



HAL
open science

Epimutations in both the TESK2 and MMACHC promoters in the Epi-cblC inherited disorder of intracellular metabolism of vitamin B12

Abderrahim Oussalah, Youssef Siblini, Sébastien Hergalant, Céline Chéry, Pierre Rouyer, Catia Cavicchi, Renzo Guerrini, Pierre-Emmanuel Morange, David Trégouët, Mihaela Pupavac, et al.

► To cite this version:

Abderrahim Oussalah, Youssef Siblini, Sébastien Hergalant, Céline Chéry, Pierre Rouyer, et al.. Epimutations in both the TESK2 and MMACHC promoters in the Epi-cblC inherited disorder of intracellular metabolism of vitamin B12. *Clinical Epigenetics*, 2022, 14 (1), pp.52. 10.1186/s13148-022-01271-1 . hal-03664165

HAL Id: hal-03664165

<https://hal.univ-lorraine.fr/hal-03664165>

Submitted on 23 Jan 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

RESEARCH

Open Access



Epimutations in both the *TESK2* and *MMACHC* promoters in the Epi-*cbIC* inherited disorder of intracellular metabolism of vitamin B₁₂

Abderrahim Oussalah^{1,2,3}, Youssef Siblini¹, Sébastien Hergalant¹, Céline Chéry^{1,2,3}, Pierre Rouyer¹, Catia Cavicchi⁴, Renzo Guerrini^{4,5}, Pierre-Emmanuel Morange⁶, David Trégouët⁷, Mihaela Pupavac⁸, David Watkins⁸, Tomi Pastinen⁸, Wendy K. Chung⁹, Can Ficiocioglu¹⁰, François Feillet^{1,2}, D. Sean Froese¹¹, Matthias R. Baumgartner¹¹, Jean-François Benoit¹², Jacek Majewski⁸, Amelia Morrone^{4,5}, David S. Rosenblatt⁸ and Jean-Louis Guéant^{1,2,3,13*} 

Abstract

Background: epi-*cbIC* is a recently discovered inherited disorder of intracellular vitamin B₁₂ metabolism associating hematological, neurological, and cardiometabolic outcomes. It is produced by an epimutation at the promoter common to *CCDC163P* and *MMACHC*, which results from an aberrant antisense transcription due to splicing mutations in the antisense *PRDX1* gene neighboring *MMACHC*. We studied whether the aberrant transcription produced a second epimutation by encompassing the CpG island of the *TESK2* gene neighboring *CCDC163P*.

Methods: We unraveled the methylome architecture of the *CCDC163P*–*MMACHC* CpG island (CpG:33) and the *TESK2* CpG island (CpG:51) of 17 epi-*cbIC* cases. We performed an integrative analysis of the DNA methylome profiling, transcriptome reconstruction of RNA-sequencing (RNA-seq), chromatin immunoprecipitation sequencing (ChIP-Seq) of histone H3, and transcription expression of *MMACHC* and *TESK2*.

Results: The *PRDX1* splice mutations and activation of numerous cryptic splice sites produced antisense readthrough transcripts encompassing the bidirectional *MMACHC/CCDC163P* promoter and the *TESK2* promoter, resulting in the silencing of both the *MMACHC* and *TESK2* genes through the deposition of SETD2-dependent H3K36me3 marks and the generation of epimutations in the CpG islands of the two promoters.

Conclusions: The antisense readthrough transcription of the mutated *PRDX1* produces an epigenetic silencing of *MMACHC* and *TESK2*. We propose using the term 'epi-digenism' to define this epigenetic disorder that affects two genes. Epi-*cbIC* is an entity that differs from *cbIC*. Indeed, the *PRDX1* and *TESK2* altered expressions are observed in epi-*cbIC* but not in *cbIC*, suggesting further evaluating the potential consequences on cancer risk and spermatogenesis.

Keywords: Epi-*cbIC*, Secondary epimutation, Promoter hypermethylation, *MMACHC*, *TESK2*, Methylmalonic aciduria and homocystinuria, *cbIC* type

Introduction

Epigenetic regulation of gene expression through DNA methylation is a source of genetic variation and can induce transcriptional haploinsufficiency [1]. Epigenetic

*Correspondence: jean-louis.gueant@univ-lorraine.fr

¹³ Department of Hepato-Gastroenterology, University Hospital of Nancy, 54000, Nancy, France

Full list of author information is available at the end of the article



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

diseases can be caused by aberrant DNA methylation marks, also called epimutations, which represent an underlying molecular mechanism of disease. In the setting of inherited metabolic disorders, we have previously reported a new type of inherited defect of vitamin B₁₂ (cobalamin, cbl) metabolism with an epimutation in the promoter of the *MMACHC* gene, which we called *epi-cblC* [2]. Patients with *epi-cblC* have the same clinical presentation as *cblC* type, an autosomal recessive inherited disorder of intracellular vitamin B₁₂ metabolism with combined methylmalonic aciduria and homocystinuria (OMIM phenotype ID: 277400) due to mutations in the *MMACHC* gene (metabolism of cobalamin-associated C; OMIM gene ID, 609831). In contrast, *epi-cblC* cases harbor an epimutation with an aberrant methylation of the CpG island (CpG:33) in the *MMACHC* promoter that silences the expression of the *MMACHC* gene. *MMACHC* belongs to a gene trio in which it is a sense gene flanked by *CCDC163P* and *PRDX1* in the opposite orientation (trio with antisense (reverse, R1)/sense (forward, F2)/antisense (reverse, R3)) [2]. We found mutations in *PRDX1* that produced an antisense transcript encompassing the *MMACHC/CCDC163P* bidirectional promoter, resulting in an H3K36me3 mark and the generation of the epimutation [2]. The splice acceptor variants induced readthrough transcripts extending beyond the normal poly(A) addition site, thus skipping the transcription termination signal of *PRDX1* [2]. Most *epi-cblC* patients had a combination of alleles, with an epimutation in one allele and an *MMACHC* pathogenic genetic variant carried in *trans* [2]. One patient had a bi-allelic *MMACHC* epimutation due to the homozygous *PRDX1:c.515-1G>T* variant transmitted by both parents. In this homozygous case, we found that the bi-allelic epimutation produces the complete silencing of *MMACHC* in the patient's fibroblasts [2]. No *PRDX1* variant was detected in one of two *epi-cblC* cases reported in China, suggesting that the epimutation could also be triggered by a non-genetic mechanism [2]. Importantly, we demonstrated the presence of the *MMACHC* secondary epimutation in DNA from sperm, showing that the epimutation escaped erasure in spermatozoa [2]. This observation may be explained by the ubiquitously high expression of *PRDX1* in germ cells [2].

The aberrant antisense transcript of *PRDX1* encompasses the *CCDC163P/MMACHC* bidirectional promoter. *TESK2* is an antisense gene neighboring *CCDC163P*, with the CpG island 'CpG:51' in its promoter region. However, whether the aberrant transcription encompasses the CpG island 'CpG:51' and produces a *TESK2* epimutation was not considered. To address this hypothesis, we gathered data from the 17 *epi-cblC* patients described from Europe and North

America. We unraveled the methylome architecture of the *CCDC163P/MMACHC* CpG island (CpG:33) and the *TESK2* CpG island (CpG:51) by studying the epigenome-wide DNA methylation profile of the 17 *epi-cblC* cases [2, 3]. We performed an integrative analysis of the DNA methylome profiling, RNA-sequencing (RNA-seq) with de novo transcriptome reconstruction, reverse transcription-quantitative polymerase chain reaction (RT-qPCR), and chromatin immunoprecipitation sequencing (ChIP-Seq). We revealed epimutations in both the *CCDC163P/MMACHC* CpG island (CpG:33) and the *TESK2* CpG island (CpG:51) that produced silencing in both genes.

Methods

Overview of the study design

First, we used an EWAS approach to look for epigenomic signatures associated with the *epi-cblC* phenotype. In a second step, we investigated whether the DNA methylation signatures revealed in the EWAS translate in terms of chromatin remodeling (ChIP-seq analysis), gene expression (RNA-seq and RT-qPCR analyses), and transcript structure (splicing analysis). We studied fibroblasts from skin biopsies since most reference centers use these cells for phenotyping inherited disorders of intracellular vitamin B₁₂ metabolism.

DNA methylome study design and patients description

We performed a case-control EWAS to look for significant epigenomic signatures associated with an *epi-cblC* phenotype. The *epi-cblC* phenotype was defined by one of the three following conditions: i) composite *MMACHC* epimutation/*MMACHC* mutation, ii) heterozygous *MMACHC* epimutation, iii) homozygous *MMACHC* epimutation. We studied 17 patients with proven *MMACHC* epimutation, as previously described [2, 3]. All patients exhibited aberrant methylation on the CpG island 'CpG:33' on the *CCDC163-MMACHC* bidirectional promoter (Chr1: 45,965,587–45,966,049, GRCh37). Of the 17 patients with *MMACHC* epimutation, three were assessed at the Reference Center for Inborn Errors of Metabolism, University Hospital of Nancy, France (CHU-12122, a female patient with composite *MMACHC* epimutation/*MMACHC* mutation (composite *epi-cblC* disease) who died at 1-month of life from cardiometabolic decompensation and two relatives with heterozygous *MMACHC* epimutation [CHU-14061, the father, and CHU-14067, the grandfather]) [2] and three were assessed at the Department of Human Genetics, Montreal, Canada (WG-3838, a female patient with a composite *epi-cblC* disease who died at the age of two months from a sudden cardiac arrest with an acute renal failure, her father [CDH-867] who had a heterozygous

MMACHC epimutation, and a 59-year-old male patient with a composite *epi-cblC* disease [WG-4152]) [2]. The remaining eleven patients were assessed at the Molecular and Cell Biology Laboratory of Neurometabolic Diseases and Paediatric Neurology Unit and Laboratories, Meyer Children's Hospital, Florence, Italy. Of the eleven patients, eight had a composite *epi-cblC* disease and three corresponded to a trio composed of a proband exhibiting a homozygous *MMACHC* epimutation and the two parents with heterozygous *MMACHC* epimutation [3]. In total, of the 17 patients analyzed in the study, eleven had a composite *MMACHC* epimutation/*MMACHC* mutation, five had a heterozygous *MMACHC* epimutation, and one had a homozygous *MMACHC* epimutation. For the control group, we used in silico data generated using the Infinium Human Methylation 450 k BeadChip array from the MARTHA cohort, which included 350 unrelated European-ancestry ambulatory subjects recruited in Marseille (France) between January 1994 and October 2005 [4]. All adult patients and proband's parents assessed at the Reference Center for Inborn Errors of Metabolism at the University Hospital of Nancy gave their informed written consent for performing the analyses, as previously reported [2]. The Columbia family provided informed consent, and the study was approved by the Columbia IRB [2]. Informed consent was obtained from all participants included in the Italian study, as previously reported (Ethics Committee of the Tuscany Region (No. CS_01/2021) [3].

DNA methylome analysis, quality controls, and statistical analyses

We carried out bisulfite conversion of 600 ng of DNA extracted from whole blood using the EZ DNA Methylation kit (Zymo Research, Proteogene, Saint-Marcel, France). The genome-wide profiling of DNA methylome was determined using the Infinium Human Methylation 450 k BeadChip array (Illumina, Paris, France) of the Infinium MethylationEPIC BeadChip array (Illumina, Paris, France), according to the manufacturer's instructions. The arrays were scanned on an Illumina iScan[®] system, and raw methylation data were extracted using Illumina's Genome Studio methylation module. For each CpG probe, the methylation level was described as a β value, ranging between 0 (fully unmethylated CpG probe) and 1 (fully methylated CpG probe). Background correction and normalization were implemented using the SWAN method (R Package Minfi) [5]. Probe annotation information, including sequence and chromosome location for Infinium Human Methylation 450 k and Infinium MethylationEPIC BeadChip arrays, was retrieved from the Manifest Files. We visually inspected the genome-wide distribution of the CpG probes according to their

β value. We performed principal component analysis (PCA) to assess the clustering of methylation profiles according to the whole methylation landscape of the analyzed samples. The top ten principal components (eigenvectors, EV) were calculated with their respective eigenvalue. PCA plots were used to report on the three top eigenvalues. We compared the mean β values of each CpG probe between the two subgroups using the *t* test with Bonferroni correction. Output data included the mean β values in each subgroup, the difference of β values, the nominal *P*-value, and the Bonferroni corrected *P*-value. We used the smoothed *P*-value transformation by converting nominal *P*-values obtained from the *t* test to smoothed *P*-values using a window radius of 3, as previously reported [2, 3, 6]. All statistical analyses were performed using the SNP & Variation Suite (v8.8.1; Golden Helix, Inc., Bozeman, MT, USA) and MedCalc, version 19.5.3 (MedCalc Software, Ostend, Belgium).

Whole-genome chromatin Immunoprecipitation sequencing

ChIP-Seq was performed on patient's fibroblasts and control fibroblast lines without inherited metabolic defects in the cobalamin pathway, as previously reported [2]. According to the manufacturer's instructions, the immunoprecipitation and reverse crosslinking were performed with the IP-Star SX-8G (Diagenode) using the Auto-Histone ChIP kit (Diagenode). ChIP-Seq libraries were prepared using the Kappa Library Preparation Kit Illumina Platforms (Kappa Biosystems) and Illumina TruSeq adapters (Illumina) according to the manufacturer's instructions. Samples were sequenced using the HiSeq 2000 with a selected read length of 50 bp. Duplicated reads were removed using PICARD. Peaks were called using Model-based Analysis of ChIP-Seq MACS2 with input DNA as control and using the broad peak mod [7]. In order to generate Wiggle (WIG) and Tiled Data Format (TDF) files, HOMER (4.7) [8] and Integrative Genomics Viewer (2.3.67) [9] were used. Tags were normalized to 10 million reads to generate tracks for visualization.

RNA sequencing

As previously described, RNA depleted of rRNA transcripts was extracted from fibroblasts obtained by skin biopsies of CHU-12122 and WG-3838 *epi-cblC* cases, 3 *cblC* cases with the *c.270_271insA* mutation, 3 *cblG* cases (another inherited defect of vitamin B₁₂ intracellular metabolism due to mutations in methionine synthase (*MTR*) gene) and 4 control fibroblasts using RiboMinus[™] (Thermo Scientific, Villebon, France) [2]. cDNA libraries were prepared using the TruSeq[™] RNA Sample Preparation Kit (Illumina, San Diego, CA, USA). RNA

sequencing was performed using the Illumina Hi-Scan sequencer. Reads were classified according to known 5' and 3' boundaries of annotated genes. RNA-sequencing FASTQ files for the two composite epi-*cbIC* samples compiled 150-nucleotide-long paired-end reads. The control group originated from a previous study [10]. All samples were regrouped and analyzed using the same bioinformatics pipeline, with quality control, adapter removal, read alignment, and manipulation, as previously described [11]. The alignment step was performed on the human reference genome GRCh38, with two splice-aware tools, HISAT v2.0.4 [12] and STAR v2.5.1b [13], that accounted for splicing junctions and genetic polymorphisms. From this point on, as we observed and hypothesized that the RNA splicing mechanisms were abnormal in the genomic region spanning from *TESK2* to *PRDX1*, we could not rely on reference-based transcriptome reconstruction methods, which would not efficiently report on the real isoform population and abundances in this region. We extracted the high-quality reads aligning inside the genomic interval chr1:45,443,800–45,543,000 (*TESK2* to *PRDX1*) and performed de novo transcriptome assembly with Trinity v2.6.5 [14]. The Trinity pipeline was launched with default parameters for paired-end and unstranded reads, with the '-jacard_clip' flag to account for high gene density, with possible overlapping at these genomic coordinates. Besides the two composite epi-*cbIC* samples, 4 controls were suitable for the analysis and were used as controls against the composite epi-*cbIC* cases. All samples presented with enough coverage in high-quality reads in the region of interest (>10,000) to achieve transcript reconstruction, providing enough read depth for unbiased estimation of their expression levels. Reconstructed transcripts were then aligned with blastn (with parameters '-evaluate 1e-10' and '-max_target_seqs 3') against a cDNA database obtained with BioMart (<https://www.ensembl.org/biomart/>) and comprising all known isoforms of the four genes *TESK2*, *CCDC163*, *MMACHC*, and *PRDX1*. Criteria for a successful transcript assignment to a known gene product of interest were as follows: i) biotype = protein-coding; ii) select the highest alignment length among candidates; iii) subject length = alignment length and is > 300 nt; iv) a number of mismatches allowed < 4; and v) a maximum number of gaps = 1. Finally, all transcripts were quantified using Kallisto v0.43 [15], which reported the normalized expression levels as estimated read counts and transcript-per-million (TPM) unit.

Quantification of *MMACHC*, *TESK2*, and *PRDX1* aberrant transcripts mRNA expression

Besides quantification from RNA-seq data, we also quantified the expression of *MMACHC* and *TESK2* transcripts

and *PRDX1* aberrant transcript using reverse transcription-quantitative polymerase chain reaction (RT-qPCR). Fibroblasts from an epi-*cbIC* case (CHU-12122) and control fibroblasts were cultured in DMEM medium supplemented with 10% v/v heat-inactivated fetal bovine serum, 1% v/v pyruvate, and 1% v/v penicillin–streptomycin. Cells were maintained at 37 °C and in 5% CO₂. All the reagents were obtained from Sigma-Aldrich. RNA was extracted using NucleoSpin RNA Plus (Macherey–Nagel, Hoerd, France). After the extraction, a DNase digestion step was carried out to remove DNA contamination using the DNA-free™ DNA Removal kit (Thermo Fisher Scientific France, Illkirch-Grattenstaden, France). RNA was reverse-transcribed using PrimeScript™ RT Master Mix (Takara Bio Europe, Saint-Germain-en-Laye, France); 2 μL of cDNA was used for qPCR with TB Green Premix Ex Taq (Tli RNase H Plus) (Takara Bio Europe, Saint-Germain-en-Laye, France) in a 20 μL reaction volume with the forward and the reverse primers specific for each of the studied genes (Additional file 3: Table S1) at a concentration of 0.2 μM. PCRs were carried out in 96-well plates using the CFX Connect Real-Time PCR Detection System (Bio-Rad, Marnes-la-Coquette, France) with the following temperature cycling: 95 °C for 30 s followed by 40 cycles consisting of 95 °C for 5 s followed by 60 °C for 30 s and finally a melt curve analysis from 65 °C to 95 °C to detect unspecific PCR products. All steps were done following the manufacturer's instructions. Statistical analyses for RT-q-PCR were done using the CFX Maestro software. The forward and reverse primers for reverse transcription-quantitative polymerase chain reaction (RT-qPCR) of *MMACHC*, *TESK2* transcripts, and *PRDX1* aberrant transcript are reported in Additional file 3: Table S1.

Results

Epigenome-wide association study for the epi-*cbIC* phenotype

All the DNA methylome profiles passed the quality checks and exhibited a valid β value density distribution (Additional file 1: Figure S1). In PCA on genome-wide DNA methylome profiles, we found a clustered distribution according to patients' gender (EV2) and the epi-*cbIC* phenotype (EV1) (Fig. 1). Additionally, we performed a PCA analysis that only considered CpG probes on chromosome 1. The PCA plot reporting PC1 vs. PC2 from chromosome 1-based PCA analysis was similar to that obtained from the genome-wide PCA analysis (PC1 vs. PC3) (Additional file 1: Figure S2). The EWAS revealed a significant locus in chromosome 1 in association with the epi-*cbIC* phenotype (Fig. 2A). The visualization of this top epigenomic signature confirmed the significant association at the CpG island 'CpG:33'

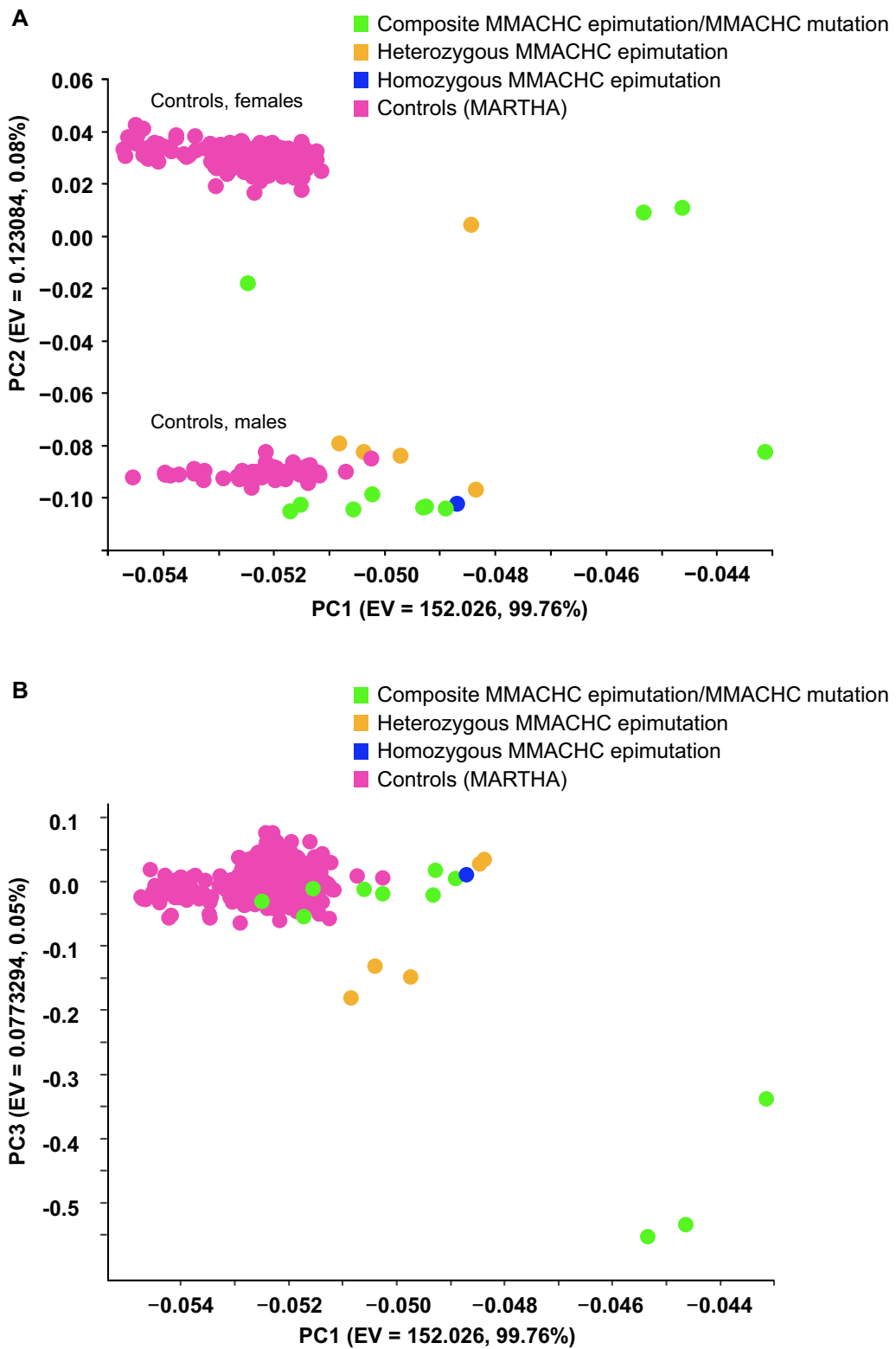
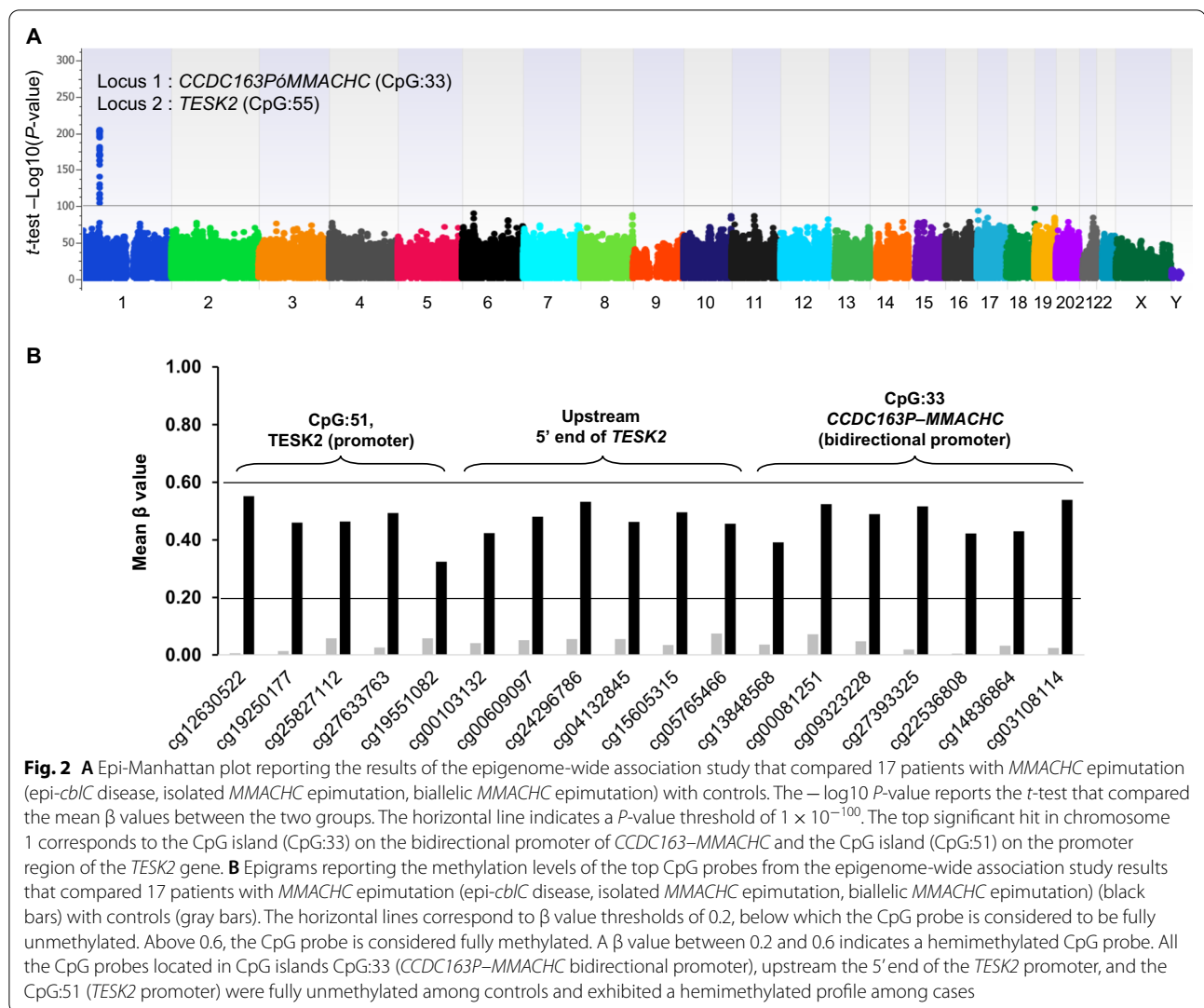


Fig. 1 **A** 2-D plot using the two top eigenvectors (PC1, PC2) derived from the primary component analysis on the genome-wide methylome landscape of the studied patients and controls. **B** 2-D plot using the PC1 and PC3 eigenvectors derived from the primary component analysis on the genome-wide methylome landscape of the studied patients and controls



on the *CCDC163–MMACHC* bidirectional promoter but also revealed a second significant association at the CpG island ‘CpG:51’ on the promoter region of the *TESK2* gene (Figs. 2B and 3). The mean-beta values of the CpG probes located in the CpG islands CpG:33 and CpG:51 had a fully unmethylated profile among controls and a hemimethylated profile among cases (Table 1 and Figs. 2B and 3).

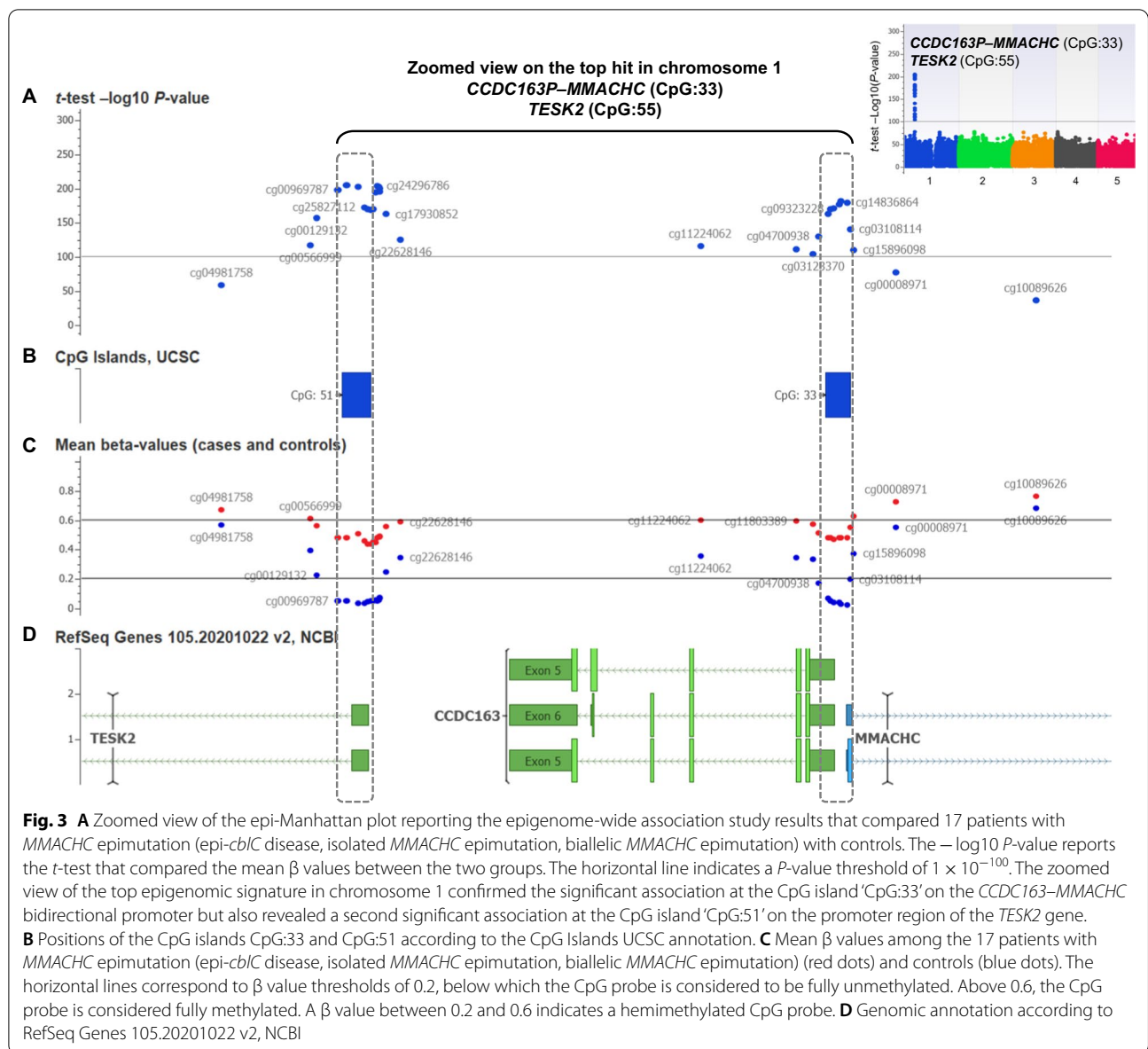
Genome-wide chromatin landscape profiling in fibroblasts of patients with epi-*cbIC*

We assessed ChIP-Seq data generated on case and control fibroblasts previously described in reference 2 to further characterize the epigenetic changes at the *MMACHC* and *TESK2* loci. We observed a significant accumulation of trimethylated lysine 36 on histone H3 (H3K36me3) and no mark of H3K4me3 in the *CCDC163–MMACHC* bidirectional promoter region (CpG:33) and in the *TESK2*

promoter region (CpG:51) among patients with an epi-*cbIC* phenotype in comparison with controls (Fig. 4). Overall, the region spanning from mid-*PRDX1* to *TESK2* harbored a continuous enrichment of H3K36me3 marks in epi-*cbIC* patients as compared to controls (Fig. 4).

The epimutations in *CCDC163–MMACHC* bidirectional promoter and *TESK2* promoter result from *PRDX1* antisense transcription

The RNA-seq analyses showed aberrant splicing and wrong splice junction usage in the genomic region encompassing *TESK2*, *CCDC163*, *MMACHC*, and *PRDX1* (Fig. 5). The RNA-seq analyses showed the absence of *MMACHC* sense transcripts in case WG-3838, a result which may be consistent with a splicing defect produced by the c.80A>G variant in *MMACHC*, which may then lead to total degradation of the mRNA (Fig. 5). In contrast, in case CHU-12122,



we detected transcripts with the *c.270_271insA* mutation (heterozygous *c.270_271insA*, p.Arg91LysfsTer14) (Fig. 5). The RNA-Seq and RT-qPCR analyses of case fibroblasts showed a *PRDX1* readthrough transcription through the *CCDC163–MMACHC* bidirectional promoter region (CpG:33) but also through the *TESK2* promoter region (CpG:51) (Figs. 5 and 6). In epi-*cbIC* fibroblasts, after de novo transcriptome reconstruction in the region spanning from *PRDX1* to *TESK2*, we observed a dramatic increase in the *PRDX1* aberrant transcripts as compared with control fibroblasts (Fig. 5). We further assessed the expression of *MMACHC*, *TESK2*, and *PRDX1* aberrant transcripts

in fibroblasts of patients with composite epi-*cbIC*. In comparison with controls, fibroblasts from the CHU-12122 patient with epi-*cbIC* showed a 22-fold increase of *PRDX1* aberrant transcript and a dramatic decrease of both *MMACHC* (12-fold decrease) and *TESK2* (fourfold decrease) mRNA, in RT-qPCR analyses normalized to *GAPDH* and *TBP* (Fig. 6B). The canonical transcriptions of *TESK2* and *MMACHC*, but not *PRDX1*, were also decreased in the RNA-seq analysis of CHU-12122 and WG-3838 fibroblasts (Fig. 6C). In contrast, the canonical transcription of *MMACHC* and *TESK2* was similar to that of *PRDX1* in RNA-seq and RT-qPCR analysis of control cells (Fig. 6C).

Table 1 Top significant CpG probe in the epigenome-wide association study on the epi-*cbIC* phenotype

CpG probe	Chr	Position*	CpG island	Locus	t-test, P-value	t-test, Bonf. P-value	β-value (Cases)	β-value (Controls)	Δβ-value
cg12630522	1	45956424	CpG:51	<i>TESK2</i> (promoter)	3.86E-223	1.74E-217	0.55	0.01	0.54
cg19250177	1	45956646	CpG:51	<i>TESK2</i> (promoter)	7.56E-204	3.42E-198	0.46	0.01	0.45
cg25827112	1	45956773	CpG:51	<i>TESK2</i> (promoter)	4.96E-192	2.25E-186	0.46	0.06	0.41
cg27633763	1	45956828	CpG:51	<i>TESK2</i> (promoter)	1.22E-94	5.53E-89	0.49	0.03	0.47
cg19551082	1	45956882	CpG:51	<i>TESK2</i> (promoter)	3.62E-148	1.64E-142	0.32	0.06	0.27
cg00103132	1	45956932	Upstream 5' end CpG:51	Upstream 5' end <i>TESK2</i>	4.42E-212	2.00E-206	0.42	0.04	0.38
cg00609097	1	45956974	Upstream 5' end CpG:51	Upstream 5' end <i>TESK2</i>	6.61E-195	2.99E-189	0.48	0.05	0.43
cg24296786	1	45957014	Upstream 5' end CpG:51	Upstream 5' end <i>TESK2</i>	2.75E-199	1.24E-193	0.53	0.05	0.48
cg04132845	1	45957038	Upstream 5' end CpG:51	Upstream 5' end <i>TESK2</i>	1.96E-218	8.85E-213	0.46	0.06	0.41
cg15605315	1	45957053	Upstream 5' end CpG:51	Upstream 5' end <i>TESK2</i>	3.07E-196	1.39E-190	0.50	0.03	0.46
cg05765466	1	45957060	Upstream 5' end CpG:51	Upstream 5' end <i>TESK2</i>	8.34E-203	3.77E-197	0.46	0.08	0.38
cg13848568	1	45965625	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	1.87E-138	8.44E-133	0.39	0.04	0.35
cg00081251	1	45965679	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	2.89E-182	1.31E-176	0.52	0.07	0.45
cg09323228	1	45965727	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	1.18E-171	5.33E-166	0.49	0.05	0.44
cg27393325	1	45965846	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	2.16E-195	9.79E-190	0.52	0.02	0.50
cg22536808	1	45965870	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	7.73E-167	3.50E-161	0.42	0.00	0.42
cg14836864	1	45965990	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	2.33E-167	1.05E-161	0.43	0.03	0.40
cg03108114	1	45966048	CpG:33	<i>CCDC163P</i> – <i>MMACHC</i> (bidirectional promoter)	1.51E-208	6.82E-203	0.54	0.02	0.51

Chr chromosome; Bonf. Bonferroni; Δβ-value difference between case and control β values

* Genomic positions are reported according to GRCh37

Discussion

We found that the two *PRDX1* mutations reported in 17 epi-*cbIC* cases produced antisense readthrough transcripts encompassing the *CCDC163P/MMACHC* bidirectional promoter and the *TESK2* promoter, resulting in H3K36me3 marks, generation of epimutations in the two CpG islands and silencing of *MMACHC* and *TESK2* genes. These results showed that epi-*cbIC* is a clinical entity that must be distinguished from *cbIC* with regard to the potential consequences that may be produced by *TESK2* silencing. Epi-*cbIC* is an example of an altered expression of two genes through a common

epigenetic mechanism, which led us to introduce the term 'epi-digenism'.

The previous reports of the clinical and metabolic presentations of the 17 epi-*cbIC* cases showed similar manifestations, compared to the *cbIC* type of inherited disorders of cobalamin metabolism, with combined methylmalonic aciduria and homocystinuria, hypotonia, failure to thrive, megaloblastic anemia, pulmonary hypertension, and fatal neonatal cardio-metabolic decompensation [2, 3, 16–18]. Of note, the clinical phenotype of the epi-*cbIC* homozygote appeared to be more severe than homozygous cases with *MMACHC* c.271dupA, which is the most common

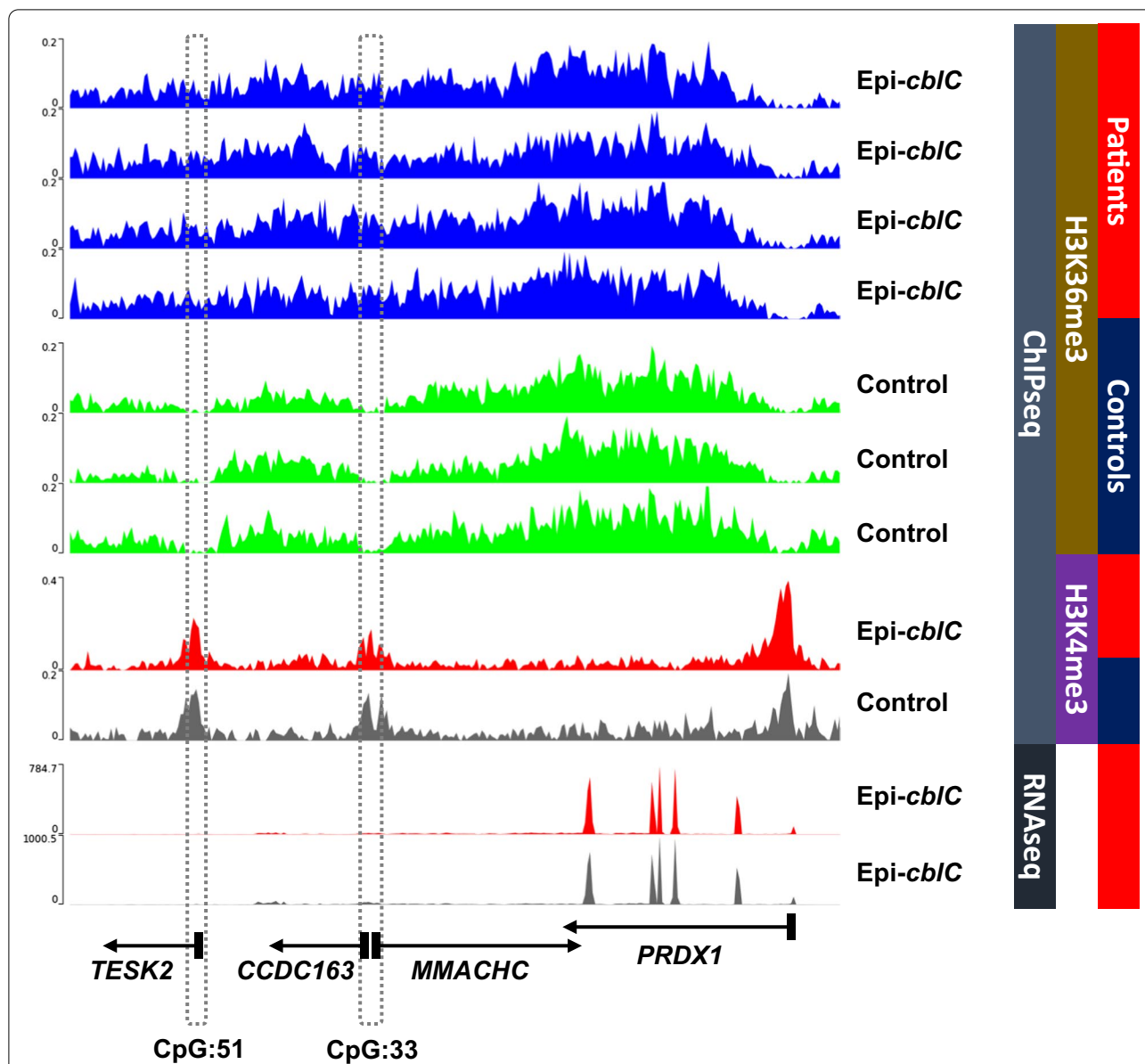
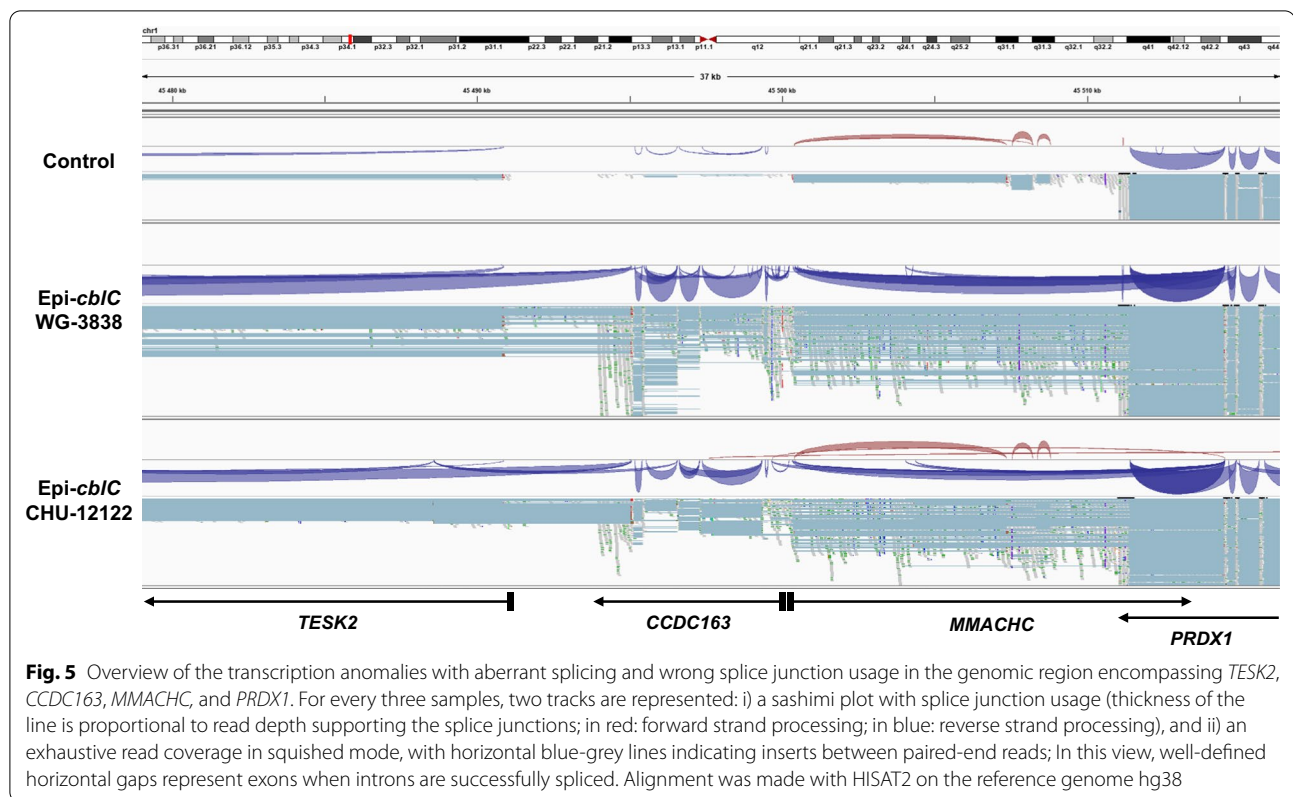


Fig. 4 Results of ChIP-Seq analyses at the genomic region encompassing the *CCDC163*–*MMACHC* bidirectional promoter region (CpG:33) and in the *TESK2* promoter region (CpG:51). Genomic panels show normalized coverage for histone H3 trimethylated lysine 36 (H3K36me3) and H3K4me3 marks in patients with an *epi-cbIC* phenotype and controls. The dashed rectangles indicate the *CCDC163*–*MMACHC* bidirectional promoter region (CpG:33) and the *TESK2* promoter region (CpG:51). The same scale has been set in all panels. ChIP-Seq showed a significant accumulation of the H3K36me3 and a mirrored profile of H3K4me3 in the *CCDC163*–*MMACHC* bidirectional promoter region (CpG:33) and in the *TESK2* promoter region (CpG:51) among patients with an *epi-cbIC* phenotype in comparison with controls. In contrast, the histone H3K36me3 and H3K4me3 marks are similar in the *PRDX1* promoter region. The RNA-Seq showed a high expression of *PRDX1* exons and low or no expression of *MMACHC* exons in case WG-3838 *epi-cbIC* and *cbIC* fibroblasts

mutation reported in European patients with *cbIC* [3, 18]. In addition, some manifestations are frequent in *epi-cbIC*, including skeletal deformity, metabolic acidosis with or without hyperammonemia, and recurrent severe infections [3]. The presence of the *PRDX1* mutation and the potential clinical consequences of *TESK2* silencing

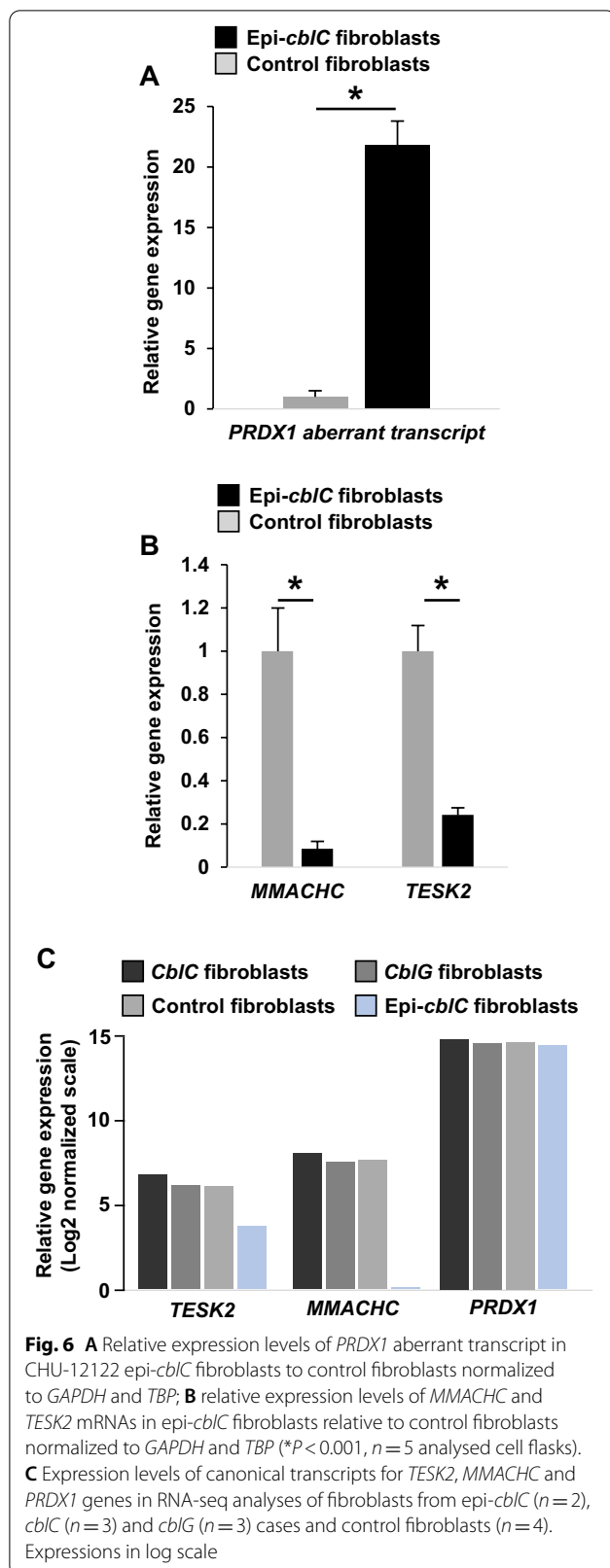
in *epi-cbIC* cases suggest that it should be considered as a distinct entity. *PRDX1* encodes Peroxiredoxin 1, a versatile protein involved in cell defense against cellular oxidative stress, influencing cell growth, differentiation, and apoptosis [19]. *PRDX1* enhances the natural killer cell cytotoxicity [20] and inhibits the function of



oncoproteins such as c-Abl [21] and c-Myc [19]. The role of *PRDX1* in suppressing tumors has been confirmed in *Prdx1*-knockout mouse models [22, 23]. We suggest periodically monitoring subjects bearing the *c.515-1G>T* variant to test the hypothesis of a potential increased risk of cancer. This potential risk could be related to the decreased expression of *PRDX1* evidenced in RNA-seq analyses (Fig. 5). The *PRDX1:c.515-1G>T* variant leads to the skipping of the last exon, which encodes one of the two cysteine residues which are essential for the catalytic activity [2, 3]. We also observed a clear reduction of the expression of *TESK2*, which could impact the disease course of epi-*cblC* cases. *TESK2* encodes a putative 555-amino acid protein with a kinase domain that exhibits a dual specific protein kinase activity on both serine/threonine and tyrosine residues [24]. The low expression of *TESK2* is associated with poor survival of patients with lung adenocarcinoma and premetastatic stage in human lung-to-brain metastasis [25]. *TESK2* is mainly expressed in the testis and prostate and influences cofilin phosphorylation and actin scaffold in testicular Sertoli cells [24, 26]. It also influences myogenic differentiation through actin remodeling [27]. *CCDC163P* was also silenced and was predicted to be the coding gene of a transmembrane protein, which has a main transcriptional expression in the thyroid, brain, and testis [28]. However, the protein

has not been characterized and it is not associated with pathological outcomes [28].

The RNA-seq data analysis showed that the readthrough transcription of *PRDX1* was prolonged through the *MMACHC/CCDC163P* bidirectional promoter and the *TESK2* promoter in fibroblasts of epi-*cblC* patients (Fig. 5). The H3K36me3 mark was the predominant common characteristic of histone marks at both *MMACHC* and *TESK2* promoters (Fig. 4). This mark is deposited only by the histone-lysine N-methyltransferase SETD2 at K36 of histone H3, where it binds the active form of RNA polymerase II [29]. Subsequently, the H3K36me3 mark allows the recruitment of DNMT3B1 through the binding of the heterochromatin protein 1 (HP1). This explains why the de novo methylation of CpG islands is preferentially targeted to genomic regions with elevated H3K36me3 levels through the recruitment of DNMT3B1 in mouse stem cells [30]. Based on these data and our data on RNA-seq and ChIP-seq of patient fibroblasts, we propose a common mechanism that produces the writing of the two epimutations through the successive recruitment of SETD2, HP1, and DNMT2B in epi-*cblC* disease. The RNA-seq analyses showed the activation of numerous cryptic splice sites that participated in the readthrough transcription of *PRDX1* and its prolongation through



the *MMACHC*, *CCDC163P*, and *TESK2* genes. The activation of these cryptic splice sites could involve SETD2. Indeed the SETD2 methyltransferase not only mediates the co-transcriptional methylation in histone H3 but it also has other functions that include the regulation of pre-mRNA splicing [31].

Digenic inheritance (DI) concerns pathologies with multigenic etiology implicating more than one gene [32]. Examples of unequivocal digenism in known diseases have been reviewed previously [32]. One of the categories of digenism is the inheritance of a single primary mutation that establishes the diagnosis and a second DNA variant, which modifies the phenotype [32]. In the case of epi-*cbIC*, the epimutation in the *CCDC163P/MMACHC* promoter produces the main phenotype of the disease while the epimutation in the promoter of *TESK2* produces its decreased expression with potential clinical consequences [25]. Therefore, we propose introducing the term ‘epi-digenism’ and considering epi-*cbIC* as an example of epidigenism since the silencing of *MMACHC* and *TESK2* are produced by a shared epigenetic mechanism on the two promoters.

Recently, a comprehensive genome-wide analysis of human epivariations analyzed in silico data generated from 23,116 individuals with the Illumina 450 k methylation array and reported 4,452 unique autosomal epivariations, including 384 in disease-causing OMIM genes [33]. The epivariation in the *CCDC163P/MMACHC* promoter was the most frequent among the 384 hypermethylated in the studied individuals [17]. Of note, one of the subjects had epivariations in *TESK2* and *CCDC163P/MMACHC* promoters [17]. This suggests that both epivariations could be triggered by environmental factors, as reviewed recently for *CCDC163P/MMACHC* promoter [17]. In addition, several EWAS from the EWAS catalog (<http://ewascatalog.org/?cpg=cg0036120>) showed the association of hypermethylated CpG in *CCDC163P/MMACHC* and *TESK2* promoters with sex, age, child abuse, rheumatoid arthritis, and five-year increase in epigenomic biological age of subjects with chronic HIV Infection [34–37].

In conclusion, our results show that epi-*cbIC* should be distinguished from *cbIC*, with potential consequences on spermatogenesis and cancer risk produced by *TESK2* silencing. The coverage of readthrough transcripts through a large region that encompasses *MMACHC*, *CCDC163P* and *TESK2* involves the activation of numerous splice cryptic sites. Epi-*cbIC* is an example of altered expression of two neighboring genes through a shared epigenetic pathomechanism. We propose introducing the term ‘epi-digenism’ to characterize this type of disorder.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13148-022-01271-1>.

Additional file 1. Supplemental Figure S1. Genome-wide density distribution of CpG probes in the 17 DNA methylome profiles of the 17 patients with *MMACHC* epimutation (epi-*cbIC* disease, isolated *MMACHC* epimutation, biallelic *MMACHC* epimutation).

Additional file 2. Supplemental Figure S2. (A) 2-D plot using the two top eigenvectors (PC1, PC3) derived from the primary component analysis on the genome-wide methylome landscape of the studied patients and controls. **(B)** 2-D plot using the PC1 and PC2 eigenvectors derived from the primary component analysis on the methylome landscape of chromosome 1 of the studied patients and controls.

Additional file 3. Supplemental Table S1. Forward and reverse primers for reverse transcription-quantitative polymerase chain reaction (RT-qPCR) of *MMACHC*, *TESK2* transcripts and *PRDX1* aberrant transcript.

Acknowledgements

We would like to thank the mother, father, and relatives of cases for their valuable contribution and help in the collection of data and samples used to study the entire families, and the scientists of the McGill University and Genome Quebec and the Genomic Platform of the FR3209 CNRS-Inserm, University of Lorraine, for expert advice and performing high throughput sequencing.

Author contributions

AO contributed to methodology; software; validation; formal analysis; investigation; resources; writing of the draft; visualization; CCh, CCa, YS, SH, PR, DSF, LF, AG, SG, SM, MRB, GP, AT, CM, FM, FF, MD, SM, GM, MAD, RG, PEM, DT, MP, AB, DW, TP, AM, FH, BAR, WKC, FF, JM, DSR, and AM contributed to investigation; resources; writing—review and editing; JLG contributed to conceptualization; methodology; validation; formal analysis; investigation; resources; writing of the draft—review and editing; visualization; supervision; project administration; funding acquisition. All authors read and approved the final manuscript.

Funding

INSERM UMR_S 1256, Nutrition, Genetics, and Environmental Risk Exposure (NGERE). The methylome analyses were funded by FHU ARRIMAGE and the French Agence Nationale de la Recherche, PIA project 'Lorraine Université d'Excellence' (ANR-15-IDEX-04-LUE). Institutional grants were received from the Region Lorraine, i-SITE Lorraine University of Excellence (LUE) and FEDER (fonds européen de développement régional). Canadian Institutes for Health Research. W.K.C received support from the Simons Foundation and the JPB Foundation.

Availability of data and materials

Data are available for use in collaborative studies to researchers upon reasonable request (jean-louis.gueant@univ-lorraine.fr). Data will be provided following the review and approval of a research proposal (including a statistical analysis plan) and the completion of a data-sharing agreement. Responses to the request for the raw data will be judged by the IRB of INSERM UMR_S 1256.

Declarations

Ethics approval and consent to participate

All adult patients and proband's parents assessed at the Reference Center for Inborn Errors of Metabolism at the University Hospital of Nancy gave their informed written consent for performing the analyses, as previously reported [2]. Informed consent was obtained from all participants included in the Italian study, as previously reported (Ethics Committee of the Tuscany Region (No. CS_01/2021) [3].

Consent for publication

Not applicable.

Competing interests

The authors declare no competing financial interests.

Author details

¹INSERM UMR_S 1256, Nutrition, Genetics, and Environmental Risk Exposure (NGERE), Faculty of Medicine of Nancy, University of Lorraine, 9 Avenue de la Forêt de Haye, 54000 Nancy, France. ²Reference Center for Inborn Errors of Metabolism (ORPHA67872), University Hospital of Nancy, 54000 Nancy, France. ³Department of Molecular Medicine, Division of Biochemistry, Molecular Biology and Nutrition, University Hospital of Nancy, 54000 Nancy, France. ⁴Molecular and Cell Biology Laboratory of Neurometabolic Diseases, Paediatric Neurology Unit and Laboratories, Meyer Children's Hospital, Viale Pieraccini 24, 50139 Florence, Italy. ⁵Department of NEUROFARBA, University of Florence, Florence, Italy. ⁶INSERM UMR_S 1263, Center for CardioVascular and Nutrition Research (C2VN), Aix-Marseille University, 13385 Marseille, France. ⁷INSERM, BPH, U1219, Université Bordeaux, 33000 Bordeaux, France. ⁸Department of Human Genetics, McGill University and Research Institute, McGill University Health Centre, Montreal, QC H4A 3J1, Canada. ⁹Departments of Pediatrics and Medicine, Columbia University, New York, USA. ¹⁰Children's Hospital of Philadelphia, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, PA, USA. ¹¹Division of Metabolism, University Children's Hospital, University of Zürich, Zürich, Switzerland. ¹²Biochemistry Hormonology Laboratory, Robert-Debré University Hospital, APHP, 48 bd Serurier, 75019 Paris, France. ¹³Department of Hepato-Gastroenterology, University Hospital of Nancy, 54000, Nancy, France.

Received: 31 December 2021 Accepted: 5 April 2022

Published online: 19 April 2022

References

- Zhou H, Brockington M, Jungbluth H, Monk D, Stanier P, Sewry CA, Moore GE, Muntoni F. Epigenetic allele silencing unveils recessive RYR1 mutations in core myopathies. *Am J Hum Genet*. 2006;79(5):859–68.
- Gueant JL, Chery C, Oussalah A, Nadaf J, Coelho D, Josse T, Flayac J, Robert A, Kosciński I, Gastin I, et al. *APRDX1* mutant allele causes a *MMACHC* secondary epimutation in *cbIC* patients. *Nat Commun*. 2018;9(1):67.
- Cavicchi C, Oussalah A, Falliano S, Ferri L, Gozzini A, Gasperini S, Motta S, Rigoldi M, Parenti G, Tummolo A, et al. *PRDX1* gene-related epi-*cbIC* disease is a common type of inborn error of cobalamin metabolism with mono- or bi-allelic *MMACHC* epimutations. *Clin Epigenet*. 2021;13(1):137.
- Dick KJ, Nelson CP, Tsaprouni L, Sandling JK, Aissi D, Wahl S, Meduri E, Morange PE, Gagnon F, Grallert H, et al. DNA methylation and body-mass index: a genome-wide analysis. *Lancet*. 2014;383(9933):1990–8.
- Aryee MJ, Jaffe AE, Corrada-Bravo H, Ladd-Acosta C, Feinberg AP, Hansen KD, Irizarry RA. Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*. 2014;30(10):1363–9.
- Gallet P, Oussalah A, Pouget C, Dittmar G, Chery C, Gauchotte G, Jankowski R, Gueant JL, Houllgatte R. Integrative genomics analysis of nasal intestinal-type adenocarcinomas demonstrates the major role of *CACNA1C* and paves the way for a simple diagnostic tool in male woodworkers. *Clin Epigenet*. 2021;13(1):179.
- Zhang Y, Liu T, Meyer CA, Eeckhoutte J, Johnson DS, Bernstein BE, Nusbaum C, Myers RM, Brown M, Li W, et al. Model-based analysis of ChIP-Seq (MACS). *Genome Biol*. 2008;9(9):R137.
- Heinz S, Benner C, Spann N, Bertolino E, Lin YC, Laslo P, Cheng JX, Murre C, Singh H, Glass CK. Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. *Mol Cell*. 2010;38(4):576–89.
- Robinson JT, Thorvaldsdottir H, Winckler W, Guttman M, Lander ES, Getz G, Mesirov JP. Integrative genomics viewer. *Nat Biotechnol*. 2011;29(1):24–6.
- Quintana AM, Yu HC, Brebner A, Pupavac M, Geiger EA, Watson A, Castro VL, Cheung W, Chen SH, Watkins D, et al. Mutations in *THAP11* cause an inborn error of cobalamin metabolism and developmental abnormalities. *Hum Mol Genet*. 2017;26(15):2838–49.
- Zgheib R, Battaglia-Hsu SF, Hergalant S, Quere M, Alberto JM, Chery C, Rouyer P, Gauchotte G, Gueant JL, Namour F. Folate can promote the methionine-dependent reprogramming of glioblastoma cells towards pluripotency. *Cell Death Dis*. 2019;10(8):596.

12. Kim D, Paggi JM, Park C, Bennett C, Salzberg SL. Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. *Nat Biotechnol.* 2019;37(8):907–15.
13. Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, Batut P, Chaisson M, Gingeras TR. STAR: ultrafast universal RNA-seq aligner. *Bioinformatics.* 2013;29(1):15–21.
14. Haas BJ, Papanicolaou A, Yassour M, Grabherr M, Blood PD, Bowden J, Couger MB, Eccles D, Li B, Lieber M, et al. De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. *Nat Protoc.* 2013;8(8):1494–512.
15. Bray NL, Pimentel H, Melsted P, Pachter L. Near-optimal probabilistic RNA-seq quantification. *Nat Biotechnol.* 2016;34(5):525–7.
16. Zhang X, Chen Q, Song Y, Guo P, Wang Y, Luo S, Zhang Y, Zhou C, Li D, Chen Y, et al. Epimutation of MMACHC compound to a genetic mutation in cblC cases. *Mol Genet Genomic Med.* 2021;9(6):e1625.
17. Gueant JL, Sibilini Y, Chery C, Schmitt G, Gueant-Rodriguez RM, Coelho D, Watkins D, Rosenblatt DS, Oussalah A. Epimutation in inherited metabolic disorders: the influence of aberrant transcription in adjacent genes. *Hum Genet.* 2022.
18. Huemer M, Diodato D, Schwahn B, Schiff M, Bandeira A, Benoist JF, Burlina A, Cerone R, Couce ML, Garcia-Cazorla A, et al. Guidelines for diagnosis and management of the cobalamin-related remethylation disorders cblC, cblD, cblE, cblF, cblG, cblJ and MTHFR deficiency. *J Inher Metab Dis.* 2017;40(1):21–48.
19. Ledgerwood EC, Marshall JW, Weijman JF. The role of peroxiredoxin 1 in redox sensing and transducing. *Arch Biochem Biophys.* 2017;617:60–7.
20. Shau H, Gupta RK, Golub SH. Identification of a natural killer enhancing factor (NKEF) from human erythroid cells. *Cell Immunol.* 1993;147(1):1–11.
21. Wen ST, Van Etten RA. The PAG gene product, a stress-induced protein with antioxidant properties, is an Abl SH3-binding protein and a physiological inhibitor of c-Abl tyrosine kinase activity. *Genes Dev.* 1997;11(19):2456–67.
22. Neumann CA, Krause DS, Carman CV, Das S, Dubey DP, Abraham JL, Bronson RT, Fujiwara Y, Orkin SH, Van Etten RA. Essential role for the peroxiredoxin Prdx1 in erythrocyte antioxidant defence and tumour suppression. *Nature.* 2003;424(6948):561–5.
23. Egler RA, Fernandes E, Rothermund K, Sereika S, de Souza-Pinto N, Jaruga P, Dizdaroglu M, Prochownik EV. Regulation of reactive oxygen species, DNA damage, and c-Myc function by peroxiredoxin 1. *Oncogene.* 2005;24(54):8038–50.
24. Rosok O, Pedeutour F, Ree AH, Aasheim HC. Identification and characterization of TESK2, a novel member of the LIMK/TESK family of protein kinases, predominantly expressed in testis. *Genomics.* 1999;61(1):44–54.
25. Singh M, Venugopal C, Tokar T, McFarlane N, Subapanditha MK, Qazi M, Bakhshinyan D, Vora P, Murty NK, Jurisica I, et al. Therapeutic targeting of the premetastatic stage in human lung-to-brain metastasis. *Cancer Res.* 2018;78(17):5124–34.
26. Toshima J, Toshima JY, Takeuchi K, Mori R, Mizuno K. Cofilin phosphorylation and actin reorganization activities of testicular protein kinase 2 and its predominant expression in testicular Sertoli cells. *J Biol Chem.* 2001;276(33):31449–58.
27. Kawauchi K, Tan WW, Araki K, Abu Bakar FB, Kim M, Fujita H, Hirata H, Sawada Y. p130Cas-dependent actin remodelling regulates myogenic differentiation. *Biochem J.* 2012;445(3):323–32.
28. Fagerberg L, Hallstrom BM, Oksvold P, Kampf C, Djureinovic D, Odeberg J, Habuka M, Tahmasebpoor S, Danielsson A, Edlund K, et al. Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics. *Mol Cell Proteom.* 2014;13(2):397–406.
29. Krogan NJ, Kim M, Tong A, Golshani A, Cagney G, Canadien V, Richards DP, Beattie BK, Emili A, Boone C, et al. Methylation of histone H3 by Set2 in *Saccharomyces cerevisiae* is linked to transcriptional elongation by RNA polymerase II. *Mol Cell Biol.* 2003;23(12):4207–18.
30. Baubec T, Colombo DF, Wirbelauer C, Schmidt J, Burger L, Krebs AR, Akalin A, Schubeler D. Genomic profiling of DNA methyltransferases reveals a role for DNMT3B in genic methylation. *Nature.* 2015;520(7546):243–7.
31. McDaniel SL, Strahl BD. Shaping the cellular landscape with Set2/SETD2 methylation. *Cell Mol Life Sci.* 2017;74(18):3317–34.
32. Deltas C. Digenic inheritance and genetic modifiers. *Clin Genet.* 2018;93(3):429–38.
33. Garg P, Jadhav B, Rodriguez OL, Patel N, Martin-Trujillo A, Jain M, Metsu S, Olsen H, Paten B, Ritz B, et al. A survey of rare epigenetic variation in 23,116 human genomes identifies disease-relevant epimutations and CGG expansions. *Am J Hum Genet.* 2020;107(4):654–69.
34. Mulder RH, Neumann A, Cecil CAM, Walton E, Houtepen LC, Simpkin AJ, Rijlaarsdam J, Heijmans BT, Gaunt TR, Felix JF, et al. Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. *Hum Mol Genet.* 2021;30(1):119–34.
35. Yang BZ, Zhang H, Ge W, Weder N, Douglas-Palumberi H, Perepletchikova F, Gelernter J, Kaufman J. Child abuse and epigenetic mechanisms of disease risk. *Am J Prev Med.* 2013;44(2):101–7.
36. Liu Y, Aryee MJ, Padyukov L, Fallin MD, Hesselberg E, Runarsson A, Reinius L, Acevedo N, Taub M, Ronninger M, et al. Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. *Nat Biotechnol.* 2013;31(2):142–7.
37. Gross AM, Jaeger PA, Kreisberg JF, Licon K, Jepsen KL, Khosroheidari M, Morse BM, Swindells S, Shen H, Ng CT, et al. Methylome-wide analysis of chronic HIV infection reveals five-year increase in biological age and epigenetic targeting of HLA. *Mol Cell.* 2016;62(2):157–68.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

