	p, ca, c
MPHOSPH6	1.34833083	1.34833083	6.12845204	29.2602877	6.33E-08	4.68E-06	2.54617367	
MPZL3	-1.2454389	1.24543886	4.0557192	22.8024002	1.80E-06	7.62E-05	0.42177958	p, ca, c
MRPL13	-1.0153962	1.01539618	3.89741519	21.0062329	4.58E-06	0.0001668	0.49469246	
MRPL42	-2.0400146	2.0400146	1.99927586	7.40515599	0.00650372	0.04781743	0.24316128	
MS4A6A	1.17844039	1.17844039	6.00932377	23.5899414	1.19E-06	5.45E-05	2.26331971	
MS4A7	1.11365809	1.11365809	5.489179	39.4807499	3.31E-10	4.05E-08	2.16393639	
MT1G	2.22774483	2.22774483	2.16672753	12.9033921	0.00032799	0.00502862	4.68401219	
MTA3	-2.4998014	2.49980136	1.29485295	7.42354924	0.00643757	0.04740822	0.17680104	
MTHFR	1.54105695	1.54105695	2.6182009	7.32408665	0.00680365	0.04941946	2.91007625	p, ca
MTMR3	1.21633817	1.21633817	2.96379044	9.26632078	0.00233406	0.02270245	2.32356204	p, ca, c
MNAT1	-1.3621175	1.36211746	3.56717273	12.9332436	0.0003228	0.00771641	0.38901091	
MPHOSPH6	1.29654751	1.29654751	6.12845204	20.7637989	5.20E-06	0.00032156	2.45640342	
MPZL3	-1.3030985	1.30309849	4.0557192	15.2619624	9.36E-05	0.00298802	0.40525489	p, ca, c
MRPS28	-1.2824463	1.28244627	3.67943982	12.6285726	0.0003799	0.00864668	0.41109785	
MRS2	-2.8065474	2.80654742	1.49702351	8.15211456	0.0043011	0.04722323	0.14293713	
MS4A4A	3.11146316	3.11146316	1.8264729	13.162905	0.00028555	0.00708844	8.64258661	
MS4A6A	1.09952803	1.09952803	6.00932377	15.2852943	9.24E-05	0.0029618	2.1428458	
MS4A7	1.59600854	1.59600854	5.489179	61.8289861	3.75E-15	2.82E-12	3.02305776	
MSRB1	1.09961481	1.09961481	6.61427139	41.7579695	1.03E-10	3.11E-08	2.14297469	p, ca, c
MT1G	3.27690073	3.27690073	2.16672753	23.1521112	1.50E-06	0.00012759	9.6927143	
MTHFD1	-4.1379088	4.13790876	1.08358146	8.32585529	0.00390847	0.04429006	0.05680222	
NAGA	1.02790827	1.02790827	4.04320768	9.61769169	0.00192712	0.02662605	2.03906571	
NCF2	1.02943709	1.02943709	5.73465821	11.0413981	0.000891	0.01569404	2.04122766	p, ca, c
NDRG1	1.14747096	1.14747096	6.7480751	20.4169051	6.23E-06	0.00036944	2.21525221	p
NDUFAF4	-1.4420603	1.44206031	3.60826958	13.1639123	0.00028539	0.00708844	0.36804133	
NEDD9	1.02779815	1.02779815	6.99922598	14.0786293	0.00017532	0.00487456	2.03891008	p, ca, c
NGDN	-1.0198906	1.01989057	5.11367705	22.7918269	1.81E-06	0.00014185	0.49315376	
NLRP12	1.92998957	1.92998957	1.63326946	8.37874817	0.00379634	0.04331277	3.81052444	p, ca, c
NOL9	2.21421632	2.21421632	1.42634954	8.25727724	0.0040589	0.04544756	4.64029432	
NPL	1.62998216	1.62998216	3.32115052	16.027567	6.24E-05	0.00216957	3.09509172	p, ca, c
NQO2	-1.0785551	1.07855514	4.00390423	9.21757873	0.00239702	0.03110613	0.4735028	p, ca, c
NRIP3	1.10914057	1.10914057	6.19100552	30.3067923	3.69E-08	5.76E-06	2.15717105	
NRM	1.28051347	1.28051347	3.252714	10.4425305	0.00123146	0.01972963	2.42925422	
NTSR1	2.89874975	2.89874975	1.21135333	8.06571854	0.00451106	0.04829612	7.45779816	p, ca
OFD1	-1.509884	1.50988399	3.65659956	20.6620444	5.48E-06	0.00033228	0.35113945	p
OLR1	1.21225964	1.21225964	5.6656029	9.74004755	0.00180296	0.02561567	2.31700257	p, ca, c
OSBPL5	1.04940607	1.04940607	4.31982178	12.985329	0.00031394	0.00756473	2.06967762	
OSCAR	1.36871956	1.36871956	3.15287189	8.68393318	0.00321027	0.03820845	2.58241267	p, ca
OSM	1.72128559	1.72128559	5.93502877	16.620389	4.57E-05	0.0017048	3.297301	p, ca, c
P2RY10	-1.225998	1.22599798	3.29269715	10.2820745	0.00134329	0.02099992	0.42750169	
PAIP1	-3.2195664	3.21956641	2.25941963	12.544599	0.00039735	0.00886539	0.10735294	
PAM	1.32102538	1.32102538	3.19499814	9.94240349	0.00161515	0.02393333	2.49843621	
PAPSS2	1.05152242	1.05152242	3.7831335	8.61099692	0.00334139	0.03931358	2.07271595	
PARP8	-1.3674148	1.36741483	5.22400015	16.779303	4.20E-05	0.00160767	0.38758514	p, ca, c
PCSK1N	-2.8989933	2.89899333	1.98788961	8.22133304	0.00414008	0.04613866	0.1340652	
PDCD2L	-2.1534724	2.15347238	2.59762564	9.06045631	0.00261197	0.03319514	0.22477097	
PDLIM7	1.04680388	1.04680388	6.0824092	14.0089995	0.00018194	0.00495921	2.06594791	p, ca, c
PFKFB4	2.97770111	2.97770111	1.29534068	9.22342066	0.00238939	0.03110613	7.87729937	p, ca, c
PHF3	-1.2335301	1.23353007	4.5989272	22.5784067	2.02E-06	0.00015319	0.42527558	p, ca, c
PHLDB3	-2.2623804	2.26238041	2.66104772	12.4049044	0.00042821	0.00930117	0.2084278	
PITPNC1	-1.502095	1.50209496	3.35332634	8.40247428	0.00374711	0.04280512	0.35304036	p, ca
PLA2G15	-1.8094954	1.80949536	2.39490207	8.51692971	0.00351858	0.04086614	0.2852907	
PLEKHB1	-3.9161011	3.91610106	2.26266719	21.2532907	4.02E-06	0.00026262	0.06624241	
PLEKHO2	1.6233435	1.6233435	3.68753023	12.1794814	0.00048318	0.01018043	3.08088216	p, ca, c
PLXDC2	1.25529246	1.25529246	4.07358663	10.806614	0.00101138	0.01727569	2.38715536	p, ca, c
PML	1.00848064	1.00848064	4.97591275	11.1589847	0.00083626	0.0149372	2.01179129	
PNPT1	-2.2187322	2.21873217	3.19916071	9.13589949	0.00250642	0.03226215	0.21483007	
POLD3	-1.6571322	1.65713222	2.93270353	10.4017473	0.00125896	0.02006345	0.31706879	
PPCDC	1.45844683	1.45844683	3.33675719	14.2291417	0.00016184	0.00459883	2.74812349	p, ca, c
PPIL1	-2.5061279	2.50612794	2.32208678	8.44081232	0.00366892	0.04218842	0.17602742	p, ca, c
PPM1K	-1.344182	1.34418196	4.18756241	10.1179452	0.00146833	0.02244974	0.39387726	
PPP1R18	1.05462777	1.05462777	6.04739056	10.1562721	0.00143811	0.02221329	2.0771822	
PPP5C	-1.5871696	1.58716962	3.03793156	11.7072784	0.00062256	0.01210539	0.33282377	
PRKAG2	1.194051	1.194051	6.33508018	25.276543	4.97E-07	5.09E-05	2.28794282	p, ca, c
PRKAR1B	-1.5953062	1.59530615	2.71239992	10.0640045	0.00151194	0.0229206	0.33095199	
PRKCDBP	1.69051593	1.69051593	3.57600317	11.496736	0.00069719	0.01293586	3.22772112	
PRKCH	-1.062222	1.06222199	3.87139624	10.0646134	0.00151144	0.0229206	0.47889392	p
PROK2	1.70568494	1.70568494	3.039456	16.2752477	5.48E-05	0.00197189	3.26183758	p, ca, c
PTGDS	-1.3727366	1.37273658	6.15033869	10.6760072	0.00108534	0.0181278	0.38615807	
PTPRK	-4.2185029	4.21850286	1.24793652	9.04209992	0.00263832	0.03338921	0.05371605	
QSOX1	1.02626964	1.02626964	4.24783315	8.9290069	0.00280677	0.03498202	2.03675103	p, ca, c

ACCEPTED MANUSCRIPT

MTX2	-2.1110148	2.11101475	1.64758424	9.01284842	0.00268088	0.02538878	0.23148414	
MVP	1.12820115	1.12820115	4.05753246	11.302999	0.00077382	0.00967114	2.18586022	p
MXI1	-2.4429403	2.44294026	1.84001833	12.1184961	0.00049924	0.00702671	0.18390846	p
MYC	-1.2135664	1.21356641	5.21179134	24.8846495	6.09E-07	3.09E-05	0.43120135	
MYO1C	-3.9197325	3.91973251	1.21687989	12.3297715	0.00044579	0.00639392	0.06607588	p
N4BP1	1.87312498	1.87312498	1.58722687	11.5757993	0.00066816	0.00866208	3.66325207	p, ca, c
NAA35	-1.4996372	1.4996372	2.26062584	7.60744172	0.00581279	0.04406407	0.35364231	p
NAGA	1.05897012	1.05897012	4.04320768	14.478142	0.0001418	0.0026095	2.08344371	
NAIP	1.61820678	1.61820678	3.35154757	15.9736767	6.42E-05	0.00141901	3.06993218	p, ca, c
NAP1L5	-2.9136091	2.91360912	1.46663051	8.79510326	0.0030204	0.02751245	0.13271385	
NAPB	2.73772761	2.73772761	1.17173052	8.152582	0.00429999	0.03552773	6.67018887	
NDUFAF4	-1.5762616	1.57626156	3.60826958	23.6230124	1.17E-06	5.43E-05	0.33534975	
NDUFAF6	-1.7206284	1.72062842	2.27361803	14.7221587	0.00012457	0.0023451	0.30341653	p
NEDD9	1.1802393	1.1802393	6.99922598	25.2782338	4.96E-07	2.62E-05	2.26614362	p, ca, c
NELL2	-2.3941103	2.39411029	2.86272854	19.7373975	8.88E-06	0.00027779	0.19023963	
NEURL3	1.53980869	1.53980869	2.57094348	9.63636674	0.00190762	0.01963243	2.90755944	
NEXN	-1.707367	1.707367	2.8970492	10.43946	0.00123351	0.01416268	0.30621843	
NFAM1	1.40358796	1.40358796	2.95704272	11.6452588	0.00064366	0.00850314	2.64558718	p, ca, c
NFIL3	2.96437818	2.96437818	1.1662791	9.70252344	0.00184015	0.01915623	7.80488937	p, ca, c
NLRP1	-1.2776086	1.27760858	4.47808968	12.6015156	0.00038543	0.00569087	0.41247867	p
NLRP12	3.77377652	3.77377652	1.63326946	33.4013998	7.50E-09	7.06E-07	13.6779159	p, ca, c
NOL4L	1.61940349	1.61940349	3.41889595	10.8712628	0.00097668	0.01165822	3.07247973	p
NOL8	-1.1033797	1.10337968	2.71478885	8.04770348	0.00455614	0.03695373	0.46542491	
NOL9	-2.2688191	2.2688191	1.42634954	9.00862247	0.00268709	0.02538878	0.20749966	
NOP2	-1.1354237	1.13542367	3.40409964	9.60201705	0.00194364	0.01991237	0.45520122	p, ca, c
NPL	2.38039258	2.38039258	3.32115052	42.6903576	6.41E-11	9.82E-09	5.20678409	p, ca, c
NPRL2	-1.0193586	1.01935861	3.02029768	7.33969678	0.00674482	0.04925638	0.49333563	
NR1D1	-2.4251164	2.4251164	3.49725777	14.1216286	0.00017136	0.00303019	0.18619466	p, ca, c
NSUN3	-1.4872938	1.4872938	2.3506255	10.2553581	0.00136288	0.01527546	0.35668098	p
NT5DC1	-1.4592441	1.45924408	2.59483797	9.7971801	0.0017478	0.01836406	0.36368364	
NTPCR	-1.0572741	1.05727411	3.07507828	8.17303291	0.00425178	0.03537665	0.48053915	
NUCB2	-1.0106218	1.01062179	4.84346905	21.6519872	3.27E-06	0.00012786	0.49633229	p
NUDT16	1.19076452	1.19076452	3.64029938	11.0655592	0.00087946	0.01071188	2.28273679	
NUP107	-2.0320839	2.03208388	1.91131711	10.0930704	0.00148828	0.01624166	0.24450165	
OLR1	1.13431931	1.13431931	5.6656029	12.4054127	0.00042809	0.00618507	2.19514967	p, ca, c
OSBPL3	2.35375595	2.35375595	1.54481785	9.09748726	0.00255961	0.02456607	5.1115327	
OSCAR	1.34633976	1.34633976	3.15287189	11.7869043	0.00059649	0.00800872	2.54266211	p, ca
OXR1	-2.0526959	2.05269593	1.3845221	7.43716881	0.00638903	0.04735955	0.24103325	
P2RY10	-1.8124242	1.81242419	3.29269715	29.586373	5.35E-08	4.20E-06	0.28471212	
PADI4	1.46814623	1.46814623	2.30497319	8.64191834	0.00328515	0.02921717	2.76666166	p, ca, c
PAK4	-2.2972784	2.29727838	2.29210669	9.38457031	0.00218819	0.02172804	0.20344654	
PAM	1.03751863	1.03751863	3.19499814	9.04239851	0.00263789	0.02506415	2.05269408	
PARK2	-3.3807581	3.38075812	1.15626568	8.5926073	0.0033753	0.02981354	0.09600424	
PARP8	-1.1939165	1.19391651	5.22400015	21.4643299	3.60E-06	0.0001398	0.43711461	p, ca, c
PCSK1N	-3.0267011	3.02670114	1.98788961	16.6609455	4.47E-05	0.00105993	0.1227078	
PDPK1	-1.165444	1.16544404	3.25887127	8.54295608	0.00346862	0.03048875	0.44582702	p, ca, c
PEA15	1.26327004	1.26327004	5.51386082	8.4399086	0.00367075	0.03195328	2.40039202	
PFN2	-4.3499623	4.34996227	1.09285405	10.2424731	0.00137243	0.01527762	0.04903779	
PHLDB3	-1.8117072	1.81170723	2.66104772	13.5003608	0.00023852	0.00389737	0.28485364	
PIK3IP1	-1.3779291	1.37792909	6.87099539	51.6684696	6.57E-13	1.60E-10	0.38477072	p, ca
PLAGL1	1.20690709	1.20690709	2.89205169	9.64767336	0.00189592	0.0195565	2.30842217	p, ca, c
PLBD1	1.13298274	1.13298274	5.41549093	18.0925613	2.10E-05	0.00055759	2.19311694	p, ca, c
PLEC	1.25106857	1.25106857	3.82529557	14.0108685	0.00018176	0.00314628	2.38017652	p, ca, c
PLEK	1.01957889	1.01957889	7.45001468	45.8658742	1.27E-11	2.29E-09	2.02732711	p, ca, c
PLEKHB1	-2.9176283	2.91762827	2.26266719	16.8859606	3.97E-05	0.00095928	0.13234465	
PLEKHF2	1.04960878	1.04960878	3.32099323	10.0678857	0.00150876	0.01636634	2.06996845	p, ca, c
PLIN3	1.23798895	1.23798895	5.57520469	41.8880909	9.66E-11	1.41E-08	2.35869512	p
PLXDC2	1.45199403	1.45199403	4.07358663	19.2344645	1.16E-05	0.00034363	2.73585929	p, ca, c
POP5	-1.2115567	1.2115567	4.02186345	22.5570591	2.04E-06	8.42E-05	0.43180244	p, ca, c
PPIF	1.0220257	1.0220257	7.37374789	26.4693536	2.68E-07	1.52E-05	2.03076838	p, ca, c
PRAM1	1.44272562	1.44272562	4.20931	19.5211446	9.95E-06	0.00030522	2.71833945	p, ca, c

RAB13	1.06832278	1.06832278	4.57543233	15.8078624	7.01E-05	0.00236388	2.09699407	p, ca, c
RAB20	1.14772724	1.14772724	4.17612031	10.8429418	0.00099173	0.01710167	2.21564576	p, ca, c
RAB31	1.15756567	1.15756567	9.34869645	19.6697115	9.20E-06	0.00050409	2.23080695	p, ca
RAB39B	-2.2808948	2.28089478	2.88936389	18.3487752	1.84E-05	0.00088407	0.20577009	p, ca, c
RAMP1	-2.2009183	2.20091826	3.40589272	9.60558607	0.00193986	0.02667977	0.21749916	
RASD1	2.96564873	2.96564873	2.3322604	13.6492618	0.00022033	0.00580146	7.81176597	
RBFA	-1.6208736	1.62087363	2.45534129	9.58169113	0.00196527	0.02686567	0.32513852	
RBM11	-4.4826056	4.48260565	2.35641785	21.4474049	3.64E-06	0.00024523	0.04473024	p
RBP7	1.0781312	1.0781312	4.66302054	15.4093676	8.66E-05	0.00282361	2.11129944	p, ca, c
REEP4	1.26235482	1.26235482	4.90620106	21.2614111	4.01E-06	0.00026262	2.39886975	
RETN	2.20712893	2.20712893	5.05354167	33.0216559	9.11E-09	1.72E-06	4.6175543	p, ca, c
RGL2	1.90785737	1.90785737	4.62636769	15.1069275	0.00010159	0.00319315	3.75251377	
RNASE1	1.63920746	1.63920746	2.51570791	12.849468	0.00033758	0.00796431	3.11494666	p
RNF130	1.00368454	1.00368454	5.08704466	19.2992154	1.12E-05	0.00058709	2.00511439	p, ca, c
RPAP1	-4.5771173	4.57711735	1.24362163	9.79809783	0.00174692	0.02501618	0.04189386	
RRAGD	2.02474502	2.02474502	2.12519329	10.3903116	0.00126678	0.02011713	4.06919952	p, ca, c
RRM2	-2.6962372	2.69623718	2.70909411	14.2852592	0.00015709	0.00449199	0.15429496	p, ca, c
RSAD2	1.11132652	1.11132652	7.5135656	33.8798226	5.86E-09	1.26E-06	2.16044204	p
RSBN1	-2.7736914	2.77369137	2.18801325	13.9378612	0.00018895	0.00512729	0.14622974	p, ca, c
RUNX1	1.10951689	1.10951689	5.20203942	9.89816423	0.00165444	0.02430812	2.15773381	p, ca, c
S100A2	2.38225986	2.38225986	3.16607401	27.4206234	1.64E-07	2.05E-05	5.21352759	p
S100B	-4.0902775	4.09027746	6.08190808	13.02589	0.00030721	0.00745542	0.05870888	
S100P	2.39733329	2.39733329	4.42289684	67.0639898	2.63E-16	2.37E-13	5.26828463	p, ca, c
SAMM50	-1.1060145	1.10601453	3.79465208	12.6561853	0.00037433	0.00854804	0.46457566	
SCAF1	1.38502492	1.38502492	3.08329724	8.21216504	0.00416105	0.04613866	2.6117647	p, ca
SCML1	-2.696171	2.69617104	2.39091619	13.7679833	0.00020683	0.00551306	0.15430203	
SDC2	1.21361228	1.21361228	3.60692986	8.93908115	0.00279133	0.03483766	2.31917596	
SDS	2.07866114	2.07866114	2.75038629	10.6564126	0.0010969	0.01828705	4.22415021	
SEC14L2	-1.2972719	1.29727191	3.60565247	9.28272343	0.00231325	0.03042583	0.4068949	
SECTM1	1.49777083	1.49777083	4.98571285	13.0293323	0.00030665	0.00745542	2.82406018	p
SEPSECS	-3.083984	3.08398404	2.31691809	9.24507904	0.00236129	0.03096753	0.11793109	
SERGEF	-2.0956321	2.09563211	2.22817532	8.28677418	0.00399349	0.04496742	0.23396553	
SERPINB8	1.14880589	1.14880589	5.18524617	19.4565251	1.03E-05	0.00055685	2.21730294	p, ca, c
SERPINE1	2.8672618	2.8672618	3.05132248	16.6558232	4.48E-05	0.00168196	7.29678934	
SETD1A	3.43027065	3.43027065	1.46781416	11.5583938	0.00067444	0.01263762	10.7798908	p
SGK1	1.0139585	1.0139585	5.90153916	26.7991149	2.26E-07	2.52E-05	2.0194445	p, ca, c
SH2D1B	-2.0439364	2.04393637	4.06598288	17.7637322	2.50E-05	0.00108652	0.24250117	
SH3BP2	1.2775152	1.2775152	4.87126459	14.9495879	0.00011042	0.00339379	2.42421087	p, ca
SHROOM1	3.13427305	3.13427305	1.78310065	11.787227	0.00059639	0.01176623	8.78031714	
SLC22A4	1.41785927	1.41785927	4.54769227	23.6897421	1.13E-06	0.00010436	2.67188751	p, ca, c
SLC25A37	1.14788581	1.14788581	6.24234034	19.4052495	1.06E-05	0.00056524	2.21588931	p, ca, c
SLC2A9	2.6652065	2.6652065	1.38487434	8.23518163	0.00410861	0.04589044	6.34318098	p, ca, c
SLC35B2	3.38602141	3.38602141	3.22535942	14.2425198	0.0001607	0.00458066	10.4542772	
SLC35B3	-3.3534943	3.35349427	1.84481179	7.9968812	0.0046858	0.04950121	0.09783576	
SLC35E4	2.45874614	2.45874614	3.38949023	8.81408473	0.00298914	0.03674813	5.49738738	
SLC44A2	-1.113038	1.11303798	4.89329351	9.12853536	0.00251653	0.03230025	0.46231947	p, ca, c
SLC6A6	1.24031398	1.24031398	5.53547158	17.8624508	2.37E-05	0.00104316	2.36249943	p, ca, c
SLC7A5	2.18308027	2.18308027	2.28207371	10.518035	0.00118215	0.01927454	4.54122106	p, ca, c
SLC7A7	1.33039043	1.33039043	5.49263725	18.3241221	1.86E-05	0.00088616	2.51470721	p
SLFN11	1.37473343	1.37473343	3.13236598	12.1455596	0.00049205	0.01029202	2.5931999	p
SMARCC1	-2.9998099	2.99980988	2.73800434	14.3792044	0.00014944	0.00434203	0.12501647	
SMC4	-1.8536387	1.85363869	2.66007015	11.8897969	0.00056442	0.01125855	0.27669362	
SMCO4	1.49598411	1.49598411	3.27733149	15.5295214	8.12E-05	0.00267871	2.82056486	p
SMIM14	1.78233578	1.78233578	2.55847777	11.9611358	0.00054322	0.01100563	3.43982646	p
SMOX	1.32538017	1.32538017	4.67952579	11.0863945	0.00086963	0.01540787	2.50598916	
SNX20	1.13077402	1.13077402	4.46383245	18.4593985	1.74E-05	0.00084774	2.18976192	p, ca, c
SOCS3	1.40247035	1.40247035	5.60962066	17.2273897	3.32E-05	0.00134523	2.64353851	p, ca
SPI1	1.04392925	1.04392925	8.17120995	14.6413126	0.00013003	0.00389064	2.06183552	p, ca, c
SPINK1	2.23514159	2.23514159	2.61177573	8.45485592	0.0036407	0.04196094	4.70808899	p, ca, c
SSTR2	3.82108287	3.82108287	3.44999719	41.7890505	1.02E-10	3.11E-08	14.1338527	
STARD5	1.4015229	1.4015229	2.94534496	10.5448061	0.00116515	0.01909436	2.64180303	

ACCEPTED MANUSCRIPT

PROCR	1.4352571	1.4352571	2.39835114	7.54437892	0.00601976	0.04521573	2.70430355	p
PRSS57	-3.1434158	3.14341581	2.05227709	18.2353755	1.95E-05	0.000525	0.11317163	
PTAFR	1.14857064	1.14857064	5.95369786	29.2325711	6.42E-08	4.68E-06	2.21694141	p, ca, c
PTGDS	-1.2531931	1.25319314	6.15033869	14.3124036	0.00015484	0.00280953	0.41951865	
PTK2	-2.233427	2.23342696	1.65470661	11.9521214	0.00054585	0.00753026	0.21265299	
PUS3	-1.4221078	1.42210782	3.12682127	13.8120558	0.00020204	0.00341233	0.37316671	
QPCT	1.0791268	1.0791268	3.230018	8.4382321	0.00367413	0.03195328	2.11275694	p, ca, c
QSOX1	1.25347303	1.25347303	4.24783315	18.4708943	1.73E-05	0.00047818	2.38414673	p, ca, c
RAB13	1.34609582	1.34609582	4.57543233	36.7756132	1.33E-09	1.50E-07	2.54223223	p, ca, c
RAB20	1.18515234	1.18515234	4.17612031	12.4399058	0.00042026	0.00612491	2.27387405	p, ca, c
RAB32	1.00442273	1.00442273	6.16478255	29.324431	6.12E-08	4.59E-06	2.00614061	p
RABL2A	-2.6738165	2.67381647	1.6377627	10.0091927	0.00155761	0.01675541	0.15671156	
RACGAP1	-2.8545632	2.85456317	1.64604926	13.7314435	0.00021089	0.00353551	0.13825819	p, ca, c
RAD51C	-1.0140177	1.01401767	3.84938569	10.9410153	0.00094059	0.01127206	0.49516537	
RAMP1	-2.2055518	2.20555185	3.40589272	15.0803519	0.00010303	0.00203716	0.21680173	
RANGAP1	-1.128716	1.12871604	4.16857106	16.1921555	5.72E-05	0.00128962	0.45732255	
RASD1	2.25859179	2.25859179	2.3322604	11.2478996	0.00079713	0.00986696	4.78524169	
RASGRP4	2.5896857	2.5896857	3.25357411	33.6328841	6.66E-09	6.40E-07	6.01967541	
RBBP8	1.32922844	1.32922844	2.25947822	10.1029904	0.00148029	0.01617399	2.51268259	
RBM11	-2.2443265	2.24432649	2.35641785	18.313107	1.87E-05	0.00051317	0.21105245	p
RBMS1	-1.637341	1.63734101	2.58545808	16.2609077	5.52E-05	0.00125618	0.32144838	
RBP4	2.48618627	2.48618627	1.5957789	8.56723046	0.00342267	0.03014355	5.60294865	
RBP7	1.25413696	1.25413696	4.66302054	28.5627108	9.07E-08	6.16E-06	2.38524418	p, ca, c
RDH13	-2.4755842	2.47558418	1.93592483	13.8596082	0.00019699	0.00335844	0.17979388	
REC8	-2.6211291	2.6211291	1.10924135	10.0246065	0.00154463	0.01663557	0.16254047	p, ca, c
REEP6	-4.6197559	4.6197559	1.20156227	23.8619779	1.03E-06	4.92E-05	0.04067381	p
RETN	2.24145486	2.24145486	5.05354167	42.5016536	7.06E-11	1.06E-08	4.72873687	p, ca, c
RGCC	1.30697198	1.30697198	2.91456833	8.72083691	0.00314594	0.02831342	2.47421691	
RIC3	-3.3869002	3.38690023	2.17264268	19.518178	9.96E-06	0.00030522	0.09559638	
RIPK3	-3.2360677	3.23606768	1.74936381	16.4751698	4.93E-05	0.00114793	0.10613205	p, ca, c
RNASE1	1.81947756	1.81947756	2.51570791	12.759909	0.00035413	0.0053243	3.52953362	p
RNASEK	1.00627821	1.00627821	4.73787661	23.5869498	1.19E-06	5.45E-05	2.00872242	p
RNF14	-1.1511359	1.15113592	2.58839128	8.24749659	0.00408082	0.03442981	0.45027057	
RRAD	4.34145045	4.34145045	1.6717438	25.5858567	4.23E-07	2.26E-05	20.2724767	
RRM2	-1.9880119	1.9880119	2.70909411	14.6372913	0.00013031	0.00243282	0.25208604	p, ca, c
RUVBL1	-1.1353118	1.13531179	3.19351131	7.82207351	0.00516119	0.04034304	0.45523652	
S100A12	1.14459671	1.14459671	8.34459845	16.5051837	4.85E-05	0.00113282	2.2108432	p, ca, c
S100A2	1.54488604	1.54488604	3.16607401	13.9899153	0.00018379	0.00316335	2.9178102	p
S100A8	1.04596624	1.04596624	10.1995268	14.1256492	0.000171	0.00302965	2.06474876	p, ca, c
S100A9	1.00659293	1.00659293	11.6147091	13.8333728	0.00019976	0.00338649	2.00916066	p, ca, c
S100B	-3.3610182	3.36101821	6.08190808	17.2741507	3.24E-05	0.00080542	0.09732686	
S100P	2.59684024	2.59684024	4.42289684	107.991033	2.70E-25	4.88E-22	6.04960202	p, ca, c
S100PBP	-1.3506817	1.35068168	2.36461933	8.37049042	0.00381363	0.03281898	0.39210673	
SATB1	-1.4457712	1.44577119	2.7979038	8.28904647	0.00398849	0.03384375	0.36709587	
SCGB3A1	-3.7512221	3.75122213	1.32437209	9.89274372	0.00165932	0.0176188	0.07426251	
SCML4	-1.2463152	1.24631523	3.73746659	22.6468475	1.95E-06	8.12E-05	0.42152344	p, ca, c
SCPEP1	1.15361678	1.15361678	3.92657477	17.8336699	2.41E-05	0.00062062	2.22470922	
SDS	1.91582155	1.91582155	2.75038629	29.4277035	5.80E-08	4.44E-06	3.77328624	
SEC14L2	-2.0098324	2.00983241	3.60565247	30.3787198	3.55E-08	2.84E-06	0.24830197	
SEPHS2	-1.5812395	1.58123952	3.397586	8.08440615	0.00446478	0.03645434	0.33419464	p, ca, c
SERPINB8	1.19114969	1.19114969	5.18524617	27.6065738	1.49E-07	9.33E-06	2.28334632	p, ca, c
SETX	2.31602515	2.31602515	1.84717754	8.45671979	0.00363697	0.03169111	4.97958376	p, ca
SH2D1B	-2.8276717	2.82767171	4.06598288	48.4091335	3.46E-12	7.10E-10	0.14085945	
SH3BP2	1.04755181	1.04755181	4.87126459	12.4834491	0.00041057	0.00602263	2.06701924	p, ca
SH3YL1	-1.2710488	1.27104875	2.69398593	9.10477709	0.00254943	0.02455745	0.41435845	
SHARPIN	-1.1720652	1.17206517	2.51819909	7.92094176	0.00488658	0.0387501	0.44378562	p, ca, c
SHROOM1	2.61006347	2.61006347	1.78310065	10.8361191	0.00099539	0.01183468	6.10530541	
SIAH1	2.19427681	2.19427681	2.18242449	9.41110276	0.00215675	0.02146304	4.57660191	p
SIRPB2	2.99721039	2.99721039	1.67805499	14.7318252	0.00012394	0.00233798	7.98454605	p, ca
SIRPG	-3.0577759	3.05777586	1.39338826	13.2221529	0.00027666	0.00437586	0.12009301	p, ca, c
SKAP2	1.06519658	1.06519658	2.82408702	8.42943749	0.00369195	0.03207733	2.09245497	p, ca, c
STK40	1.1347097	1.1347097	4.17374585	9.12953134	0.00251516	0.03230025	2.19574375	p, ca, c
STMN3	-1.1690065	1.16900652	3.07631032	9.30388149	0.00228669	0.03012029	0.44472749	
STX3	1.20667279	1.20667279	4.11724678	20.1030358	7.34E-06	0.00041966	2.3080473	p, ca, c
SULT1A1	1.96725463	1.96725463	3.54075016	36.7975238	1.31E-09	3.20E-07	3.91023315	p, ca, c
SUSD3	-1.5277677	1.52776768	3.93479792	16.0037914	6.32E-05	0.00218857	0.34681358	p
SYCE1	4.90977146	4.90977146	1.29708341	17.5053453	2.87E-05	0.00119853	30.0599658	
SYK	1.07776755	1.07776755	4.88591675	16.542546	4.76E-05	0.00176167	2.11076731	p
TBC1D1	-2.6453948	2.64539475	2.63411797	8.27555576	0.00401824	0.04516018	0.15982946	p, ca, c
TCF7	-1.933669	1.93366896	5.57200871	26.9371467	2.10E-07	2.42E-05	0.26176263	
TCN2	1.46117614	1.46117614	3.52173752	9.80847614	0.00173709	0.02499424	2.75332734	
TESPA1	-1.5692284	1.56922845	3.88465542	21.0893285	4.38E-06	0.000277	0.33698857	
TFPI	2.55216187	2.55216187	1.90925591	11.5334689	0.00068354	0.01270885	5.86512506	p
TGFBI	1.04769945	1.04769945	4.73031133	9.74568489	0.00179744	0.02561567	2.06723078	p
THEM4	-1.5629564	1.56295641	3.25612892	11.6280042	0.00064966	0.01243718	0.3384568	
THOC2	-1.9867941	1.98679409	2.71875755	10.0639792	0.00151196	0.0229206	0.25229892	
THRA	-1.8492581	1.84925808	2.53968485	8.1435241	0.00432152	0.04738989	0.27753506	p
THUMPD1	-1.0120102	1.01201023	4.03550599	9.80194379	0.00174328	0.02500355	0.49585485	
TICAM1	1.06160355	1.06160355	6.7752569	12.4738104	0.0004127	0.00907332	2.08725021	
TLE3	1.52348914	1.52348914	3.8515741	9.71400387	0.00182869	0.02585925	2.8748549	
TLR4	1.73611082	1.73611082	3.67193956	13.074217	0.00029939	0.00739146	3.33135897	p, ca, c
TMEM243	-1.0217006	1.02170056	4.81825835	21.6885786	3.21E-06	0.00022121	0.49253544	
TMEM63A	-3.3294266	3.32942657	2.02988514	10.3783268	0.00127503	0.02021261	0.09948159	p, ca, c
TNF	1.10560557	1.10560557	6.01464449	25.2248242	5.10E-07	5.09E-05	2.15189185	p, ca
TNFAIP6	1.01147191	1.01147191	6.4751805	14.0282318	0.00018009	0.00495204	2.01596684	p, ca, c
TNFRSF1A	1.37911439	1.37911439	6.33611297	30.7121662	2.99E-08	4.83E-06	2.60108653	p, ca, c
TNFRSF25	-1.6769576	1.67695758	3.08326495	7.97217956	0.00475017	0.04996804	0.31274147	
TNFRSF4	-3.4283289	3.42832894	2.25026124	10.5523979	0.00116037	0.01909436	0.09289025	
TNNI2	1.23652858	1.23652858	3.2302122	9.81109123	0.00173463	0.02499424	2.35630873	p
TP53I3	1.92307969	1.92307969	2.12893352	11.6129081	0.00065496	0.01248563	3.79231734	
TPM1	-1.620838	1.62083799	4.45959664	9.66217238	0.00188101	0.02631085	0.32514655	
TPM2	1.9094775	1.9094775	2.24365853	8.64168879	0.00328557	0.03875768	3.75673019	p
TPSAB1	5.92936769	5.92936769	2.31869964	53.6382813	2.41E-13	1.21E-10	60.9421162	
TRAT1	-1.4075785	1.40757849	3.74786054	14.4199169	0.00014625	0.00426287	0.37694384	
TREM1	1.15091528	1.15091528	7.88148683	31.968714	1.57E-08	2.89E-06	2.22054726	p, ca, c
TRIB1	2.54763821	2.54763821	3.33316482	17.1266522	3.50E-05	0.00139195	5.84676341	p, ca, c
TRIM16	3.13162507	3.13162507	1.18656325	8.32449264	0.00391141	0.04429006	8.76421618	
TRIP10	2.47546345	2.47546345	1.46251491	8.01627503	0.00463588	0.04928216	5.56145915	p, ca
TRMT10C	-1.2557439	1.25574391	5.29028734	36.572792	1.47E-09	3.50E-07	0.41877757	p, ca, c
TRMT13	-3.8674982	3.86749816	1.31799816	9.71784869	0.00182487	0.02584565	0.06851206	
TRMU	-2.3249093	2.32490935	1.92973487	10.1708975	0.00142675	0.02207551	0.19958714	
TRNT1	-3.127232	3.12723202	2.49816461	17.7247078	2.55E-05	0.00110115	0.1144483	
TSGA10	-1.8813146	1.88131459	2.6805114	12.9421806	0.00032126	0.00770003	0.27143627	p
TSHZ2	-2.1330881	2.13308809	4.58556693	23.3043142	1.38E-06	0.00012152	0.22796937	
TSR1	-1.3804919	1.38049187	3.98261251	14.0960156	0.00017371	0.00484462	0.38408782	
TTC3	-1.4760636	1.47606362	3.14664986	12.8119812	0.00034441	0.0080456	0.35946828	p
TUBA1C	1.33321392	1.33321392	7.28388689	85.8903007	1.90E-20	5.73E-17	2.51963354	p, ca, c
TUBB3	2.45142516	2.45142516	2.69505574	12.1068214	0.00050238	0.01039564	5.46956144	
TUBB4B	1.0049504	1.0049504	7.88329416	75.9075244	2.97E-18	6.72E-15	2.0068745	
TUBB6	1.12385607	1.12385607	5.03399787	21.2321244	4.07E-06	0.00026262	2.1792868	
TUBE1	-2.1334816	2.13348155	1.88144605	9.23558769	0.00237356	0.03099351	0.22790721	
TUBGCP5	-3.8055166	3.80551659	2.26223228	14.1559818	0.00016826	0.00475128	0.07151965	
TXK	-2.5125749	2.51257493	3.26089925	17.7071441	2.58E-05	0.00110115	0.17524256	
VASP	1.91542749	1.91542749	6.27874965	26.3533872	2.84E-07	3.10E-05	3.77225574	p, ca
VAT1	1.11989404	1.11989404	3.24435879	8.85783053	0.00291834	0.03609533	2.1733101	p
VCAN	1.1171384	1.1171384	4.39522132	11.706107	0.00062295	0.01210539	2.16916291	
VMO1	2.59571134	2.59571134	4.10855348	49.6940469	1.80E-12	7.38E-10	6.0448701	p, ca, c
WRN	-1.3183237	1.3183237	3.19497333	10.1098545	0.00147479	0.02251042	0.4010006	
XCL2	-4.1005472	4.10054717	3.57160391	35.7531863	2.24E-09	5.19E-07	0.05829245	
YPEL3	-1.2278601	1.2278601	3.54991007	8.49717166	0.00355699	0.04120636	0.42695026	p
ZC3H7A	-3.6985669	3.69856694	1.45610656	11.5612412	0.00067341	0.01263762	0.077023	p
ZCCHC7	-1.7907193	1.79071934	3.37881956	14.5454971	0.00013682	0.00405332	0.2890279	

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SLC25A1	-1.0685279	1.0685279	2.59420007	8.73001976	0.00313013	0.02822741	0.47680527	
SLC25A37	1.0154553	1.0154553	6.24234034	20.514929	5.92E-06	0.00020484	2.02154077	p, ca, c
SLC25A46	-2.2128992	2.21289917	1.71197292	7.87241067	0.00501947	0.03950865	0.21570041	
SLC30A5	-1.8322222	1.83222219	3.08228895	12.2258186	0.00047133	0.00671753	0.28083172	
SLC31A2	1.01924152	1.01924152	5.76199107	49.2833278	2.22E-12	4.66E-10	2.02685309	
SLC35E3	-1.6321872	1.63218722	2.8359129	11.6058168	0.00065746	0.00858497	0.32259876	p, ca, c
SLC35E4	2.77651865	2.77651865	3.38949023	23.3144529	1.38E-06	6.15E-05	6.85196913	
SLC37A2	2.28859964	2.28859964	1.82254622	8.87388395	0.00289279	0.02664552	4.88581635	p, ca
SLC43A3	1.09397845	1.09397845	5.22544916	24.6419992	6.90E-07	3.48E-05	2.13461879	p
SLC7A7	1.1856105	1.1856105	5.49263725	19.9396638	7.99E-06	0.00025519	2.27459627	p
SLC9B1	-2.8519743	2.85197432	1.12878538	7.65546181	0.00566007	0.04323279	0.13850651	p, ca, c
SMOX	1.30495354	1.30495354	4.67952579	13.9848659	0.00018429	0.00316583	2.47075771	
SNAI3	1.25622447	1.25622447	3.28349896	11.6213406	0.00065199	0.00856248	2.388698	p, ca, c
SNAPC5	-1.4307984	1.43079836	3.48133565	17.0375528	3.66E-05	0.00089986	0.37092557	p
SPG21	1.39077984	1.39077984	2.95973755	13.1842387	0.00028231	0.00442112	2.62220385	
SPHK1	1.21024224	1.21024224	4.75183234	11.5407381	0.00068088	0.00878914	2.31376483	
SPON2	-1.2467131	1.24671305	4.82443631	20.285884	6.67E-06	0.00022237	0.42140722	p, ca, c
SPPL2A	1.25941738	1.25941738	4.37706068	25.5982245	4.20E-07	2.26E-05	2.39399042	
SSH1	1.02718735	1.02718735	2.62632221	8.33862941	0.00388109	0.03320975	2.03804704	p, ca
SSTR2	2.1145687	2.1145687	3.44999719	27.9225825	1.26E-07	8.15E-06	4.33060532	
ST7	1.26517661	1.26517661	2.13948914	8.06065307	0.00452369	0.03679212	2.40356633	
STAM	-1.3705225	1.37052245	3.39985363	13.8559565	0.00019737	0.00335864	0.38675117	
STMN3	-1.0329644	1.03296441	3.07631032	11.8407334	0.00057949	0.00783873	0.48870494	
STX6	1.14559824	1.14559824	3.51681366	8.50784007	0.0035362	0.0309323	2.21237852	p, ca, c
SUCLA2	-1.7833472	1.78334723	2.29908531	11.1174175	0.00085521	0.01045691	0.2905086	
SULT1A1	1.26434039	1.26434039	3.54075016	20.6647073	5.47E-06	0.00019238	2.40217355	p, ca, c
SUPV3L1	-1.3947926	1.39479258	3.15538447	13.6618899	0.00021885	0.0036486	0.38029936	p
SUSD3	-1.7369341	1.7369341	3.93479792	39.482666	3.31E-10	4.05E-08	0.30000655	p
SYCE1	4.33399588	4.33399588	1.29708341	16.3082715	5.38E-05	0.0012345	20.1679967	
SYK	1.20023669	1.20023669	4.88591675	27.3989709	1.66E-07	1.02E-05	2.29777366	p
TAF3	-1.0462342	1.04623418	3.9157849	21.4528167	3.63E-06	0.0001399	0.48423049	
TASP1	-1.1471235	1.14712354	2.72476365	8.15804943	0.00428705	0.03550664	0.45152459	
TAZ	-1.2764845	1.27648452	2.77811557	8.07799262	0.00448061	0.03650744	0.41280017	p
TC2N	-1.3468627	1.34686266	2.80371849	8.04295497	0.0045681	0.03695373	0.39314607	
TCAF2	-2.7644289	2.76442893	1.53756504	8.85608924	0.00292113	0.02677009	0.14717159	
TCEA3	-2.1019311	2.10193114	2.02235071	10.6686054	0.00108969	0.01278761	0.23294623	
TCF7	-1.9426606	1.94266058	5.57200871	42.754715	6.21E-11	9.67E-09	0.26013626	
TESC	1.2654412	1.2654412	4.46696228	18.3957303	1.79E-05	0.00049289	2.40400717	
TESPA1	-1.3454654	1.34546538	3.88465542	25.3011883	4.90E-07	2.61E-05	0.39352702	
TGFB2	4.66997894	4.66997894	1.34621101	23.1278388	1.52E-06	6.71E-05	25.4567958	
THBS1	1.05422995	1.05422995	5.12925062	9.33106058	0.00225302	0.02227383	2.0766095	
THEM4	-2.2871102	2.2871102	3.25612892	27.37999	1.67E-07	1.03E-05	0.2048855	
THEMIS2	1.03586624	1.03586624	7.44051461	10.9376313	0.00094231	0.01127771	2.05034437	p, ca, c
THG1L	1.14349696	1.14349696	2.82889972	9.83228241	0.00171475	0.01812225	2.20915855	
TIMM21	-2.3935328	2.39353279	1.67645112	9.80727671	0.00173823	0.01832744	0.1903158	
TLE1	-1.4431423	1.44314234	3.20326608	13.9361203	0.00018913	0.00324283	0.3677654	
TLR4	1.18012265	1.18012265	3.67193956	7.93420904	0.00485088	0.03858501	2.26596039	p, ca, c
TM4SF1	2.23222083	2.23222083	1.79045518	10.1813732	0.00141866	0.01570963	4.69856704	
TMC8	-2.5164016	2.51640164	2.93009483	15.3417038	8.97E-05	0.0018258	0.17477835	
TMEM106C	-1.0438038	1.04380381	3.00612388	7.54837438	0.00600642	0.04519071	0.48504691	
TMEM192	-2.2424148	2.24241483	1.99315742	11.7733016	0.00060086	0.00804944	0.2113323	
TMEM204	-2.9269546	2.92695461	2.00155944	13.7337674	0.00021063	0.00353551	0.13149186	
TMEM69	-1.4349258	1.43492579	2.92319479	16.4236827	5.06E-05	0.00117048	0.3698659	p
TMIGD2	-2.0867569	2.08675686	2.72372933	20.6258378	5.58E-06	0.00019481	0.23540929	
TNFRSF1A	1.15303753	1.15303753	6.33611297	27.7790844	1.36E-07	8.65E-06	2.22381616	p, ca, c
TNFRSF25	-1.996436	1.99643604	3.08326495	16.4010027	5.13E-05	0.00117855	0.25061835	
TNFSF13	1.05699112	1.05699112	5.13507001	18.2078637	1.98E-05	0.00052983	2.08058772	p, ca, c
TNNI2	1.00012929	1.00012929	3.2302122	7.8884639	0.00497511	0.03929641	2.00017924	p
TNS1	1.38514854	1.38514854	2.99752921	8.36303628	0.0038293	0.03289123	2.6119885	
TOP3B	-3.4463249	3.44632489	1.20235319	10.5886839	0.00113782	0.01324915	0.09173875	p, ca, c
TP53I3	1.52233985	1.52233985	2.12893352	9.29579627	0.0022968	0.02256107	2.87256562	
ZEB1	-1.5474319	1.54743191	4.18368361	18.8257105	1.43E-05	0.00072706	0.34211852	
ZFP62	-3.589168	3.58916803	1.60510652	10.5179858	0.00118218	0.01927454	0.08309077	p, ca
ZNF211	-4.3197874	4.31978741	1.67395406	8.84262152	0.00294276	0.03622724	0.05007425	
ZNF280B	-4.2481159	4.2481159	1.25444281	8.65461618	0.00326234	0.03853397	0.05262471	
ZNF331	-1.2155081	1.21550811	5.15968286	24.8188585	6.30E-07	6.19E-05	0.43062139	
ZNF33A	-1.7354192	1.73541915	2.8599936	8.34554245	0.00386635	0.04394505	0.30032175	
ZNF346	-1.8283927	1.82839272	2.11637657	8.21349312	0.004158	0.04613866	0.28157815	p, ca, c
ZNF385A	1.03321355	1.03321355	7.39661326	11.3890147	0.0007388	0.01345921	2.04657785	p, ca, c
ZNF530	-3.8129527	3.8129527	1.17613918	8.8517675	0.00292805	0.03609533	0.07115196	
ZNF580	1.17046745	1.17046745	3.12024683	8.78092396	0.00304397	0.03707424	2.25084615	p
ZNF587	-4.2570655	4.25706548	1.279989	8.96591386	0.00275063	0.03447254	0.05229927	
ZNF761	-1.7609116	1.76091162	2.56413229	9.74186435	0.00180118	0.02561567	0.29506166	
ZNF789	-4.3497043	4.34970433	1.83889411	11.4641498	0.00070952	0.01308407	0.04904656	p, ca, c
ZNF83	-1.6017037	1.60170371	2.62269125	10.4704757	0.00121297	0.0195175	0.32948765	

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TP53INP2	2.08063188	2.08063188	1.90446913	9.09539425	0.00256254	0.02456607	4.2299244	p, ca, c
TPM1	-1.1333295	1.13332947	4.45959664	7.7904325	0.00525236	0.04094939	0.45586246	
TPPP	-2.847138	2.84713797	1.97840364	12.0332834	0.00052259	0.00728722	0.1389716	
TPRA1	1.01093728	1.01093728	3.49484051	7.77290347	0.00530357	0.04118415	2.01521991	
TPSAB1	3.37525846	3.37525846	2.31869964	20.7020171	5.37E-06	0.00019014	10.3765753	
TRABD2A	-3.2856662	3.28566616	1.31574646	9.41426688	0.00215304	0.02144965	0.10254534	p
TRAT1	-1.3004332	1.30043321	3.74786054	15.6802613	7.50E-05	0.00159696	0.40600426	
TREM1	1.13869759	1.13869759	7.88148683	41.8244617	9.98E-11	1.43E-08	2.20182161	p, ca, c
TRIB1	1.89548329	1.89548329	3.33316482	9.19324847	0.00242909	0.02355075	3.72046589	p, ca, c
TRIM68	-2.8537144	2.85371445	1.32107926	10.6900272	0.00107715	0.0126733	0.13833955	
TRMT1	-1.0202313	1.02023132	3.86504307	9.32259968	0.00226345	0.02232806	0.49303729	p, ca, c
TRMT10B	-1.3326078	1.33260778	4.20828149	14.0702018	0.00017611	0.00307804	0.3970499	p, ca, c
TRPT1	1.55049088	1.55049088	2.58570459	10.1679704	0.00142901	0.01576628	2.92916789	p
TSHZ2	-1.6804989	1.68049893	4.58556693	25.9516413	3.50E-07	1.91E-05	0.31197473	
TTC13	-4.7238165	4.72381646	1.88312438	26.7327738	2.34E-07	1.35E-05	0.03784335	
TUBA1C	1.13571903	1.13571903	7.28388689	82.0502105	1.33E-19	9.22E-17	2.19728046	p, ca, c
TUBB2A	1.25048025	1.25048025	5.16719959	51.8386003	6.03E-13	1.56E-10	2.37920609	
TUBB3	1.90713627	1.90713627	2.69505574	10.1449618	0.00144696	0.01590602	3.75063863	
TUBB6	1.10781977	1.10781977	5.03399787	28.367099	1.00E-07	6.72E-06	2.15519704	
TXK	-2.9778512	2.97785124	3.26089925	39.2538575	3.72E-10	4.48E-08	0.12693385	
UBASH3A	-1.8148235	1.8148235	2.47011106	10.121721	0.00146532	0.01604926	0.28423902	
UBE2Q2	1.67502389	1.67502389	2.60864129	19.9819214	7.82E-06	0.00025353	3.19324643	
ULBP1	2.52900722	2.52900722	1.61944674	10.4486147	0.00122741	0.01414244	5.77174365	
ULBP2	1.22205849	1.22205849	2.89689881	11.5188185	0.00068895	0.00885543	2.33279332	
ULBP3	2.89146084	2.89146084	1.31989944	9.38570014	0.00218685	0.02172804	7.42021423	
UNC93B1	1.75473354	1.75473354	3.1879726	8.1078111	0.00440749	0.03613983	3.37463986	
USP20	-1.7604475	1.76044745	2.25162689	7.85331873	0.00507275	0.03985858	0.29515661	p, ca, c
UTP3	-1.2600283	1.26002832	3.45643476	12.1282578	0.00049663	0.00700093	0.41753576	
VCAN	1.14461334	1.14461334	4.39522132	17.1480886	3.46E-05	0.00085362	2.21086869	
VHL	-1.1173153	1.11731532	3.63614016	8.86240996	0.00291103	0.02673177	0.4609508	p, ca
VMO1	2.89629642	2.89629642	4.10855348	77.341267	1.44E-18	8.66E-16	7.44512678	p, ca, c
VNN3	2.31848244	2.31848244	1.71641559	12.8652214	0.00033475	0.00508502	4.98807253	p, ca, c
VPS37C	1.97496136	1.97496136	2.43787991	8.6451649	0.0032793	0.02919389	3.9311771	p, ca, c
VPS9D1	1.4940163	1.4940163	2.27536272	8.24938911	0.00407657	0.03442608	2.81672028	p, ca, c
VSTM1	1.7345152	1.7345152	3.74112863	10.2418618	0.00137289	0.01527762	3.32767652	p, ca
WLS	3.6802008	3.6802008	1.32413099	22.8870788	1.72E-06	7.32E-05	12.8189021	p, ca, c
WNT10A	-2.8807528	2.88075277	1.47548834	9.58211978	0.00196481	0.02003844	0.135771	p
WWP1	-2.0291037	2.02910371	2.15760546	7.57022955	0.00593402	0.04478043	0.24500724	
XCL2	-1.9367238	1.93672382	3.57160391	33.9381536	5.69E-09	5.53E-07	0.26120894	
XRCC6BP1	-1.4840152	1.48401517	2.9566386	12.8826962	0.00033163	0.00505337	0.35749249	p, ca, c
ZAP70	-1.7134066	1.71340661	4.09452917	32.5933576	1.14E-08	1.03E-06	0.30493917	
ZC3H10	1.19303243	1.19303243	4.32556167	14.7942911	0.0001199	0.00227127	2.28632806	p, ca, c
ZC3H6	-1.1366051	1.13660505	4.13188411	15.0088941	0.00010701	0.0020974	0.45482862	p
ZEB1	-1.4221236	1.42212362	4.18368361	26.7215617	2.35E-07	1.35E-05	0.37316262	
ZNF165	-1.2752938	1.27529383	3.16422801	7.68957361	0.00555407	0.0426757	0.41314101	
ZNF169	-1.4921347	1.49213465	2.41583126	7.54570969	0.00601531	0.04521573	0.35548617	
ZNF264	-1.1512997	1.15129969	2.46495659	8.01753424	0.00463266	0.0373423	0.45021945	
ZNF32	-1.0648811	1.06488111	2.96785365	8.49322049	0.00356472	0.03112158	0.47801205	
ZNF354B	-2.8858152	2.88581516	1.09166169	9.56456786	0.00198369	0.02014001	0.13529541	
ZNF385A	1.0052146	1.0052146	7.39661326	14.5003545	0.00014013	0.00259707	2.00724205	p, ca, c
ZNF490	1.30948961	1.30948961	2.42000436	8.74614071	0.00310258	0.02809109	2.4785384	
ZNF551	-3.5455243	3.54552428	1.12845232	9.03172038	0.00265335	0.02515807	0.0856428	
ZNF552	-2.8502876	2.85028758	1.93857012	11.3030709	0.00077379	0.00967114	0.13866854	
ZNF576	1.01256832	1.01256832	3.03364643	9.88423854	0.00166701	0.01767964	2.0174995	
ZNF692	-3.1731029	3.17310289	1.14588135	7.74019001	0.00540051	0.04177999	0.11086663	p, ca, c
ZNF714	-3.0029347	3.0029347	1.53541814	12.1939771	0.00047944	0.0068224	0.12474599	
ZNF76	-1.778656	1.77865605	2.25304325	11.6839722	0.00063041	0.00840172	0.29145478	
ZNF787	1.23463802	1.23463802	3.13256851	11.2565753	0.00079341	0.00983442	2.35322296	p
ZSCAN18	-3.681697	3.68169705	1.53983891	13.2154287	0.00027765	0.0043785	0.07792894	
ZSCAN9	-1.637325	1.637325	2.0109248	9.09454967	0.00256372	0.02456607	0.32145195	p

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Table E8.

The interferon scores of CAIN patients. mRNA levels of selected IFN-marker genes from two patients' and age and sex matched healthy controls' PBMC cells were measured using Nanostring and the average fold changes between the patients and controls are listed in the table. Interferon scores were calculated as Rice et al. 2013* by taking the median fold change from interferon signature genes. No clear signatures for type I interferonopathy were found (interferon scores <2).

Interferon signature genes	Patient1	Patient2
IFI27	0.922992	1.305603
IFI44	2.929098	0.793661
IFI44L	5.275569	0.649852
IFI6	1.514945	0.670349
IFIT1	1.402317	0.521123
IFIT2	0.952393	1.563095
IFIT3	2.314059	1.965553
ISG15	1.243071	0.684931
MX1	2.014627	0.589092
OAS1	1.545809	0.855401
Interferon score	**1.530377**	**0.739296**

*21. Rice GI, Forte GMA, Szynkiewicz M, et al. Assessment of interferon-related biomarkers in Aicardi-Goutières syndrome associated with mutations in TREX1, RNASEH2A, RNASEH2B, RNASEH2C, SAMHD1, and ADAR: a case-control study. The Lancet Neurology 2013;12:1159-69

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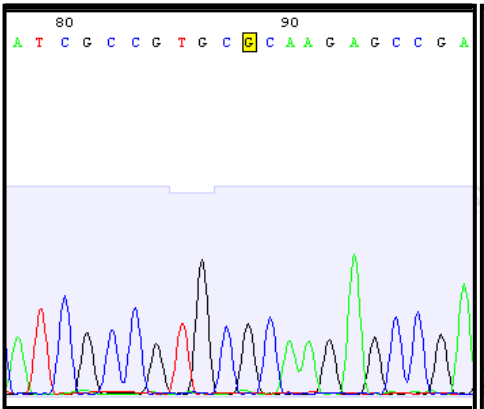
Table E9.
Sequences of the primers used in quantitative real-time RT-PCR. F, forward primer; R, reverse primer.

Target gene	Primer	Sequence 5' -> 3'
caspase-5	CASP5_F	CTTCAAGGCCTGGGCTACAC
	CASP5_R	TCAGCACTGACTCCATATCCCTG
interferon induced protein with tetratricopeptide repeats 2	IFIT2_F	GCCGAACAGCTGAGAATTGC
	IFIT2_R	AGGCCAGTAGGTTGCACATTG
MX dynamin like GTPase 1	MX1_F	CGAGATGTCCCGGATCTGACT
	MX1_R	CACCACCAGGCTGATTGTCT
MX dynamin like GTPase 2	MX2_F	AGAGGCAGCGGAATCGTAAC
	MX2_R	ATTCCCGGCCATGACGTTCT
ribosomal protein lateral stalk subunit P0	RPLP0_F	GAAATCCTGAGTGATGTGCAGC
	RPLP0_R	TCGAACACCTGCTGGATGAC

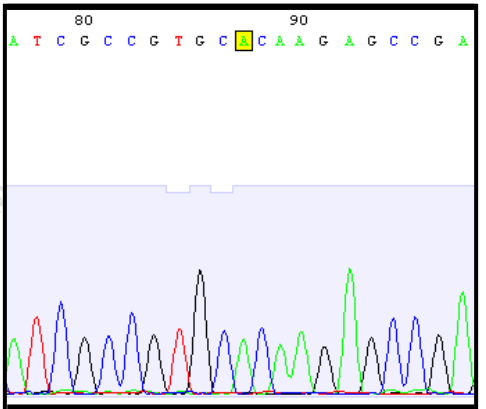
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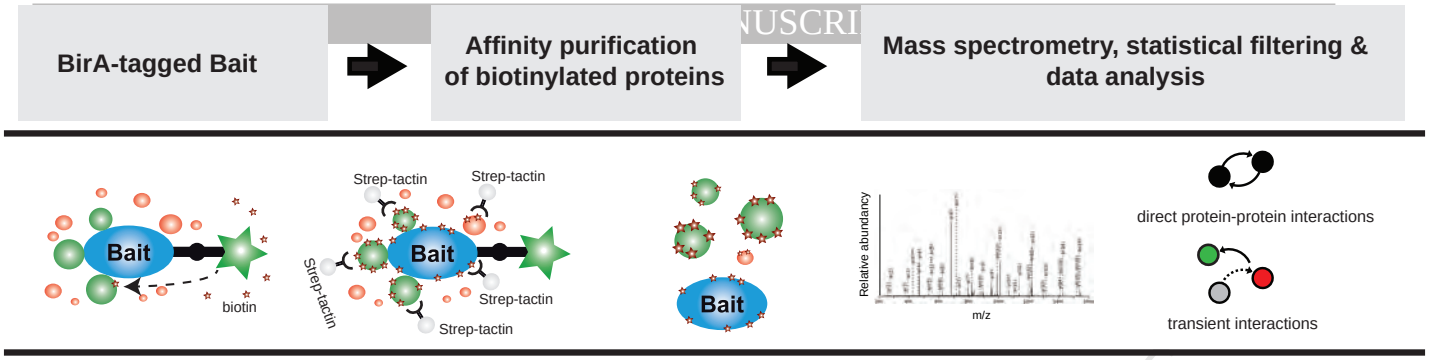
Control



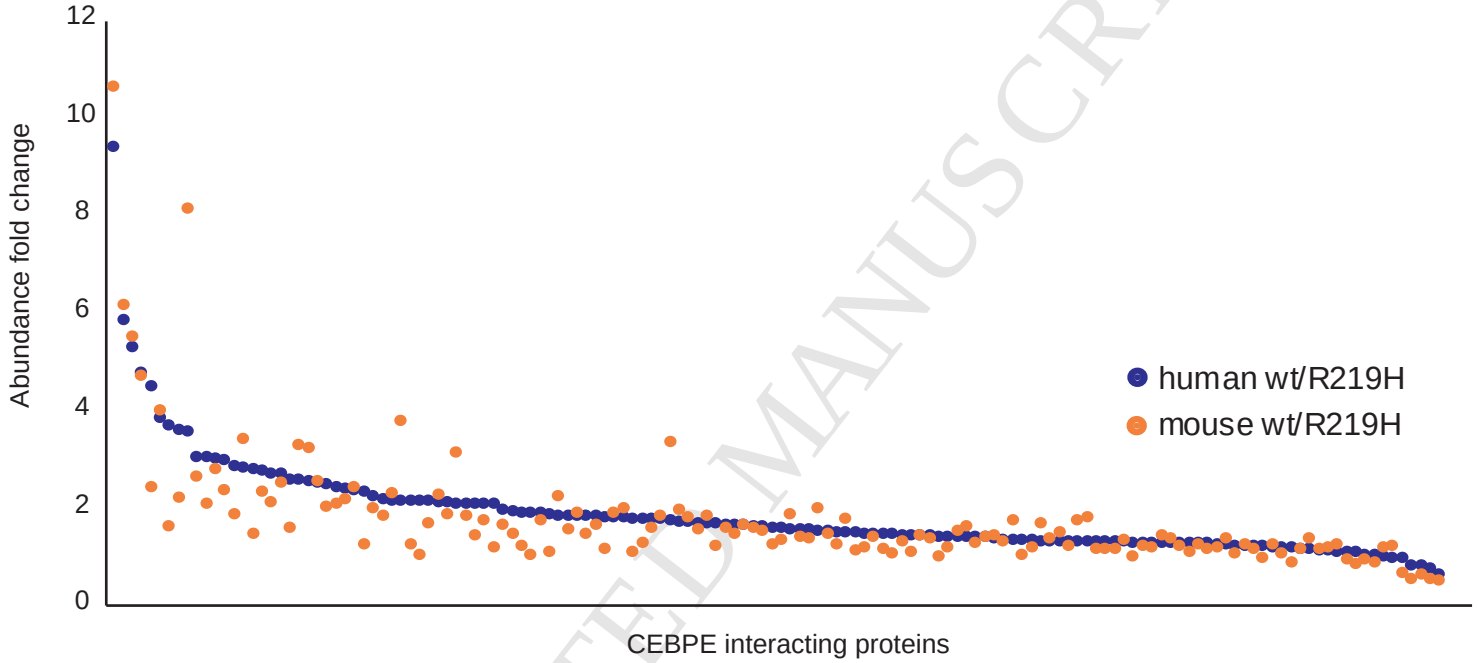
Patient



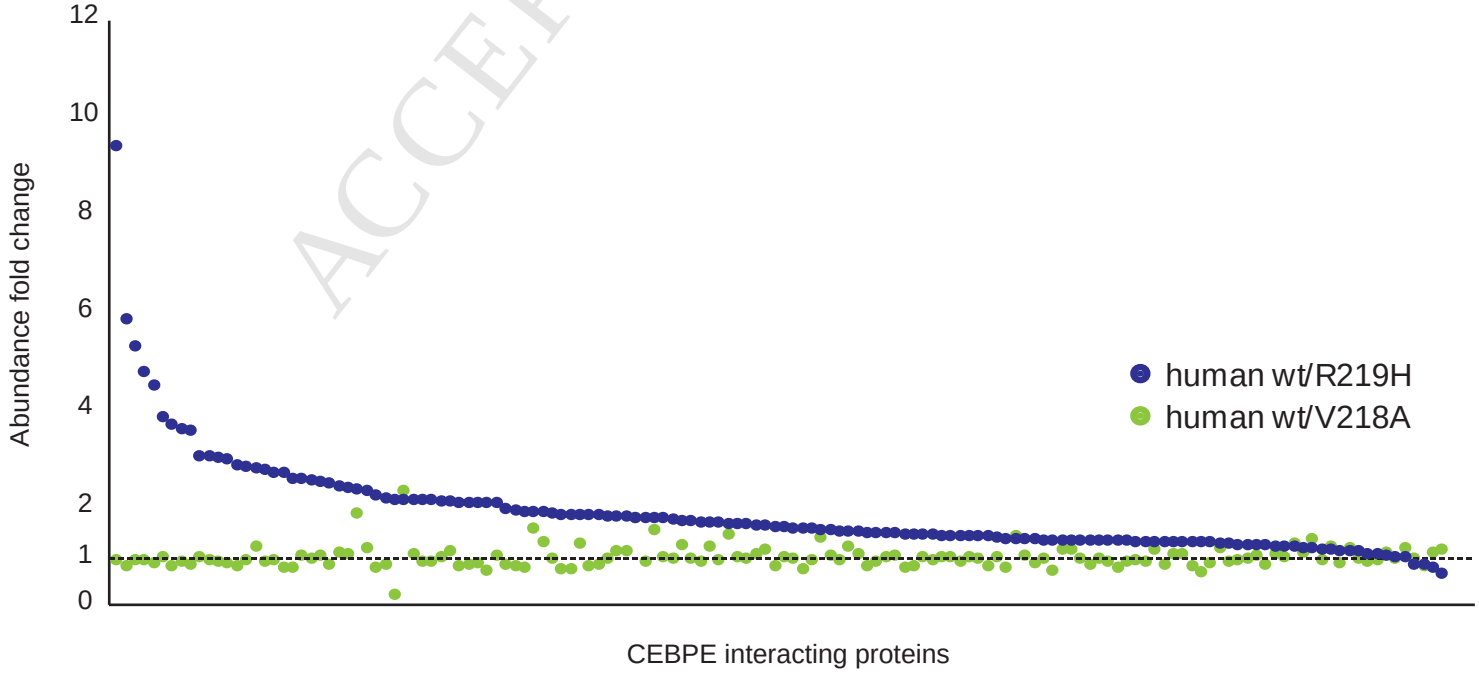
A



B

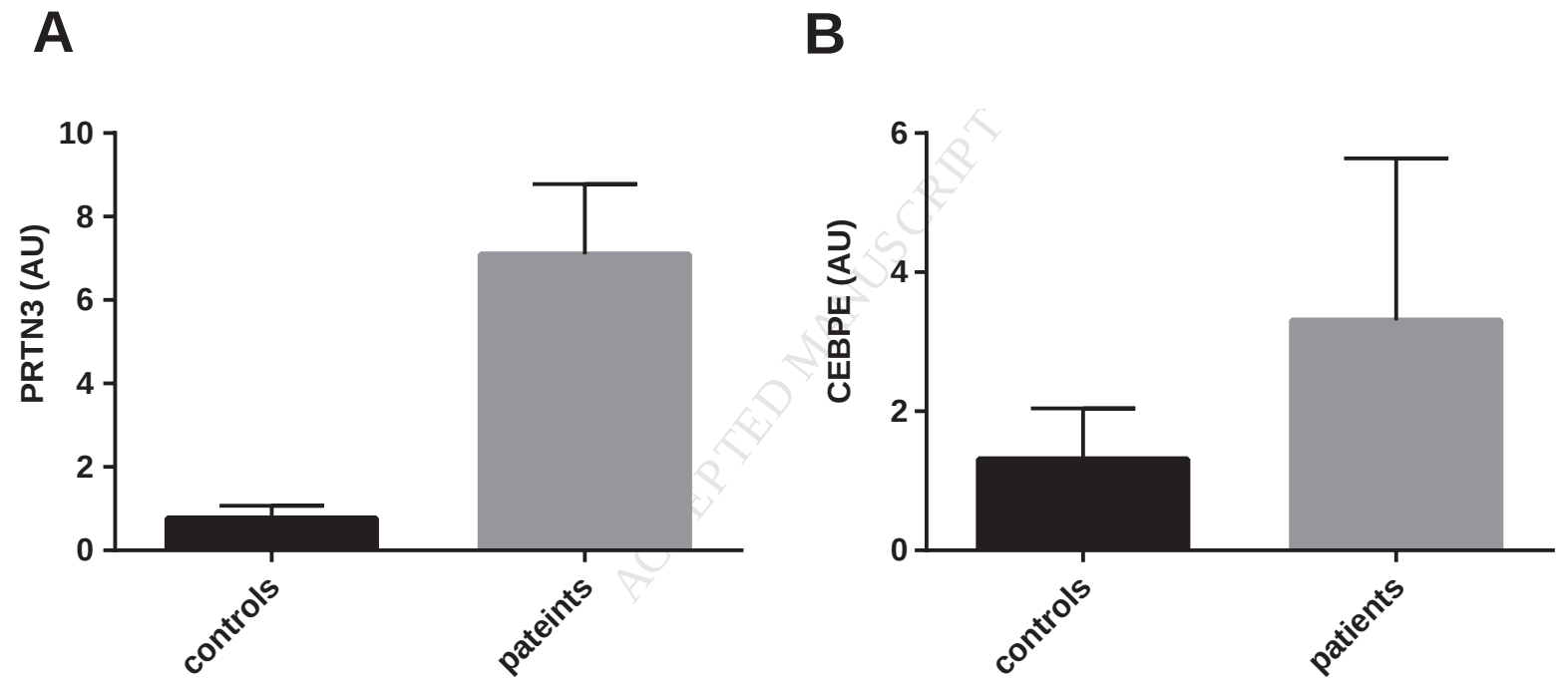


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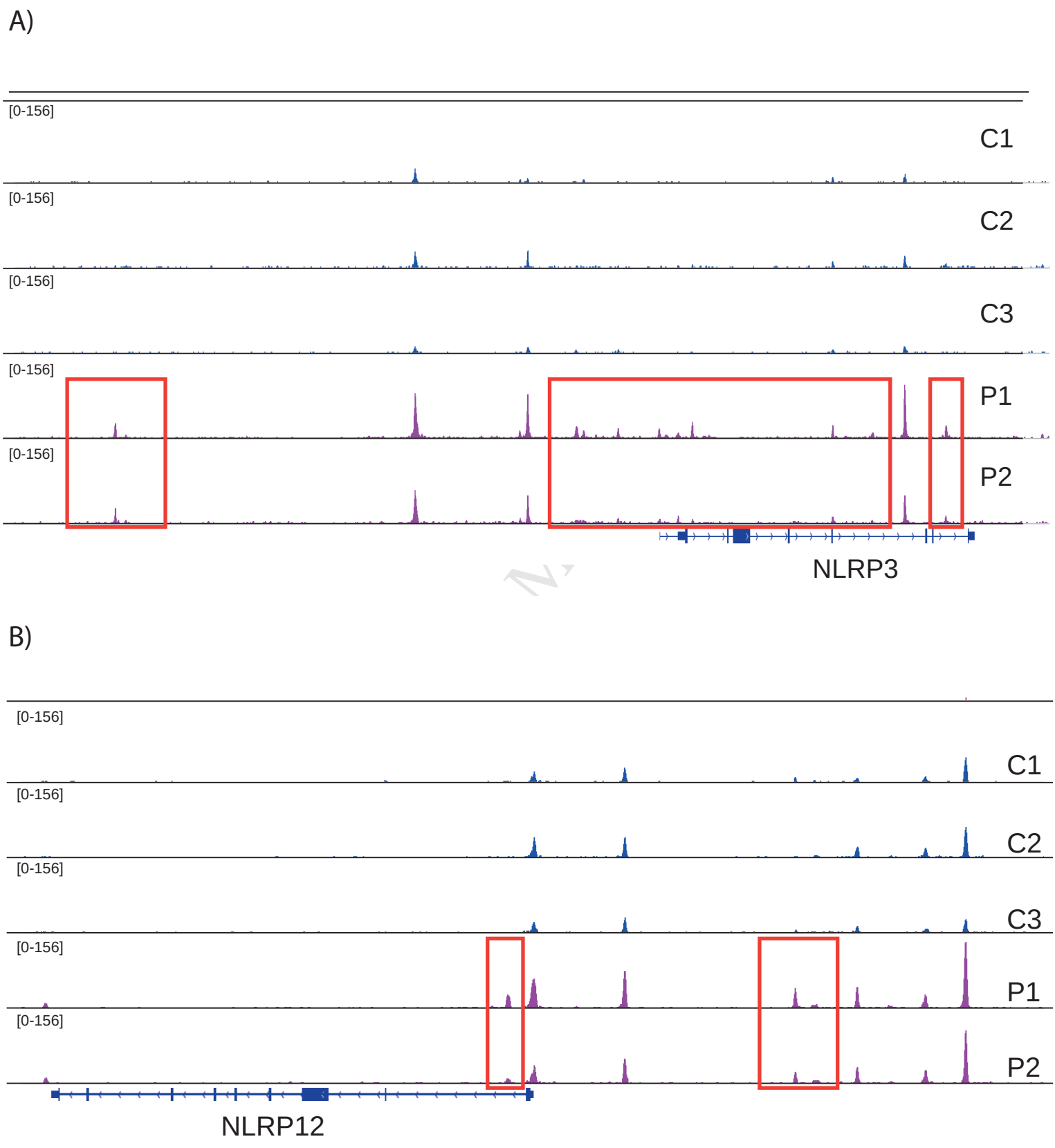


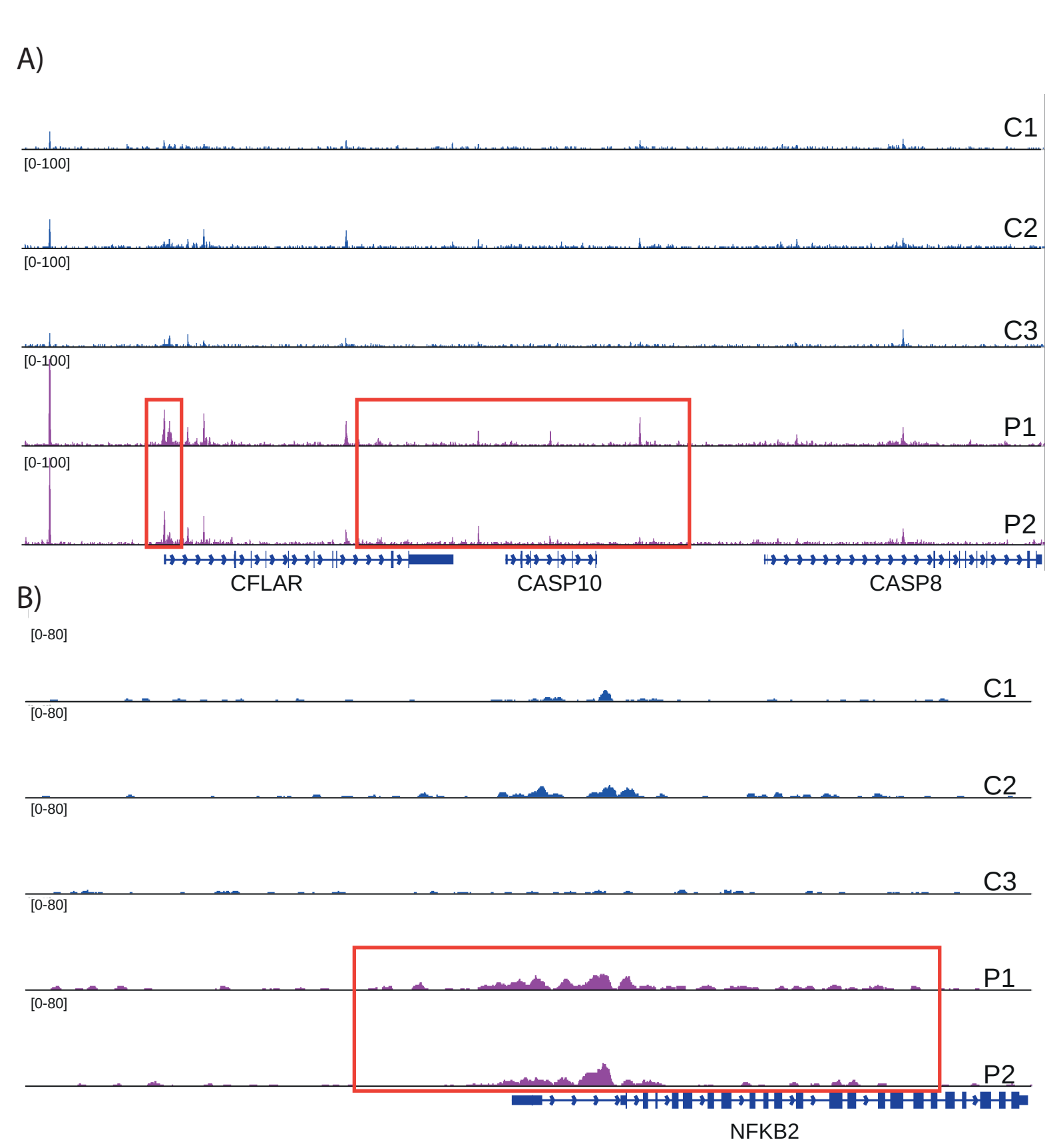
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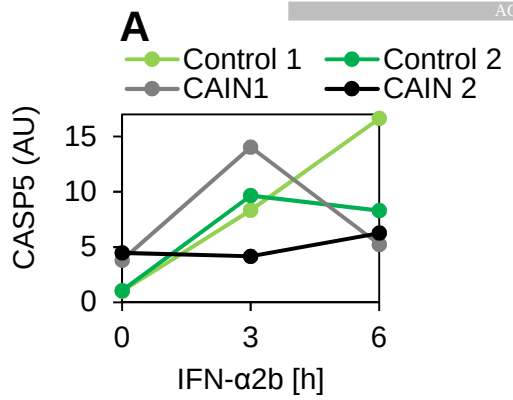


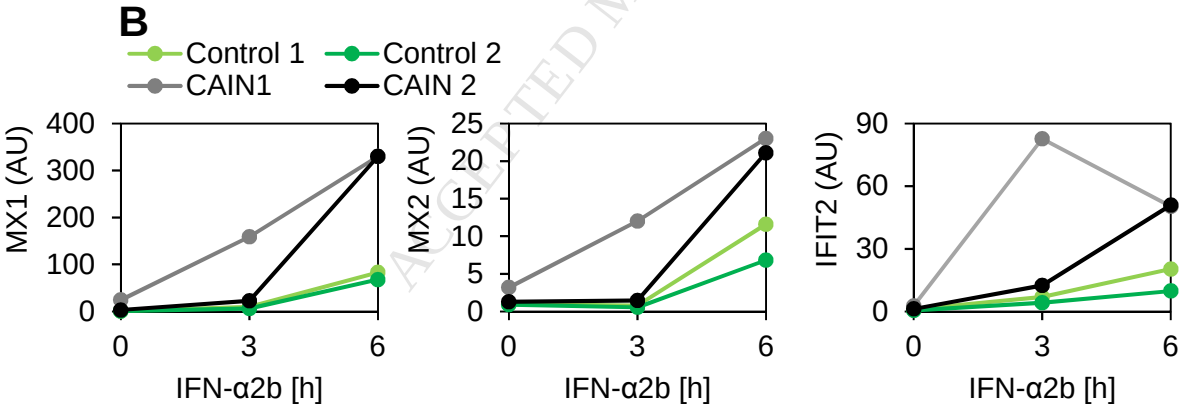
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C2
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C3
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P1
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P2
NLRP3
B)
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C1
[0-156]
C2
[0-156]
C3
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P1
[0-156]
P2
NLRP12

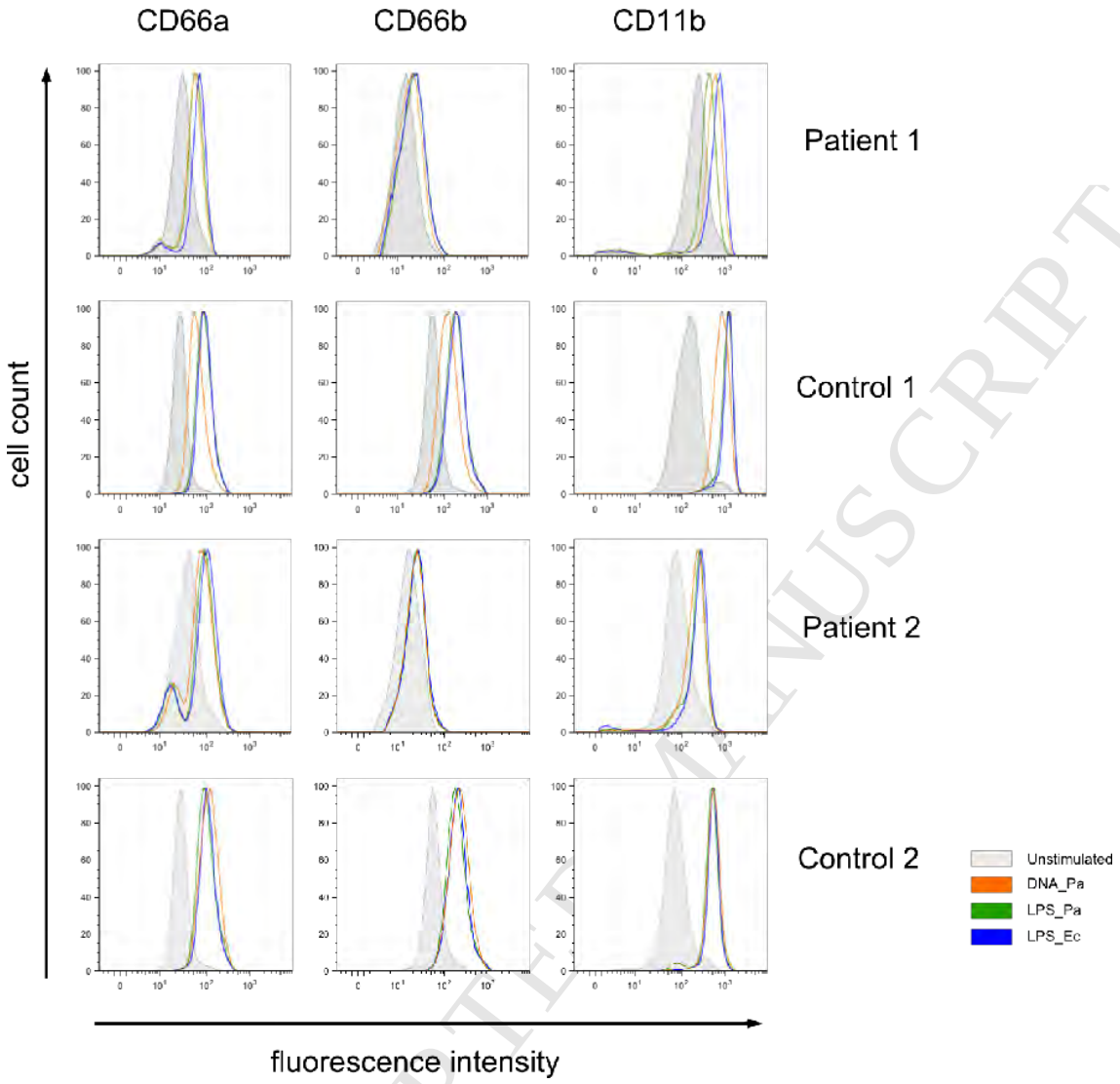

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C2
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C3
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P1
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P2
CFLAR
CASP10
CASP8
B)
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C1
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C2
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C3
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P1
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P2
NFKB2

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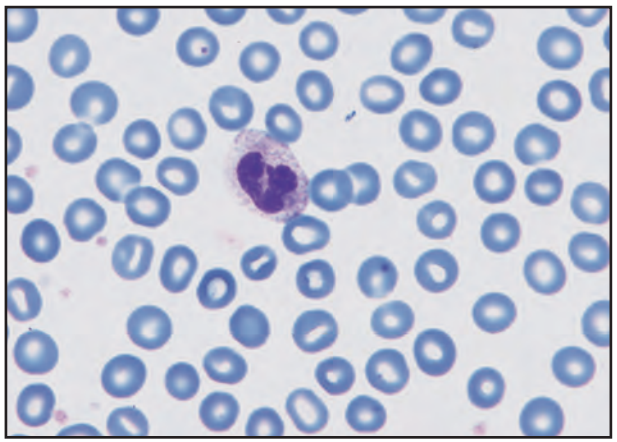


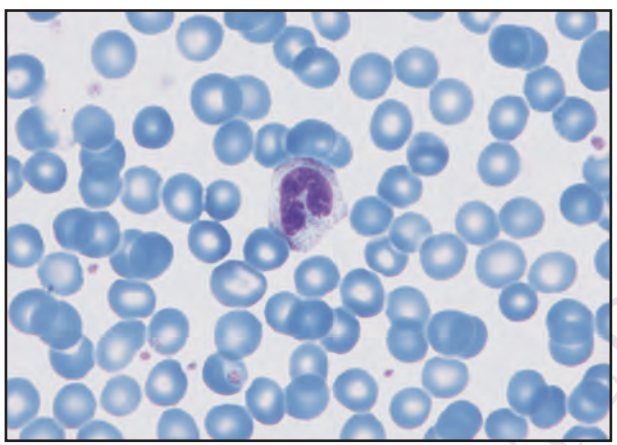
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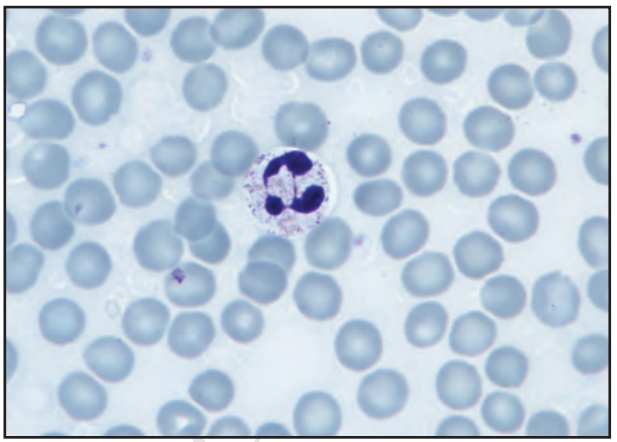
A

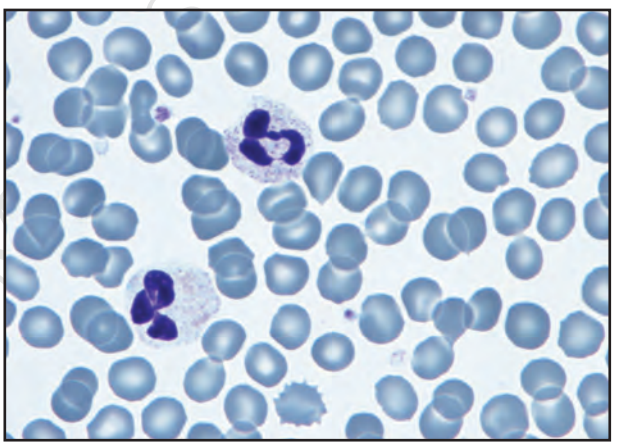
Patient granulocytes





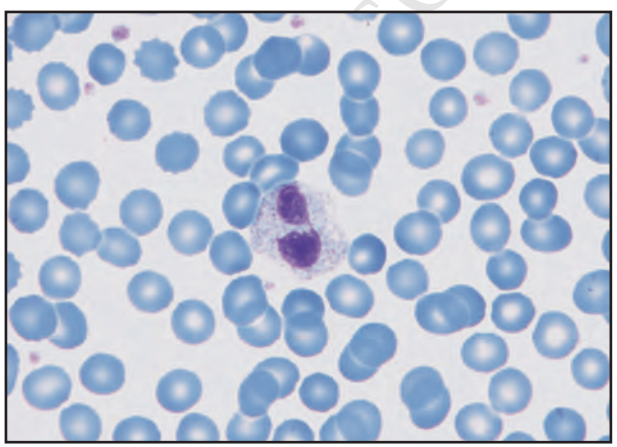
Control granulocytes





B

Patient hyposegmented granulocyte



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Supplementary Appendix

To: Gain-of-function *CEBPE* mutation causes non-canonical autoinflammatory inflammasomopathy

Helka Göös*, Christopher L. Fogarty*, Biswajyoti Sahu*, Vincent Plagnol, Kristiina Rajamäki, Katariina Nurmi, Xiaonan Liu, Elisabet Einarsdottir, Annukka Jouppila, Tom Pettersson, Helena Vihinen, Kaarel Krjutskov, Päivi Saavalainen, Asko Järvinen, Mari Muurinen, Dario Greco, Giovanni Scala, James Curtis, Dan Nordström, Robert Flaumenhaft, Outi Vaarala, Panu E. Kovanen, Salla Keskitalo, Annamari Ranki, Juha Kere, Markku Lehto, Luigi D Notarangelo, Sergey Nejentsev, Kari Eklund¤, Markku Varjosalo¤, Jussi Taipale¤, Mikko RJ Seppänen¤

*/¤ These authors contributed equally to this work.

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Extended case reports

Our index family has no known consanguinity, while I.1 and I.2 came from the same restricted geographical area. Unlike the four unaffected children of them, the affected four female family members displayed painful recurrent tongue abscesses soon after birth. Patient records from that time contain no references to positive bacterial cultures other than normal oral commensals from superficial samples. Patients did not recall any help from antibiotics. In adolescence, tongue abscesses were replaced by painful crater-like buccal ulcers healing slowly, again failing to clearly respond to antibiotics. No information on attempts to treat these with glucocorticoids were found.

Throughout follow up, they suffered from frequently recurring paronychia, more prominent on fingers. These frequently progressed into ascending lymphangitis. Constant careful hand hygiene seemed to decrease their frequency. In occasional bacterial cultures, mainly *Staphylococcus aureus* and other staphylococci were noted. They also suffered from delayed wound healing, frequent pus formation and positive *Staphylococcus aureus* cultures of their skin wounds compared to other family members, throughout follow up. Patients' paronychia and pus formation responded well to topical and systemic antibiotics against staphylococci. In addition, they displayed a moderate bleeding tendency without an identifiable cause in repeated testing. This manifested as frequent nose bleeds, need for prolonged compression after needle sticks and prominent early postoperative hematomas.

At puberty, all four affected family members developed recurrent high fever with abdominal pain, with an average duration of 4-5 days. These recurred every 2-4 weeks during adolescence and early adulthood, somewhat decreasing in frequency with advancing age. Attacks were frequently accompanied by bouts of skin lymphangitis. Other symptoms during febrile attacks included vomiting, myalgia, pleurisy, arthralgia, scleritis and episcleritis (Table 1). Typically, both plasma

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C-reactive protein and erythrocyte sedimentation rate increased to > 100 mg/L and >50-70 mm/h, respectively. Throughout adult age, they received only occasionally low dose oral glucocorticoid courses, with mild symptom relief. In addition, II.2 also suffered from surgically treated recurrent gluteal and submandibular abscesses between ages 38-39 y. She died of complications associated with Alzheimer's dementia at age 78. At menopause, the febrile attacks stopped in II.2 and II.7, while in II.13 these abated somewhat.

For II.3, there was no genetic or autopsy material available for testing, but she displayed pronounced neutrophil hyposegmentation in her blood smears (Murros, Konttinen). She acquired rheumatic fever causing significant mitral and aortic valve insufficiency and cardiac arrhythmias at age 18 y. At age 23 y, she developed a subacute *Streptococcus viridans* endocarditis and died at age 34 of ventricular fibrillation. In autopsy statement, "substantial numbers of calcified mesenteric lymph nodes with nonspecific inflammation" were found.

II.7 developed pyoderma gangrenosum at age 43 y and was radically operated for ileal leiomyosarcoma at age 35 y. While all three sisters surviving beyond early adulthood had undergone repeated gastroduodenoscopies and ileocolonoscopies, these were usually performed outside febrile attacks. However, at age 55 y II.7 had ileocolonoscopy during fever and "few aphthae" were noted in descending colon, but these were not biopsied.

II.13 suffered from recurrent upper and lower respiratory tract infections from age 42 y. At age 55 y, she developed prolonged cough, abdominal pain, malaise and bilateral upper lobe lung infiltrates together with a mass lesion between her portal vein and vena cava and somewhat thick ileal wall. Her mesenterial lymph node biopsy, taken during laparotomy, showed sterile non-necrotic granulomatous lymphadenitis. Systemic glucocorticoid therapy was started, first with daily oral 40mg of prednisolone, offering good and rapid symptom relief. Her oral prednisolone dose was thereafter tapered slowly to 12.5-7.5 mg. After menopause, she still developed febrile attacks

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unless continuous daily low dose oral prednisolone 2.5-7.5 mg was used. Currently the dose has been tapered down to 2.5 mg daily. Patient II.13 refused all experimental therapy outside prednisolone due to good disease control with it after menopause.

In T cell differential at age 68 y, II.13 was noted to have somewhat low CD3+CD4+CD45RA+CD3+CD4+ (10%) and CD3+CD8+ (9%) CD45RACCR7+ naïve T cells. Also, low percentages of recent thymic emigrant CD3+CD4+CD45RA+CD62L+CD31+ T cells (6%) were noted. 76% of her CD3+CD8+ T cells and 63% of her CD3+CD4+ displayed terminally differentiated effector memory (TEMRA) CD45RA+CCR7- subtype, suggesting advanced age and immune exhaustion, while age-matched reference values are not available for such advanced age.

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Supplementary Methods

Subjects

Two patients, two asymptomatic carriers and eight [different numbers for different analyses] age-matched controls were analyzed. Patient samples were processed concurrently with their matched controls. Written informed consent was obtained from study participants and the study was approved by the institutional ethical review board (138/13/03/00/2013).

Genetic analysis of a de novo C/EBPε germ-line mutation

We analyzed DNA from three affected family members (Fig. 1a) by whole exome sequencing. Library preparation, exome capture and sequencing were done according to the manufacturers' instructions. For exome target enrichment, Agilent SureSelect (Agilent Technologies) 50 Mb kit was used. Sequencing was done on Illumina HiSeq instruments (Illumina) using paired-end 75 bp reads. Reads from raw FASTQ files were aligned to the hg19 reference genome using Novoalign version 2.08.03. Duplicate reads were marked using Picard tools MarkDuplicates. Calling was performed using the haplotype caller module of GATK (https://www.broadinstitute.org/gatk), creating gVCF formatted files for each sample. The individual gVCF files were combined into gVCF files containing 100 samples each. The final variant calling was performed using the GATK "GenotypegVCFs" module jointly for all cases and controls. Variants' quality scores were then re-calibrated according to GATK best practices separately for indels and SNPs. Resulting variants were annotated using ANNOVAR.

In the exome data, we identified between 20,638 and 21,313 single nucleotide variants and small insertions/deletions in each patient. A total of 149 variants were very rare, i.e. those not seen in the 6,500 NHLBI Exomes, 1000 Genomes database (April 2012 data release) and 2,500 exomes

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analyzed internally using the same bioinformatics pipeline. Of these, 22 variants were shared between all three patients. Only one of these variants was homozygous in all three patients (ENSG00000092067:ENST00000206513: exon2:c.G656A;p.Arg219His), in the *CEPBE* gene. The novel homozygous CEBPE 14:23586886 C>T mutation co-segregated perfectly with the disease phenotype. Arg219His was predicted to be detrimental and not listed in major public or in-house databases. It resided in the highly conserved basic zipper (bZIP) region's carboxyl terminal DNA binding domain (DBD), shared by all four C/EBPε isoforms.

Sanger sequencing

Identified homozygous or heterozygous novel germline mutations were validated by Sanger sequencing. We used primers GGTGTCTAGCTCCTGGGTGA and CTGCAGTCCCCTCCTGAA to amplify the fragment of the CEBPE.

Protein-protein interactions

Flp-In™ T-REx™ 293 cell lines stably expressing mutant or wild type (WT) C/EBPε were generated and used to investigate protein-protein interactions (PPIs) by proximity-dependent biotin identification coupled to mass spectrometry (BioID-MS)[1].

Generation of expression constructs and inducible Flp-In™ 293 T-REx cell lines

The WT human or mouse CEBPE full length coding sequence without stop codon were commercially cloned into a Gateway®-compatible pDONR221 entry-vector (GenScript). The Arg219His mutant constructs were generated by PCR (primers: human_forward GCAACAACATCGCCGTGCACAAGAGCCGAGA, human_reverse GCCTTGTCTCGGCTCTTGTGCACGGCGATGT, mouse_forward: GTAACAACATCGCGGTGCACAAGAGCCGGGA and mouse_reverse

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GCCTTGTCCCGGCTCTTGTGCACCGCGATGT), and the corresponding point mutation was verified by sequencing. Val218Ala mutation construct was generated similarly (primers: forward: GCAACAACATCGCCGCGCGCAAGAGCCGAG and reverse: CTCGGCTCTTGCGCGCGGCGATGTTGTTGCG). For the generation of a tetracycline-inducible C/EBPε expressing cell line, both WT and mutant constructs were cloned in to a pTO_HA_StrepIII_BirA-N_GW_FRT (MAC-tag) vector and recombined into Flp-In™ T-REx™ 293 cells (Life Technologies), as previously described[1, 2].

Affinity purification and mass spectrometry analysis

For affinity purification, approx. 5×107 Flp-In™ T-REx™ 293 cells stably expressing human or mouse C/EBPε (WT, Arg219His or Val218Ala) were induced with 2 µg/ml tetracycline and 50 µM biotin for 24 hours, pelleted, snap frozen with liquid nitrogen and stored at -80 °C. Pellets were then suspended in 3 ml of lysis buffer (50 mM HEPES pH 8.0, 5 mM EDTA, 150 mM NaCl, 50 mM NaF, 0.5 % NP40, 1.5 mM Na3VO4, 1 mM PMSF, 1× protease inhibitors cocktail; Sigma, 0.1 % SDS and 80 U/ml Benzonase Nuclease (Santa Cruz Biotechnology) and incubated on ice for 15 min. This was followed by three cycles of sonication (3 min) and incubation (5 min) on ice, prior to sample cleanup by centrifugation. Supernatants were loaded in to spin columns (Bio-Rad) containing 200 µl of Strep-Tactin beads (IBA, GmbH) and allowed to drain under gravity. The beads were washed with 3× 1ml lysis buffer and 4× 1ml lysis buffer without the detergents and inhibitors (wash buffer). The purified proteins were eluted from the beads with 600 µl of wash buffer supplemented with 0.5 mM biotin. For reduction and alkylation of cysteine bounds, samples were treated to final concentration of 5 mM TCEP (Tris(2-carboxyethyl) phosphine) and 10 mM iodoacetamide. Proteins were digested with 1 µg sequencing grade trypsin (Promega) overnight at 37 °C and the peptides were purified using C-18 microspin columns (The Nest Group Inc. USA)

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according manufacturer's instructions. The vacuum-dried samples were dissolved in 30 µl of buffer A (0.1% trifluoroacetic acid and 1% acetonitrile in MS grade water).

The mass spectrometry analysis was performed on an EASY-nLC II –system coupled to an Orbitrap Elite ETD hybrid mass spectrometer (Thermo Fisher Scientific), as described earlier[3].

Proteome Discoverer™ software with SEQUEST search engine (version 1.4, Thermo Fisher Scientific) were used for protein identification. Raw data was searched against the human component of the UniProt-database (release 2016_02; 20144 entries) complemented with trypsin, BSA, GFP, mouse CEBPE and tag sequences. Carbamidomethylation (+57.021464 Da) of cysteine residues was used as static modification whereas oxidation (+15.994491 Da) of methionine and biotinylation (+226.078 Da) of lysine residues or N-terminus were used as dynamic modification. Maximum two missed cleavages were allowed, and maximum of 15 ppm monoisotopic mass error was allowed. Peptide false discovery rate (FDR) was set to <0.05. Identified proteins were compared against the control BioID database. Only interactions with <20% frequency and 2-fold higher abundance, compared to the corresponding protein values in the controls database, where classified as high-confidence interactions. The Cytoscape software platform[4] was used to visualize the high-confidence protein-protein interactions.

Protein-protein interaction validation in Jurkat cells

Jurkat cells were transfected with pTO_HA_StrepIII_BirA-N_GW_FRT vector inserted with CEBPE (WT or mutant) or GFP using Neon® Transfection system (Invitrogen) according manufacturer's instructions. Shortly, in one Neon 100 µl tip, 15 µg of construct DNA and approximately 5×10^6 suspension Jurkat cells were transfected using electroporation with 1,350 volts, 10 ms pulse width and three cycles. Cells from 10 tips (~ 5×10^7 cells) were combined for PPI analysis for each construct. The following day, transfected cells were treated with 50 µM biotin for

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24 hours. The cells were subsequently collected and affinity purification, MS analysis and data interpretation were performed as previously described with Flp-In™ T-REx™ 293 cells.

White blood cell fractionation and isolation for ChIP-seq and RNA-seq

Plasma was separated from the blood cell fraction by centrifugation at 400×g for 15 min. Plasma was removed and centrifuged at 1500×g for 10 min at room temperature (rt) to pellet out the platelets. Platelet-depleted plasma was collected. The cell fraction was carefully mixed with dextran (Sigma Aldrich) and the erythrocytes were allowed to settle for 30 min at rt. The leukocyte fraction was collected, washed, re-suspended in platelet-depleted plasma, and carefully layered atop FICOLL (GE Healthcare, UK) and centrifuged at 700×g for 15 min. After FICOLL gradient centrifugation, the granulocytes and peripheral blood mononuclear cells (PBMCs) were separately collected. The PBMCs were stored in liquid nitrogen until further use. The remaining erythrocytes in the granulocyte fraction were lysed using a lysing buffer containing 1 mM EDTA, 150 mM NH4CL, 10 mM NaHCO3 in water for 3 min followed by centrifugation at 483×g for 8 min at rt. Cells were washed twice using 0.9% NaCl and then re-suspended in Hanks balanced salt solution (Thermo Fisher Scientific) medium until use. Trypan blue exclusion assay was used to assess the viability of the isolated cells.

Chromatin immunoprecipitation followed by sequencing (ChIP-seq)

Chromatin immunoprecipitation

Chromatin immunoprecipitation (ChIP) was performed as previously described with minor modifications[5]. Briefly, the extracted PBMCs were fixed in 1% formaldehyde for 10 min at rt followed by addition of 0.125 M glycine. The cells were twice washed with ice-cold PBS and collected in lysis buffer (5 mM PIPES (pH 8.0), 85 mM KCl, and 0.5% NP-40). The cell suspension was centrifuged and the pellet resuspended for lysis in 300 µl RIPA buffer (1% NP-40, 0.5%

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sodium deoxycholate, 0.1% SDS in 1 × PBS) containing protease inhibitors (Roche). The chromatin was sonicated to an average fragment size of 100–300 bp using Bioruptor UCD-300-TO (Diagenode), after which the samples were centrifuged at 13000 rpm for 15 min at +4 °C to collect the supernatant. Dynal protein-G magnetic beads (Invitrogen) were pre-washed with 5 mg/ml BSA in PBS for a total of 5 times and resuspended in 100 ul of wash buffer. Antibodies specific for the protein of interest were coupled to magnetic beads overnight with rotation at 4 °C. For each immunoprecipitation (IP), 100 µl of sonicated chromatin was diluted 1:10 with 900 µl of RIPA buffer containing PIC and 10% of it was stored as input fraction. Into the remaining 90%, 100 µl of antibody-coupled magnetic beads were added and incubated on a rotator overnight at 4 °C. After incubation, beads were washed 5 times with LiCl wash buffer (100 mM Tris- HCl (pH 7.5), 500 mM LiCl, 1% NP-40, and 1% sodium deoxycholate) and followed by two washes with 10 mM Tris-HCl (pH 8.0) containing 1 mM EDTA. Chromatin-antibody samples were eluted from beads by incubating for 1 h at 65°C in IP elution buffer (1% SDS, 0.1 M NaHCO3), followed by overnight incubation at 65°C to reverse cross-linking. The eluted DNA was purified using phenol-chloroform followed by library preparation for Illumina sequencing.

ChIP-sequencing

Granulocytes were isolated from two homozygous patients, two heterozygous carriers and three sex- and age-matched controls, and chromatin immunoprecipitation followed by sequencing (ChIP-seq) was used to assess C/EBPε binding to chromatin in freshly isolated and LPS stimulated cells.

The ChIP was performed in PBMCs with anti-CEBPE (sc-25770 X), anti-CEBPB (sc-150 X) and rabbit anti-IgG (sc-2027). Immunoprecipitated samples together with input samples were processed for library preparation as previously described, with minor modifications5. In brief, DNA samples were end-repaired, dA-tailed and ligated to sequencing adapters. Adapter-ligated DNA fragments (size range 200–350 bp) were size-selected using AMpure XP beads (Beckman Coulter) and further

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amplified by PCR (12 cycles). The PCR-amplified ChIP libraries were quantified on Bioanalyzer/Qubit and run on a HiSeq2000 (Illumina).

Data analysis

The raw sequencing data was demultiplexed using bcl2fastq and quality analyzed by FastQC. The fastq files were aligned to human genome version GRCh37/hg19 using bowtie and the ChIP-seq peak calling was performed with MACS2[6] against rabbit IgG and input as controls. The tag density maps and motif analysis were performed with Cistrome pipeline[7] and MEME[8].

RNA-seq

RNA sequencing (RNA-seq) was used for genome-wide transcriptional profiling of freshly isolated untreated granulocytes from patients and controls. In addition, 5-end RNA-seq was used to identify the genes differentially expressed in granulocytes after three different stimulation: 1. DNA (DNA_Pa) or 2. LPS (LPS_Pa) extracted from *Pseudomonas aeruginosa* or 3. LPS from *E. coli* (LPS_Ec). Moreover, granulocytes were stimulated with IFNα2 and IFNγ followed by transcriptional profile analysis by 5-end RNA-seq.

RNA-seq of untreated granulocytes

cDNA libraries were prepared using to Illumina TruSeq Stranded mRNA LT Kit, (Part Number RS-122-2101). In summary, mRNA was purified from total RNA using poly-T oligo–attached magnetic beads, RNA was then fragmented and primed for cDNA synthesis using random primers. Superscript II was used during first strand synthesis. The 3’ end of the cDNA was then adenylated and Illumina adapters were ligated to allow pooling of libraries. cDNA libraries were then enriched by conventional PCR and finally purified using AMPure XP beads. Libraries were then analysed using Agilent Bioanalyzer 2100 to determine the average size distribution of the cDNA libraries.

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Quantitative PCR with KAPA Library Quantification Kit (part number KK4824) was performed to quantify the libraries prior to normalisation for sequencing; any library below 5 nmol was considered a fail and library preparation was repeated. Sequencing was done on Illumina HiSeq machines using SE50 reads.

5-end RNA-seq of stimulated granulocytes

Granulocytes were seeded into wells at a concentration of 1×106 cells/ml and incubated for 1 h at +37 °C with either 100ng/ml LPS from 0111:B4 E. coli (Sigma Aldrich), 100ng/ml LPS from P. aeruginosa (P.a; Sigma Aldrich), 12.5µg/ml DNA_Pa, 500 ng/ml IFNα2b (Immuno Tools), 500 ng/ml IFNγ (Immuno Tools) or buffer as a control. DNA_Pa was isolated using the QIAamp DNA Mini and Blood Mini prep kit (Qiagen, Hilden, Germany) according to manufacturer's instructions. LAL tests showed the final bacterial DNA solution to have no detectable LPS activity.

Following the incubation, samples were centrifuged at 5000 rpm for 3 min at +4 °C. Cells were lysed in buffer RLT (Qiagen) supplemented with 1% β-mercaptoethanol. Cell lysate was stored at -80 °C.

Total-RNA samples from isolated granulocytes as well as stimulated granulocytes were analyzed using 5'end RNA-seq[9] with modifications[10] except that 10 ng total-RNA from granulocytes rather than single cells were used. The STRTprep pipeline version 2.0.0, available at https://github.com/shka/STRTprep, was used to processing the raw sequenced reads as previously described[10].

For the standard RNA-seq, paired-end reads from the raw RNA-seq data were aligned using TopHat (version 2.0.6) against the h19 genome build using the bowtie 1 option, and quality control assessments were made using RSeQC software. Gene counts were generated using HTSeq software and gene annotation files were obtained from Illumina.

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For all RNA-seq experiments, genes with low counts in more than three samples were removed before the identification of differentially expressed genes using the Bioconductor package edgeR v3.14.0. A false discovery rate (FDR) method was employed to correct for multiple testing. Differential expression was defined as fold cahnge $| \geq 2$ with the FDR set to 5%. Genes related to IFN signaling were identified using Interferome v.2.01 (www.interferome.org).

Nanostring analysis of selected genes' RNA levels in patient PBMCs

We used Nanostring[11] in peripheral blood mononuclear cells (PBMC) to analyze the mRNA levels of selected genes. Patients' and their age- and gender-matched controls' blood samples were collected in Vacutainer® CPT™- Cell preparation tubes with Sodium HeparinN (BD) and the PBMCs were purified according manufacturer's instructions. Approximately 10 million fresh PBMCs were snap frozen without media and stored at -80 °C until RNA extraction. RNA was extracted using the RNeasy® Mini Kit (Qiaqen) according to the manufacturer's instructions and quantified using a Qubit fluorometer (Thermo Fisher Scientific).

A total 100 ng of RNA in 5 µl per sample was analyzed on the NanoString nCounter gene expression platform (NanoString Technologies). A custom set gene panel (50 genes) containing genes involved in IFN, inflammasome, JAK/STAT and NFKB signaling was used in the analysis. RNA samples were mixed with 5' reporter probes, tagged with fluorescent barcodes of targeted genes, and 3' biotinylated capture probes and the samples were hybridized overnight at 65 °C following the manufacturer's protocol.

After the hybridization step, the reactions were purified and immobilized on the sample cartridge surface by using the Prep Station (NanoString Technologies). Finally, the cartridge was scanned, in triplicate, using the nCounter Digital Analyzer (NanoString Technologies).

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Gene expression data were analyzed using nSolver™ 4.0 analysis software (Nanostring Technologies). As recommended by manufacturer, raw gene counts were normalized in two steps. First, the positive control normalization within samples was performed to adjust the possible variation of sample preparation, analysis and scanning. Secondly, to adjust the variance in input materials and RNA degradation states, normalization to housekeeping genes was performed. Both normalizations were implemented using the default settings of nSolver™ 4.0.

Normalized gene counts from three replicates were further used to calculate the fold changes between the patients and control. The Student's t-test was used to assess significance of the results.

Inflammasome analyses in human monocyte-derived macrophages

For inflammasome analyses, levels of caspase-5 were analyzed by quantitative PCR and IL-1β/IL-18 secretion by ELISA from cultured macrophages. PBMCs were isolated from sodium heparin anticoagulated blood after dextran sedimentation using density gradient centrifugation in FICOLL-Paque PLUS (GE Healthcare) and used fresh for macrophage culture. After 1 h adherence of PBMCs and three washes, the adherent monocytes were differentiated into macrophages via 7-day culture in Macrophage-SFM medium (Gibco), supplemented with penicillin-streptomycin (Gibco) and 10 ng/ml recombinant human GM-CSF (Miltenyi Biotec). Macrophages were primed for 6 h with 1 μg/ml LPS from E.coli O111:B4 (Sigma Aldrich), 1 μg/ml Pam3Cys-SKKK (EMC microcollections), or 100 IU/ml IFNα2b (ImmunoTools). After priming, the NLRP3 inflammasome was activated with 5 mM ATP (Sigma, canonical activation) for 45 min or by transfection of 2 μg/ml UltraPure LPS from E.coli O111:B4 (Invivogen) with 5 μl/ml Lipofectamine2000 (Invitrogen) for 5 h (non-canonical activation). The mature, cleaved forms of IL-1β and IL-18 were detected in macrophage culture media supernatants using Human IL-1β/IL-1F2 DuoSet ELISA and Human Total IL-18 DuoSet ELISA (R&D Systems). For quantitative real-time PCR, RNA was isolated using the RNeasy Plus Mini Kit (Qiagen), followed by cDNA synthesis with the iScript kit

(Bio-Rad). Quantitative PCR was performed on 10 ng of cDNA per reaction using LightCycler480 SYBR Green I master (Roche) and LightCycler96 instrument (Roche). See Supplementary Table E9 for the primer sequences. Relative gene expression was calculated using the 2(-ΔΔCt) method using RPLP0 as a housekeeping gene.

Caspase 5 western blot

The protein expression of caspase-5 was detected by western blot from non-stimulated snap frozen CAIN patients' and healthy control's PBMCs. PBMCs were lysed in 1x lysis buffer (Cell Signaling Technology, 9803S), containing 1x phosphatase inhibitor (Pierce, A32957) and 1x protease inhibitor (Sigma Aldrich, 04 693 116 001) and sonicated 3x15s in a bath sonicator. The lysates were then resolved by SDS-PAGE (Biorad, 1610183) and transferred to a PVDF membrane that was incubated o/n at +4 °C with anti-human caspase-5 antibody (Novus Biologicals, NBP1-77209). The bands are normalized against the stain free loading control (Biorad) that quantitates the total protein loading in the lane. The normalized bands of procaspase-5 (48 kDa) and processed intermediate caspase-5 (~30 kDa) bands are expressed as fold changes to the control.

Flow cytometry

Caspase-1 activity measurement from blood immune cells

For inflammasome activity analyses, Caspase-1 activity was measured by flow cytometry from blood immune cells. EDTA-anticoagulated blood was aliquoted freshly after sampling and incubated for 6 h at 37 °C under gentle rocking with or without 10 ng/ml LPS from E.coli O111:B4 (Sigma). ATP (Sigma) at 5 mM was added for 20 min, followed by incubation with FAM-FLICA Caspase-1 substrate (ImmunoChemistry Technologies) for 2 h at 37 °C according to manufacturer instructions. After red blood cell lysis and staining with anti-human CD14-APC (Miltenyi Biotec) for 15 min at +4 °C, the cells were analyzed using BD Accuri C6 flow cytometer (BD Biosciences;

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instrument maintained by Biomedicum Flow Cytometry Unit). Monocyte and granulocyte populations were identified based on their scatter properties and the intensity of CD14-APC staining.

Surface markers

We assessed granule exocytosis and granulocyte responsiveness by flow cytometry. Immediately after blood sampling, 100 µl of heparinized whole blood was mixed with either 100 ng/ml LPS from 0111:B4 E. coli (LPS_Ec; Sigma-Aldrich), 100 ng/ml LPS from P. aeruginosa (LPS_Pa; Sigma-Aldrich), 12.5 µg/ml DNA from P. aeruginosa (DNA_Pa) or carrier as a control, and incubated at 37 °C for 60 min. Surface marker antibodies were then added and incubated for 20 min in the dark at rt. The red blood cells were then lysed by incubating the whole blood in 1 ml of FACS Lysing Solution (Becton Dickinson) for 10 min. White blood cells were then pelleted out of the solution by centrifugation (500×g for 5 min at rt) and washed twice with a washing solution of 5% inactivated fetal calf serum (FCS) (sterile, 0.22 µm filtered), 0.02% NaN3 and PBS. The washed cells were then fixed with 1% paraformaldehyde in PBS and stored overnight in the dark at 4 °C. Compensation matrices were prepared using OneComp eBeads (eBiosciences, France) using one test volume of each antibody per tube, according to manufacturer's instructions. Data were acquired with FACSCalibur (BD Biosciences). The maximum number of events (300,000-500,000) was collected for each sample. The raw flow cytometry data were analyzed using FlowJo (Treestar, Inc.). Statistical analyses were performed using SPSS (v.19; IBM Armonk). The Mann-Whitney U and Wilcoxon signed-rank tests were used to determine group effect.

Intracellular NF-kB staining and LPS stimulation

We assessed neutrophilic and monocytic NFκB1 phosphorylation by flow cytometry. After blood sampling, 100 µl of heparinized whole blood was mixed with either 100 ng/ml LPS_Ec (Sigma

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Aldrich), 100 ng/ml LPS_Pa (Sigma Aldrich), 12.5 µg/ml DNA_Pa or carrier, as a control and incubated at +37 °C for 30 min. After the stimulation, the cells were permeabilized using PerFix Expose (Beckman Coulter) according to manufacturer's instructions. Briefly, following stimulation, 50 µl of buffer 1 was added, samples were then mixed and incubated for 10 min at rt. Samples were then briefly vortexed followed by the addition of 1 ml of buffer 2 and a 5-minute incubation at +37 °C. Permeabilized white blood cells were pelleted out of solution by centrifugation (300×g for 5 min at rt), lysed erythrocyte-containing supernatant was aspirated. Cells were re-suspended in 100 µl of buffer 3, premixed antibodies were then added and incubated for 30 min in the dark at rt. Following the incubation, 3 ml of 1× reagent was added and white blood cells were pelleted out of solution by centrifugation (300 g for 5 min, rt). Washed cells were re-suspended in 300 µl 1× reagent and stored in the dark at +4 °C until analysis. Data were acquired with FACSCalibur (BD Biosciences). The maximum number of events (300,000-500,000) was collected for each sample. The raw flow cytometry data were analyzed using FlowJo (Treestar, Inc.). Statistical analysis was performed using SPSS (v.19; IBM Armonk). The Mann-Whitney U and Wilcoxon signed-rank tests were used to determine group effect.

Electron microscope

TEM of platelets

Previous reports have shown C/EBPε to be involved in platelet granule formation[12, 13]. Alpha granules carry a cargo of hemostatically essential proteins and factors and the lack of those may serve to explain the postoperative bleeding observed in the patients. Additionally, platelets play a role in inflammation e.g alpha granules contain chemokines, cytokines, TGFB, P-selectin[14, 15]. We therefore assayed platelet structure on transmission electron microscope[16]. Blood was collected via a venipuncture, from the antecubital vein with 18-gauge cannula (BD Venflon Pro, Becton Dickinson and Company, Franklin Lakes). First 2.7 ml blood was discarded and followed by blood

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collection into 131 mM acidic citric dextrose (ACD; 1:6). Blood was centrifuged at 180×g for 12 min at 22 ℃ to collect the platelet rich plasma (PRP). PRP was supplemented with apyrase (0.1 U/ml; Sigma-Aldrich) and prostaglandin E1 (PGE1 25 ng/ml, Sigma-Aldrich). Platelets were pelleted at 1,200×g for 10 min and supernatant was discarded. Platelets were gently suspended in Hepes-Tyrode buffer (Hepes 3.5 mM, NaCl 137 mM, KCl 2.7 mM, NaH2PO4 3 mM, Glucose 5.5 mM, pH 7.35), supplemented with apyrase (0.1 U/ml) and PGE1 (25 ng/ml) and kept at 37 ℃ for 20 min. The pelleting and washing step were repeated twice after which platelets were suspended in 4% paraformaldehyde in PBS pH 7.4 for 2 h at 22 ℃. The subsequent sample fixation and embedding in resin was according to the procedure described by J.G. White[16]. Samples were imaged with JEOL 1400 Transmission Electron Microscope (JEOL Inc.) equipped with high resolution Morada CCD camera Olympus-SIS (Olympus Corp, Japan).

TEM of granulocytes

To determine possible structural changes in mutated neutrophils, we analyzed ER size/shape and mitochondrial size using transmission electron microscopy. No clear differences were seen between patient and control samples (data not shown).

Wright staining

Peripheral blood samples were collected using Ethylene Diaminetetraacetic acid (EDTA) and Sodium citrate and smears were prepared shortly thereafter, air-dried and stained with the Wright method[17] to detect leukocyte granules. For microscopy Nikon Microscope was used with Eyepiece Lens CFI 10x/22 with Nikon Apochromatic 100x (N.A. 1.40) lateral magnification (oil immersion) resulting in 1000x total magnification.

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Supplementary Figure E1. Genetic analysis of *de novo* C/EBPε germ-line mutation. Whole exome sequencing was performed for a healthy control and affected patients. This revealed a novel germ line mutation in the *CEPBE* gene (ENSG00000092067:ENST00000206513: exon2:c.G656A;p.Arg219His).

Supplementary Figure E2. Schematic illustration of the BioID workflow and mouse C/EBPε interacting proteins. A) Bait protein is tagged with minimal biotin ligase. Once activated by the addition of biotin to the cell culture media, the interacting proteins are biotinylated, allowing for their affinity purification using Strep-tactin resin. The affinity purified interacting proteins are identified with LC-MS/MS and the high-confidence protein-protein interactions are resolved with statistical data analysis. B) The average fold-change between WT and Arg219His for human and mouse C/EBPε interacting proteins. C) The average fold-change between WT and Val219Ala C/EBPε interacting proteins. All the BioID analyses were performed in four replicates.

Supplementary Figure E3. Expression levels of *PRTN3* and *CEBPE* in CAIN patients' neutrophils. Relative expression of *PRTN3* (A) and *CEBPE* (B) of untreated granulocytes of CAIN patients (n=2) and healthy controls (n=6) determined by quantitative PCR. AU, arbitrary units.

Supplementary Figure E4. C/EBPε DNA binding sites at *NLRP3* and *NLRP12* gene loci. C/EBPε binding sites from ChIP-seq in controls' (C) and patients' (P) *NLRP3* (A) and *NLRP12* (B) gene loci. The patients have increased binding of C/EBPε compared to controls. Patient-specific C/EBPε binding sites are highlighted by red boxes.

Supplementary Figure E5. C/EBPε DNA binding sites at *CASP8* and *NFKB2* gene loci. C/EBPε binding sites from ChIP-seq in controls' (C) and patients' (P) *CASP8* (A) and *NFKB2* (B) gene loci. The patients have increased binding of C/EBPε compared to controls. Patient-specific C/EBPε binding sites are highlighted by red boxes.

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Supplementary Figure E6. Enhanced expression of *CASP5* and classical interferon-regulated genes in macrophages of CAIN patients. (A-B) Peripheral blood monocyte-derived macrophages left untreated or treated with IFNα2b for 3-6 hours. Relative expression of *CASP5*, *MX1/2* and *IFIT2* determined by quantitative PCR. AU, arbitrary units.

Supplementary Figure E7. Flow cytometry analysis surface marker expression. Filled histograms represent unstimulated samples. Orange histograms represent samples stimulated with *Pseudomonas aeruginosa* (Pa) DNA, green histograms represent samples stimulated with Pa LPS, and blue histograms represent samples stimulated with *Escherichia coli* (Ec) LPS. Each patient sample is shown directly above representative age and gender-matched control analyzed simultaneously.

Supplementary Figure E8. Wright staining of patient's neutrophils. A) Representative patient (lower and upper left panel) and control subject (lower and upper right panel) neutrophils from smears stained with the Wright method presenting both primary and secondary granules (1000x magnification). Two hundred consecutive neutrophils were studied in both cases and observed for granule morphology as well as for nuclear segmentation. No consistent differences were observed in granules whereas (B) 20 % of patient neutrophils were hyposegmented.

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