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BRIEF REPORT



Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells

Nadia Boutaoui^a, Sandeep Puranik ^{*a}, Rong Zhang^{a,b}, Ting Wang ^c, Daniel H. Hui^d, John Brehm^e, Erick Forno ^a, Wei Chen^a, and Juan C. Celedón ^a

^aDivision of Pediatric Pulmonary Medicine, UPMC Children's Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, PA, USA; ^bDepartment of Statistics, University of Pittsburgh, Pittsburgh, PA, USA; ^cFred Hutchinson Cancer Research Center, Seattle, WA, USA; ^dBrigham and Women's Hospital, Harvard Medical School, Broad Institute, Boston, MA, USA; ^eDivision of Pulmonary and Critical Care Medicine, University of Pittsburgh Medical Center- St. Margaret's Hospital, University of Pittsburgh, Pittsburgh, PA, USA

ABSTRACT

Vitamin D is a nutrient and a hormone with multiple effects on immune regulation and respiratory viral infections, which can worsen asthma and lead to severe asthma exacerbations. We set up a complete experimental and analytical pipeline for ATAC-Seq and RNA-Seq to study genome-wide epigenetic changes in human bronchial epithelial cells of asthmatic subjects, following treatment of these cells with calcitriol (vitamin D3) and Poly (I:C) (a viral analogue). This approach led to the identification of biologically plausible candidate genes for viral infections and asthma, such as DUSP10 and SLC44A1.

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To the editor

Vitamin D may prevent or attenuate severe asthma exacerbations and viral respiratory infections through epigenetic regulation of innate and adaptive immune mechanisms [1] through processes such as chromatin folding. Genome-wide chromatin accessibility assays such as ATAC-Seq (Assay for Transposase Accessible Chromatin and high-throughput sequencing) [2] can identify transcriptionally active sections of chromosomes, thus helping us define the binding status of transcription factors, determine nucleosome occupancy, and construct gene regulatory networks. We report the use of ATAC-Seq and total RNA-Seq to evaluate the genome-wide effects of vitamin D, with and without a viral analogue (Poly (I:C)) on asthmatic bronchial epithelial cells.

Asthmatic (AHBEC) bronchial epithelial cells were cultured and stimulated with sham (culture media), calcitriol, poly (I:C) (to simulate viral infection), or both. ATAC-Seq was performed using one sample per treatment to detect chromatin sections open for transcription; the resultant DNA fragments were purified, amplified, and sequenced. Sequencing

data was aligned to the reference genome with Bowtie2 [3], and peaks were called with MACS2 [4] and annotated with HOMER. Chromatin accessibility was quantified as read coverage within the merged ATAC-Seq peak regions for each sample, and the count matrix was normalized with library sizes and transformed to counts per million (CPM) using edgeR [5]. Pairwise fold-change of the chromatin accessibility was then calculated based on CPM. Pathway enrichment analysis was performed on genes annotated to the differential peaks, using Fisher's exact test.

RNA-Seq was performed using the same conditions as for ATAC-Seq. RNA-Seq was performed in three biological replicates where cell line AHBEC obtained from ATCC was cultured from different passages and on different dates, and in one set of three technical replicates to confirm that the open chromatin determined by ATAC-Seq corresponds to changes in gene expression. The RNA-Seq data was further validated using real-time PCR of detected genes using three biological and three technical replicates. RNA-Seq reads were aligned to the reference genome with STAR [6], and TPM (Transcripts Per Kilobase Million) value was quantified for each gene

CONTACT Juan C. Celedón  juan.celedon@chp.edu  Division of Pediatric Pulmonary Medicine, UPMC Children's Hospital of Pittsburgh, 4401 Penn Avenue, Pittsburgh, PA 15224

*These authors contributed equally to this work.

 Supplemental data for this article can be accessed [here](#).

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in each sample using RSEM [7]. Bigwig files containing the read coverage information of every sequencing sample were generated for the visualization in the UCSC Genome Browser [8].

The quality of the ATAC-Seq data is shown in Figures S1 and S2. The mapping rates were high (>95%), and the average number of ATAC-Seq peaks (accessible chromatin regions) was 17,125 (detected by MACS2 *callpeak*), but with wide variation depending on treatment protocol and library size (Table S1).

Clustering analysis on the chromatin accessibility indicated clustering of: Sham and Calcitriol treated cells, Poly I:C and Calcitriol +Poly I:C treated samples (Figure S3). Differential peaks were identified between six pairwise comparisons among the four treatments for Asthma AHBEC (n = 616) (Figure 1)

with more than a three-fold absolute change on the log2 transformation of CPM in any of the pairwise comparisons. Among these differential peaks, 52 were highly correlated (absolute correlation >0.9) to the expression of corresponding annotated genes (Table S2). The top 4 correlated ATAC-Seq differential peaks and RNA-Seq genes are shown in Figure 2. We used QRT-PCR to validate the top 4 genes from RNA-Seq (Figure S5). We also performed analyses for differential gene expression between each treatment (Calcitriol, Poly I:C, and Calcitriol +Poly I:C) versus Sham (Table S3) using the R package DESeq2. We summarized the log fold-changes for the differentially expressed genes from RNA-Seq using adjusted p-value <0.05 and the corresponding differential peaks from ATAC-Seq that share the same gene symbol annotations. For Calcitriol vs Sham,

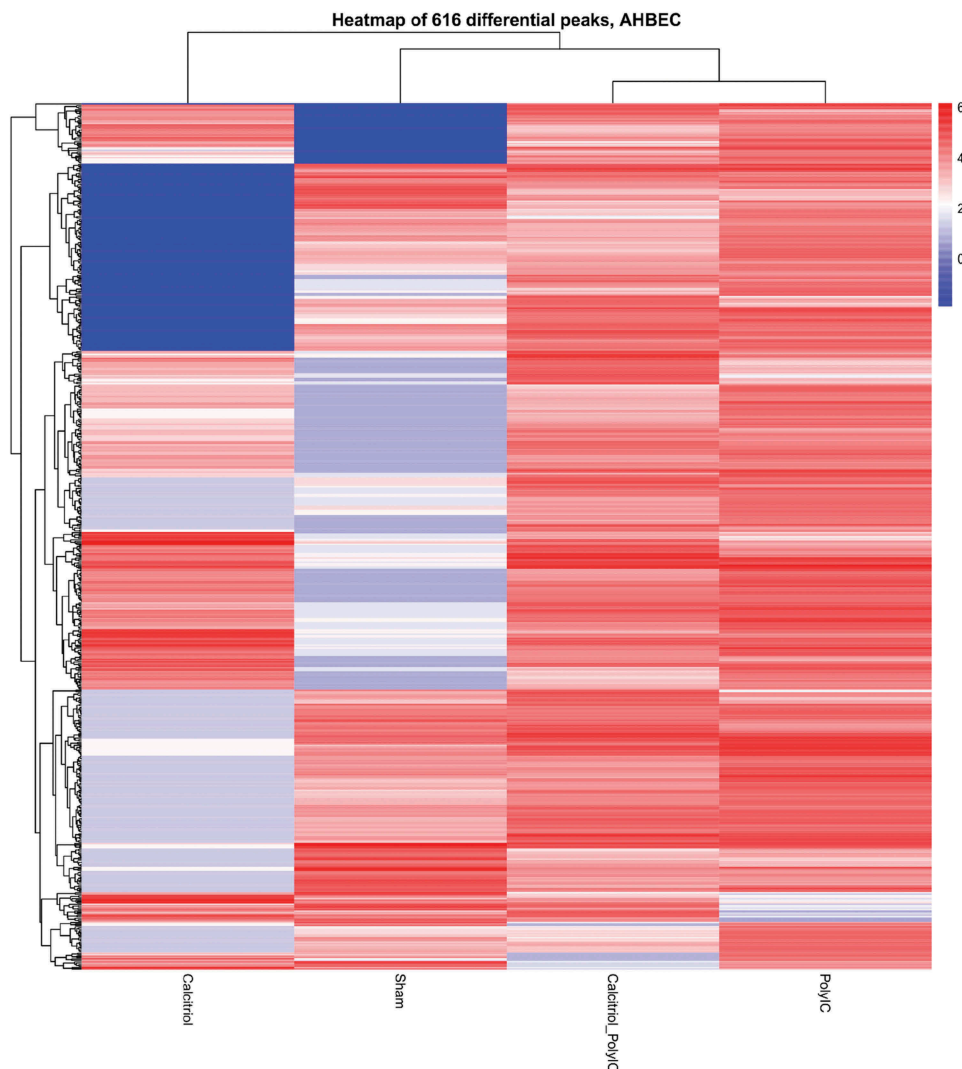


Figure 1. Heatmap of chromatin accessibility in the differential peaks for AHBEC.

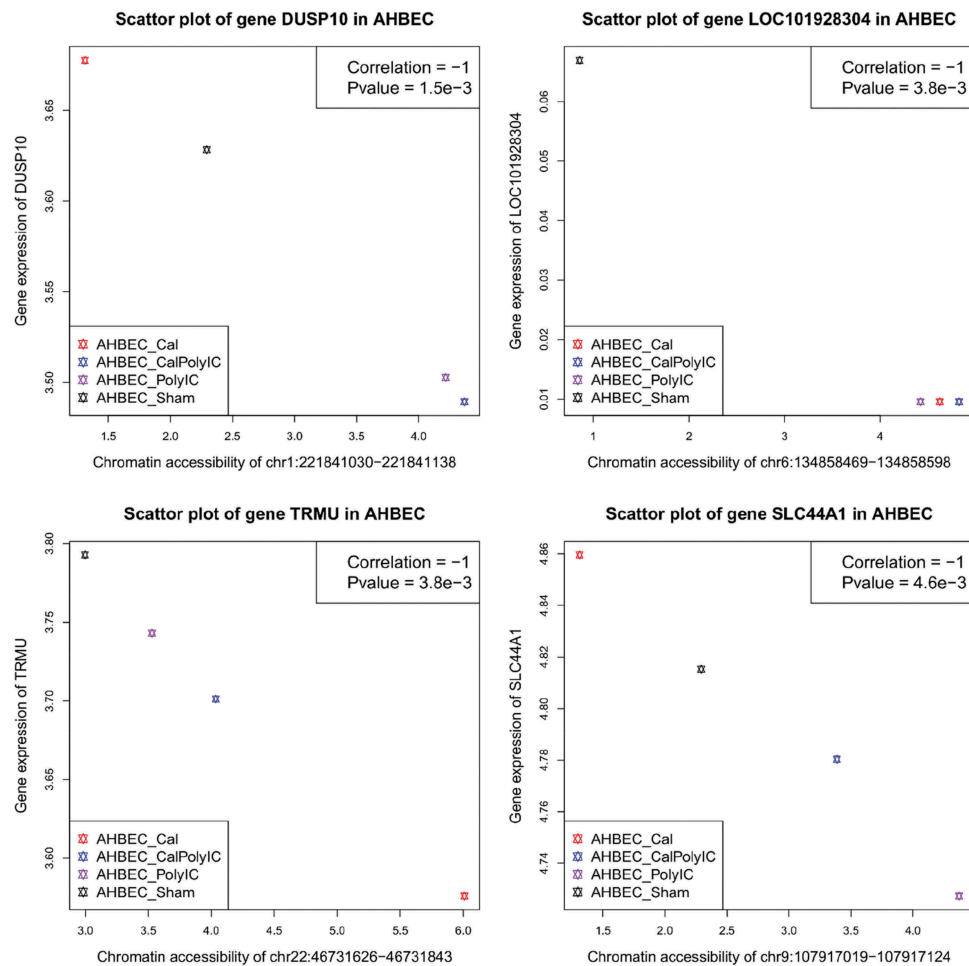


Figure 2. Scatter plots of top correlated ATAC-Seq differential peaks and RNA-Seq genes.

there were no differentially expressed genes. We have 92 differentially expressed genes between Poly I:C vs. Sham and 364 differentially expressed genes between Calcitriol+PolyI:C vs. Sham. The corresponding peaks from ATAC-Seq that share same gene annotations (table S3) include 4 and 11 overlapped peaks with corresponding genes between PolyIC vs. Sham and Calcitriol+PolyIC vs. Sham, respectively. TBX3 gene has a log fold-change of 3.56 between PolyIC vs. Sham. In addition, the peak annotated with SLC8A1 gene also has a relatively high log fold-change of 2.72. For Calcitriol+PolyI:C vs. Sham, we can also notice that the peaks annotated to TBX3 and SLC8A1 are differential based on more than three-fold absolute changes. Besides, the significant differential peak also includes the one annotated to the ZCCHC2 gene. In a genome-wide study of a gene by environment interaction (GWIS) of depressive symptoms and stressful life events, a single nucleotide

polymorphism (SNP) intronic to ZCCHC2 (rs17070072) was significant ($p = 1.46 \times 10^{-8}$) [9].

Large absolute log fold changes (near 3 or >3) for differential peaks between PolyI:C vs. Sham (genes SLC8A1 and TBX3) and Calcitriol+PolyI:C vs. Sham (genes SLC8A1, TBX3 and ZCCHC2) and those for the corresponding differentially expressed genes annotated to them are shown in Figure S6.

Through pathway enrichment analysis of genes annotated to the differential peaks, we identified 101 pathways significantly enriched ($FDR < 0.05$) by the differentially accessible genes. The pathway analysis in the asthma cell line 'AHBEC' showed enrichment in cancer-related and metabolic pathways (Table S4). Genes with the highest fold-change between treatments included *DUSP10*, *LOC101928304*, *TRMU*, and *SLC44A1* (Table S2). Dual specificity phosphatase 10 (DUSP10), also known as MAP kinase phosphatase 5 (MKP5) is a key negative regulator of IL-33-induced

cytokine production in Th2 cells [10]. Mkp5-deficient cells produced greatly enhanced levels of pro-inflammatory cytokines during innate immune responses and exhibited greater T-cell activation than their wild-type counterparts [11]. MKP5 was shown to protect against sepsis-induced acute lung injury [12]. Furthermore, deficiency of MKP5 results in reduced influenza virus replication in the lung, which is associated with increased type I IFN production [13] while overexpression of MKP2 and MKP5 inhibited IFN β promoter activity in response to LPS or poly (I:C) stimulation [14]. DUSP10 negatively regulates the inflammatory response to rhinovirus through IL-1 β signalling [15].

DUSP10 is a primary vitamin D target is expressed in human peripheral blood mononuclear cells (PBMCs) [16]. showed that changes in the expression of DUSP10 and 11 other VitD target genes in human PBMCs at the start and the end of the 5 months vitamin D-intervention (VitDmet study) were systematically correlated with the alteration in the circulating form of vitamin D₃, 25-hydroxyvitamin D₃ (25(OH)D₃). Furthermore, VDR target gene DUSP10 gene expression appears to be the most comprehensive biomarker for vitamin D₃ responsiveness of human individual [17].

LOC101928304 is an uncharacterized non-coding RNA, and TRMU (tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase) is a nuclear gene that encodes a mitochondrial tRNA-modifying enzyme. *SLC44A1* (solute carrier family 44 members 1) also called Choline like transporter family is proposed to supply choline for the synthesis of cell membrane phospholipids in an NA(+)-independent manner. The physiological relevance of *SLC44A1* is indicated by its likely involvement in membrane synthesis for cell growth or repair, and also by its role in phospholipid production for the generation of lung surfactant. In transfusion-related acute lung injury, antibodies to *SLC44A2* cause a deleterious aggregation of granulocytes [18].

In the analysis of differential gene expression between each treatment (Calcitriol, Poly I:C, and Calcitriol +Poly I:C) versus Sham, there were no differentially expressed genes, based on the adjusted p-value, for Calcitriol vs. Sham. We extracted the log fold-change in ATAC-Seq for the top 5 differentially expressed genes from the results of all the peaks (not

the 616 differential peaks we reported) between PolyIC vs Sham and Calcitriol + PolyIC vs Sham. For the genes with multiple peaks, we took the peak with the largest absolute log fold-change (Table S5).

In comparing Poly IC vs Sham we identified dual specificity phosphatase 4 (DUSP4), Activin A receptor type 2B (ACVR2B) and T-Box3 (TBX3). DUSP4 belongs to the same family as DUSP10, the top 1 gene we report in our correlation analysis. It regulates corticosteroid sensitivity via dephosphorylation of JNK1 and GR-Ser²²⁶. DUSP4 activation by formoterol restores impaired corticosteroid sensitivity, indicating that DUSP4 is crucial in regulating corticosteroid sensitivity, and therefore might be a novel therapeutic target in severe asthma [19]. ACVR2B, a member of the transforming growth factor (TGF)- β superfamily of secreted factors, is a potent negative regulator of muscle growth. Systemic Blockade of ACVR2B Ligands Protects Myocardium from Acute Ischaemia-Reperfusion Injury [20]. T-box genes encode transcription factors involved in the regulation of developmental processes. TBX3 is the earliest expressed member of the T-box transcription factor family and is involved in the maintenance and induction of pluripotency [21].

In comparing Calcitriol + PolyIC vs. Sham we identified DUSP4, TBX3 and Macrophage Migration Inhibitory Factor (MIF). MIF plays a role in the regulation of macrophage function in host defense through the suppression of anti-inflammatory effects of glucocorticoids. MIF also antagonizes glucocorticoid inhibition of T-cell proliferation in vitro by restoring IL-2 and IFN- γ production [22]. Furthermore, MIF overexpression promotes the proliferation and migration of Airway Smooth Muscle Cells (ASMCs) by upregulating the activity of the ERK1/2 and FAK signalling and the expression of matrix metalloproteinase (MMP)-2 [23]. In mouse models of allergic asthma, the lack of MIF causes an almost complete abrogation of the cardinal signs of the disease including mucus secretion, eosinophilic inflammation, and airway hyper-responsiveness. Additionally, blocking the expression of MIF in animal models leads to a significant reduction of pathological signs of eosinophilic inflammation [24].

We uploaded the bam and bigwig files to the NSF-funded site CyVerse Discovery Environment

(<https://de.cyverse.org/de/>) that supports free data hosting and created custom tracks on UCSC Genome Browser to visualize read coverage in these matched ATAC-Seq and RNA-Seq samples (http://genome.ucsc.edu/s/zhangr100/AHBEC_VitD). Our chromatin accessibility patterns were similar to the reference DNase I hypersensitivity clusters in the ENCODE database. For instance, integration of ATAC-Seq and RNA-Seq data indicated the effect of chromatin accessibility on the expression of *DUSP10* (Figure S4).

Vitamin D is a hormone with multiple effects on immune regulation and respiratory viral infections, which may affect asthma morbidity. We set up an experimental and analytical approach to ATAC-Seq and RNA-Seq to study genome-wide epigenetic changes in human bronchial epithelial cells of asthmatic subjects, following treatment of these cells with vitamin-D and Poly I:C. This approach led to the identification of biologically plausible candidate genes for viral infections and asthma (*DUSP10*) a Vitamin D Receptor 'VDR' target gene is a key negative regulator of IL-33-induced cytokine production in Th2 cells [10]. For instance, deficiency of MKP5 results in reduced influenza virus replication in the lung, which is associated with increased type I IFN production [13]. Type I IFN signalling promotes the maintenance of lung epithelial tight junctions during *S. pneumoniae* infection thereby reducing the passage of the pathogen from alveoli into the lung parenchyma [25,26].

SLC44A1 gene is involved in phospholipid production for the generation of lung surfactants. Surfactant Proteins play a role in: (1) lowering surface pressure of the alveolus [27], (2) enhancing bacterial and viral clearance by opsonizing pathogens and facilitate their phagocytosis immune cells such as macrophages and monocytes [28] and (3) immunomodulation: studies have shown that surfactants proteins SP-A and SP-D bind directly to allergens and particles such as pollen grains [29], house dust mite allergen [30], and *Aspergillus fumigatus* allergen [31], inhibiting specific IgE binding to allergens and subsequently decreasing allergen-induced histamine release.

Additional experiments are needed to validate our findings, ideally on a larger set of cells from

subjects with asthma and matching control subjects.

Disclosure statement

No potential conflict of interest was reported by the authors.

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ORCID

Sandeep Puranik  <http://orcid.org/0000-0002-8771-3593>

Ting Wang  <http://orcid.org/0000-0003-4712-6658>

Erick Forno  <http://orcid.org/0000-0001-6497-9885>

Juan C. Celedón  <http://orcid.org/0000-0002-6139-5320>

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ONLINE SUPPLEMENT

Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells

Nadia Boutaoui PhD^{1,*}, Sandeep Puranik MD^{1,*}, Rong Zhang^{1,3}, Ting Wang PhD⁵, Daniel H. Hui⁴, John Brehm MD², MPH, Erick Forno MD, MPH¹, Wei Chen PhD¹, Juan C. Celedón MD, DrPH¹

¹Division of Pediatric Pulmonary Medicine, UPMC Children’s Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, Pennsylvania, U.S.A.

²Division of Pulmonary and Critical Care Medicine, University of Pittsburgh Medical Center- St. Margret’s Hospital, University of Pittsburgh, Pittsburgh, Pennsylvania, U.S.A.

³Department of Statistics, University of Pittsburgh, Pittsburgh, Pennsylvania, U.S.A.

⁴Brigham and Women's Hospital, Harvard Medical School, Broad Institute of MIT, Boston, Massachusetts, U.S.A

⁵Fred Hutchinson Cancer Research Center, Seattle, Washington, U.S.A

*These authors contributed equally to this work.

Corresponding author:

Juan C. Celedón, MD, DrPH

Division of Pediatric Pulmonary Medicine

UPMC Children’s Hospital of Pittsburgh

4401 Penn Avenue, Pittsburgh, PA 15224

Phone: 412.692.8429; Fax: 412.692.7636

Email: juan.celedon@chp.edu

METHODS

ATAC-Seq was performed to evaluate the epigenome-wide response to vitamin D and/or Poly I:C (as a surrogate for viral infection) on primary asthma human bronchial epithelial cells (AHBEC).

Cell culture treatments

AHBEC were cultured according to ATCC (American Type Culture Collection)-recommended protocols. After flask treatment with coating mixture (0.01 mg/mL fibronectin, 0.03 mg/mL bovine collagen type I and 0.01 mg/mL bovine serum albumin [BSA] dissolved in Bronchial Epithelial Growth Medium [BEGM™]), cells were inoculated at 3000 cells per cm² with BEGM without antibiotics, and incubated at 37° C with 5% carbon dioxide. Cells were inspected daily and culture media was changed every 2-3 days. Once the cells reached 70-80% confluence, four treatments were performed on cells in 4 different wells: 1) BEGM complete media at time 0 and 20 min (“Sham”); 2) 100 nM of calcitriol at time 0 and 20 min (“Calcitriol”); 3) BEGM complete media at time 0 then 10 µg/ml poly I:C at 20 min (“Poly I:C”); and 4) 100nM Calcitriol at time 0 followed by 10 µg/ml poly I:C and 100nM Calcitriol at 20 min (“Calcitriol/Poly I:C”). Cells were incubated for 20 minutes prior to harvesting and counting. Cells are detached by adding 1 ml of 0.25% trypsin – 0.53mM EDTA solution with 0.5% PVP to each well and incubate at 37C for 5 minutes. 3 mls of complete growth media is then added to well and cells where aspirated by pipetting prior to transfer to 15 ml tube. Cells where then centrifuged at 130x g for 10 minutes. Supernatant is removed and cells are resuspended in 1 ml complete growth media prior to counting cells using Countess™ cell counter (ThermoFisher Scientific, Pittsburgh, PA) and 50,000 cells were used for ATAC-Seq.

ATAC-Seq and RNA-Seq

ATAC-Seq was performed using a protocol modified from Buenrostro *et al.* Briefly, cells (50,000) were spun down at 500×g for 5 min at 4°C, washed with 50 µl cold 1x PBS buffer, and spun again. Cells were re-suspended in 50 µl cold lysis buffer and spun immediately at 500×g for 10 min at 4°C. Transposition reaction (25 µl TD, 2.5 µl TDE1, 22.5 µl Nuclease Free H₂O) was performed immediately and incubated at 37°C for 30 min. Transposed DNA was purified using the MinElute PCR Purification Kit (Qiagen, Germantown, MD) prior to PCR amplification for 6 cycles (1 cycle: 5 min 72°C, 30 sec 98°C; then 5 cycles: 10 sec 98°C, 30 sec 63°C, 1min 72°C). To reduce PCR GC and size bias, the appropriate number of additional PCR cycles was determined using qPCR; this method has the additional benefit of serving as an estimate of library complexity. Amplified DNA fragments were purified using the Qiagen MinElute PCR Purification Kit, and purified DNA library quality assessment was performed using a high-sensitivity DNA chip on Bio-Analyzer (Agilent technologies,

Santa Clara, CA). As large fragments (>1kb) are relatively hard to quantify and may result in reduced clustering efficiency during sequencing, we carried out size selection prior to sequencing, in order to eliminate the potentially confounding long fragments and maintain high library complexity. We excised fragments in window of 140-650 bp using pippin prep (Sage Science, Beverly, MA). The size-selected library was checked on the Bio-Analyzer and library quantitation was performed using the KAPA Library Quant Kit for Illumina Sequencing Platforms (KAPA Biosystems, Wilmington, MA) according to manufacturer's protocol. DNA libraries were then submitted for 75bp paired-end sequencing on the Illumina NextSeq 500 sequencer.

Total RNA was extracted using RNeasy micro kit (Qiagen, Germantown, MD) The concentration and quality of DNase I-treated RNA was determined using RNA 6000 Nano chip on the Agilent 2100 BioAnalyzer (Agilent Technologies, Santa Clara, CA). Samples with high quality RNA (RNA Integrity Number >8) were 500 ng of each DNase I-treated RNA sample was used for library construction with the Illumina's TruSeq Total Stranded RNA sample preparation kit (ribosome depleted) according to the manufacturer's protocol. Adaptor-ligated fragments were amplified by PCR. The quality and size of the final library preparations were analyzed on an Agilent TapeStation. Sequencing was performed on the Illumina NextSeq 500 NGS platform, generating approximately 40 million paired-end 75 bp reads per sample.

Data analysis

After ATAC-Seq, quality control was performed with FastQC (Supplementary Figure S2). Low quality reads and 3' adapters were trimmed with Trim Galore! and Cutadapt. Trimmed reads were aligned to the reference human genome hg19 using Bowtie2. Reads with low mapping quality (MAPQ < 20) or aligned to chrM were filtered out; duplicated reads were removed with Picard [<http://broadinstitute.github.io/picard/>]; and reads in blacklisted genomic regions annotated by ENCODE were also removed. Peak calling was performed with MACS2 *callpeak* using “-f BAMPE” for paired-end mode and “-B --trackline --SPMR” to generate bedGraph files, which were subsequently converted into bigwig format using the UCSC Genome Browser tool *bedGraphToBigWig* for coverage visualization. These peaks (i.e. open chromatin regions) were annotated with HOMER.

Similarly, after quality control and trimming, the RNA-Seq reads were aligned to reference genome with the RNA-seq aligner STAR. Subsequently, gene expression for each sample was quantified as TPM (Transcripts Per Kilobase Million) using RSEM. The alignment results (bam files) were converted to bigwig format using the bam2wig tool of RSeQC, for the visualization of read coverage in genome browser. The total read coverage of each sample was normalized to 10Mbp, so that the peak values of different samples are comparable.

Pathway enrichment analysis was performed on the genes annotated to the 616 differential peaks which have more than a three-fold absolute change in any of six pairwise comparisons from ATAC-Seq data. We used a total of 318 pathways specifically for human beings from *Kegg.gsets* function in the R package gage and 60118 background or reference genes with Entrez gene identifiers that are mapped to a gene symbol generated from the R package org.Hs.eg.db for Fisher’s exact test. The enriched significant pathways and their involved annotated genes are presented in Table S4.

Figure S1: Quantitative PCR amplification plot demonstrating calculation of the correct number of additional cycles to perform for four ATAC-Seq libraries.

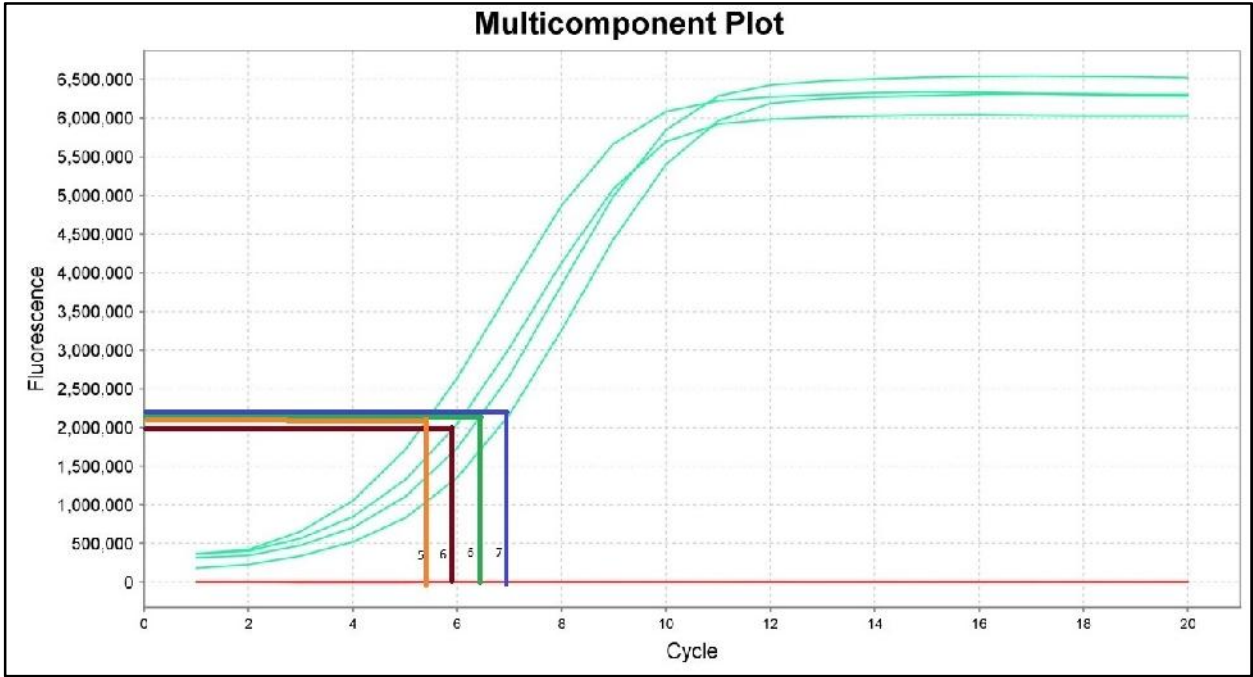


Figure S2: QC and contamination screening results: The figure of Per base sequence quality shows the range of quality values across all bases at each position in the FastQ file, green range means a very good quality; the figure of Per sequence quality scores shows that almost all sequences have overall high quality; the figure of Per sequence GC content shows that the distribution of GC content across the whole length of each sequence is similar to a theoretical distribution; the figure of contamination screening shows that almost all reads can be mapped to human genome, hence there is no contamination.

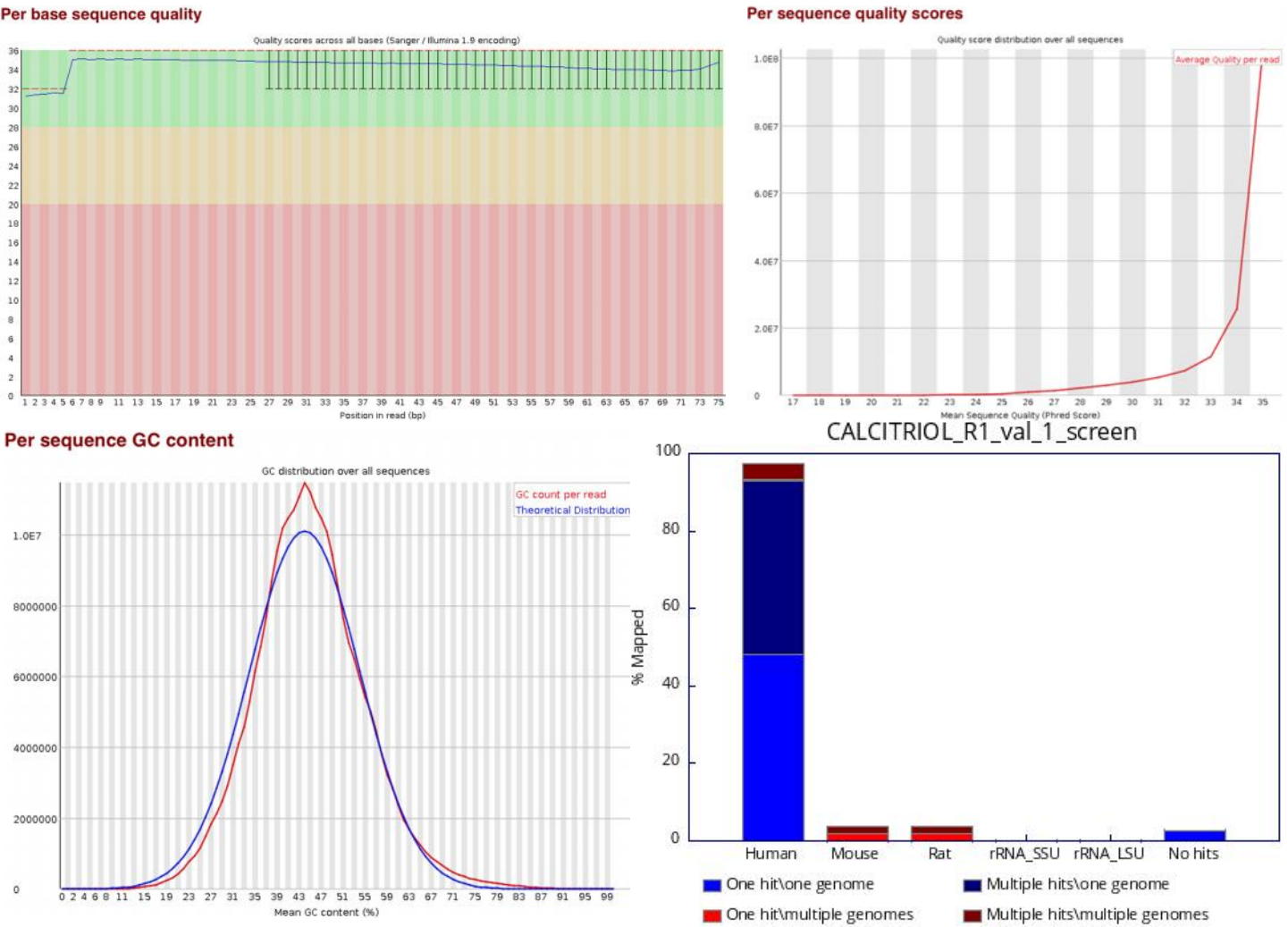


Figure S3: Clustering dendrogram of samples using data of chromatin accessibility in AHBEC cells

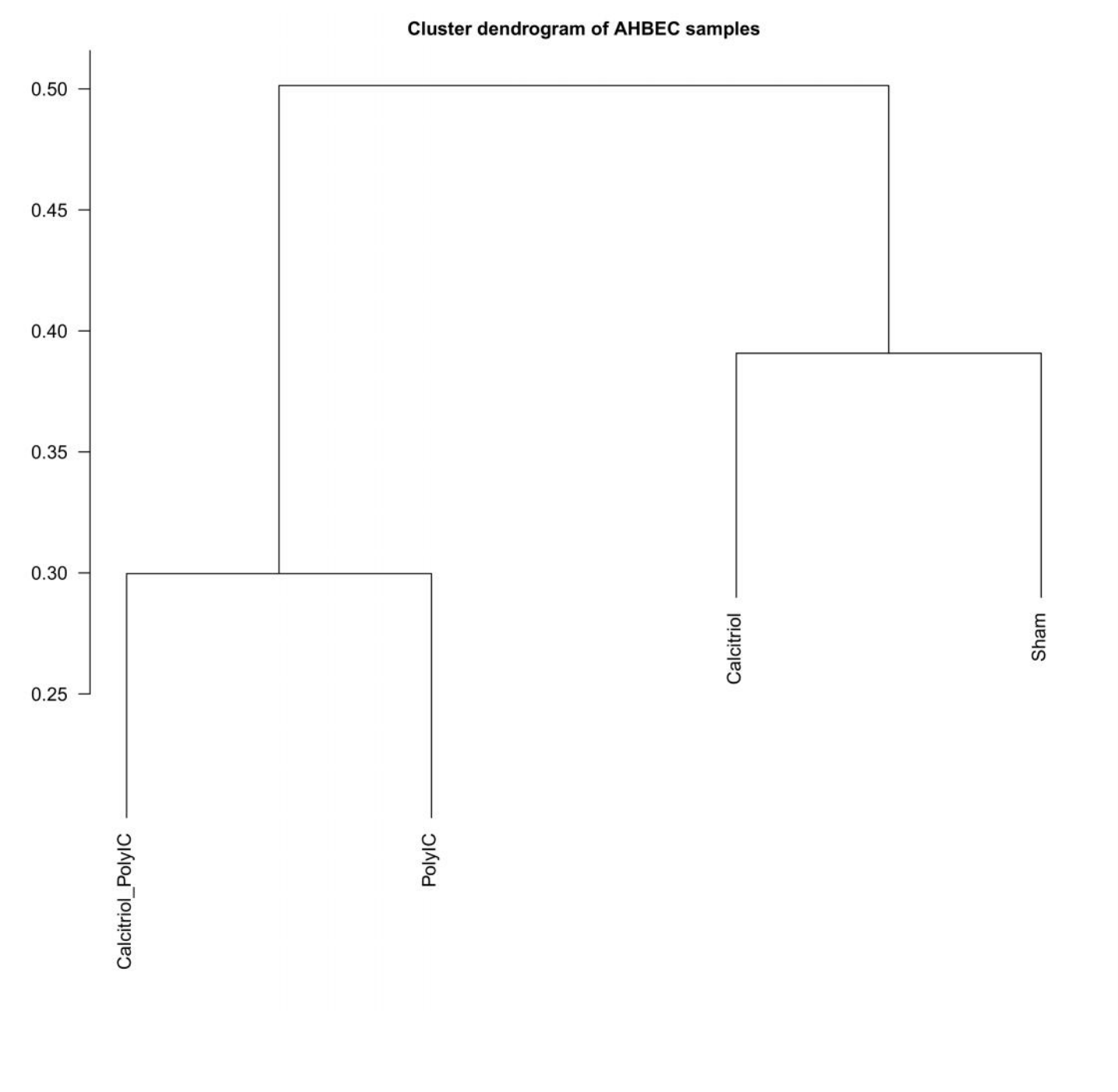


Figure S4: Figure of UCSC Genome Browser for *DUSP10*, showing read coverage of our ATAC-Seq data (the top four tracks), RNA-Seq data (the next four tracks), along with other annotation and reference DNaseI hypersensitivity clusters from ENCODE database.

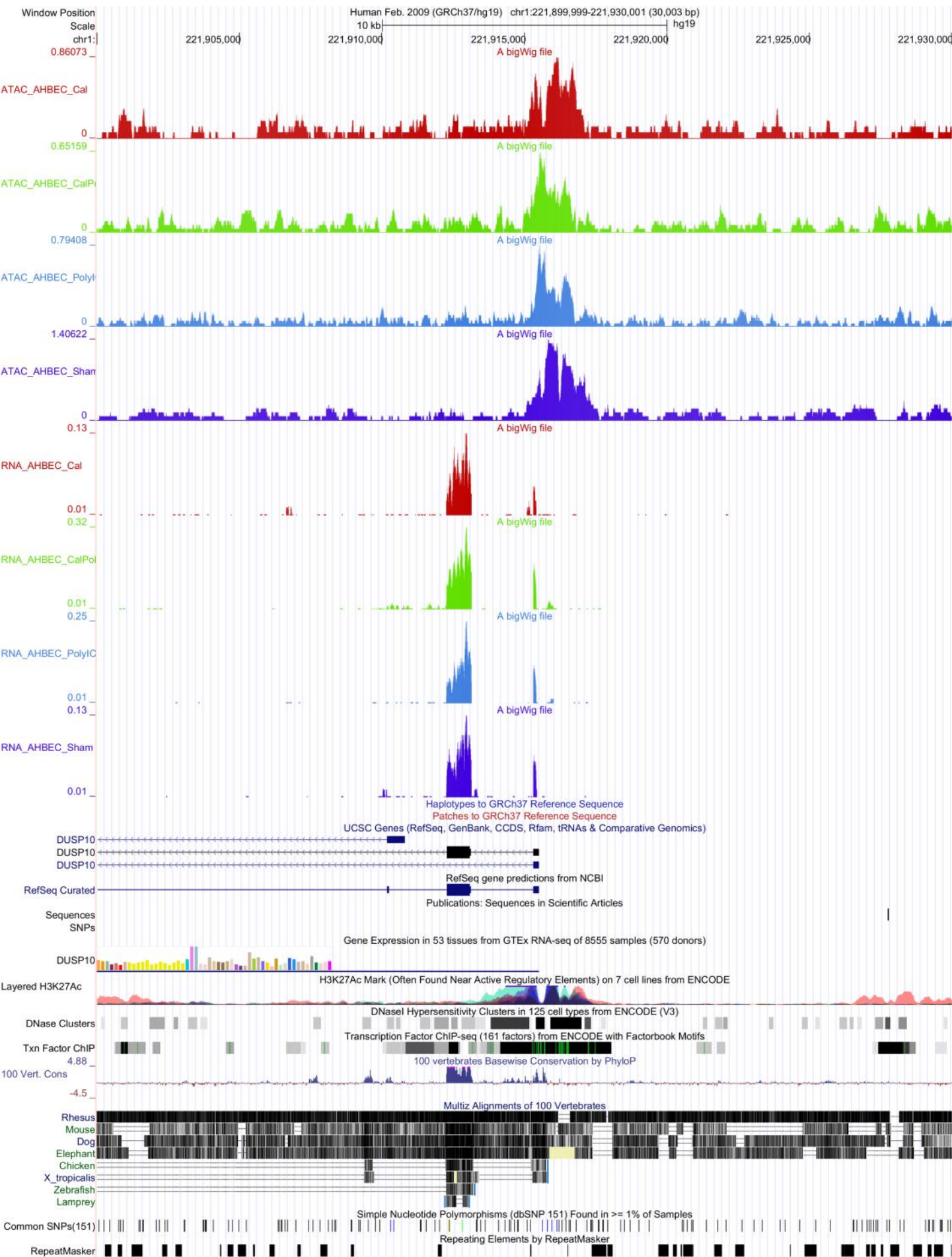


Figure S5: Correlation between RNA-Seq and QRT-PCR of the top four correlated ATAC-Seq differential peaks and RNA-Seq genes.

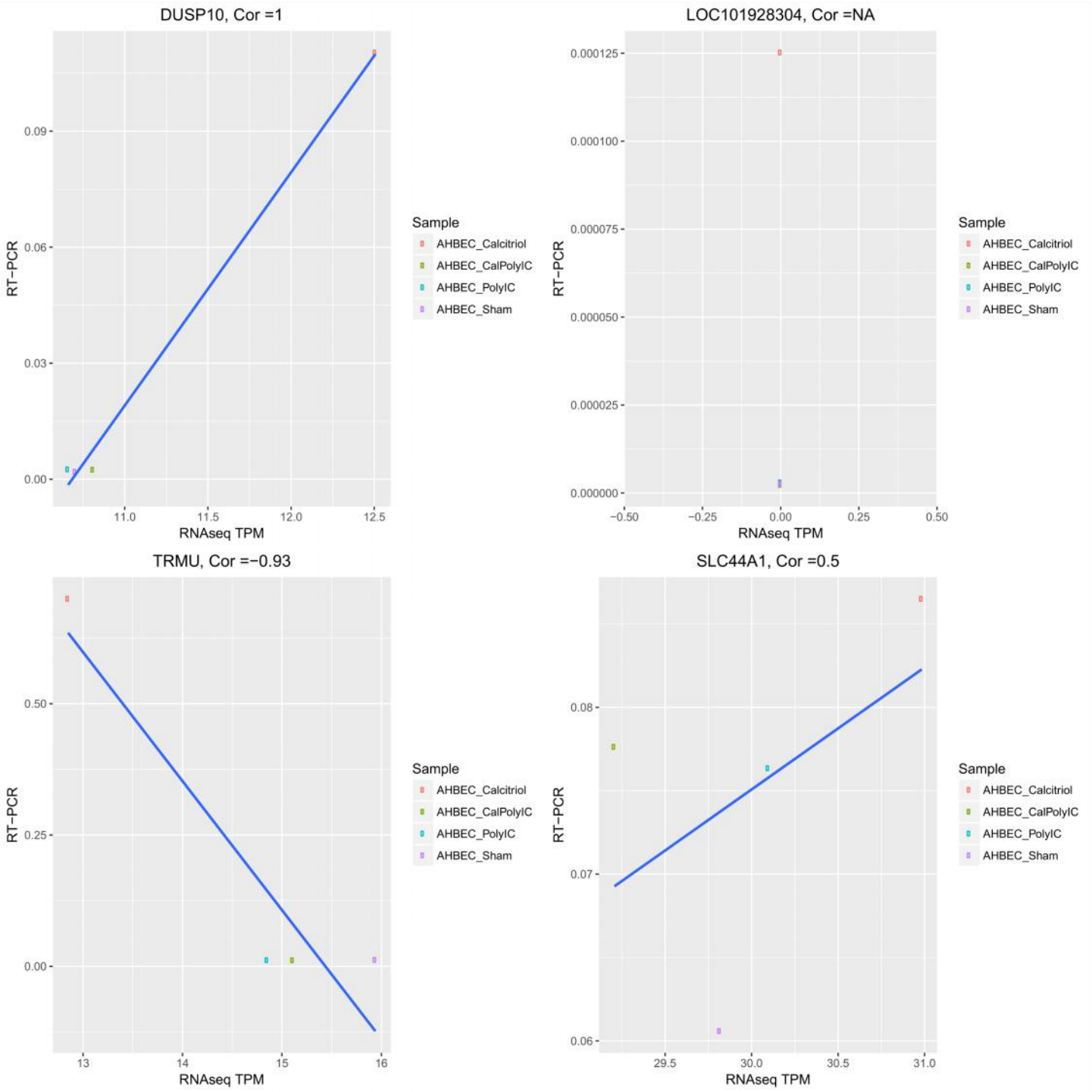


Figure S6 : Differentially-expressed genes with adjusted p-value < 0.05 and corresponding peaks which share same gene annotations

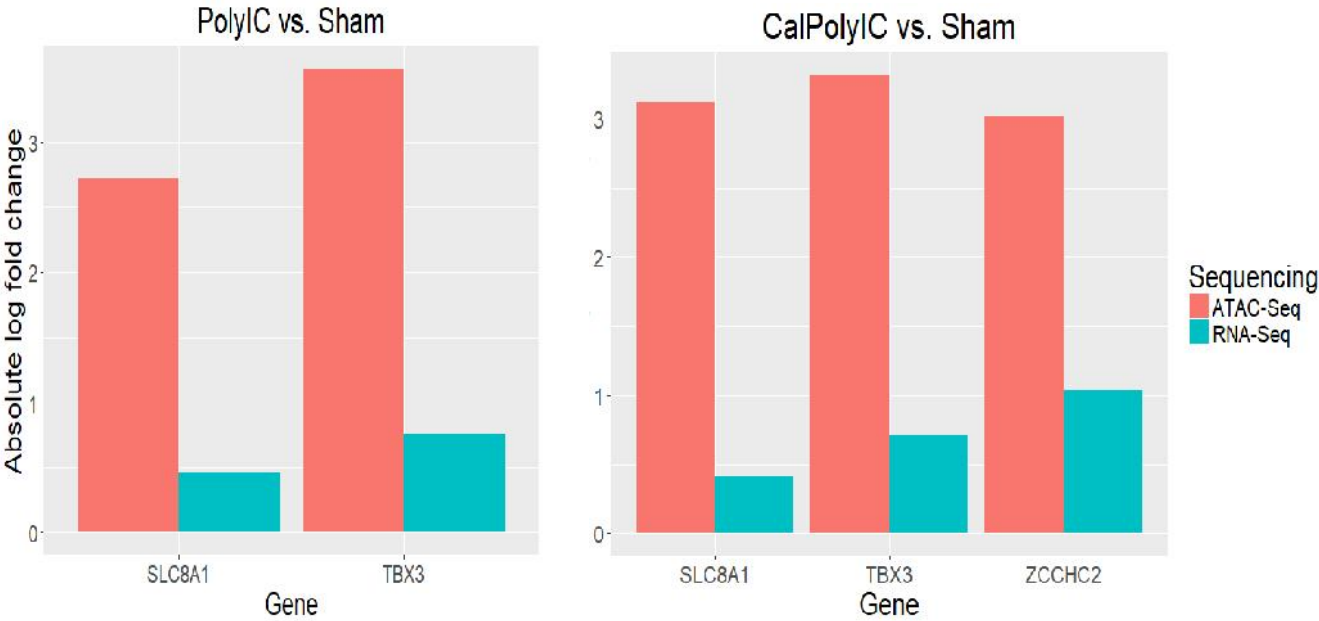


Table S1: Summary statistics of data and alignment in asthma human bronchial epithelial cells.

Sequencing type		Treatment			
		Sham	Calcitriol	PolyIC	Cal+PolyIC
ATAC-Seq	Total Reads	25,837,041	26,172,888	70,283,356	62,036,897
	Mapping Rate	96.20%	95.88%	95.33%	95.93%
	# Peaks	13,402	3,072	18,561	10,773
RNA-Seq (Experiment 1)	Total Reads	38,539,641	34,182,797	39,162,242	34,855,259
	Mapping Rate	76.93%	73.93%	78.92%	72.56%
	# Genes	16,272	16,091	16,513	16,144
RNA-Seq (Experiment 2)	Total Reads	73,483,156	68,523,088	66,729,115	67,219,947
	Mapping Rate	61.94%	64.19%	78.84%	79.49%
	# Genes	16,690	15,390	15,642	17,075
RNA-Seq (Experiment 3)	Total Reads	48,438,502	49,808,207	50,722,329	41,426,537
	Mapping Rate	63.34%	59.60%	62.03%	93.88%
	# Genes	15,489	16,573	15,669	15,488

Table S2: Fold-change of the differential peaks and correlation with gene expressions in AHBEC.

#	CHR	START	END	Cal_vs_CalPolyIC	Cal_vs_PolyIC	Cal_vs_Sham	CalPolyIC_vs_PolyIC	CalPolyIC_vs_Sham	PolyIC_vs_Sham	Gene	Cor
1	chr1	221841030	221841138	-3.06	-2.90	-0.98	0.15	2.08	1.92	DUSP10	-1.00
2	chr6	134858469	134858598	-0.20	0.20	3.76	0.40	3.96	3.56	LOC101928304	-1.00
3	chr22	46731626	46731843	1.97	2.48	3.01	0.51	1.04	0.53	TRMU	-1.00
4	chr9	107917019	107917124	-2.07	-3.06	-0.98	-0.99	1.09	2.08	SLC44A1	-1.00
5	chr2	127758564	127758870	-2.25	-3.00	-2.41	-0.75	-0.16	0.59	BIN1	0.99
6	chr3	122612244	122612378	-2.72	-3.59	-2.66	-0.86	0.06	0.93	LOC100129550	-0.99
7	chr1	85680552	85680756	-5.49	-6.16	-5.36	-0.67	0.13	0.80	SYDE2	0.99
8	chr12	28126561	28126742	-0.46	0.96	2.74	1.42	3.20	1.78	PTHLH	-0.99
9	chr6	122972635	122973010	-2.48	-2.67	-3.65	-0.19	-1.17	-0.98	PKIB	-0.98
10	chr5	138089703	138089846	0.24	3.14	0.96	2.90	0.71	-2.18	CTNNA1	0.98
11	chr9	91079920	91080034	-2.87	-3.29	-2.92	-0.42	-0.05	0.37	NXNL2	-0.98
12	chr1	174784294	174784446	-3.79	-3.72	-2.35	0.07	1.44	1.37	RABGAP1L	-0.98
13	chr3	78188455	78188554	-2.57	-3.11	-2.66	-0.54	-0.09	0.45	ROBO1	-0.98
14	chr16	33515102	33515231	-6.52	-5.23	-5.14	1.30	1.39	0.09	ENPP7P13	-0.98
15	chr2	10678772	10678907	-1.85	-1.77	1.93	0.08	3.78	3.70	LOC101929715	-0.98
16	chr8	116729006	116729192	-3.59	-3.92	-2.51	-0.33	1.08	1.41	TRPS1	-0.97
17	chr20	31961623	31961784	-1.03	-0.77	2.64	0.27	3.68	3.41	CDK5RAP1	-0.97
18	chr6	158895972	158896229	-2.72	-3.66	-1.69	-0.93	1.04	1.97	TMEM181	-0.97
19	chr5	130664335	130664445	-2.65	-3.16	-2.35	-0.51	0.30	0.81	CDC42SE2	-0.97
20	chr20	4493660	4493846	-3.17	-3.20	-2.66	-0.03	0.51	0.54	PRNP	-0.97
21	chr18	49049321	49049454	-1.63	-1.61	1.44	0.03	3.08	3.05	LOC100287225	0.97
22	chr5	101331467	101331569	-1.32	-3.20	-2.51	-1.88	-1.19	0.69	SLCO4C1	-0.97
23	chr2	190272094	190272341	3.67	1.50	2.08	-2.17	-1.59	0.57	WDR75	-0.97
24	chr2	167841484	167841591	-3.06	-3.01	-0.44	0.05	2.62	2.58	XIRP2	0.96
25	chr18	60119570	60119702	-2.57	-3.06	0.45	-0.49	3.02	3.51	ZCCHC2	-0.96
26	chr8	99837611	99837856	-6.57	-6.44	-5.99	0.13	0.58	0.45	STK3	-0.96
27	chr4	185669395	185669492	0.37	-0.82	5.39	-1.19	5.02	6.21	CENPU	0.96
28	chr18	43608182	43608377	-0.77	-0.79	2.33	-0.02	3.10	3.12	PSTPIP2	-0.96
29	chr20	19865636	19865999	-1.14	1.58	-1.78	2.71	-0.64	-3.36	RIN2	0.95
30	chr18	77267599	77267913	-0.84	2.05	-1.24	2.90	-0.40	-3.30	NFATC1	0.95

31	chr1	243962145	243962281	-6.87	-6.53	-5.54	0.35	1.33	0.98	AKT3	-0.95
32	chr19	16770966	16771165	-1.50	-2.07	2.33	-0.57	3.83	4.40	SMIM7	0.95
33	chr3	48594294	48594440	-1.67	-0.60	1.76	1.06	3.42	2.36	PFKFB4	-0.94
34	chr14	62134881	62135246	-3.55	-3.89	-1.69	-0.34	1.87	2.21	HIF1A	-0.94
35	chr16	79908458	79908614	0.49	-0.84	2.90	-1.33	2.41	3.74	LINC01229	-0.94
36	chr18	66589431	66589794	-5.02	-4.76	-6.85	0.26	-1.83	-2.09	CCDC102B	-0.94
37	chr3	85807712	85807857	-3.00	-3.24	-2.66	-0.25	0.33	0.58	CADM2	0.94
38	chr10	18971217	18971324	-2.48	-3.20	-0.44	-0.72	2.05	2.77	ARL5B	-0.94
39	chr2	129562882	129563019	0.51	-0.28	2.87	-0.79	2.36	3.15	LOC101927881	-0.94
40	chr1	233652283	233652452	-1.52	-1.25	1.93	0.26	3.45	3.18	KCNK1	-0.93
41	chr6	143206582	143206718	-2.48	-3.16	-1.94	-0.67	0.54	1.21	HIVEP2	-0.93
42	chr8	123135103	123135259	-2.20	-1.87	1.37	0.32	3.57	3.24	LOC105375734	0.93
43	chr7	53678947	53679216	-0.03	-0.88	2.90	-0.85	2.93	3.78	LINC01446	0.93
44	chr8	57869809	57869964	-2.20	-1.01	1.37	1.19	3.57	2.38	IMPAD1	-0.93
45	chr5	114579235	114579334	-2.19	-3.06	-0.44	-0.87	1.75	2.63	PGGT1B	-0.93
46	chr16	83859886	83860103	-0.61	-1.02	2.45	-0.41	3.07	3.48	HSBP1	0.93
47	chr2	31109014	31109207	-2.46	-3.06	-1.88	-0.60	0.58	1.18	CAPN13	0.92
48	chr14	75517909	75518173	1.53	3.70	2.33	2.17	0.79	-1.37	MLH3	0.92
49	chr7	117720955	117721210	-3.00	-3.20	-1.94	-0.20	1.06	1.26	LSM8	-0.92
50	chr10	5666409	5666572	-6.37	-5.01	-5.71	1.36	0.66	-0.70	ASB13	0.92
51	chr15	57899835	57899994	0.38	-0.21	2.87	-0.59	2.50	3.08	MYZAP	0.92
52	chr7	78923069	78923215	-7.05	-6.79	-5.54	0.27	1.51	1.24	MAGI2-AS3	-0.92
53	chr6	20811384	20811522	-3.22	-2.38	0.45	0.84	3.68	2.84	CDKAL1	-0.89
54	chr2	136002826	136002928	-3.28	-3.37	-2.16	-0.09	1.12	1.21	RAB3GAP1	-0.89
55	chr6	13002259	13002445	-0.83	-0.01	5.65	0.82	6.47	5.66	PHACTR1	-0.89
56	chr15	34447209	34447314	-1.16	-1.93	1.37	-0.77	2.53	3.30	PGBD4	-0.89
57	chr8	95030864	95030980	-2.80	-3.01	-1.69	-0.21	1.11	1.32	PDP1	-0.89
58	chr2	33456112	33456218	-2.29	-3.24	-2.66	-0.95	-0.37	0.58	LTBP1	-0.89
59	chr11	95256146	95256254	-2.29	-3.16	-0.44	-0.86	1.86	2.72	FAM76B	-0.89
60	chr18	12336925	12337142	-3.28	-3.45	-2.16	-0.17	1.12	1.29	TUBB6	0.89
61	chr12	80836759	80836881	-1.32	-3.33	-1.38	-2.00	-0.05	1.95	PTPRQ	0.89
62	chr1	198940145	198940297	-1.35	-0.85	2.33	0.49	3.68	3.18	MIR181A1HG	-0.88
63	chr15	51173503	51173774	-3.42	-2.96	-2.66	0.46	0.76	0.30	AP4E1	-0.88
64	chr14	23624634	23624754	-6.25	-6.68	-4.18	-0.43	2.08	2.50	SLC7A8	-0.88

65	chr6	153359619	153359783	-2.93	-3.48	-3.03	-0.55	-0.10	0.45	MTRF1L	0.88
66	chr20	52199572	52199743	-6.19	-6.53	-3.63	-0.33	2.56	2.89	ZNF217	-0.88
67	chr18	19928855	19929036	1.10	1.63	4.21	0.52	3.10	2.58	CTAGE1	0.88
68	chr9	73539979	73540080	-2.48	-3.01	3.20	-0.53	5.68	6.21	TRPM3	-0.87
69	chr2	168109605	168109825	-2.46	-3.03	-1.59	-0.57	0.86	1.44	XIRP2	0.87
70	chr4	7727595	7727877	0.23	2.60	3.03	2.37	2.80	0.43	AFAP1-AS1	0.87
71	chr7	130615201	130615356	-2.19	-3.06	-0.44	-0.87	1.75	2.63	LOC100506860	0.87
72	chr17	11733200	11733393	-0.92	0.50	2.64	1.42	3.57	2.15	DNAH9	0.87
73	chr4	123686912	123687080	-6.31	-5.32	-5.54	0.99	0.77	-0.22	BBS12	-0.86
74	chr6	26328625	26328838	2.27	3.02	1.43	0.75	-0.84	-1.59	BTN3A2	-0.86
75	chr14	32841378	32841668	0.46	-0.42	2.59	-0.88	2.13	3.01	AKAP6	0.86
76	chr5	139511632	139511762	-6.06	-6.26	-5.36	-0.19	0.71	0.90	IGIP	-0.86
77	chr2	222382754	222383079	0.13	3.42	-0.64	3.29	-0.77	-4.06	EPHA4	0.86
78	chr12	117699125	117699240	-0.87	-1.10	2.64	-0.23	3.51	3.74	NOS1	-0.86
79	chr12	7096316	7096427	-5.59	-5.87	-4.18	-0.28	1.41	1.69	EMG1	0.86
80	chr11	64918353	64918533	-2.65	-3.16	-1.69	-0.51	0.96	1.47	SYVN1	-0.86
81	chr15	66194888	66195016	-0.49	0.12	2.59	0.61	3.08	2.47	RAB11A	0.86
82	chr12	39630903	39631072	-3.51	-3.72	-2.51	-0.21	1.00	1.21	KIF21A	-0.86
83	chr8	95022523	95022622	-4.71	-6.21	-5.14	-1.50	-0.43	1.07	PDP1	-0.85
84	chr12	51180702	51180814	-2.48	-3.24	-0.98	-0.76	1.50	2.26	ATF1	-0.85
85	chr3	189949850	189950001	-0.80	0.00	2.23	0.80	3.03	2.23	CLDN1	0.84
86	chr9	32627609	32627720	-5.27	-6.31	-5.71	-1.03	-0.44	0.60	TAF1L	0.84
87	chr20	18171757	18171945	-6.13	-5.58	-3.63	0.55	2.50	1.95	CSRP2BP	0.84
88	chr12	50561260	50561397	-6.95	-6.72	-4.88	0.23	2.06	1.83	CERS5	-0.84
89	chr10	123816302	123816434	-6.19	-6.61	-4.88	-0.41	1.31	1.72	TACC2	-0.84
90	chr16	53779727	53779826	-1.12	-1.41	2.33	-0.29	3.45	3.74	FTO	-0.83
91	chr2	200715364	200715542	1.80	3.02	1.43	1.22	-0.37	-1.59	FTCDNL1	0.83
92	chrX	97006735	97006956	-6.25	-6.61	-4.57	-0.35	1.68	2.03	DIAPH2-AS1	0.83
93	chr1	148931171	148931275	-2.93	-3.37	-2.80	-0.44	0.14	0.57	LOC645166	0.83
94	chr17	55453364	55453470	-1.37	-2.14	1.37	-0.77	2.74	3.51	MSI2	-0.83
95	chr5	32236679	32236830	-1.95	-3.01	0.45	-1.06	2.41	3.46	GOLPH3	0.83
96	chr10	102295582	102295738	-1.25	-0.98	1.93	0.26	3.18	2.91	HIF1AN	-0.83
97	chr7	21404596	21404696	-1.95	-3.24	-1.69	-1.29	0.27	1.56	SP4	-0.83
98	chr5	16736465	16736600	0.37	-0.44	3.12	-0.82	2.74	3.56	FAM134B	0.82

99	chr6	17864557	17864712	-6.66	-6.35	-5.54	0.31	1.12	0.81	KIF13A	-0.82
100	chr8	55181506	55181737	-6.19	-6.44	-4.18	-0.25	2.01	2.26	MRPL15	0.82
101	chr20	15201557	15201656	-1.51	-3.29	-1.38	-1.78	0.13	1.91	MACROD2	-0.81
102	chr8	80673374	80673571	-2.29	-3.01	-0.98	-0.72	1.31	2.03	HEY1	-0.81
103	chr3	87000615	87000744	-0.33	-0.39	3.12	-0.06	3.45	3.51	VGLL3	-0.81
104	chr1	78291098	78291253	-2.93	-3.33	-2.35	-0.40	0.59	0.98	FAM73A	-0.80
105	chr11	13396965	13397366	-4.87	-5.12	-6.77	-0.25	-1.90	-1.65	BTBD10	-0.80
106	chr12	68704218	68704348	-6.57	-5.93	-2.75	0.64	3.83	3.18	MDM1	0.80
107	chr9	108043133	108043405	-3.95	-3.72	-3.33	0.24	0.62	0.39	SLC44A1	-0.80
108	chr1	145698095	145698241	-2.65	-3.29	-1.94	-0.64	0.71	1.35	CD160	0.80
109	chr7	77022724	77022856	0.78	-0.45	6.37	-1.23	5.59	6.82	LOC101927243	0.80
110	chr10	4746367	4746476	-5.59	-5.80	-4.57	-0.21	1.01	1.23	LINC00704	0.80
111	chr14	79836179	79836366	-2.30	-3.00	-0.77	-0.70	1.54	2.24	NRXN3	-0.80
112	chr7	155446661	155446775	-2.93	-3.06	-3.03	-0.13	-0.10	0.03	RBM33	-0.80
113	chr2	40629161	40629270	-6.52	-6.40	-5.14	0.13	1.39	1.26	SLC8A1	-0.79
114	chr20	25317335	25317489	-5.59	-6.21	-5.14	-0.62	0.45	1.07	ABHD12	0.79
115	chr10	19467907	19468220	-4.87	-6.68	-5.14	-1.81	-0.27	1.54	MALRD1	0.79
116	chr11	87562310	87562458	0.56	-0.77	3.31	-1.33	2.74	4.08	RAB38	0.79
117	chr8	31002907	31003120	-2.07	-3.75	-2.35	-1.67	-0.27	1.40	PURG	0.79
118	chr9	10059246	10059390	-2.65	-3.06	-1.94	-0.41	0.71	1.12	PTPRD	-0.78
119	chr9	87863546	87863720	-3.17	-3.24	-2.35	-0.07	0.82	0.90	AGTPBP1	-0.78
120	chr13	24327783	24327895	0.37	-1.04	2.90	-1.41	2.53	3.94	C1QTNF9B-AS1	0.78
121	chr5	91854127	91854267	-2.65	-3.16	-2.35	-0.51	0.30	0.81	NR2F1-AS1	-0.77
122	chr12	6539998	6540177	-5.15	-5.66	-5.99	-0.51	-0.84	-0.34	CD27	-0.77
123	chr5	38541425	38541523	-5.27	-6.35	-4.88	-1.08	0.39	1.47	LIFR	-0.77
124	chr1	70152957	70153060	0.37	-1.37	2.33	-1.74	1.96	3.70	LRRC7	-0.77
125	chr10	101736884	101737002	-6.19	-6.35	-5.54	-0.16	0.65	0.81	DNMBP	-0.77
126	chr2	196716448	196716663	0.20	-1.18	2.33	-1.39	2.13	3.51	SLC39A10	-0.77
127	chr2	127617093	127617328	-0.33	-0.39	3.12	-0.06	3.45	3.51	GYPC	-0.77
128	chr19	21265010	21265305	-5.02	-5.87	-6.61	-0.85	-1.60	-0.75	ZNF714	-0.76
129	chr3	5036370	5036689	-5.85	-6.31	-6.85	-0.46	-1.00	-0.54	BHLHE40-AS1	-0.76
130	chr4	143874203	143874484	-1.64	1.53	-2.10	3.17	-0.46	-3.63	INPP4B	0.76
131	chr3	174580011	174580122	0.85	-0.70	5.86	-1.55	5.02	6.57	NAALADL2	-0.75
132	chr10	28543451	28543757	-6.52	-6.16	-5.71	0.37	0.81	0.45	MPP7	-0.74

133	chr2	151462355	151462455	-3.55	-2.60	-0.98	0.95	2.57	1.62	LOC101929282	0.74
134	chr10	52931852	52931959	-1.82	-3.20	-1.94	-1.38	-0.12	1.26	PRKG1	-0.74
135	chr3	118803722	118803844	1.50	0.44	6.37	-1.06	4.87	5.93	IGSF11	-0.74
136	chr2	67675952	67676114	1.35	-0.70	2.42	-2.05	1.07	3.12	ETAA1	0.74
137	chr1	164582525	164582631	-2.48	-3.55	-1.94	-1.07	0.54	1.61	PBX1	-0.73
138	chr4	24596586	24596740	-2.87	-3.52	-1.69	-0.65	1.18	1.83	DHX15	-0.73
139	chr1	166572634	166572848	-6.87	-7.04	-5.54	-0.16	1.33	1.49	FMO9P	0.73
140	chrX	9319927	9320048	-2.29	-3.33	-0.44	-1.04	1.86	2.89	TBL1X	-0.73
141	chr7	39627118	39627240	-0.56	-3.24	-1.38	-2.68	-0.81	1.87	YAE1D1	0.73
142	chr7	149156748	149156916	-0.29	0.96	3.63	1.25	3.92	2.67	ZNF777	0.73
143	chr13	53256885	53257283	0.94	2.51	-1.40	1.57	-2.34	-3.91	SUGT1	-0.73
144	chr17	77373264	77373393	-5.02	-6.10	-4.57	-1.09	0.44	1.53	RBFOX3	-0.73
145	chr3	169698033	169698175	0.43	0.30	4.00	-0.13	3.57	3.70	SEC62	-0.73
146	chr5	147278466	147278595	-6.13	-5.87	-6.34	0.26	-0.21	-0.47	C5orf46	-0.72
147	chr11	122060021	122060125	-2.48	-3.29	-2.35	-0.81	0.14	0.94	MIR100HG	-0.72
148	chr17	49841886	49842014	-1.90	-0.34	1.93	1.56	3.83	2.27	CA10	0.72
149	chr1	90331729	90331942	1.22	1.28	3.03	0.07	1.82	1.75	LRRC8D	0.72
150	chr10	116298261	116298389	-3.17	-2.30	-1.69	0.87	1.48	0.62	ABLM1	-0.72
151	chr16	8824204	8824343	-3.59	-2.67	-2.35	0.93	1.25	0.32	ABAT	-0.72
152	chr9	99622239	99622376	-0.50	-0.06	3.12	0.44	3.62	3.18	ZNF782	-0.72
153	chr14	65095869	65096034	-0.20	-1.00	2.01	-0.80	2.21	3.01	PLEKHG3	-0.71
154	chr4	143272182	143272286	-3.00	-3.16	-1.69	-0.16	1.31	1.47	INPP4B	-0.71
155	chr12	132354729	132354860	-3.51	-3.20	-1.38	0.31	2.13	1.82	ULK1	-0.71
156	chr12	2905071	2905242	-2.50	-2.41	-3.05	0.09	-0.55	-0.64	FKBP4	0.71
157	chr12	19267652	19267985	-2.29	-1.41	-3.33	0.88	-1.04	-1.92	PLEKHA5	-0.71
158	chr16	21530386	21530542	-2.65	-3.24	0.45	-0.60	3.10	3.70	SLC7A5P2	-0.71
159	chr4	167953232	167953587	3.36	1.62	0.51	-1.74	-2.85	-1.11	SPOCK3	0.71
160	chr4	143294812	143295039	-0.69	-1.45	2.33	-0.76	3.02	3.78	INPP4B	-0.70
161	chr3	153860555	153860656	-5.39	-5.80	-5.14	-0.41	0.25	0.66	ARHGEF26	-0.70
162	chr1	83616943	83617094	-5.27	-6.21	-5.54	-0.94	-0.27	0.67	LINC01361	0.70
163	chrX	54835344	54835486	-3.17	-2.30	-2.66	0.87	0.51	-0.36	MAGED2	-0.69
164	chr7	7759020	7759188	-3.51	-3.41	-1.38	0.10	2.13	2.03	RPA3	0.69
165	chr8	116951358	116951489	-0.90	-2.53	1.37	-1.63	2.27	3.90	TRPS1	-0.69
166	chr5	15540192	15540325	1.33	-1.01	5.39	-2.34	4.06	6.40	FBXL7	0.68

167	chr2	47100847	47100975	0.19	-0.58	3.12	-0.76	2.93	3.70	MCFD2	-0.68
168	chr18	10530916	10531049	-0.28	-1.07	2.01	-0.79	2.29	3.08	NAPG	-0.68
169	chr3	69419538	69419807	-2.29	-2.38	-3.33	-0.09	-1.04	-0.95	FRMD4B	-0.68
170	chr3	158548296	158548413	-2.93	-3.24	-0.44	-0.31	2.50	2.81	MFSD1	-0.68
171	chr2	35963	36074	-1.67	-3.20	-2.16	-1.53	-0.48	1.04	FAM110C	-0.67
172	chr1	173131142	173131247	-5.76	-5.80	-5.14	-0.04	0.63	0.66	TNFSF4	0.67
173	chrX	14523240	14523402	-2.57	-3.11	-1.38	-0.54	1.19	1.73	GLRA2	-0.67
174	chr9	136150547	136150733	-2.87	-3.29	-2.16	-0.42	0.71	1.13	ABO	0.67
175	chr13	44880704	44880838	-3.22	-3.20	-1.69	0.02	1.54	1.51	SERP2	0.67
176	chr12	115779236	115779349	-0.42	-0.66	2.90	-0.24	3.32	3.56	TBX3	-0.67
177	chr10	76559671	76559803	-0.20	-1.01	5.39	-0.81	5.59	6.40	KAT6B	-0.67
178	chr19	21788166	21788263	0.37	-1.45	2.33	-1.82	1.96	3.78	ZNF429	0.67
179	chr1	39452444	39452542	-2.57	-3.20	-1.94	-0.63	0.63	1.26	AKIRIN1	-0.66
180	chr10	17688051	17688244	-2.94	-3.11	-2.32	-0.17	0.62	0.79	STAM	-0.66
181	chr6	4135399	4135505	0.37	0.32	3.31	-0.05	2.93	2.99	ECI2	0.66
182	chr21	16564700	16564898	-1.35	-2.10	1.44	-0.75	2.79	3.54	NRIP1	-0.66
183	chr7	115812486	115812663	-2.29	-3.11	-2.16	-0.82	0.13	0.95	TES	-0.66
184	chr14	24299395	24299549	-3.22	-3.78	-1.94	-0.56	1.28	1.84	DHRS4	-0.66
185	chr8	484471	484687	-0.33	0.00	2.67	0.33	3.00	2.67	TDRP	-0.65
186	chr12	9839942	9840058	-1.03	-1.99	1.37	-0.95	2.41	3.36	CLEC2D	0.65
187	chr2	96426973	96427077	-4.87	-6.05	-5.36	-1.18	-0.48	0.69	LINC00342	-0.65
188	chr12	71003810	71004048	-6.57	-5.87	-6.77	0.71	-0.20	-0.91	PTPRB	0.65
189	chr8	119917494	119917644	-4.87	-6.57	-5.36	-1.70	-0.48	1.21	TNFRSF11B	0.65
190	chrX	102696901	102697075	-3.51	-2.53	-3.14	0.98	0.37	-0.61	NGFRAP1	-0.64
191	chr3	101875403	101875509	-0.08	-1.41	2.33	-1.33	2.41	3.74	LOC152225	-0.64
192	chr13	43632514	43632628	0.30	-0.18	3.48	-0.48	3.18	3.65	DNAJC15	0.64
193	chr20	54949118	54949294	-3.07	-1.81	-0.06	1.25	3.00	1.75	FAM210B	-0.64
194	chr2	13149274	13149382	2.21	-1.23	-0.28	-3.44	-2.49	0.95	LOC100506474	-0.63
195	chr1	152724814	152724956	-3.17	-3.52	0.45	-0.35	3.62	3.97	KPRP	0.63
196	chr2	226928533	226928670	-6.57	-6.16	-5.99	0.42	0.58	0.16	LOC646736	0.63
197	chr9	117996383	117996560	-6.62	-5.87	-3.63	0.75	2.99	2.23	1-Dec	0.63
198	chr1	223603026	223603326	-2.80	-3.01	-2.51	-0.21	0.29	0.50	CCDC185	-0.63
199	chr3	38038406	38038520	-6.00	-7.01	0.00	-1.01	6.00	7.01	VILL	-0.62
200	chr9	27499553	27499710	-6.87	-4.27	-4.18	2.61	2.69	0.09	IFNK	0.62

201	chr18	42320122	42320294	-0.67	-1.63	1.47	-0.96	2.13	3.09	SETBP1	-0.62
202	chr12	29581802	29581923	-6.13	-6.31	-5.36	-0.18	0.78	0.95	OVCH1-AS1	-0.62
203	chr6	129958547	129958707	-5.59	-6.31	-4.57	-0.72	1.01	1.73	ARHGAP18	-0.62
204	chr10	135132641	135132799	-6.31	-5.50	-5.14	0.81	1.17	0.36	TUBGCP2	0.62
205	chr6	13725700	13725931	-5.27	-5.80	-6.92	-0.53	-1.64	-1.12	RANBP9	-0.61
206	chr8	40207601	40207791	-3.51	-3.41	-1.94	0.10	1.57	1.47	C8orf4	-0.61
207	chr6	110419777	110420037	-0.70	-0.62	3.00	0.08	3.70	3.62	WASF1	-0.61
208	chr11	120417484	120417642	-3.67	-3.33	-1.38	0.35	2.30	1.95	GRIK4	0.61
209	chr17	41176931	41177075	1.36	-0.12	3.00	-1.48	1.64	3.12	RND2	-0.61
210	chr10	75503987	75504088	0.63	-0.34	2.90	-0.97	2.27	3.24	SEC24C	-0.61
211	chr17	33760283	33760524	-5.02	-5.23	-6.70	-0.21	-1.68	-1.47	SLFN12	0.61
212	chr2	36015552	36015664	-0.13	0.06	5.86	0.20	6.00	5.80	LOC100288911	0.60
213	chr9	109984401	109984511	-5.15	-6.10	-5.14	-0.95	0.01	0.96	RAD23B	-0.60
214	chr4	109457810	109457981	-7.15	-7.22	-6.12	-0.07	1.03	1.11	RPL34-AS1	0.60
215	chr1	223963856	223963969	2.06	0.81	3.03	-1.25	0.97	2.22	CAPN2	-0.59
216	chr9	94766127	94766225	1.36	0.90	6.63	-0.46	5.27	5.73	ROR2	0.59
217	chr5	119781777	119781917	-0.82	-1.48	1.93	-0.67	2.74	3.41	PRR16	-0.58
218	chr11	67771509	67771657	-2.65	-3.01	-1.94	-0.36	0.71	1.07	UNC93B1	0.58
219	chr3	127522514	127522677	-3.33	-3.37	-2.51	-0.04	0.81	0.86	MGLL	0.58
220	chr1	53642244	53642392	-0.67	-0.84	2.90	-0.17	3.57	3.74	CPT2	0.58
221	chr1	226667266	226667402	-0.05	0.03	3.11	0.08	3.16	3.08	C1orf95	0.58
222	chr2	60779641	60779770	0.78	-0.05	3.31	-0.83	2.53	3.36	BCL11A	0.58
223	chr7	105986812	105987247	-1.65	-1.61	-3.40	0.03	-1.76	-1.79	NAMPT	-0.58
224	chr1	69724534	69724650	-0.29	-0.66	2.64	-0.37	2.93	3.30	LRRC7	-0.57
225	chr10	25162317	25162483	0.61	-0.31	2.74	-0.92	2.13	3.05	PRTFDC1	0.57
226	chr12	26844615	26844785	-0.68	-1.05	2.64	-0.38	3.32	3.70	ITPR2	-0.57
227	chr6	17233871	17234047	-0.03	-1.00	2.01	-0.97	2.05	3.01	RBM24	-0.57
228	chrX	39767553	39767721	-0.39	-0.24	5.86	0.15	6.25	6.10	BCOR	-0.57
229	chr7	139013281	139013406	-5.39	-6.21	-5.54	-0.82	-0.16	0.67	LUC7L2	-0.56
230	chr6	26572019	26572255	1.70	0.89	3.11	-0.81	1.41	2.22	ABT1	0.56
231	chr6	157098373	157098550	0.18	-0.42	3.63	-0.59	3.45	4.04	ARID1B	-0.56
232	chr6	125269237	125269382	-0.65	0.19	2.42	0.84	3.08	2.23	RNF217	-0.56
233	chr3	123204877	123205034	-4.71	-6.35	-3.63	-1.65	1.07	2.72	ADCY5	-0.55
234	chr6	71891326	71891494	-2.72	-3.20	-1.43	-0.49	1.29	1.78	OGFRL1	-0.55

235	chr3	156032873	156032988	0.28	-0.62	3.12	-0.90	2.84	3.74	KCNAB1	-0.55
236	chr5	27450866	27451008	-5.85	-6.31	-3.63	-0.46	2.21	2.67	LINC01021	0.55
237	chr6	43670714	43670878	-1.16	0.19	1.87	1.35	3.04	1.69	MRPS18A	-0.55
238	chr14	78610010	78610109	-6.00	-6.16	-5.86	-0.16	0.14	0.30	NRXN3	-0.54
239	chr3	32955727	32955901	-5.27	-6.57	-5.36	-1.29	-0.08	1.21	CCR4	0.54
240	chr12	3802122	3802219	0.85	-0.06	5.86	-0.91	5.02	5.93	CRACR2A	-0.54
241	chr10	128947294	128947415	-2.65	-3.62	-2.35	-0.97	0.30	1.28	FAM196A	-0.54
242	chr11	116693838	116693973	-6.37	-4.61	-5.36	1.76	1.01	-0.74	APOA4	0.54
243	chr18	7871734	7872158	-2.41	-2.74	-3.92	-0.33	-1.52	-1.19	PTPRM	-0.54
244	chr5	96144064	96144225	-2.55	-3.16	-1.88	-0.61	0.67	1.28	ERAP1	-0.54
245	chr5	78908248	78908434	1.04	-0.25	3.31	-1.29	2.27	3.56	PAPD4	0.54
246	chr21	16596733	16596897	-0.56	-1.33	1.68	-0.78	2.24	3.02	NRIP1	-0.53
247	chr2	142715126	142715543	-2.48	-1.81	-3.33	0.67	-0.85	-1.52	LRP1B	0.53
248	chr4	91364502	91364712	-3.67	-4.44	-3.24	-0.76	0.44	1.20	CCSER1	0.52
249	chr8	139739744	139739859	-3.17	-3.41	-2.51	-0.24	0.66	0.90	COL22A1	-0.52
250	chr8	92373133	92373253	-1.16	-2.19	1.37	-1.03	2.53	3.56	SLC26A7	0.52
251	chr9	129119521	129119644	-5.15	-5.99	-5.36	-0.84	-0.20	0.63	MVB12B	-0.52
252	chr15	85113741	85114012	-2.93	-2.60	-3.42	0.33	-0.48	-0.81	LINC00933	-0.52
253	chr1	86016630	86016770	-3.47	-3.41	-1.94	0.06	1.53	1.47	DDAH1	-0.51
254	chr4	68064358	68064705	-2.07	-3.20	-3.24	-1.13	-1.16	-0.04	LOC101927237	0.51
255	chr1	236629448	236629594	-3.42	-3.37	-3.14	0.05	0.28	0.23	LGALS8	-0.51
256	chr6	15949952	15950109	-5.02	-6.44	-5.86	-1.43	-0.84	0.58	MYLIP	-0.51
257	chr1	181002517	181002802	2.48	-0.06	-0.57	-2.55	-3.05	-0.51	MR1	0.51
258	chr2	38143937	38144057	-2.39	-2.90	0.45	-0.52	2.84	3.36	RMDN2	0.51
259	chr6	121786359	121786532	-1.82	-3.11	-2.35	-1.29	-0.53	0.76	GJA1	-0.51
260	chr17	67594677	67594782	-6.06	-6.16	-5.86	-0.09	0.21	0.30	LINC01483	0.51
261	chr1	232266676	232266805	-6.66	-5.80	-4.88	0.86	1.78	0.92	DISC1-IT1	0.51
262	chr1	237262277	237262537	-6.47	-5.32	-5.36	1.15	1.12	-0.03	RYR2	0.50
263	chr17	17206709	17206895	-1.14	0.63	2.64	1.77	3.78	2.01	NT5M	0.50
264	chr19	16770798	16770935	0.38	1.14	3.63	0.77	3.25	2.48	SMIM7	0.50
265	chr12	89338146	89338344	-0.08	-1.81	2.33	-1.73	2.41	4.14	LOC728084	-0.50
266	chr12	30957094	30957241	0.37	-0.13	5.86	-0.50	5.49	5.99	LINC00941	0.49
267	chr4	103737231	103737356	0.12	-0.66	2.64	-0.77	2.53	3.30	UBE2D3	-0.49
268	chr3	56501235	56501382	-1.23	-1.29	1.76	-0.06	2.99	3.05	ERC2	0.49

269	chr2	8870230	8870336	-0.61	-0.66	2.64	-0.05	3.25	3.30	ID2	0.49
270	chr10	66716272	66716433	-0.70	-0.47	6.05	0.22	6.75	6.53	ANXA2P3	-0.49
271	chr15	23092567	23092812	-3.33	-3.24	-2.16	0.08	1.17	1.09	NIPA1	-0.49
272	chr21	36570380	36570492	-0.71	-1.43	4.67	-0.72	5.39	6.10	RUNX1	-0.49
273	chr21	32739276	32739397	-0.60	-1.85	1.93	-1.25	2.53	3.78	TIAM1	-0.48
274	chr13	22125213	22125337	-2.39	-3.29	-1.38	-0.90	1.01	1.91	MICU2	-0.48
275	chr9	80893343	80893513	-1.58	-1.97	1.04	-0.39	2.62	3.01	PSAT1	0.48
276	chr1	24127482	24127666	2.00	3.87	1.45	1.87	-0.55	-2.42	GALE	-0.47
277	chr6	83041147	83041375	-2.63	-1.53	0.50	1.09	3.12	2.03	TPBG	0.47
278	chr1	247537144	247537302	-3.11	-1.81	-2.35	1.30	0.77	-0.53	ZNF496	-0.47
279	chr2	66617042	66617187	-3.63	-2.79	-2.51	0.84	1.12	0.28	LOC729348	0.47
280	chr4	89455201	89455333	-6.06	-6.53	-4.88	-0.46	1.18	1.64	PYURF	0.47
281	chr1	116336769	116336979	2.35	3.01	4.88	0.66	2.53	1.87	CASQ2	0.46
282	chr14	67653977	67654106	-2.93	-2.38	0.45	0.55	3.39	2.84	FAM71D	0.46
283	chr4	188136683	188136855	-0.29	1.05	6.37	1.34	6.66	5.32	LOC339975	0.46
284	chr6	113975975	113976297	0.45	2.56	-0.48	2.11	-0.92	-3.04	LOC101927686	-0.46
285	chr8	122862439	122862536	-0.10	-0.82	2.64	-0.72	2.74	3.46	HAS2	-0.46
286	chr12	75571883	75572002	-0.87	-0.77	2.64	0.10	3.51	3.41	KCNC2	0.45
287	chr2	187874644	187874799	-6.37	-6.26	-5.14	0.11	1.23	1.12	ZSWIM2	0.45
288	chr7	17108895	17109058	-0.15	-0.46	2.59	-0.31	2.73	3.05	AGR3	0.45
289	chr4	121614275	121614432	-2.80	-3.16	-3.42	-0.36	-0.62	-0.26	PRDM5	0.45
290	chr10	54212029	54212274	-1.95	-2.22	-3.24	-0.26	-1.28	-1.02	LINC01468	0.45
291	chr8	122361123	122361254	-6.31	-6.31	-5.86	0.01	0.45	0.45	HAS2-AS1	-0.45
292	chr3	27058746	27058982	-1.99	-0.08	1.04	1.91	3.03	1.12	NEK10	-0.45
293	chr6	126226142	126226343	-6.13	-6.79	-4.18	-0.66	1.95	2.61	NCOA7	-0.45
294	chr11	11863963	11864183	-1.99	0.86	1.04	2.85	3.03	0.18	USP47	-0.44
295	chr6	47699110	47699363	-0.26	0.20	3.32	0.46	3.58	3.12	ADGRF4	-0.44
296	chr3	133515834	133515946	0.37	-0.22	2.90	-0.59	2.53	3.12	SRPRB	-0.44
297	chr2	167315301	167315437	-6.25	-6.57	-5.71	-0.31	0.54	0.86	SCN7A	0.44
298	chr13	96296419	96296579	-4.52	-6.53	-6.44	-2.00	-1.91	0.09	DZIP1	-0.44
299	chr10	106099747	106099910	-5.49	-6.05	-5.86	-0.56	-0.37	0.19	ITPRIP	-0.44
300	chr3	162437626	162437728	-5.76	-6.26	-3.63	-0.49	2.13	2.63	LINC01192	0.43
301	chr5	127563828	127563974	-3.51	-3.01	-3.03	0.50	0.48	-0.02	SLC12A2	-0.43
302	chr4	141549310	141549426	-4.87	-6.31	-5.36	-1.44	-0.48	0.95	TNRC18P1	-0.43

303	chr18	34430593	34430732	-0.45	-0.78	2.23	-0.33	2.68	3.01	TPGS2	0.43
304	chr5	53872	54000	-3.06	-2.85	-1.94	0.21	1.12	0.91	PLEKHG4B	0.42
305	chr11	74654177	74654310	-3.47	-2.03	-1.69	1.44	1.78	0.34	XRRA1	-0.42
306	chr6	79880782	79880899	-1.67	-3.16	-1.94	-1.48	-0.27	1.21	HMGN3-AS1	-0.42
307	chr18	52379615	52379785	-2.80	-3.24	-1.69	-0.45	1.11	1.56	RAB27B	-0.42
308	chr3	59757618	59757719	0.85	-0.39	3.12	-1.24	2.27	3.51	C3orf67	0.42
309	chr1	86570856	86570977	-2.48	-3.11	-0.98	-0.63	1.50	2.13	COL24A1	-0.42
310	chr15	66849032	66849189	-5.15	-6.40	-5.36	-1.25	-0.20	1.04	LCTL	0.41
311	chr6	67086076	67086185	-5.68	-5.73	-4.57	-0.05	1.10	1.16	SLC25A51P1	0.41
312	chr2	40662101	40662251	0.10	0.50	3.22	0.40	3.12	2.72	SLC8A1	-0.41
313	chr5	16778304	16778508	-0.34	-0.85	6.37	-0.52	6.71	7.22	MYO10	-0.40
314	chr3	136612808	136612915	-1.37	-2.04	4.12	-0.67	5.49	6.16	NCK1	-0.40
315	chr11	99239509	99239622	0.12	-0.96	2.64	-1.08	2.53	3.61	CNTN5	-0.40
316	chr7	76052791	76052953	-0.42	-0.66	2.42	-0.24	2.84	3.08	ZP3	-0.40
317	chr11	15145487	15145701	0.71	-0.78	2.45	-1.49	1.74	3.23	INSC	0.40
318	chr12	120875665	120875797	-3.42	-2.46	-3.14	0.96	0.28	-0.68	COX6A1	0.40
319	chr13	26960289	26960499	-0.86	-1.17	1.87	-0.31	2.73	3.04	CDK8	0.40
320	chr2	133188570	133188704	-0.40	1.33	3.48	1.73	3.87	2.15	GPR39	0.40
321	chr1	243911772	243912144	2.67	0.47	-0.47	-2.20	-3.15	-0.95	AKT3	0.40
322	chr16	23436091	23436219	-3.42	-3.06	-1.38	0.36	2.05	1.68	COG7	0.40
323	chr10	125607898	125608238	-2.07	-2.38	-3.33	-0.31	-1.25	-0.95	CPXM2	-0.40
324	chr19	10812199	10812369	1.07	1.47	3.50	0.41	2.43	2.02	QTRT1	-0.40
325	chr5	93769286	93769685	-1.65	-2.77	-3.05	-1.12	-1.40	-0.28	KIAA0825	-0.40
326	chr6	24428570	24429126	-2.51	-2.30	-3.01	0.21	-0.51	-0.71	MRS2	0.40
327	chr20	56347633	56347848	-2.03	-2.30	4.67	-0.27	6.71	6.98	PMEPA1	-0.40
328	chr12	48357293	48357393	1.45	1.41	3.03	-0.04	1.59	1.62	TMEM106C	-0.40
329	chr8	51260559	51260820	-5.15	-5.80	-5.71	-0.65	-0.56	0.09	SNTG1	0.39
330	chr2	26578445	26578653	-0.09	-0.46	2.59	-0.37	2.68	3.05	ADGRF3	0.39
331	chr9	93733011	93733138	0.33	0.03	3.22	-0.30	2.89	3.19	LOC100129316	0.38
332	chr1	95440455	95440636	-0.60	-2.04	1.04	-1.44	1.64	3.08	LOC729970	0.38
333	chr6	7425254	7425375	-4.71	-6.31	-3.63	-1.60	1.07	2.67	RIOK1	0.37
334	chr11	1568215	1568367	-1.17	-1.48	1.93	-0.31	3.10	3.41	DUSP8	0.37
335	chr5	33401693	33401845	-1.51	-3.29	-1.69	-1.78	-0.18	1.60	TARS	-0.36
336	chr5	143963323	143963463	-5.76	-5.87	-6.44	-0.10	-0.67	-0.57	KCTD16	-0.36

337	chr14	35839145	35839251	-0.31	-0.91	5.08	-0.60	5.39	5.99	NFKBIA	0.35
338	chr6	7441439	7441542	1.61	0.70	6.63	-0.91	5.02	5.93	RIOK1	-0.35
339	chr1	116420255	116420374	-6.42	-6.95	-4.88	-0.53	1.54	2.06	NHLH2	0.35
340	chr13	106636834	106636985	-5.02	-6.44	-2.75	-1.43	2.27	3.70	LINC00343	0.35
341	chr15	60700418	60700658	-3.22	-1.07	-2.92	2.16	0.30	-1.85	ANXA2	0.34
342	chr6	142644646	142644919	-0.37	-0.72	2.33	-0.35	2.69	3.04	ADGRG6	0.34
343	chr5	148650974	148651158	1.37	3.05	1.64	1.68	0.27	-1.41	AFAP1L1	-0.34
344	chr4	88025055	88025207	-0.77	-1.13	5.08	-0.36	5.85	6.21	AFF1	-0.34
345	chr15	66084409	66084521	-0.03	-0.28	2.90	-0.25	2.93	3.18	DENND4A	-0.34
346	chr4	81883966	81884399	-5.76	-5.23	-6.77	0.54	-1.01	-1.55	BMP3	-0.33
347	chr14	32976977	32977113	-3.51	-3.33	-2.80	0.18	0.71	0.53	AKAP6	0.33
348	chr2	117957925	117958271	2.01	-0.34	-1.66	-2.35	-3.67	-1.32	DDX18	0.33
349	chr7	156562202	156562392	-3.11	-2.13	-1.69	0.99	1.43	0.44	LMBR1	-0.33
350	chr10	69857049	69857184	-5.49	-6.16	-4.57	-0.67	0.92	1.58	MYPN	0.32
351	chr4	11587277	11587513	-0.50	-1.17	3.12	-0.67	3.62	4.29	HS3ST1	-0.32
352	chr3	108139876	108140037	-3.37	-2.96	-2.51	0.42	0.86	0.45	MYH15	-0.32
353	chr12	123616550	123616728	1.26	1.52	3.11	0.26	1.86	1.59	PITPNM2	0.32
354	chr8	1972241	1972385	-1.02	0.23	5.65	1.25	6.66	5.42	MYOM2	0.32
355	chr17	4047049	4047245	-0.66	3.23	0.98	3.89	1.64	-2.25	CYB5D2	-0.31
356	chr20	43803424	43803537	0.99	-0.13	3.12	-1.12	2.13	3.24	PI3	0.31
357	chr9	119572116	119572286	0.21	-0.05	6.05	-0.26	5.85	6.10	TRIM32	-0.30
358	chr11	132113713	132113876	-0.61	0.76	5.65	1.36	6.25	4.89	NTM-IT	-0.29
359	chr7	123403355	123403516	1.81	-1.63	-0.21	-3.44	-2.02	1.42	WASL	0.29
360	chr10	69579692	69579791	-5.27	-6.53	-4.18	-1.25	1.09	2.35	DNAJC12	0.29
361	chr19	37329357	37329488	-2.65	-2.90	-3.14	-0.26	-0.49	-0.23	ZNF790	-0.28
362	chr19	8400417	8400577	-3.33	-1.69	-2.16	1.63	1.17	-0.46	KANK3	-0.28
363	chr11	105590243	105590469	-0.17	-0.26	3.50	-0.09	3.67	3.76	GRIA4	0.28
364	chr14	67885658	67885835	-2.59	-3.13	-2.11	-0.54	0.48	1.02	PLEK2	0.28
365	chr19	49376435	49376606	-1.27	-2.33	4.12	-1.06	5.39	6.44	PPP1R15A	0.28
366	chr18	9117354	9117493	0.16	-0.56	2.90	-0.72	2.74	3.46	NDUFV2	0.28
367	chr2	216878175	216878332	0.71	0.70	6.63	-0.01	5.92	5.93	MREG	0.27
368	chr9	12798244	12798355	-0.20	-0.85	2.33	-0.66	2.53	3.18	LURAP1L-AS1	0.27
369	chr9	132586459	132586566	-1.46	-1.25	1.93	0.20	3.39	3.18	TOR1A	0.27
370	chr2	145167092	145167378	-2.39	-1.93	-3.33	0.46	-0.94	-1.40	GTDC1	-0.27

371	chr11	33744363	33744582	1.35	0.01	3.31	-1.34	1.96	3.30	CD59	-0.27
372	chr18	26415056	26415312	-3.06	-2.73	-2.66	0.33	0.40	0.07	CDH2	-0.26
373	chr1	173098040	173098285	0.50	0.68	3.58	0.18	3.08	2.89	TNFSF4	0.26
374	chr14	81462758	81462864	-0.61	-0.40	5.65	0.21	6.25	6.05	TSHR	0.26
375	chr8	6405194	6405365	-6.62	-6.61	-6.44	0.01	0.18	0.17	ANGPT2	-0.26
376	chr8	87496199	87496540	-1.88	-3.11	-1.88	-1.23	0.00	1.23	RMDN1	0.26
377	chr18	21851980	21852101	0.71	-0.18	5.86	-0.90	5.15	6.05	OSBPL1A	-0.25
378	chr3	115541609	115541776	-3.71	-2.67	-1.94	1.04	1.77	0.73	GAP43	0.25
379	chr3	45008385	45008532	-3.51	-3.01	-2.80	0.50	0.71	0.21	ZDHHC3	0.24
380	chr19	17611708	17611902	-0.08	-1.13	2.33	-1.06	2.41	3.46	PGLS	0.24
381	chr4	106912389	106912504	-5.68	-6.26	-3.63	-0.58	2.05	2.63	LOC101929577	-0.23
382	chr9	107635470	107635634	-2.25	-2.83	4.12	-0.58	6.37	6.95	ABCA1	0.23
383	chr13	33792291	33792395	-3.17	-3.11	-2.16	0.06	1.01	0.95	STARD13	-0.23
384	chr9	113046278	113046636	-6.25	-6.26	-7.05	0.00	-0.79	-0.79	TXN	0.22
385	chr7	90209541	90209639	-0.81	-1.10	5.39	-0.29	6.19	6.49	CDK14	0.21
386	chr20	278674	278914	-2.48	-2.60	-3.03	-0.12	-0.55	-0.43	ZCCHC3	0.21
387	chr1	169105924	169106202	1.62	2.95	3.58	1.32	1.95	0.63	ATP1B1	0.21
388	chr12	42326174	42326435	-2.48	-2.38	-3.03	0.10	-0.55	-0.65	GXYLT1	-0.21
389	chr6	11318663	11318773	-6.19	-6.40	-2.75	-0.20	3.45	3.65	NEDD9	-0.21
390	chr10	50758665	50758783	-1.52	-2.11	1.04	-0.59	2.56	3.15	ERCC6-PGBD3	-0.21
391	chr2	190228454	190228558	0.16	-0.61	2.90	-0.77	2.74	3.51	WDR75	-0.21
392	chr3	66789480	66789593	3.88	0.64	2.57	-3.24	-1.32	1.92	LRIG1	-0.20
393	chr2	174049206	174049303	1.73	0.44	3.11	-1.29	1.38	2.67	MLK7-AS1	-0.19
394	chr7	148762109	148762313	-0.88	2.13	0.29	3.01	1.17	-1.84	ZNF786	0.19
395	chr19	8478058	8478168	-3.17	-2.46	-1.38	0.71	1.79	1.08	2-Mar	-0.19
396	chr2	73980794	73981128	0.95	4.00	0.40	3.04	-0.55	-3.60	TPRKB	0.19
397	chr8	116680920	116681265	0.38	0.06	3.63	-0.31	3.25	3.56	TRPS1	-0.18
398	chr7	98928325	98928480	-6.06	-6.31	-5.71	-0.24	0.35	0.60	ARPC1A	0.18
399	chr11	85532799	85532962	-6.66	-6.68	-6.70	-0.02	-0.03	-0.02	SYTL2	0.17
400	chr8	636909	637072	0.37	-0.06	3.12	-0.44	2.74	3.18	ERICH1	-0.17
401	chr8	117457082	117457304	-2.87	-3.13	-1.74	-0.27	1.12	1.39	LINC00536	0.17
402	chr3	174311019	174311482	0.47	2.54	-0.56	2.07	-1.03	-3.10	NAALADL2	0.16
403	chr7	123210596	123210701	-1.73	-2.24	4.12	-0.51	5.85	6.35	NDUFA5	-0.16
404	chr3	7829585	7829807	-2.87	-3.03	-1.24	-0.16	1.63	1.79	LOC101927394	0.16

405	chr2	37872719	37873038	-1.32	-2.22	-3.72	-0.89	-2.39	-1.50	CDC42EP3	0.16
406	chr6	16336807	16336911	3.19	-0.35	0.70	-3.54	-2.49	1.04	GMPR	0.15
407	chr13	41019779	41019889	-3.17	-3.37	-2.35	-0.20	0.82	1.02	LINC00598	0.15
408	chr5	115084839	115084987	-2.48	-3.45	-2.16	-0.97	0.32	1.29	CDO1	0.15
409	chr4	77012260	77012391	-5.02	-6.44	-5.14	-1.43	-0.12	1.30	ART3	-0.15
410	chr2	186816980	186817098	-1.00	-1.68	1.93	-0.67	2.93	3.61	LINC01473	-0.15
411	chr15	52789103	52789296	-0.96	0.06	2.04	1.03	3.00	1.98	MYO5A	-0.15
412	chr4	159823875	159824022	-3.75	-3.62	-1.94	0.13	1.81	1.68	C4orf45	-0.15
413	chr1	154989915	154990052	-0.56	1.16	2.57	1.72	3.12	1.40	ZBTB7B	-0.15
414	chr18	28572336	28572450	-0.56	-0.58	3.12	-0.02	3.68	3.70	DSC3	0.14
415	chr9	530797	530910	-6.42	-6.31	-4.18	0.12	2.24	2.13	KANK1	0.14
416	chr7	156685142	156685377	-3.59	-2.46	-2.92	1.13	0.67	-0.46	LMBR1	-0.14
417	chr12	10548416	10548552	-5.68	-6.16	-4.57	-0.48	1.10	1.58	KLRK1	-0.14
418	chr8	7252600	7252997	-4.87	-5.58	-6.61	-0.71	-1.74	-1.03	DEFB4B	0.14
419	chr9	93741453	93741601	-0.20	-0.97	2.33	-0.77	2.53	3.30	LOC100129316	0.14
420	chr4	99714921	99715070	-2.41	-1.01	1.37	1.40	3.78	2.38	TSPAN5	0.13
421	chr9	5566102	5566223	-5.68	-5.87	-5.71	-0.19	-0.03	0.16	PDCD1LG2	0.13
422	chr4	73206858	73207101	-5.59	-4.76	-6.44	0.83	-0.85	-1.68	ADAMTS3	0.13
423	chr5	157478147	157478252	-4.06	-6.40	-4.88	-2.34	-0.82	1.51	CLINT1	-0.13
424	chr22	29468780	29468902	-0.97	-1.11	5.86	-0.14	6.83	6.98	KREMEN1	0.13
425	chr19	52599025	52599174	0.73	-0.63	3.48	-1.36	2.74	4.11	ZNF841	-0.12
426	chr6	81149929	81150046	-2.19	-3.01	-1.69	-0.82	0.50	1.32	BCKDHB	0.12
427	chr2	180636610	180636772	-0.53	-1.59	1.76	-1.06	2.29	3.34	ZNF385B	0.12
428	chr15	48042760	48042912	-2.87	-3.33	-2.80	-0.46	0.07	0.53	SEMA6D	0.11
429	chr2	36788799	36788940	0.16	-0.09	3.89	-0.24	3.73	3.97	FEZ2	0.11
430	chr5	117414370	117414530	-0.41	-0.97	2.33	-0.56	2.74	3.30	HNCAT21	0.11
431	chrX	108957316	108957712	-1.51	-1.56	-3.97	-0.05	-2.46	-2.41	ACSL4	0.11
432	chr1	214755406	214755671	-5.76	-5.01	-6.12	0.75	-0.35	-1.11	CENPF	0.11
433	chr17	30677098	30677371	-0.93	0.64	3.12	1.56	4.05	2.48	ZNF207	0.11
434	chr15	70471218	70471485	-2.19	-1.93	-3.03	0.26	-0.85	-1.11	TLE3	-0.10
435	chr4	54430141	54430241	-0.61	-0.41	2.64	0.20	3.25	3.05	LNX1	-0.10
436	chr8	126558000	126558237	-6.00	-6.82	-5.14	-0.83	0.86	1.68	TRIB1	-0.10
437	chr8	49236892	49236991	-2.39	-3.33	-2.16	-0.94	0.23	1.17	LOC101929268	0.10
438	chr6	53358003	53358155	1.50	0.57	3.63	-0.93	2.13	3.05	GCLC	-0.10

439	chr3	71307537	71307702	-1.59	1.94	-0.28	3.52	1.31	-2.22	FOXP1	0.09
440	chr5	148382706	148382858	-5.15	-6.21	-4.88	-1.06	0.27	1.32	SH3TC2	0.09
441	chr13	34599986	34600108	-1.47	-2.14	1.37	-0.67	2.84	3.51	RFC3	0.09
442	chr10	34953533	34953889	-2.72	-2.53	-3.21	0.19	-0.50	-0.68	PARD3	0.08
443	chr2	180520513	180520629	-2.87	-3.29	-2.16	-0.42	0.71	1.13	ZNF385B	-0.08
444	chr1	226148502	226148756	-1.95	-2.22	-3.03	-0.26	-1.08	-0.82	LEFTY2	0.08
445	chr3	139373664	139373783	0.21	-0.73	2.42	-0.94	2.21	3.15	NMNAT3	-0.08
446	chr8	67281325	67281544	-2.57	-3.48	-2.66	-0.92	-0.09	0.82	RRS1-AS1	0.08
447	chr12	48551315	48551489	-1.02	-0.40	2.90	0.62	3.92	3.30	ASB8	0.07
448	chr4	86697836	86698013	-6.57	-6.95	-5.14	-0.38	1.43	1.81	ARHGAP24	0.07
449	chr4	166170126	166170263	-6.31	-6.31	-4.57	0.01	1.74	1.73	GK3P	-0.07
450	chr8	18067528	18067632	-0.01	-0.55	3.31	-0.54	3.32	3.86	NAT1	0.07
451	chr4	83142544	83142832	-0.12	3.01	-0.79	3.13	-0.67	-3.80	HNRNPD	0.07
452	chr11	104035035	104035534	-1.80	-2.19	-3.45	-0.38	-1.64	-1.26	PDGFD	-0.07
453	chr12	101439443	101439645	2.58	3.23	1.17	0.65	-1.41	-2.06	ANO4	0.07
454	chr15	84402100	84402239	-0.61	-1.26	1.76	-0.65	2.36	3.01	ADAMTSL3	-0.06
455	chr14	20762947	20763125	-2.72	-3.06	-0.44	-0.34	2.29	2.63	TTC5	-0.06
456	chr2	11672668	11672813	-1.59	1.27	1.44	2.85	3.03	0.18	GREB1	-0.06
457	chrX	73673139	73673274	-1.88	-1.87	1.37	0.01	3.25	3.24	SLC16A2	0.06
458	chr2	27632515	27632641	-5.59	-6.35	-5.71	-0.77	-0.12	0.64	PPM1G	-0.06
459	chr7	3629501	3629653	0.24	-0.64	3.63	-0.88	3.39	4.26	SDK1	0.06
460	chr10	120183445	120183550	-5.02	-6.16	-4.88	-1.14	0.13	1.27	LINC00867	0.05
461	chr12	90968533	90968643	-0.20	-1.58	4.67	-1.39	4.87	6.26	LINC00615	0.05
462	chr12	99231217	99231409	-3.00	-3.29	-3.14	-0.29	-0.14	0.15	ANKS1B	-0.05
463	chr11	121016439	121016581	-1.51	-3.06	-1.38	-1.55	0.13	1.68	TECTA	0.05
464	chr1	200153423	200153587	-0.47	-0.66	3.31	-0.19	3.78	3.97	NR5A2	-0.05
465	chr1	224251532	224251677	-1.18	-0.34	2.33	0.84	3.51	2.67	FBXO28	0.04
466	chr9	114364067	114364303	-5.92	-5.01	-6.34	0.91	-0.42	-1.33	PTGR1	0.04
467	chr11	7435286	7435413	-0.27	-0.78	3.12	-0.51	3.39	3.90	LOC100506258	-0.04
468	chr10	6828607	6828889	-3.28	-2.85	-3.58	0.43	-0.30	-0.73	LINC00707	0.04
469	chr9	139340103	139340370	-2.57	-2.13	-3.72	0.44	-1.15	-1.59	INPP5E	0.04
470	chr13	99719564	99719789	-0.87	0.26	2.64	1.13	3.51	2.38	DOCK9	0.04
471	chr12	109210156	109210275	-1.11	-3.33	-2.66	-2.22	-1.55	0.67	SSH1	-0.03
472	chr8	103416051	103416160	0.21	0.55	3.31	0.34	3.10	2.76	UBR5	0.03

473	chr15	92640924	92641046	-5.15	-6.26	-5.54	-1.11	-0.39	0.71	SLCO3A1	-0.03
474	chr2	75520210	75520334	-2.65	-3.20	-1.94	-0.55	0.71	1.26	TACR1	-0.02
475	chr8	90738827	90739055	1.77	1.81	3.41	0.05	1.64	1.59	LOC101929709	0.02
476	chr10	25113223	25113335	-0.08	-1.08	2.33	-1.01	2.41	3.41	ARHGAP21	0.01
477	chr5	63802196	63802328	-1.35	-0.05	2.33	1.30	3.68	2.38	RGS7BP	-0.01
478	chr8	11735249	11735367	-6.25	-6.21	-6.23	0.05	0.02	-0.02	CTSB	-0.01
479	chr3	59286459	59286647	-0.99	-1.61	2.33	-0.62	3.32	3.94	C3orf67	-0.01
480	chr1	107684027	107684193	0.84	-0.09	6.22	-0.92	5.39	6.31	NTNG1	-0.01
481	chr3	125313187	125313294	-1.32	-3.01	-1.69	-1.69	-0.36	1.32	OSBPL11	-0.01
482	chr18	21075088	21075230	0.16	-0.51	2.90	-0.67	2.74	3.41	C18orf8	0.00
483	chr1	30262718	30262871	0.37	-0.74	3.12	-1.12	2.74	3.86	LOC101929406	NA
484	chr1	62071825	62072162	-2.19	-1.93	-3.03	0.26	-0.85	-1.11	MGC34796	NA
485	chr1	96116282	96116482	-2.29	-4.12	-2.35	-1.83	-0.05	1.78	LOC100996635	NA
486	chr1	143462818	143462927	-0.90	-2.14	1.37	-1.24	2.27	3.51	MIR6077	NA
487	chr1	163141270	163141652	1.33	1.58	-1.89	0.25	-3.22	-3.47	LOC101928404	NA
488	chr1	185410778	185410927	1.16	-0.74	3.12	-1.90	1.96	3.86	GS1-279B7.1	NA
489	chr1	196471294	196471468	-3.42	-2.96	-1.38	0.46	2.05	1.58	MIR4735	NA
490	chr10	14026877	14027066	-1.32	-1.05	1.76	0.27	3.08	2.81	LOC101928453	NA
491	chr10	44696341	44696641	-5.76	-5.87	-6.53	-0.10	-0.76	-0.66	C10orf142	NA
492	chr10	54577855	54577954	-1.00	-1.19	1.93	-0.19	2.93	3.12	MBL2	NA
493	chr10	79222593	79222690	-0.82	-1.58	1.93	-0.77	2.74	3.51	KCNMA1-AS3	NA
494	chr10	106569113	106569389	-2.17	-1.18	0.90	0.99	3.07	2.08	SORCS3-AS1	NA
495	chr10	107344992	107345160	1.44	1.03	4.54	-0.41	3.10	3.51	LOC101927549	NA
496	chr10	115911350	115911486	-0.65	-0.42	2.59	0.23	3.24	3.01	MIR2110	NA
497	chr10	122263851	122264093	-0.26	-1.22	1.87	-0.96	2.13	3.09	PLPP4	NA
498	chr11	17838312	17838461	-1.18	0.38	2.64	1.56	3.83	2.27	KCNC1	NA
499	chr11	48329372	48329567	1.25	-2.09	-1.59	-3.34	-2.85	0.50	OR4S1	NA
500	chr11	57669325	57669441	-3.11	-3.48	-0.44	-0.37	2.68	3.05	OR9Q1	NA
501	chr11	77271886	77272096	-2.93	-3.41	-2.51	-0.48	0.42	0.90	LOC646029	NA
502	chr11	91029910	91030050	-5.85	-6.64	-5.86	-0.80	-0.01	0.78	MIR1261	NA
503	chr11	92570921	92571037	-0.27	-0.39	3.12	-0.13	3.39	3.51	MTNR1B	NA
504	chr11	126862073	126862220	-3.22	-3.33	-1.94	-0.10	1.28	1.39	MIR3167	NA
505	chr11	126887496	126887616	-6.19	-6.31	-4.57	-0.11	1.62	1.73	KIRREL3-AS3	NA
506	chr11	127069370	127069549	-3.17	-3.55	-0.44	-0.38	2.73	3.12	LOC101929497	NA

507	chr11	127521154	127521260	-5.68	-5.93	-5.71	-0.25	-0.03	0.22	LOC101929497	NA
508	chr12	5457600	5457889	-2.87	-3.75	-3.42	-0.88	-0.55	0.33	NTF3	NA
509	chr12	7791492	7791813	-5.27	-5.93	-6.77	-0.66	-1.50	-0.84	APOBEC1	NA
510	chr12	16391689	16391818	-1.45	-0.15	2.33	1.30	3.78	2.48	SLC15A5	NA
511	chr12	16399324	16399451	-3.06	-3.24	-0.98	-0.19	2.08	2.26	SLC15A5	NA
512	chr12	43173463	43173578	1.53	-0.05	3.31	-1.58	1.78	3.36	LOC101927058	NA
513	chr12	79960359	79960533	-3.75	-3.16	0.45	0.59	4.20	3.61	MIR5692B	NA
514	chr12	92471983	92472088	-5.15	-6.16	-5.14	-1.01	0.01	1.02	LINC01619	NA
515	chr12	102591703	102591805	-2.19	-3.01	-0.44	-0.82	1.75	2.58	PMCH	NA
516	chr12	128055583	128055912	-1.32	-2.60	-3.50	-1.28	-2.17	-0.90	LOC101927637	NA
517	chr13	37980332	37980445	0.33	0.50	3.22	0.17	2.89	2.72	LINC01048	NA
518	chr13	60121844	60122056	0.28	-0.44	3.12	-0.72	2.84	3.56	DIAPH3-AS1	NA
519	chr13	67508199	67508428	-1.53	-1.12	1.48	0.42	3.01	2.60	PCDH9-AS3	NA
520	chr13	72636851	72637083	1.11	0.68	3.18	-0.43	2.08	2.50	DACH1	NA
521	chr13	94499583	94499712	-0.53	0.42	2.59	0.95	3.12	2.17	GPC6-AS2	NA
522	chr13	98867079	98867212	-2.87	-3.20	-2.66	-0.33	0.21	0.54	MIR3170	NA
523	chr13	105061225	105061328	-1.09	-1.93	4.67	-0.84	5.76	6.61	LINC01309	NA
524	chr14	31964129	31964279	-1.56	-1.87	4.12	-0.31	5.68	5.99	GPR33	NA
525	chr14	57968066	57968220	1.20	-0.04	3.48	-1.24	2.27	3.51	C14orf105	NA
526	chr14	83346441	83346567	-2.07	-3.11	-1.94	-1.03	0.13	1.17	LINC01467	NA
527	chr14	101222028	101222140	-5.85	-6.89	-2.75	-1.04	3.10	4.14	DLK1	NA
528	chr15	35129571	35129688	0.55	-1.13	2.33	-1.69	1.78	3.46	ACTC1	NA
529	chr15	99346830	99346948	1.18	0.12	6.05	-1.06	4.87	5.93	MIR4714	NA
530	chr16	26485419	26485785	-1.82	-1.93	-3.33	-0.11	-1.51	-1.40	C16orf82	NA
531	chr16	65876069	65876219	-3.00	-3.16	-1.38	-0.16	1.62	1.78	LINC00922	NA
532	chr17	14942815	14942945	-0.61	-0.66	2.42	-0.05	3.03	3.08	CDRT7	NA
533	chr17	26796280	26796437	-5.39	-6.40	-5.14	-1.01	0.25	1.26	SLC13A2	NA
534	chr17	47647669	47647973	1.33	2.24	3.46	0.91	2.13	1.23	LOC100288866	NA
535	chr18	33514078	33514243	-2.12	-2.42	1.93	-0.30	4.05	4.35	MIR3929	NA
536	chr18	40892789	40893138	-2.07	-2.38	-3.78	-0.31	-1.71	-1.40	SYT4	NA
537	chr18	71984105	71984289	-2.80	-3.55	-1.94	-0.76	0.86	1.61	C18orf63	NA
538	chr19	51425653	51425760	-3.76	-6.26	-5.54	-2.50	-1.78	0.71	KLK4	NA
539	chr2	15784489	15784587	1.34	-0.49	5.86	-1.83	4.52	6.35	LOC101926966	NA
540	chr2	19052790	19052957	0.96	0.51	3.32	-0.45	2.36	2.81	NT5C1B	NA

541	chr2	19289425	19289540	0.71	-0.06	3.12	-0.78	2.41	3.18	MIR4757	NA
542	chr2	60582001	60582140	-0.78	-1.53	2.01	-0.75	2.79	3.54	MIR4432HG	NA
543	chr2	119613182	119613319	-1.52	0.78	1.76	2.30	3.28	0.98	EN1	NA
544	chr2	119915941	119916093	-4.87	-6.44	-4.18	-1.57	0.69	2.26	C1QL2	NA
545	chr2	189350424	189350526	-5.92	-6.10	-2.75	-0.18	3.18	3.36	MIR561	NA
546	chr2	228518336	228518444	-2.57	-3.01	0.45	-0.44	3.02	3.46	C2orf83	NA
547	chr20	7566001	7566141	-1.52	-0.74	1.93	0.78	3.45	2.67	MIR8062	NA
548	chr20	7704110	7704259	0.21	-0.15	3.31	-0.36	3.10	3.46	HAO1	NA
549	chr20	10573650	10573760	-5.76	-6.40	-6.12	-0.63	-0.35	0.28	MIR6870	NA
550	chr20	22776605	22776749	0.06	-1.41	2.33	-1.47	2.27	3.74	LINC01384	NA
551	chr20	52390501	52390633	-1.24	-0.51	2.33	0.73	3.57	2.84	SUMO1P1	NA
552	chr21	24228072	24228210	-2.57	-3.69	-2.80	-1.12	-0.23	0.89	D21S2088E	NA
553	chr21	31499035	31499213	-3.75	-2.73	-2.92	1.02	0.83	-0.19	CLDN17	NA
554	chr22	48486271	48486446	-1.51	-3.16	-2.51	-1.65	-1.00	0.64	MIR3201	NA
555	chr3	30821371	30821529	-3.33	-0.61	-2.16	2.71	1.17	-1.55	GADL1	NA
556	chr3	35377292	35377637	-2.07	-3.06	-3.72	-0.99	-1.64	-0.66	LOC101928135	NA
557	chr3	67886546	67886716	-0.60	-1.37	1.93	-0.77	2.53	3.30	FAM19A1	NA
558	chr3	171594701	171594989	-1.82	-2.38	-3.24	-0.56	-1.42	-0.85	TMEM212-AS1	NA
559	chr3	182002735	182002895	-6.13	-6.26	-5.36	-0.13	0.78	0.90	FLJ46066	NA
560	chr3	187337695	187338149	-2.29	-2.22	-3.72	0.07	-1.43	-1.50	SST	NA
561	chr3	191217652	191217809	-4.52	-6.05	-5.54	-1.53	-1.02	0.50	PYDC2	NA
562	chr4	28650582	28650967	1.25	-1.61	-2.41	-2.87	-3.66	-0.80	MIR4275	NA
563	chr4	38874431	38874568	-1.59	-0.34	1.44	1.25	3.03	1.78	MIR574	NA
564	chr4	54643498	54643639	-4.71	-6.21	-5.71	-1.50	-1.00	0.50	LOC100506444	NA
565	chr4	60478127	60478292	-2.80	-3.41	-2.80	-0.61	0.00	0.61	MIR548AG1	NA
566	chr4	84776349	84776539	-4.11	-3.66	-2.92	0.45	1.19	0.74	GPAT3	NA
567	chr4	96937942	96938040	-5.76	-6.61	-5.14	-0.84	0.63	1.47	PDHA2	NA
568	chr4	133196958	133197075	-0.53	-0.60	2.64	-0.07	3.18	3.24	LINC01256	NA
569	chr4	176046674	176046978	-2.65	-2.67	-3.24	-0.02	-0.59	-0.57	ADAM29	NA
570	chr4	179478080	179478210	-4.87	-6.21	-4.57	-1.34	0.30	1.63	LINC01099	NA
571	chr5	5105740	5105939	2.52	-1.05	1.76	-3.58	-0.77	2.81	CTD-2297D10.2	NA
572	chr5	32050071	32050250	0.37	-0.96	2.64	-1.34	2.27	3.61	MIR4279	NA
573	chr5	35029521	35029639	1.18	0.12	6.05	-1.06	4.87	5.93	AGXT2	NA
574	chr5	57555746	57555869	-1.32	-3.06	-0.98	-1.74	0.34	2.08	LOC101928569	NA

575	chr5	71195989	71196161	-1.82	-3.45	-2.16	-1.63	-0.34	1.29	CARTPT	NA
576	chr5	71203173	71203449	0.38	3.81	0.72	3.43	0.34	-3.09	CARTPT	NA
577	chr5	116283763	116283922	-5.39	-6.31	-5.86	-0.92	-0.47	0.45	LOC102467223	NA
578	chr5	123737853	123737975	-5.39	-6.21	-4.57	-0.82	0.81	1.63	LINC01170	NA
579	chr5	140105639	140105904	-4.13	-3.48	-1.94	0.65	2.19	1.54	VTRNA1-3	NA
580	chr5	143009631	143010030	2.61	0.87	-0.85	-1.74	-3.46	-1.72	MIR5197	NA
581	chr6	25505062	25505186	-5.15	-6.16	-5.54	-1.01	-0.39	0.61	SCGN	NA
582	chr6	50758239	50758589	2.21	1.10	3.18	-1.11	0.97	2.08	TFAP2B	NA
583	chr6	50958863	50959019	-2.65	-3.52	-2.51	-0.87	0.14	1.01	TFAP2B	NA
584	chr6	52742091	52742281	-6.91	-6.05	-5.54	0.86	1.37	0.50	GSTA5	NA
585	chr6	76159510	76159730	0.19	-0.89	3.12	-1.07	2.93	4.01	MIR4463	NA
586	chr6	87786715	87787166	-1.95	-1.69	-3.72	0.26	-1.77	-2.03	CGA	NA
587	chr6	89440480	89440639	-6.42	-5.93	-4.88	0.49	1.54	1.05	LOC101928936	NA
588	chr6	120150400	120150807	-5.15	-5.73	-7.11	-0.58	-1.96	-1.38	MIR3144	NA
589	chr6	149195960	149196137	-0.86	0.55	2.42	1.41	3.28	1.87	UST-AS1	NA
590	chr7	25891899	25892082	1.66	2.67	3.61	1.01	1.95	0.94	MIR148A	NA
591	chr7	52568615	52568840	-6.52	-7.04	-6.61	-0.51	-0.09	0.42	POM121L12	NA
592	chr7	81696944	81697313	-5.02	-5.12	-6.85	-0.11	-1.83	-1.72	LOC101927356	NA
593	chr7	96516862	96517018	-2.39	-3.84	-3.03	-1.45	-0.64	0.80	DLX6	NA
594	chr7	103273575	103273689	-2.29	-3.06	-1.38	-0.77	0.92	1.68	SLC26A5	NA
595	chr7	107135017	107135122	-2.14	-2.04	4.12	0.10	6.25	6.16	GPR22	NA
596	chr7	110162904	110163090	-2.39	-3.33	-1.94	-0.94	0.45	1.39	EIF3IP1	NA
597	chr7	116783899	116784210	2.78	-0.34	-0.21	-3.13	-3.00	0.13	ST7-AS2	NA
598	chr7	129493594	129493717	-1.11	-3.06	-1.38	-1.95	-0.26	1.68	MIR183	NA
599	chr7	137633030	137633279	-1.29	-0.85	2.33	0.44	3.62	3.18	LOC100130880	NA
600	chr8	8887121	8887465	-2.48	-3.20	-3.33	-0.72	-0.85	-0.13	MIR4660	NA
601	chr8	32169416	32169521	-0.20	-0.09	2.90	0.11	3.10	2.99	NRG1-IT3	NA
602	chr8	34851783	34851953	-2.55	-3.11	-1.74	-0.56	0.81	1.36	LINC01288	NA
603	chr8	124229389	124229547	-3.82	-3.41	-3.14	0.41	0.68	0.27	MIR4663	NA
604	chr8	132012798	132012969	-1.03	0.78	2.64	1.81	3.68	1.87	ADCY8	NA
605	chr8	143958946	143959101	-1.28	0.16	2.64	1.44	3.92	2.48	CYP11B1	NA
606	chr9	20220449	20220654	-2.75	-1.11	0.48	1.64	3.24	1.59	MIR4473	NA
607	chr9	30518021	30518321	-5.49	-6.26	-6.70	-0.77	-1.21	-0.44	LINC01242	NA
608	chr9	71201205	71201500	2.02	2.68	3.66	0.66	1.64	0.98	LINC01506	NA

609	chr9	98751705	98751822	-2.19	-3.01	-2.35	-0.82	-0.16	0.67	LINC00092	NA
610	chr9	118354015	118354118	-5.49	-6.61	-5.14	-1.12	0.35	1.47	LOC101928775	NA
611	chr9	123106622	123106763	0.74	-0.41	6.51	-1.15	5.76	6.92	MIR147A	NA
612	chrX	13242435	13242587	-0.69	-1.08	2.33	-0.39	3.02	3.41	GS1-600G8.3	NA
613	chrX	22968529	22968634	-5.49	-6.26	-4.57	-0.77	0.92	1.68	DDX53	NA
614	chrX	83990212	83990355	-2.29	-2.79	0.45	-0.50	2.74	3.24	UBE2DNL	NA
615	chrX	115361612	115361895	0.91	-0.83	-2.10	-1.74	-3.01	-1.27	AGTR2	NA
616	chrY	6876857	6877012	-6.52	-5.01	-4.18	1.51	2.35	0.83	TBL1Y	NA

Table S3: Top 5 differentially expressed genes between Poly I:C, and Calcitrol +Poly I:C vs Sham

Treatment comparison	Top 5 differentially expressed genes	Log fold change (ATAC-Seq)
PolyIC vs. Sham	LNPEP	-0.80
	ACVR2B	NA
	TBX3	3.56
	DUSP4	-1.99
	AZIN1	-1.10
CalPolyIC vs. Sham	LNPEP	-0.46
	BBX	NA
	DUSP4	-0.44
	MIF	NA
	TBX3	3.32

Supplementary Table S4: Top enriched pathways for genes annotated to the differential peaks in AHBEC.

Pathway	Genes within the pathway	Num_gene	Odds_ratio	Pval	FDR
hsa05200 Pathways in cancer	DVL2,IGF2,BAD,JAG2,CKS2,E2F1,BDKRB1,PTGS2,STAT2,ARAF,COL4A3,GSTT1,DAPK2,FZD4,NGT1,IKBKG,IFNA1,CXCR4,APPL1,SLC2A1,RBX1,RPS6KB1,IFNGR2,TERC,PRKCB,CDKN1A,MYC,CTNNA2,RASSF1,BIRC3,BIRC5	31	6.23	1.38E-14	1.39E-12
hsa05160 Hepatitis C	BAD,PPP2R1A,E2F1,PPP2R1B,STAT2,ARAF,CLDN16,YWHAZ,CXCL10,IKBKG,IFNA1,PPP2CB,CDKN1A,MYC	14	9.40	1.48E-09	7.50E-08
hsa05161 Hepatitis B	BAD,E2F1,STAT2,ATF6B,ARAF,YWHAZ,NFATC1,IKBKG,IFNA1,MAPK14,PRKCB,CDKN1A,MYC,BIRC5	14	8.94	2.71E-09	9.13E-08
hsa04350 TGF-beta signaling pathway	PPP2R1A,PPP2R1B,ID3,NOG,CHRD,PPP2CB,RBX1,PITX2,RPS6KB1,ACVR1,MYC	11	12.39	5.93E-09	1.50E-07
hsa05202 Transcriptional misregulation in cancer	IL1R2,H3F3B,ERG,NUPR1,BCL2A1,SPINT1,MYCN,CDK14,MLF1,CDKN1A,MYC,ATM,NGFR,BIRC3	14	7.83	1.30E-08	2.55E-07
hsa04060 Cytokine-cytokine receptor interaction	IL1R2,LTBR,TNFRSF10C,CCR1,CX3CR1,CXCL10,IFNA1,CCL3L1,IFNW1,CXCR4,IFNGR2,ACVR1,CCL25,TNFRSF12A,IL18RAP,NGFR,NGF	17	6.04	1.52E-08	2.55E-07
hsa04151 PI3K-Akt signaling pathway	IGF2,BAD,PPP2R1A,PPP2R1B,ATF6B,COL4A3,YWHAZ,NGT1,IKBKG,IFNA1,PPP2CB,ANGPT2,RPS6KB1,CDKN1A,EPHA2,MYC,NGFR,NGF	18	5.31	3.72E-08	5.36E-07
hsa01100 Metabolic pathways	SCP2,PIGL,GYG1,PKLR,ALDH5A1,PTGES,PTGS2,CYP4F2,GPX7,B4GALT4,SPTLC2,GSTT1,SDHA,COX6B1,GCNT4,PTGIS,PDHB,RENB, B3GALT4,PYCR2,MAT2A,TKT,ALDH3A2,DGKI,AKR1D1,AK1,DTYMK,COX17,ALOX15,ALPPL2,MTMR6,SD17B1,GAPDH,PIK3C2G,TGDS,UGT2B4,PTGES3,GPLD1	38	2.82	7.18E-08	9.06E-07
hsa05167 Kaposi's sarcoma-associated herpesvirus infection	HLA-F,CCR1,E2F1,PTGS2,STAT2,NGT1,NFATC1,IKBKG,IFNA1,MAPK14,ANGPT2,CDKN1A,MYC	13	7.26	9.65E-08	1.08E-06
hsa04066 HIF-1 signaling pathway	LTBR,PDHB,ANGPT2,SLC2A1,RBX1,RPS6KB1,IFNGR2,PRKCB,CDKN1A,GAPDH	10	10.35	1.37E-07	1.38E-06
hsa04062 Chemokine signaling pathway	CCR1,BAD,STAT2,CX3CR1,CXCL10,NGT1,IKBKG,CCL3L1,CXCR4,PRKCB,FGR,CCL25	12	6.55	8.25E-07	7.57E-06
hsa04014 Ras signaling pathway	IGF2,BAD,RAB5A,NGT1,IKBKG,ANGPT2,RASA3,PRKCB,EPHA2,RASSF1,NGFR,NGF,RIN1	13	5.82	1.04E-06	8.73E-06
hsa04064 NF-kappa B signaling pathway	LTBR,PTGS2,BCL2A1,LCK,IKBKG,PRKCB,CSNK2B,ATM,BIRC3	9	9.30	1.31E-06	1.02E-05
hsa04080 Neuroactive ligand-receptor interaction	GRM6,CALCB,FPR1,HTR2B,BDKRB1,GRIK3,GABRB2,GAL,P2RX3,NTSR2,TACR2,NPBWR1,NPY5R,GRIK1,ADM	15	4.61	2.52E-06	1.72E-05
hsa04010 MAPK signaling pathway	IGF2,ARAF,NFATC1,IKBKG,MAPK14,ANGPT2,CACNB2,PRKCB,CACNA2D2,EPHA2,MYC,NGFR,NGF,RPS6KA4	14	4.93	2.59E-06	1.72E-05
hsa04668 TNF signaling pathway	PTGS2,ATF6B,DNM1L,CXCL10,IKBKG,MAPK14,IRF1,BIRC3,RPS6KA4	9	8.45	2.73E-06	1.72E-05
hsa05166 HTLV-I infection	IL1R2,LTBR,HLA-F,E2F1,ATF6B,LCK,NFATC1,IKBKG,SLC2A1,CD	12	5.68	3.34E-06	1.98E-05

	KN1A,MYC,ATM				
hsa04012 ErbB signaling pathway	NRG2,BAD,ARAF,RPS6KB1,PRKCB,CDKN1A,MYC,NCK1	8	9.71	3.75E-06	2.10E-05
hsa04390 Hippo signaling pathway	DVL2,PPP2R1A,PPP2R1B,YWHAZ,FZD4,PPP2CB,MYC,CTNNA2,RASSF1,BIRC5	10	6.71	5.36E-06	2.82E-05
hsa00590 Arachidonic acid metabolism	PTGES,PTGS2,CYP4F2,GPX7,PTGIS,ALOX15,PTGES3	7	11.44	5.58E-06	2.82E-05
hsa05219 Bladder cancer	E2F1,ARAF,DAPK2,CDKN1A,MYC,RASSF1	6	15.05	6.29E-06	3.02E-05
hsa05222 Small cell lung cancer	CKS2,E2F1,PTGS2,COL4A3,IKBKG,CDKN1A,MYC,BIRC3	8	8.87	6.95E-06	3.19E-05
hsa05203 Viral carcinogenesis	LTBR,HLA-F,BAD,ACTN4,ATF6B,YWHAZ,IKBKG,HIST1H2BG,CDKN1A,GTF2A2,HIST1H2BC	11	5.66	8.60E-06	3.62E-05
hsa05205 Proteoglycans in cancer	IGF2,ARAF,FZD4,SDC2,MAPK14,ANK3,RPS6KB1,PRKCB,ANK1,CDKN1A,MYC	11	5.66	8.60E-06	3.62E-05
hsa05215 Prostate cancer	IL1R2,BAD,E2F1,ERG,ARAF,SPINT1,IKBKG,CDKN1A	8	8.50	9.26E-06	3.74E-05
hsa04726 Serotonergic synapse	HTR2B,PTGS2,ARAF,GABRB2,GNGT1,PRKCB,ALOX15,HTR3B	8	7.17	2.94E-05	1.14E-04
hsa05210 Colorectal cancer	BAD,ARAF,APPL1,RPS6KB1,CDKN1A,MYC,BIRC5	7	8.38	3.64E-05	1.36E-04
hsa04310 Wnt signaling pathway	DVL2,PRICKLE3,FZD4,NFATC1,RUVBL1,RBX1,PRKCB,CSNK2B,MYC	9	5.88	4.18E-05	1.51E-04
hsa04110 Cell cycle	E2F1,STAG2,YWHAZ,CDKN1C,RBX1,CDKN1A,MYC,ATM	8	6.65	4.87E-05	1.70E-04
hsa04380 Osteoclast differentiation	NCF4,STAT2,LILRB5,LCK,NFATC1,IKBKG,MAPK14,IFNGR2	8	6.44	6.02E-05	2.03E-04
hsa05146 Amoebiasis	IL1R2,C8B,ACTN4,SERPINB4,COL4A3,RAB5A,PRKCB	7	7.51	7.00E-05	2.21E-04
hsa04728 Dopaminergic synapse	PPP2R1A,PPP2R1B,ATF6B,GNGT1,MAPK14,PPP2CB,PRKCB,SLC6A3	8	6.29	7.02E-05	2.21E-04
hsa05221 Acute myeloid leukemia	BAD,ARAF,BCL2A1,IKBKG,RPS6KB1,MYC	6	9.35	7.45E-05	2.21E-04
hsa05223 Non-small cell lung cancer	BAD,E2F1,ARAF,PRKCB,CDKN1A,RASSF1	6	9.35	7.45E-05	2.21E-04
hsa01522 Endocrine resistance	BAD,JAG2,E2F1,ARAF,MAPK14,RPS6KB1,CDKN1A	7	7.35	7.91E-05	2.28E-04
hsa05142 Chagas disease (American trypanosomiasis)	PPP2R1A,PPP2R1B,IKBKG,CCL3L1,MAPK14,PPP2CB,IFNGR2	7	6.99	1.06E-04	2.98E-04
hsa01524 Platinum drug resistance	BAD,GSTT1,CDKN1A,ATM,BIRC3,BIRC5	6	8.45	1.25E-04	3.42E-04
hsa05212 Pancreatic cancer	BAD,E2F1,ARAF,IKBKG,RPS6KB1,CDKN1A	6	8.22	1.44E-04	3.82E-04
hsa05224 Breast cancer	DVL2,JAG2,E2F1,ARAF,FZD4,RPS6KB1,CDKN1A,MYC	8	5.61	1.50E-04	3.88E-04
hsa05220 Chronic myeloid leukemia	BAD,E2F1,ARAF,IKBKG,CDKN1A,MYC	6	8.12	1.54E-04	3.89E-04
hsa04670 Leukocyte transendothelial migration	NCF4,ACTN4,CLDN16,MAPK14,CXCR4,PRKCB,CTNNA2	7	6.43	1.73E-04	4.27E-04
hsa05169 Epstein-Barr virus infection	HLA-F,E2F1,STAT2,CXCL10,IKBKG,IFNA1,MAPK14,CDKN1A,MYC	9	4.62	2.39E-04	5.74E-04
hsa04218 Cellular senescence	HLA-F,RAD9A,E2F1,NFATC1,MAPK14,CDKN1A,MYC,ATM	8	5.15	2.59E-04	6.09E-04
hsa04015 Rap1 signaling pathway	RGS14,FPR1,MAPK14,ANGPT2,PFN2,PRKCB,EPHA2,NGFR,NGF	9	4.51	2.84E-04	6.48E-04
hsa04911 Insulin secretion	KCNMB2,ATF6B,KCNN3,VAMP2,SLC2A1,PRKC	6	7.17	2.89E-04	6.48E-04

	B				
hsa05213 Endometrial cancer	BAD,ARAF,CDKN1A,MYC,CTNNA2	5	8.85	3.77E-04	8.27E-04
hsa04658 Th1 and Th2 cell differentiation	JAG2,LCK,NFATC1,IKBKG,MAPK14,IFNGR2	6	6.70	4.06E-04	8.73E-04
hsa04730 Long-term depression	PPP2R1A,PPP2R1B,ARAF,PPP2CB,PRKCB	5	8.55	4.35E-04	9.16E-04
hsa05322 Systemic lupus erythematosus	C8B,H3F3B,ACTN4,TROVE2,HIST1H2BG,SNRPD3,HIST1H2BC	7	5.42	4.67E-04	9.62E-04
hsa03040 Spliceosome	DHX8,PRPF18,RBMXL2,SRSF10,SNRNP70,U2AF2,SNRPD3	7	5.38	4.87E-04	9.83E-04
hsa04210 Apoptosis	BAD,BCL2A1,IKBKG,ATM,NGF,BIRC3,BIRC5	7	5.30	5.30E-04	1.05E-03
hsa04360 Axon guidance	TRPC3,SLIT3,CFL2,CXCR4,SEMA4D,EPHA5,EPHA2,NCK1	8	4.55	5.68E-04	1.10E-03
hsa04550 Signaling pathways regulating pluripotency of stem cells	DVL2,ONECUT1,ID3,FZD4,MAPK14,ACVR1,MYC	7	5.18	5.99E-04	1.14E-03
hsa04020 Calcium signaling pathway	HTR2B,BDKRB1,CXCR4,P2RX3,TNNC2,RYR3,PRKCB,TACR2	8	4.38	7.21E-04	1.35E-03
hsa04261 Adrenergic signaling in cardiomyocytes	PPP2R1A,PPP2R1B,ATF6B,MAPK14,PPP2CB,CACNB2,CACNA2D2	7	4.97	7.60E-04	1.40E-03
hsa05211 Renal cell carcinoma	BAD,ARAF,SLC2A1,RBX1,CDKN1A	5	7.44	7.91E-04	1.43E-03
hsa04622 RIG-I-like receptor signaling pathway	CXCL10,IKBKG,IFNA1,IFNW1,MAPK14	5	7.33	8.41E-04	1.49E-03
hsa04144 Endocytosis	ARF3,RAB10,EEA1,HLA-F,RAB5A,CYTH4,VPS45,CXCR4,PSD	9	3.80	9.13E-04	1.59E-03
hsa03010 Ribosome	RPL3,RPL15,RPL39,RPS15A,RPL35A,RPL32,RPS29	7	4.71	1.03E-03	1.73E-03
hsa04921 Oxytocin signaling pathway	PTGS2,NFATC1,CACNB2,RYR3,PRKCB,CACNA2D2,CDKN1A	7	4.71	1.03E-03	1.73E-03
hsa04918 Thyroid hormone synthesis	ATF6B,GPX7,ALB,TTR,PRKCB	5	6.93	1.06E-03	1.73E-03
hsa05140 Leishmaniasis	NCF4,PTGS2,MAPK14,IFNGR2,PRKCB	5	6.93	1.06E-03	1.73E-03
hsa01230 Biosynthesis of amino acids	PKLR,PYCR2,MAT2A,TKT,GAPDH	5	6.84	1.13E-03	1.80E-03
hsa01521 EGFR tyrosine kinase inhibitor resistance	NRG2,BAD,ARAF,RPS6KB1,PRKCB	5	6.49	1.40E-03	2.21E-03
hsa04071 Sphingolipid signaling pathway	PPP2R1A,PPP2R1B,SPTLC2,MAPK14,PPP2CB,PRKCB	6	5.18	1.45E-03	2.26E-03
hsa04810 Regulation of actin cytoskeleton	ACTN4,BDKRB1,ARAF,FGD1,CFL2,CXCR4,PFN2,CYFIP2	8	3.85	1.60E-03	2.45E-03
hsa04146 Peroxisome	SCP2,CRAT,PEX11B,MPV17,PEX7	5	6.18	1.72E-03	2.59E-03
hsa04650 Natural killer cell mediated cytotoxicity	ARAF,LCK,NFATC1,IFNA1,IFNGR2,PRKCB	6	4.70	2.31E-03	3.43E-03
hsa04621 NOD-like receptor signaling pathway	MEFV,STAT2,DNM1L,IKBKG,IFNA1,MAPK14,BIRC3	7	4.04	2.35E-03	3.44E-03
hsa05034 Alcoholism	H3F3B,ATF6B,ARAF,GNGT1,HIST1H2BG,HIST1H2BC,SLC6A3	7	4.00	2.50E-03	3.60E-03
hsa05418 Fluid shear stress and atherosclerosis	IL1R2,GSTT1,SDC2,IKBKG,MAPK14,ACVR1	6	4.43	3.06E-03	4.36E-03
hsa05012 Parkinson's disease	UBA1,SDHA,COX6B1,NDUFB6,UCHL1,SLC6A3	6	4.34	3.39E-03	4.75E-03
hsa04750 Inflammatory mediator regulation of TRP channels	HTR2B,BDKRB1,MAPK14,PRKCB,NGF	5	5.13	3.71E-03	5.13E-03
hsa04660 T cell receptor signaling pathway	LCK,NFATC1,IKBKG,MAPK14,NCK1	5	5.08	3.86E-03	5.27E-03
hsa04723 Retrograde endocannabinoid signaling	PTGS2,GABRB2,GNGT1,NDUFB6,MAPK14,PRKCB	6	4.16	4.11E-03	5.54E-03
hsa04620 Toll-like receptor signaling pathway	CXCL10,IKBKG,IFNA1,CCL3L1,MAPK14	5	4.93	4.35E-03	5.78E-03

hsa04659 Th17 cell differentiation	LCK,NFATC1,IKBKG,MAPK14,IFNGR2	5	4.79	4.88E-03	6.40E-03
hsa05145 Toxoplasmosis	BAD,IKBKG,MAPK14,IFNGR2,BIRC3	5	4.54	6.07E-03	7.84E-03
hsa04217 Necroptosis	STAT2,DNM1L,IFNA1,IFNGR2,ALOX15,BIRC3	6	3.80	6.25E-03	7.84E-03
hsa04630 Jak-STAT signaling pathway	STAT2,IFNA1,IFNW1,IFNGR2,CDKN1A,MYC	6	3.80	6.25E-03	7.84E-03
hsa04724 Glutamatergic synapse	GRM6,GRIK3,GNGT1,PRKCB,GRIK1	5	4.50	6.29E-03	7.84E-03
hsa01200 Carbon metabolism	PKLR,SDHA,PDHB,TKT,GAPDH	5	4.42	6.74E-03	8.26E-03
hsa03013 RNA transport	RPP30,NUP153,NUP50,SRRM1,PRMT5,CYFIP2	6	3.73	6.79E-03	8.26E-03
hsa05164 Influenza A	STAT2,CXCL10,IKBKG,IFNA1,IFNGR2,PRKCB	6	3.69	7.17E-03	8.63E-03
hsa04152 AMPK signaling pathway	RAB10,PPP2R1A,PPP2R1B,PPP2CB,RPS6KB1	5	4.27	7.70E-03	9.15E-03
hsa05010 Alzheimer's disease	BAD,SDHA,COX6B1,NDUFB6,RYR3,GAPDH	6	3.60	7.98E-03	9.38E-03
hsa04114 Oocyte meiosis	PPP2R1A,PPP2R1B,YWHAZ,PPP2CB,RBX1	5	4.10	9.04E-03	1.05E-02
hsa05152 Tuberculosis	EEA1,BAD,RAB5A,IFNA1,MAPK14,IFNGR2	6	3.44	9.80E-03	1.12E-02
hsa04140 Autophagy – animal	BAD,DAPK2,RUBCN,PPP2CB,RPS6KB1	5	4.01	9.91E-03	1.13E-02
hsa05206 MicroRNAs in cancer	E2F1,PTGS2,FSCN1,PRKCB,CDKN1A,MYC,ATM ,RASSF1	8	2.75	1.09E-02	1.23E-02
hsa04068 FoxO signaling pathway	RAG2,ARAF,MAPK14,CDKN1A,ATM	5	3.88	1.12E-02	1.23E-02
hsa04270 Vascular smooth muscle contraction	CALCB,KCNMB2,ARAF,PRKCB,ADM	5	3.88	1.12E-02	1.23E-02
hsa04371 Apelin signaling pathway	UCP1,GNGT1,BORCS8-MEF2B,RPS6KB1,RYR3	5	3.74	1.29E-02	1.40E-02
hsa05162 Measles	BAD,STAT2,IKBKG,IFNA1,CSNK2B	5	3.71	1.32E-02	1.42E-02
hsa05016 Huntington's disease	POLR2H,POLR2G,SDHA,COX6B1,UCP1,NDUFB 6	6	3.19	1.37E-02	1.45E-02
hsa04514 Cell adhesion molecules (CAMs)	HLA-F,CLDN16,SDC2,CD274,SELPLG	5	3.51	1.64E-02	1.73E-02
hsa04145 Phagosome	NCF4,EEA1,HLA-F,RAB5A,MSR1	5	3.37	1.91E-02	1.99E-02
hsa04022 cGMP-PKG signaling pathway	BAD,KCNMB2,ATF6B,NFATC1,BORCS8-MEF2B	5	3.09	2.64E-02	2.70E-02
hsa05168 Herpes simplex infection	HLA-F,ZNF26,BAD,ZNF133,STAT2,PILRA,IKBKG,IFN A1,IFNGR2,BIRC3	10	2.09	2.64E-02	2.70E-02
hsa04530 Tight junction	ACTN4,PPP2R1A,PPP2R1B,CLDN16,PPP2CB	5	3.01	2.87E-02	2.90E-02
hsa04510 Focal adhesion	BAD,ACTN4,COL4A3,PRKCB,BIRC3	5	2.57	4.99E-02	4.99E-02

Table S5: Top differentially expressed genes between Poly I:C, and Calcitrol +Poly I:C vs Sham
 ith corresponding peaks which share same gene annotations with those identified genes

Treatments comparison	Gene	Log fold-change (ATAC-Seq)	Log fold-change (RNA-Seq)	P-value (RNA-Seq)	Adjusted P-value (RNA-Seq)
PolyIC vs. Sham	TBX3	3.56	-0.75	3.55E-07	1.95E-03
	FOXP1	-2.22	-0.74	9.07E-06	8.78E-03
	SLC8A1	2.72	-0.45	1.98E-04	4.64E-02
	ATP1B1	0.63	-0.70	2.55E-04	4.84E-02
CalPolyIC vs. Sham	TBX3	3.32	-0.71	5.24E-07	1.72E-03
	FOXP1	1.31	-0.79	1.98E-06	3.27E-03
	ATP1B1	1.95	-0.76	8.10E-05	1.50E-02
	PGGT1B	1.75	-0.68	1.40E-04	1.67E-02
	PTPRD	0.71	-0.50	2.89E-04	2.59E-02
	MSI2	2.74	-0.64	3.07E-04	2.67E-02
	SEC24C	2.27	-0.34	3.48E-04	2.80E-02
	ZNF217	2.56	-0.99	4.39E-04	3.07E-02
	RAD23B	0.01	-1.21	4.77E-04	3.19E-02
	ZCCHC2	3.02	-1.04	6.29E-04	3.65E-02
	SLC8A1	3.12	-0.41	6.87E-04	3.82E-02