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This is a copy of the final article, which was originally published in:

Journal of Experimental Medicine
2017 JUL 03 ; 214(7): 2089-2101
2017 MAY 30 (first published online)
doi: 10.1084/jem.20161093

Publisher: Rockefeller University Press

Gene silencing and a novel monoallelic expression pattern in distinct CD177 neutrophil subsets

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CD177 presents antigens in allo- and autoimmune diseases on the neutrophil surface. Individuals can be either CD177-deficient or harbor distinct CD177^{neg} and CD177^{pos} neutrophil subsets. We studied mechanisms controlling subset-restricted CD177 expression in bimodal individuals. CD177^{pos}, but not CD177^{neg} neutrophils, produced CD177 protein and mRNA. Haplotype analysis indicated a unique monoallelic *CD177* expression pattern, where the offspring stably transcribed either the maternal or paternal allele. Hematopoietic stem cells expressed both *CD177* alleles and silenced one copy during neutrophil differentiation. ChIP and reporter assays in HeLa cells with monoallelic *CD177* expression showed that methylation reduced reporter activity, whereas demethylation caused biallelic *CD177* expression. HeLa cell transfection with c-Jun and c-Fos increased *CD177* mRNA. Importantly, CD177^{pos} human neutrophils, but not CD177^{neg} neutrophils, showed a euchromatic *CD177* promoter, unmethylated CpGs, and c-Jun and c-Fos binding. We describe epigenetic mechanisms explaining the two distinct CD177 neutrophil subsets and a novel monoallelic *CD177* expression pattern that does not follow classical random monoallelic expression or imprinting.

The Journal of Experimental Medicine

INTRODUCTION

CD177 is a neutrophil-specific receptor with clinical significance in allo- and autoimmune diseases (Stroncek, 2007). CD177 harbors the human neutrophil antigen 2 (HNA-2; formerly neutrophil antigen B1 or NB1). Alloantibodies to HNA-2, either actively generated or acquired from blood products, can cause severe neutropenia in newborns (Lalezari et al., 1971), graft failure in bone marrow recipients (Stroncek et al., 1993), drug-induced neutropenia (Stroncek et al., 1994), and transfusion-related lung injury (TRALI; Bux et al., 1996; Sachs et al., 2006). In addition, CD177 presents proteinase 3 (PR3), a major autoantigen in antineutrophil cytoplasmic antibodies (ANCA)-associated small vessel vasculitis on the neutrophil surface (Bauer et al., 2007; von Vietinghoff et al., 2007). PR3-ANCA bind to membrane-exposed PR3 (mPR3) and activate the neutrophil—a central process for subsequent vascular injury (Kettritz, 2012). Above and beyond its role in immune conditions, CD177 facilitates neutrophil endothelial transmigration involving heterophilic PECAM-1 interactions and catalytic membrane PR3 activity (Sachs et al., 2007; Bayat et al., 2010; Kuckleburg et al., 2012).

CD177 is a glycosyl-phosphatidyl inositol–linked glycoprotein of the urokinase plasminogen activator receptor/CD59/Ly6 snake toxin superfamily (Kissel et al., 2001). CD177 protein is stored in secondary granules and is presented on the neutrophil plasma membrane (von Vietinghoff et al., 2008; Rørvig et al., 2013). CD177 shows a peculiar distribution pattern in that ∼95% of all healthy individuals produce CD177^{pos} neutrophils, whereas 5% are CD177 deficient (Goldschmeding et al., 1992; Matsuo et al., 2000; Li et al., 2015; Wu et al., 2016). However, even the CD177-producing individuals show a stable bimodal CD177 pattern over time, with distinct membrane CD177^{neg} and CD177^{pos} (mCD177) neutrophil subsets. The size of the latter ranges from a few, to >90% (Goldschmeding et al., 1992). Despite the strong clinical implications, the mechanisms controlling subset-restricted *CD177* gene expression in bimodal individuals are incompletely understood.

Most diploid cells express both parental alleles of each gene, whereas some genes are monoallelically expressed. To date, two basic monoallelic expression (MAE) mechanisms in autosomes are distinguished. Imprinting describes a parent-of-origin MAE with exclusive silencing of either the maternal or the paternal allele (Barlow and Bartolomei, 2014). In contrast, classical random MAE occurs stochastically, so that

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Abbreviations used: ANCA, anti-neutrophil cytoplasmic autoantibodies; HSC, hematopoietic stem cell; MAE, monoallelic expression; SNP, single nucleotide polymorphism; TF, transcription factor.

The Rockefeller University Press $30.00
J. Exp. Med. 2017 Vol. 214 No. 7 2089–2101
https://doi.org/10.1084/jem.20161093

clonal cells derived from a given cell type express either the maternal or the paternal, or even both parental alleles (Gimelbrant et al., 2007; Deng et al., 2014).

We CD177-phenotyped a large cohort of healthy individuals and studied genetic and epigenetic mechanisms that control *CD177* expression using sorted neutrophil CD177 subsets, parent-offspring trios, neutrophil-differentiated $CD34^+$ hematopoietic stem cells (HSCs), neonatal cord blood neutrophils, and a HeLa cell model. We demonstrate that disparate CpG and histone methylation, and AP-1 (c-Jun/c-Fos) transcription factor (TF) binding explain the two distinct CD177 neutrophil subsets. We observed MAE of *CD177* with a novel pattern that follows neither classical random MAE nor imprinting.

RESULTS

Neutrophil mCD177 phenotypes in normal controls

We first characterized the CD177 neutrophil phenotype in 165 normal individuals (66 men and 99 women). We assessed mCD177 on viable blood neutrophils by flow cytometry and found that 6% (10/165) of the individuals were completely CD177 deficient. In contrast, 94% (155/165) showed a bimodal pattern with varying percentages of $mCD177^{pos}$ neutrophils. The median size of the $mCD177^{pos}$ subset was 60% (Fig. 1 A). Our subsequent studies focused on the molecular basis for the CD177 bimodality that involves the vast majority of healthy individuals and has major disease implications for allo- and autoantigen presentation.

CD177 protein and mRNA expression is restricted to the $CD177^{pos}$ neutrophil subset

To gain insight into the molecular basis of the two distinct mCD177 phenotypes, we analyzed CD177 protein and mRNA expression in bimodal mCD177 individuals. For these studies, we isolated highly pure $CD177^{neg}$ and $CD177^{pos}$ blood neutrophils by magnetic cell sorting (Fig. 1 B). Immunoblotting showed CD177 protein (Fig. 1 C) and qRT-PCR detected full-length mRNA (Fig. 1 D) in $CD177^{pos}$, but not in $CD177^{neg}$ neutrophils. To precisely check *CD177* transcription in $CD177^{neg}$ neutrophils, we used three different primer pairs to exclude truncated *CD177* mRNAs by qRT-PCR (Fig. 1 E). Thus, *CD177* full-length mRNA is actively transcribed in $CD177^{pos}$ neutrophils, whereas both mRNA and protein are absent in the $CD177^{neg}$ subset.

CD177 is monoallelically expressed in neutrophils and neutrophil-differentiated $CD34^+$ HSCs

The human *CD177* gene resides on chromosome 19q13.31, 8.4-kb downstream to a *CD177* pseudogene (Bettinotti et al., 2002; Caruccio et al., 2006; Li et al., 2015). We next investigated the *CD177* gene locus to determine whether or not structural aberrations, such as frame shifts, deletions, or alternative splice sites explained the lack of *CD177* mRNA in $CD177^{neg}$ neutrophils. We sequenced the *CD177* gene in the two separated CD177 subsets ($mCD177^{neg}$ and $mCD177^{pos}$ neutrophils) and detected no DNA mutations or major substitutions in the nine exons, exon–intron transitions, 5′ UTR (−1,000 bp), and in 3′ UTR (+200 bp). In addition, a genome-wide single nucleotide polymorphisms (SNPs) analysis using an Affimetrix SNP array 6.0, revealed an almost identical SNP and copy number variation (CNV) concordance in both neutrophil subsets (five biological replicates, 99.9% concordance by Fisher's exact test; Fig. S1).

Because no *CD177* DNA sequence alterations or CNVs were found to explain the distinct *CD177* mRNA and protein patterns, we performed a systematic haplotype analysis for the *CD177* locus with 17 trios from 12 healthy families. We first sequenced the *CD177* exons from parents and offspring. Long-range PCR was used to amplify the complete *CD177* gene, thereby excluding the highly homologous pseudogene (exons 4–9) in reverse orientation on the antisense strand. Sequencing and SNP analysis of the PCR-amplicon (13 kb) detected all 9 *CD177* exons confirming that the product was not contaminated by the *CD177* pseudogene. Within the *CD177* exons, we found 22 heterozygous SNPs in 15/17 offspring (Table S1) ranging from 1 to 6 in a given child. The remaining two offspring had noninformative homozygous SNPs. Only heterozygous SNPs analyzed in DNA and corresponding mRNA from neutrophils enabled us to distinguish the two parental *CD177* alleles and to determine whether or not both alleles were actively transcribed. To our surprise, we found MAE in all 15 offspring with heterozygous SNPs. The parental origin of the actively transcribed allele was identified in 12/15 children, whereas three offspring had no informative SNP. 3/5 daughters expressed the maternal and 2/5 the paternal *CD177* allele, whereas 5/7 sons expressed the maternal and 2/7 the paternal allele. These data indicate that the parental choice occurred independently of the offspring's gender. Remarkably, siblings from two of the 12 families inherited the expressed *CD177* allele from a different parent (Fig. 1 F and S2 A). One of these two families allowed sibling testing that confirmed the full-sibling status (Fig. S2 A). We complemented Sanger sequencing in the family shown in Fig. 1 F, with more quantitative approaches, namely digital PCR with informative SNP-specific probes and pyrosequencing, respectively. Results from both assays were >70% cut-off used for a monoallelic call (Reinius and Sandberg, 2015) and strengthen the observation of monoallelic *CD177* expression (Fig. 1, G and H). The haplotypes of all remaining trios are shown in Fig. S1 B. We then studied MAE in a given individual over a 7-d period at days 0, 3, and 7, respectively. We observed that the allelic choice was stable and did not change over the observation period (Table 1). Together, these data indicate monoallelic *CD177* expression in $CD177^{pos}$ neutrophils. The expressed *CD177* transcript in a given individual was derived randomly either from the maternal or paternal allele with variation even within one family and the allelic choice remained stable over time.

To elucidate the mechanism of *CD177* MAE, we studied $CD34^+$ hematopoietic stem cell (HSC)–derived neu-

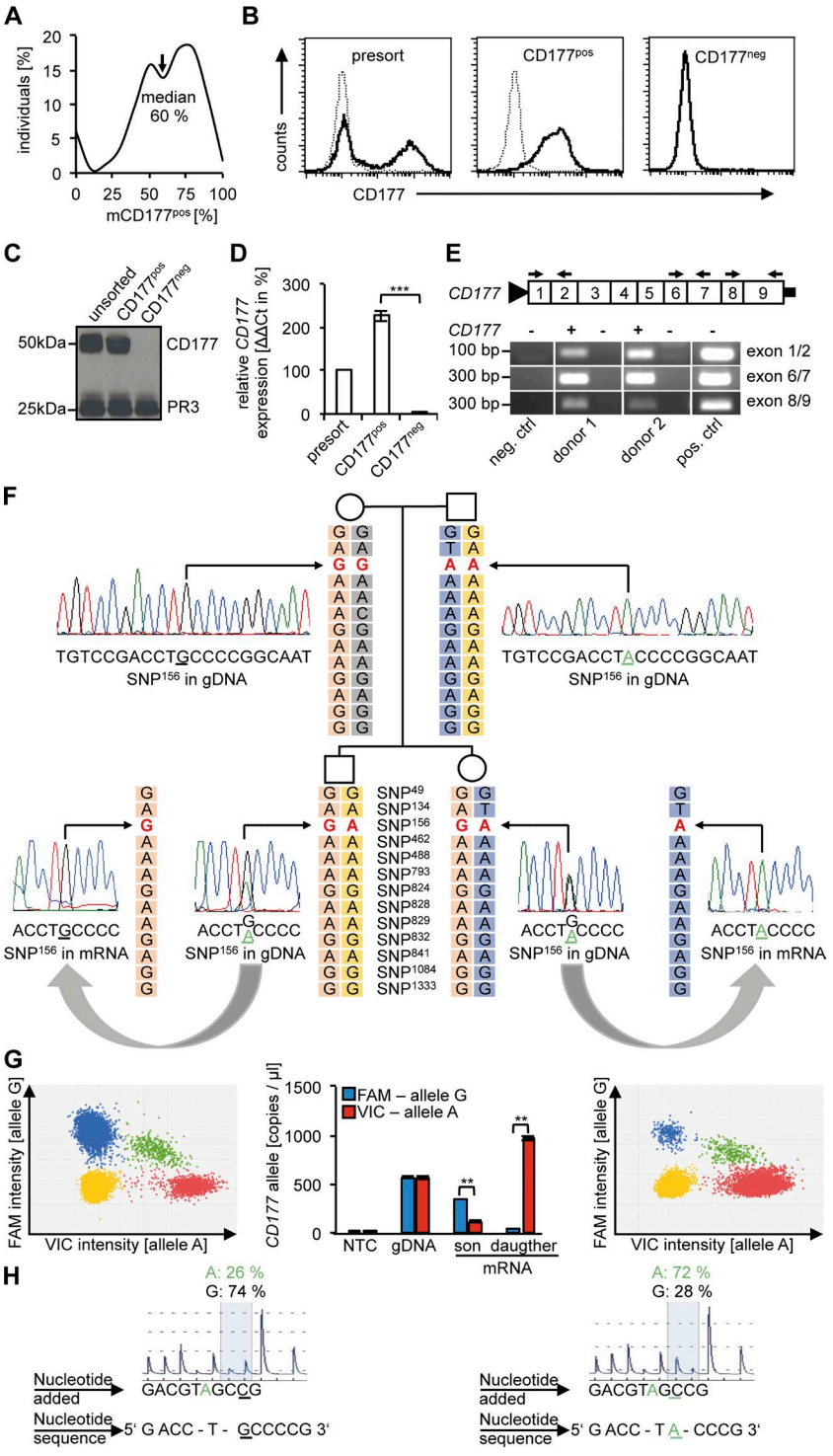

Figure 1. **CD177^{pos} neutrophils from bimodal individuals contain CD177 protein and express only one *CD177* allele either of paternal or maternal origin, whereas CD177^{neg} neutrophils produce neither CD177 protein nor mRNA.** (A) The percentage of CD177^{pos} neutrophils by flow cytometry in 165 normal controls is shown as percentage of individuals per decile. (B) A typical flow cytometry experiment before (presort) and after magnetic cell sorting yielding CD177^{pos} and CD177^{neg} neutrophil subsets is given. Samples obtained as shown in B were subjected (C) to immunoblotting for CD177 and proteinase 3 (PR3) as a control protein (n = 4 different donors), and (D) to *CD177* gene expression analysis by qRT-PCR. *CD177* mRNA of presorted neutrophils was set at 100% (n = 3 different donors). (E) RT-PCR with different *CD177* exon-spanning primers (black arrows) was performed in CD177^{pos} and CD177^{neg} neutrophils from two neutrophil donors to exclude truncated *CD177* mRNAs (n = 2 different donors). (F) An example for monoallelic *CD177* gene expression in a family with two offspring is depicted. Haplotype analysis showed an informative heterozygous GA SNP (in red, rs45571738) in the genomic DNA (gDNA) of both offspring whereas maternal gDNA showed homozygous GG and paternal gDNA AA. At mRNA, the son monoallelically expressed the maternal G and the daughter the paternal A allele as demonstrated by Sanger sequencing. The parental haplotype that is inherited by the offspring is boxed in light orange (maternal) and blue (paternal). (G) Digital PCR for the monoallelically expressed G allele for SNP^{156} in the son (left) and A allele in the daughter (right). Dot plots are depicted with each dot representing one of the 20,000 analyzed wells on the digital PCR chip. Blue dots represent the G (FAM-labeled) and red dots the A (VIC-labeled) allele, whereas yellow and green dots do not allow unequivocal allele identification. Quantitative assessment (middle) shows 75% G allele expression for the son and 96% for the daughter. gDNA was assessed as a control showing even distribution of both alleles (n = 2). (H) Pyrosequencing reveals MAE of the G allele (74%) for the son and the A allele (72%) for the daughter, respectively. Note that quantitative assays for assessment of MAE use a threshold of ~70% for the monallelic call (Reinius and Sandberg, 2015). Data in D were displayed as mean± SEM and were analyzed using one-way ANOVA. ***, P < 0.001. Data in G were given as Poisson plus ratio with confidence intervals and were analyzed using Student's t test. **, P < 0.01.

trophils and neonatal neutrophils of the identical donor. We questioned whether or not *CD177* MAE was already determined in the pluripotent HSCs. Thus, we selected umbilical cord blood donors with heterozygous DNA SNPs that allowed us to determine whether or not both alleles were expressed in the *CD177* mRNA transcripts. G-CSF induced neutrophil differentiation and the HSC-derived neutrophils expectantly expressed the maturation markers CD11b and CD18 on the surface, showed bimodal CD177 populations (Fig. 2 A), and progressively transcribed *CD177* mRNA over the 7-d observation period (Fig. 2 B). Analyzing heterozygous SNPs in *CD177* DNA and mRNA by sequencing, we

found that both *CD177* alleles were transcribed in undifferentiated $CD34^+$ HSCs. However, biallelic *CD177* expression changed to MAE with neutrophil differentiation at day 7 (Fig. 2 C). When we compared neutrophil-differentiated HSCs with the mature neonatal neutrophils obtained from the same cord blood, we validated MAE and found that the identical *CD177* allele was monoallelically transcribed in in vitro G-CSF differentiated and in in vivo natively differentiated neutrophils (Fig. 2 D). Our findings indicate that one of two *CD177* alleles is silenced during neutrophil differentiation resulting in MAE in mature neutrophils. These observations support the notion that epigenetic mechanisms control the *CD177* allele-silencing process.

Epigenetic modifications control *CD177* gene expression in a HeLa cell model

Neutrophils are short-lived and hard to transfect cells that are not suitable for genetic manipulation. Looking for alternative cell models, we successfully induced *CD177* transcription in HeLa cells by phorbol myristate acetate (PMA) treatment (Fig. 3 A). A SNP analysis by *CD177* exon and mRNA sequencing showed that PMA-stimulated HeLa cells expressed *CD177* in a monoallelic fashion similar to $CD177^{pos}$ neutrophils (Fig. 3 B).

To characterize the *CD177* locus, we dissected the molecular properties of the regulatory promoter region. We performed 5′ RACE and determined the transcription start site (TSS) of the *CD177* gene at 29 bp upstream of the ATG translation start site. In the *CD177* promoter, we detected a GC-rich element and 16 CpG dinucleotides. We next used the PROMO database (Messeguer et al., 2002) and rVISTA (Loots and Ovcharenko, 2004) to predict TF binding sites in the promoter region of interest. We found several conserved binding sites for the AP-1 family members c-Jun and c-Fos that were shown to be involved in PMA-activated gene transcription (Guerrini et al., 1996). In addition, c-Ets-1 binding sites were also predicted and of potential interest as a result of reported interactions with the AP-1 TF family (Kumari et al., 2015; Fig. 3 C).

First, we studied the effect of CpG-methylation on *CD177* allele expression. We cloned the 1,373-bp full-length *CD177* promoter with 16 CpGs, as well as shorter promoter regions into a CpG-dinucleotide lacking vector (Klug and Rehli, 2006). The constructs were used in HeLa luciferase reporter assays to study transcriptional activity (Fig. 3 D). The highest *CD177* reporter activity was associated with the 1,373 and 964 bp constructs and a significant loss of reporter activity was observed by shortening the construct to 178 bp (Fig. 3 E). To address the effect of CpG-methylation on *CD177* reporter activity, we treated constructs 1–4, each in the CpG-free vector, with methyltransferase. Methylation significantly reduced reporter activity (Fig. 3 F). These findings indicate that CpG-methylation in *CD177* regulatory promoter sequence silences *CD177* allele expression. In a different approach, we treated HeLa cells with the demethylation agent 5-Aza-2-deoxycytidin. By *CD177* mRNA sequencing, we found that demethylation converted monoallelic into biallelic *CD177* expression demonstrating that CpG-methylation caused indeed silencing of one *CD177* allele (Fig. 3 G).

CpG-methylation affects TF binding to gene promoters. We performed ChIP for c-Jun, c-Fos, and c-Ets-1 on chromatin of PMA-stimulated HeLa cells. We found binding of all three TFs to *CD177* promoter regions with c-Jun binding reaching statistical significance (Fig. 3 H). To test whether or not c-Jun, c-Fos, and c-Ets-1 control *CD177* transcription, we transfected HeLa cells with the TFs and quantified *CD177* mRNA by qRT-PCR. We observed that the combination of c-Jun and c-Fos caused strongly induced *CD177* mRNA. In contrast, c-Ets-1 transfection alone did not affect *CD177* transcription. Moreover, the combination of c-Ets-1 with the

Table 1. **Monoallelic *CD177* expression and the allelic choice over a 7-d period in five different individuals**

Individual	Allele in gDNA	SNP position	Expressed *CD177* allele		
			day 0	day 3	day 7
1	G/C	SNP^{49}	G	G	G
2	C/A	SNP^{793}	A	A	A
	C/G	SNP^{824}	G	G	G
	C/A	SNP^{828}	A	A	A
	T/A	SNP^{829}	A	A	A
	A/G	SNP^{832}	G	G	G
	G/A	SNP^{841}	A	A	A
3	G/C	SNP^{49}	G	G	G
4	A/T	SNP^{134}	T	T	T
	G/A	SNP^{156}	A	A	A
	C/A	SNP^{793}	A	A	A
	G/A	SNP^{1333}	A	A	A
5	C/G	SNP^{824}	G	G	G
	C/A	SNP^{828}	A	A	A
	T/A	SNP^{829}	A	A	A
	A/G	SNP^{832}	G	G	G
	G/A	SNP^{841}	A	A	A

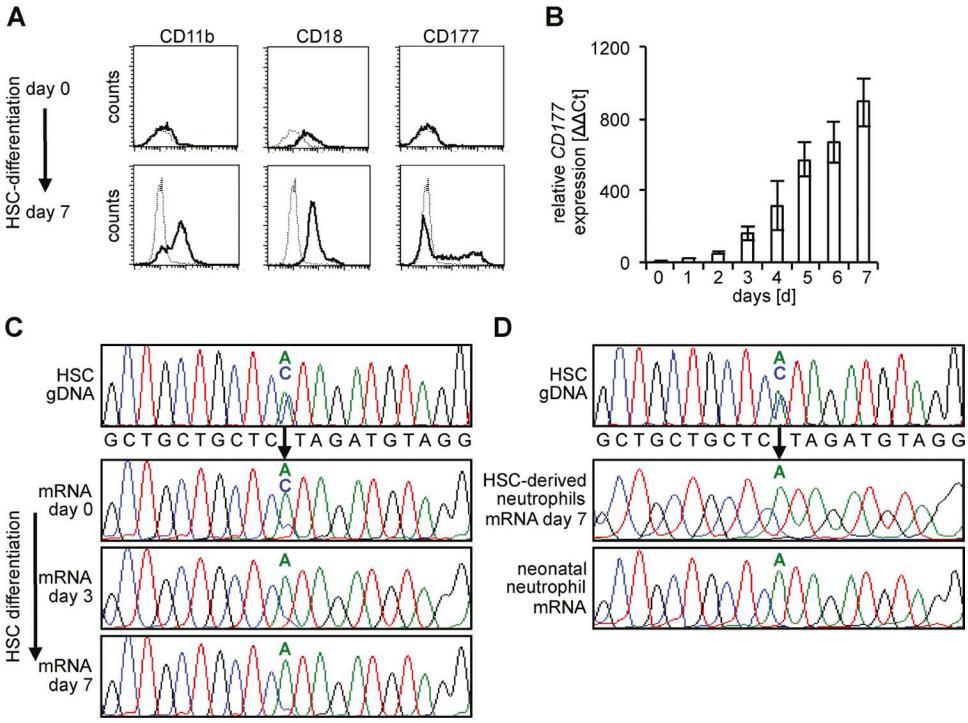

Figure 2. **Monoallelic *CD177* mRNA expression in neutrophil-differentiated CD34⁺ HSC and neonatal neutrophils.** CD34⁺ HSC were differentiated over 7 d into neutrophils and (A) acquired neutrophil surface markers CD11b and CD18, together with a bimodal CD177 phenotype. A representative flow cytometry analysis from four independent differentiation experiments is shown. Solid lines represent staining with the specific antibodies and dotted lines represent the isotype control. (B) *CD177* gene expression increased progressively in CD34⁺ HSCs during 7 d of neutrophil differentiation (qRT-PCR; $n = 4$ different CD34⁺ HSC donors). (C) Sanger sequencing of genomic DNA (gDNA) and mRNA from CD34⁺ HSC showed a heterozygous AC SNP[793] (rs10425835) in gDNA and biallelic *CD177* mRNA expression in undifferentiated cells at day 0. The C allele was silenced during neutrophil differentiation up to day 7 ($n = 4$ different CD34⁺ HSC donors). (D) Analysis of neutrophil-differentiated CD34⁺ HSCs and neonatal neutrophils from the same cord blood indicate an informative heterozygous AC SNP[793] in the gDNA from CD34⁺ HSCs.

AP-1 TFs showed no additive effect (Fig. 3 I). Finally, pharmacologic c-Jun N-terminal kinase inhibition significantly reduced G-CSF–induced *CD177* expression in human neutrophils suggesting that c-Jun controls *CD177* expression also in neutrophils (Fig. 3 J).

CpG, histone methylation, and TF binding are differentially regulated in the two CD177 neutrophil subsets

Our analysis established the importance of CpG methylation, and AP-1 TF binding in the *CD177* promoter for *CD177* gene expression in HeLa cells. We reasoned that if these epigenetic marks provided the basis for the bimodal *CD177* expression pattern in neutrophils, they should be differentially regulated in the two separated CD177 neutrophil subsets. Thus, we addressed genome-wide DNA methylation of the two CD177 neutrophil subsets unbiased by Illumina Infinium Human Methylation 450 BeadChips. The probes on this chip covered three of the 16 CpG-methylation sites of the *CD177* promoter and two further downstream in *CD177* gene body. We found significantly increased CpG methylation in the *CD177* promoter of CD177^{neg} neutrophils (paired Student's *t* test; Fig. 4 A and Table S2). H3K4me3 ChIP assay showed euchromatin in the *CD177* promoter of CD177^{pos} neutrophils, whereas nonenriched H3K4me3 indicated heterochromatin conformation in CD177^{neg} cells (Fig. 4 B). ChIP analysis revealed significantly stronger binding of c-Jun, c-Fos and c-Ets-1 in the *CD177* promoter of CD177^{pos} neutrophils, whereas no signal was obtained in the CD177^{neg} cells (Fig. 4 C). In summary, our data generated in HeLa cells and neutrophils showed that CpG and histone methylation regulated AP-1 TF-binding in the regulatory *CD177* promoter region thereby controlling *CD177* gene expression.

DISCUSSION

Our study revealed several important new findings. First, our haplotype studies in family trios shows monoallelic *CD177* gene expression with a novel pattern that differs from classical imprinting and random MAE. Using CD34⁺ HSCs, we observed that one *CD177* allele was silenced during neutrophil differentiation. Second, we show that, in contrast to CD177^{pos} neutrophils, the CD177^{neg} subset transcribed neither full-length nor truncated *CD177* mRNAs. Third, studies in HeLa cells supported the notion that *CD177* allele silencing involved DNA methylation in the *CD177* promoter re-

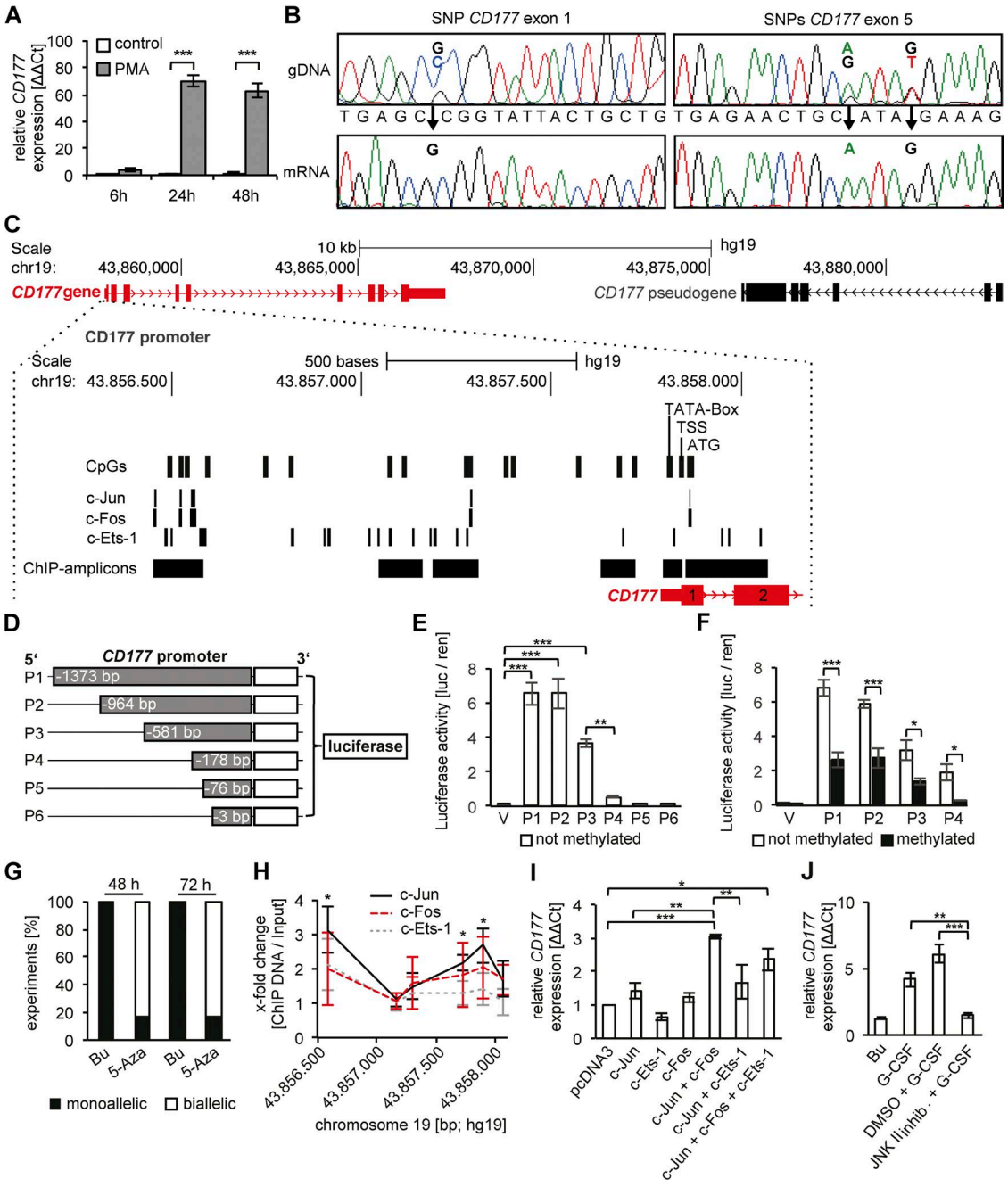

Figure 3. ***CD177* gene expression, promoter analysis, DNA methylation, and transcription factor binding in a HeLa cell model.** (A) *CD177* gene expression was induced in PMA-treated HeLa cells as shown by qRT-PCR ($n = 3$ independent experiments). (B) *CD177* haplotype analysis was performed by Sanger sequencing the genomic DNA (gDNA) and mRNA from HeLa cells ($n = 6$ independent experiments). Three heterozygous SNPs in the gDNA, one in exon 1 (SNP^{49} GC) and two in exon 5 (SNP^{652} AG and SNP^{656} GT), were found and established monoallelic *CD177* gene expression. (C) A schematic overview of the *CD177* gene (red), its promoter, and the pseudogene (black) is depicted. The *CD177* promoter region is enlarged.16 CpG dinucleotides, the c-Jun, c-Fos, and c-Ets-1 TF binding sites (PROMO database), the TATA box, the transcription start site (TSS), the translation start (ATG), and PCR amplicons of the ChIPed DNA are indicated. (D) The *CD177* promoter constructs P1 to P6 were cloned into the CpG-free luciferase vector. (E) Luciferase reporter assays were performed with the unmethylated *CD177* promoter constructs P1 to P6 ($n = 4$ independent experiments). *CD177* promoter activity was calculated from the firefly and Renilla luciferase signal. (F) Luciferase reporter assays were performed with P1 to P4 promoter constructs that were either left unmethylated (open bars) or were methylated (black bars) by incubation with methyltransferase ($n = 7$ independent experiments). (G) PMA-stimulated HeLa cells were treated with buffer (Bu) or 10 µM 5′-Aza-2-deoxycytidine (5-Aza) for 48 and 72 h, respectively ($n = 6$ independent experiments). Allele expression was analyzed using heterozygous *CD177* SNPs (SNP^{49} rs45441892, SNP^{652} rs199668750, SNP^{656} rs200662237) in gDNA and the corresponding mRNA. Black indicates the percentage of experiments where monoallelic *CD177* gene expression was detected and white indicates the percentage of experiments where

gion thereby regulating c-Jun and c-Fos binding and *CD177* gene transcription. Finally, and importantly, these mechanisms were differentially executed in the two CD177 neutrophil subsets thereby explaining the bimodal CD177 phenotype.

Almost half a century ago, clinicians were made aware of HNA-2 (named NB1 at that time), because alloantibodies to this neutrophil antigen caused neonatal neutropenia (Lalezari et al., 1971). Later, researchers showed that the CD177 glycoprotein not only harbored the HNA-2 alloantigen, but also that CD177 presented the PR3 autoantigen on the neutrophil surface (Bauer et al., 2007; von Vietinghoff et al., 2007). Alloantibodies to HNA-2 cause neutropenia (Lalezari et al., 1971; Stroncek et al., 1993, 1994) and TRALI (Sachs et al., 2006) and autoantibodies to PR3 are associated with systemic small-vessel vasculitis (van der Woude et al., 1985; Lüdemann et al., 1990). Because these conditions are associated with substantial mortality, understanding CD177 expression is clinically highly relevant. Complete CD177 deficiency is of particular interest for HNA-2 alloantibody generation because nonexpressers become immunized with pregnancies and transfusions, and the resulting alloantibodies cause disease in HNA-2 expressing individuals. Investigators showed that the genetic basis for CD177 deficiency were SNP variants leading to truncated mRNAs with premature stop codons (Kissel et al., 2002). Additionally, either the homozygous nonsense SNP (829T) that also resulted in a premature stop codon or the heterozygous SNP (829AT) where the 829A allele harbored an additional base deletion resulted in a premature stop codon (Li et al., 2015). Very recently, DNA deep sequencing confirmed this homozygous nonsense SNP (in this study named g7497T) and found that the T allele was derived from gene conversion of the neighboring *CD177* pseudogene with the *CD177* gene (Wu et al., 2016). 6% of the individuals in our healthy Caucasian cohort were CD177 deficient, whereas 94% produced a variable percentage of $CD177^{pos}$ neutrophils with a median of 60%. This bimodal CD177 expression pattern is of particular interest in patients with ANCA vasculitis, where PR3 is a major autoantigen. Membrane-presented PR3 (mPR3) is recognized by PR3-ANCA that then activates the neutrophil, leading to vascular inflammation (Kettritz, 2012). We found previously that CD177 acts as a PR3-presenting receptor supporting high mPR3 levels (von Vietinghoff et al., 2007). The CD177–PR3 complex recruits additional transmembrane molecules into a larger signaling complex (Jerke et al., 2011). The bimodal CD177 expression pattern therefore results in $CD177^{neg}/mPR3^{low}$ and $CD177^{pos}/mPR3^{high}$ neutrophil subsets. Of clinical importance, a larger percentage of $CD177^{pos}/mPR3^{high}$ neutrophils is found in ANCA vasculitis patients and is associated with worse clinical outcome (Witko-Sarsat et al., 1999; Rarok et al., 2002; Schreiber et al., 2005; Hu et al., 2009; Abdgawad et al., 2010). The molecular basis for the two distinct CD177 subsets, and therefore for the two mPR3 phenotypes is incompletely understood. We confirm data from Wolff et al. (2003), who showed that sorted $CD177^{neg}$ neutrophils from bimodal individuals lacked full-length *CD177* mRNA by PCR. We extend these data showing that multiple qRT-PCRs with exon-spanning primers excluded truncated mRNAs. In contrast, Wu et al. (2016) detected full-length mRNA in $CD177^{neg}$ sorted cells of bimodal individuals by deep sequencing. The differences could be related to different sorting algorithms and that very small amounts of contaminating material from $CD177^{pos}$ cells were analyzed by highly sensitive deep sequencing. Moreover, the g7497 SNP in the $CD177^{neg}$ sorted neutrophils in the Wu study was not homozygous for the T allele therefore not explaining the lack of CD177 protein. For individuals with bimodal CD177 neutrophils in our study, we observed that those who were homozygous for g7497A (SNP^{829}) and therefore harbored two alleles without potential stop codons showed monoallelic *CD177* expression (Fig. S1). Another interesting phenomenon that was not focus of our study is the occurrence of two $CD177^{pos}$ peaks. Our observations are in agreement with the literature in that ∼5% of individuals show this CD177 pattern (Moritz et al., 2010; Meyerson et al., 2013; Wu et al., 2016). The molecular basis of this phenomenon is unclear and needs to be elucidated in future studies.

MAE can follow a parent-of-origin pattern, where either the maternal or the paternal allele is imprinted (silenced), and all cells of a specific tissue, or even of the entire organism, actively express exclusively the other parental allele (Reik and Walter, 2001; Peters, 2014). In contrast, silencing of one allele can occur in a random fashion first recognized for X chromosomes, where female cells inactivate either the maternal or paternal X (Lyon, 1986). Recently, it became clear that random MAE also occurs in ∼5–10% of the autosomal loci (Gimelbrant et al., 2007). Our haplotype analysis revealed monoallelic *CD177* gene expression in blood neutrophils, where all neutrophils of a given individual had uniformly silenced either their maternal or paternal *CD177* allele. This issue was best illustrated in two siblings from one family who both showed MAE, but had silenced the opposite parental allele. These findings suggest a novel MAE pattern not described before. It was not truly imprinting because

biallelic *CD177* allele expression was detected. (H) ChIP assays were performed using antibodies to c-Jun, c-Fos, and c-Ets-1 in PMA-stimulated HeLa cells. (I) Nonactivated HeLa cells were transfected with empty pcDNA3 vector, c-Jun, c-Fos, c-Ets-1, and combinations thereof ($n = 3$ independent experiments). *CD177* gene expression was determined by qRT-PCR. (J) *CD177* gene expression by qRT-PCR was assessed in human blood neutrophils stimulated with buffer control (Bu) or 100 ng/ml G-CSF for 90 min, respectively. When indicated, G-CSF–stimulated cells were pretreated with buffer control (DMSO) or 20 µM JNK II inhibitor (CAS 129–56-6) for 30 min, respectively ($n = 3$ independent experiments). Data in A, E, F, I, and J were displayed as mean ± SEM and were analyzed using one-way ANOVA. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. Data in H were displayed ± SEM and were analyzed using Student's *t* test. *, $P < 0.05$.

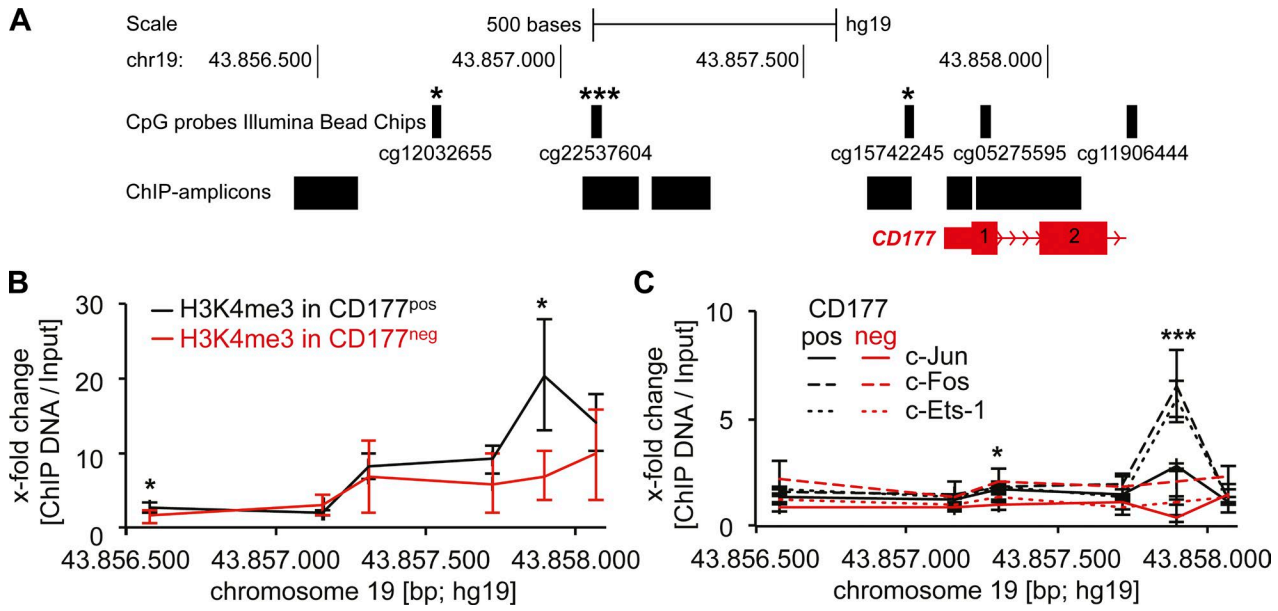

Figure 4. **Differential CpG and histone methylation, and AP-1 TF binding in the *CD177* promoter of CD177^{neg} and CD177^{pos} neutrophil subsets.** (A) Whole-genome DNA methylation analysis in CD177^{neg} versus CD177^{pos} neutrophils separated from CD177 bimodal individuals by magnetic cell sorting was performed using Illumina methylation chips. The localization of the 5 CpG probes (cg, CpG cluster number) within the *CD177* promoter and in the *CD177* gene that were present on the chip are indicated. Three of the five CpGs were significantly more methylated in the CD177^{neg} neutrophils compared with the CD177^{pos} subset (n = 6 different neutrophil donors). (B) ChIP assays were performed with the histone H3K4me3 mark for open chromatin in the *CD177* promoter region of CD177^{pos} (black lines) and CD177^{neg} (red lines) neutrophils separated from a CD177 bimodal donor (n = 3 different neutrophil donors). (C) ChIP analysis for c-Jun, c-Fos, and c-Ets-1 binding was performed in CD177^{pos} (black lines) and CD177^{neg} (red lines) neutrophils separated from CD177 bimodal donors using specific antibodies to c-Jun, c-Fos, and c-Ets-1, respectively (n = 4 different neutrophil donors). Data in A, B, and C were analyzed using Student's t test. *, P < 0.05; ***, P < 0.001; ±SEM is shown.

we observed either maternal or paternal silenced alleles. The pattern is also not truly random MAE because this pattern implies that different clonal populations derived from a particular cell type express stochastically the maternal or the paternal, and some even both alleles (Deng et al., 2014). Based on Sanger sequencing, together with two quantitative assays that used thresholds from the literature of 70% for a monoallelic call (Reinius and Sandberg, 2015), we did not find a mixed expression of maternal and paternal alleles within the entire neutrophil population of a given individual. However, if the quantitative assays were interpreted as strongly biased *CD177* transcriptional activity based on the inherited allele, two CD177^{pos} neutrophil populations with markedly different *CD177* mRNA and protein would result. In this case, one would possibly expect a more skewed peak of the CD177^{pos} neutrophils in the flow cytometry experiments. Neutrophils comprise the largest leukocyte subset with the shortest lifespan and an estimated daily production rate of 10^{11} cells (Tak et al., 2013). Despite the rapid neutrophil turnover, we found that the allelic choice did not change over time when measured in a given individual. We observed that undifferentiated CD34^{+} HSC, the neutrophil progenitors, transcribed both *CD177* alleles and that one allele was silenced during neutrophil differentiation. Thus, the decision as to which of the two parental alleles is silenced has to be made 10^{11} times per day lifelong. The fact that the choice of the activated allele remains constant during neutrophil differentiation and maturation suggests a strongly regulated silencing mechanism. *CD177* is the first neutrophil gene shown to follow such a stringent and stable MAE. Interestingly, CD177 is an antigen receptor and the initial autosomal random MAE examples came from the antigen receptors of B and T cells (Pernis et al., 1965; Rajewsky, 1996). It was subsequently suggested that surface receptors are prone to autosomal MAE (Chess et al., 1994; Pereira et al., 2003; Gimelbrant et al., 2007). Biological effects could be mediated either through dosage differences or by expressing only one out of two functionally nonequivalent parental alleles. Conceptually, these effects would increase phenotypic variation and cellular diversity, but also harbor a risk when only a dysfunctional allele is expressed (Reinius and Sandberg, 2015). It is conceivable that MAE of *CD177* has clinical relevance. In ANCA autoimmune vasculitis, heterozygous *CD177* SNPs or mutations and the choice of which allele is expressed could affect PR3 binding and thereby shape antigenicity and binding of PR3-ANCA. In fact, genes with MAE are particularly prone to mutations (Savova et al., 2016). Heterozygous *CD177* mutations and the allelic choice could also lead to incomplete penetrance of disease phenotypes. Similar mechanisms could be at work for the presentation of CD177 alloantigen epitopes.

After having excluded DNA sequence abnormalities and CNV, epigenetic modifications became candidates for allelic *CD177* gene silencing (Reik and Walter, 2001; Eckersley-Maslin and Spector, 2014; Reinius and Sandberg, 2015; Gendrel et al., 2016). Neutrophils rapidly undergo apoptosis in vivo and in culture, preventing epigenetic studies in these short-lived primary cells (Fig. S2 B). To identify these silencing mechanisms, we took advantage from the observation that activated HeLa cells expressed *CD177* in a monoallelic manner. We characterized the promoter region upstream of the *CD177* TSS that was important for gene expression and contained 16 CpGs. Our data indicate that in vitro DNA methylation at CpG dinucleotides in the promoter controlled *CD177* gene expression by c-Jun and c-Fos. Interestingly, pharmacologic HeLa cell demethylation, certainly not exclusively acting on the *CD177* promoter, activated biallelic *CD177* expression providing additional evidence for a role of DNA methylation in gene and single allele silencing. These data support the contention that DNA methylation at CpGs in the *CD177* promoter silenced two alleles in $CD177^{neg}$ and one allele in the $CD177^{pos}$ neutrophil subset, respectively. Most importantly, these epigenetic control mechanisms were differentially regulated in the two CD177 neutrophil subsets. The promoter of the $CD177^{neg}$ subset showed significantly increased CpG and histone methylation and abrogated AP-1 TF binding. In contrast, the $CD177^{pos}$ neutrophil subset actively transcribed *CD177* in a monoallelic fashion.

In summary, we have identified DNA, histone methylation and AP-1 TF binding that control *CD177* gene expression and explain the two distinct CD177 neutrophil subsets in bimodal individuals that are of clinical significance. In addition, we describe a novel MAE pattern for *CD177* that differs from classical imprinting and random MAE in its stable choice of either parental allele.

MATERIALS AND METHODS

Neutrophil isolation

Blood neutrophils from healthy human donors were obtained after due approval by IRB (Institutional Charité University Ethics Committee, EA1/277/11 and EA3/010/06) and after written, informed consent, and isolated as described previously (von Vietinghoff et al., 2007).

HeLa cell culture, stimulation, and transfection

HeLa cells were cultured in DMEM supplemented with 10% FCS, 100 U/ml penicillin, and 100 µg/ml streptomycin and treated with 100 ng/ml PMA and 10 µM 5′Aza-2-deoxycytidine (Sigma-Aldrich) as indicated. HeLa cells were transiently transfected with 67 ng c-Jun, c-Fos, and c-Ets-1 plasmids, or empty pcDNA3 vector control, respectively. All cells received a total of 2 µg plasmid using Fugene HD (Roche) according to the manufacturer's instructions.

Flow cytometry and magnetic neutrophil sorting

CD177 membrane expression was assessed by flow cytometry of either isolated neutrophils or in 100 µl whole blood after hypotonic red blood cell lysis using a FITC-labeled anti-CD177 antibody (clone MEM166; Biozol) as described before (von Vietinghoff et al., 2007). CD177 neutrophil subsets were purified using anti-CD177 abs (clone MEM166; Exbio), anti-CD66b (Dako), anti-CD9 abs (Beckman Coulter), rat anti–mouse IgG microbeads (Miltenyi Biotech), and LD columns (Miltenyi Biotech) according to the manufacturer's instructions. Highly pure neutrophils were prepared by density gradient purification, followed by depletion of CD9-positive eosinophils. $CD177^{pos}$ neutrophils were thereafter positively selected for CD177. $CD177^{neg}$ neutrophils were positively selected from this CD177-depleted preparation for CD66b. Mature neutrophil-differentiated $CD34^+$ HSC were purified by FACS using a directly labeled FITC anti-CD16 antibody (BioLegend) and an anti-CD177 antibody (Santa Cruz Biotechnology). When indicated neutrophils were stimulated with 100 µg/ml human granulocyte colony-stimulating factor (G-CSF; PeproTech) or in combination with 20 µM c-Jun N-terminal kinase inhibitor (JNK Inhibitor II, CAS 129–56-6; Merck). 10 µM 5′Aza-2-deoxycytidine was performed as described for HeLa cells. Apoptosis was measured with AnnexinV staining (BD) according to the manufacturer's manual and using flow cytometry.

Sibling testing

DNA testing was performed by an accredited laboratory for forensic genetics (Institut für Medizinische Molekulare Diagnostik und Forensische Genetik, Berlin, Germany) using the Power Plex ESX-17 system (Promega).

Differentiation of $CD34^+$ stem cells from umbilical cord blood into neutrophils

$CD34^+$ stem cells were isolated from cord blood, expanded, and differentiated as described previously (von Vietinghoff et al., 2007). Neonatal neutrophils were isolated from cord blood by density gradient centrifugation as described for blood neutrophils.

Isolation of DNA, mRNA, cDNA generation, and sequencing

Total RNA was extracted using QIAzol and the RNeasy Purification kit (QIAGEN). RNA was treated by deoxyribonuclease I (QIAGEN). cDNA synthesis was performed using hexanucleotide primers and Superscript III RT following the manufacturers protocol (Thermo Fisher Scientific). Genomic DNA was isolated using 5 M sodium perchlorate solution, DNA extraction by chloroform and DNA precipitation by isopropanol. For methylation array analysis genomic DNA was isolated using QIAGEN genomic DNA Isolation kit (QIAGEN). *CD177* long templates were amplified by PCR using 250 ng genomic DNA, specific *CD177*-43.857.788-F and *CD177*-43.870.898-R primers and Elongase (Thermo Fisher Scientific) in a total volume of 25 µl. PCR products

were purified with S.N.A.P. Purification kit (Life Technologies GmbH). *CD177* short products were amplified from 20 ng of *CD177* long templates or 50–100 ng cDNA with specific primers (Table S3) using Advantage-GC 2 PCR kit (Takara Bio Inc.). *CD177* PCR products were sequenced according to Sanger method using the Big Dye Terminator Cycle Sequencing kit v1.1 and analyzed on a 3130xl Genetic Analyzer (both from Applied Biosystems). Quantitative allele analysis by pyrosequencing was performed by the bioanalytical services laboratory (Varionostic GmbH) using four different SNP assays with template-specific PCR and sequencing primers (Table S3) and the Q24 System (QIAGEN). All SNP analyses were generated by PyroMark Q24 software.

Quantitative RT-PCR

For quantitative RT-PCR (qRT-PCR) *Taq*Man technology (Applied Biosystems) was used with oligonucleotides and probes for human *CD177* and human *18S* (Table S3), and TaqMan Fast Universal PCR Master Mix (Applied Biosystems). Each sample was measured in triplicate and expression levels were normalized to *18S* expression. Quantification was performed using an Applied Biosystems 7500 Sequence detector and data were analyzed using SDS 7500 software and ΔΔCt comparative analysis as described by Applied Biosystems.

Digital PCR

Quantification of allele-specific mRNA expression was performed using the QuantStudio 3D Digital PCR System (Thermo Fisher Scientific). SNP^{49} (rs45441892) was detected by the human TaqMan SNP Genotyping Assay C_27850890_10 and SNP^{156} (rs45571738) by the human TaqMan SNP Genotyping Assay C_27837236_10, respectively. Each reaction mix for one QuantStudio 3D Digital PCR chip v2 consisted of QuantStudio 3D Digital PCR Master Mix v2 (Thermo Fisher Scientific), specific human TaqMan SNP Genotyping Assay (primer/probe mix), template cDNA or gDNA with final concentration at 3.45 ng/µl and PCR-grade water in a final volume of 14.5 µl. PCR conditions were as follows: stage 1 enzyme activation, 96°C for 10 min; stage 2 annealing/extension and new denaturation at 54°C (SNP^{49}) or 58°C (SNP^{156}) for 2 min and 98°C for 30 s (39 cycles); stage 3 annealing/extension 60°C for 2 min and storage at 10°C. Each sample was analyzed using a separate 20,000 times compartmented QuantStudio 3D Digital PCR chip v2 and the AnalysisSuite Software (Thermo Fisher Scientific). The expressed allele amounts were presented as copy numbers per microliter PCR mixture.

DNA and cDNA sequencing

DNA and cDNA sequencing was performed from the *CD177* PCR products treated with shrimp alkaline phosphatase (SAP; Affymetrix) and exonuclease I (NEB). After enzyme inactivation, the PCR products were subjected to DNA sequencing using BigDye Terminator v1.1 Cycle Sequencing kit from Applied Biosystems. Purification of the samples was done with ZR DNA Sequencing Clean-up kit (ZYMO Research). DNA sequencing was performed with a 16-capillary sequencer 3130xl Genetic Analyzer (Applied Biosystems).

5′ RACE PCR

5′ RACE PCR was performed from neutrophil total RNA using QIAzol (QIAGEN), the GeneRacer kit, specific primers (Table S3), and reverse transcribed using Superscript III RT (Life Technologies GmbH). PCR fragments were cloned into a pDrive vector (QIAGEN) and sequenced as described in the previous section.

DNA methylation analysis

Genomic DNA was purified by using QIAGEN genomic DNA Isolation kit (QIAGEN). Genome-wide methylation analysis was performed by LIFE & BRAIN GmbH using an Infinium Human Methylation 450 BeadChip (Illumina).

SDS-PAGE, Coomassie staining, and immunoblot analysis

Cell lysis, SDS-PAGE, and immunoblots were performed as previously described (Jerke et al., 2015). Immunoblots were developed with a monoclonal rabbit anti-PR3 antibody (clone 4A5; Wieslab), an anti-CD177 mAb (clone MEM166, Exbio), or a polyclonal anti-CD177 (R&D Systems) as indicated and visualized by enhanced chemiluminescence (Thermo Fisher Scientific).

Reporter assays

10^4 cells per well were seeded into 96-well plates 24 h before transfection. HeLa cells were transiently transfected with the indicated *CD177* promoter plasmids, as well as with empty CpG-free methylation vector in equal molarities (55.14 amol). The *CD177* promoter luciferase constructs were transfected with Fugene HD according to the manufacturer's recommendations (Roche). For controlling the transfection efficiency, we transfected each well with 8 ng pRL-TK (Promega). Cell lysates were analyzed using the Dual-Luciferase Reporter Assay System (Promega) and the Infinite M200 PRO Multimode Microplate Reader from Tecan. To normalize reporter data, a quotient of the luciferase and the Renilla signal was calculated for each well.

Chromatin immunoprecipitation

3×10^7 neutrophils or 3×10^7 PMA-stimulated HeLa cells were treated with 0.4% formaldehyde to cross-link proteins and DNA. Chromatin was sonicated with Bioruptor Plus sonication device (Diagenode). 4×10^7 magnetic Dynabeads M-280 sheep anti–rabbit IgG (Thermo Fisher Scientific) were overnight preincubated with 5 µg anti-H3K4me3, 10 µg anti–c-Jun, 10 µg anti-c-Fos, 10 µg anti–c-Ets-1 or 5 µg/10 µg anti-IgG control ChIP-tested antibodies (Abcam). After washing of Dynabead-antibody samples, 50 µg chromatin was added to each sample and incubated overnight. 1 and 10% of the chromatin samples served as input. Antibody-Dynabeads bound DNA

was eluted in 1% SDS buffer and incubated with RNase A (Thermo Fisher Scientific) and Proteinase K (NEB). DNA was isolated by phenol/chloroform extraction and analyzed by quantitative RT-PCR using Fast SYBR Green Master Mix and specific and control primers (Table S3) on an ABI Prism 7500 Fast System (Applied Biosystems). The relative signals of the specific PCR product was expressed as percent of input chromatin using raw Ct values and was normalized for the control IgG.

Statistical analysis

Results are given as mean ± SEM. Comparisons between multiple groups were done using ANOVA and appropriate post-hoc tests or differences between experimental groups were analyzed by Student's *t* test. Differences were considered significant if $P < 0.05$. The dPCR results were given as poisson plus ratio with confidence intervals according to the AnalysisSuite Software (Thermo Fisher Scientific).

Online supplemental material

Fig. S1 shows the genome-wide single nucleotide polymorphisms (SNPs) analysis of sorted $CD177^{neg}$ and $CD177^{pos}$ neutrophil subsets and the haplotype analysis of the *CD177* gene. Fig. S2 presents haplotype analyses and sibling testing of an informative family with respect to the allelic choice of the *CD177* MAE as well as 5-Aza-2-deoxycytidin (5-Aza) treatment of primary human neutrophils. Table S1 lists SNPs identified in the *CD177* exons by sequencing. Table S2 shows probes in the *CD177* promoter and gene body that are covered by the Methylation450 Bead Chip. Table S3 lists all oligonucleotides for PCR assays.

ACKNOWLEDGMENTS

We thank Prof. Dr. Michael Rehli (Department of Internal Medicine III, University Hospital Regensburg, F.-J.-Strauss Allee 11, D-93053 Regensburg) for the CpG free luciferase reporter vector.

This work was supported by DFG grant KE 576/8-1 and an ECRC grant.

The authors declare no competing financial interests.

Author contributions: R. Kettritz, S. Bähring, P.G. Maass, and C. Eulenberg-Gustavus designed experiments and analyzed data. C. Eulenberg-Gustavus performed experiments and P.G. Maass and S. Bähring assisted with experiments. R. Kettritz and C. Eulenberg-Gustavus wrote the manuscript and R. Kettritz funded the study. F.C. Luft, P.G. Maass, S. Bähring, R. Kettritz, and C. Eulenberg-Gustavus revised the manuscript.

Submitted: 13 July 2016

Revised: 1 February 2017

Accepted: 12 April 2017

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SUPPLEMENTAL MATERIAL

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A

Number of individual		Number of SNPs called	Number of concordant SNPs	Percent of concordance [%]
CD177 negative neutrophils	CD177 positive neutrophils			
1	1	904728	904334	99.96
2	2	901303	899909	99.85
3	3	902183	900757	99.84
4	4	900110	897918	99,76
5	5	903039	902126	99.90
Average:				99.86 p<0.05

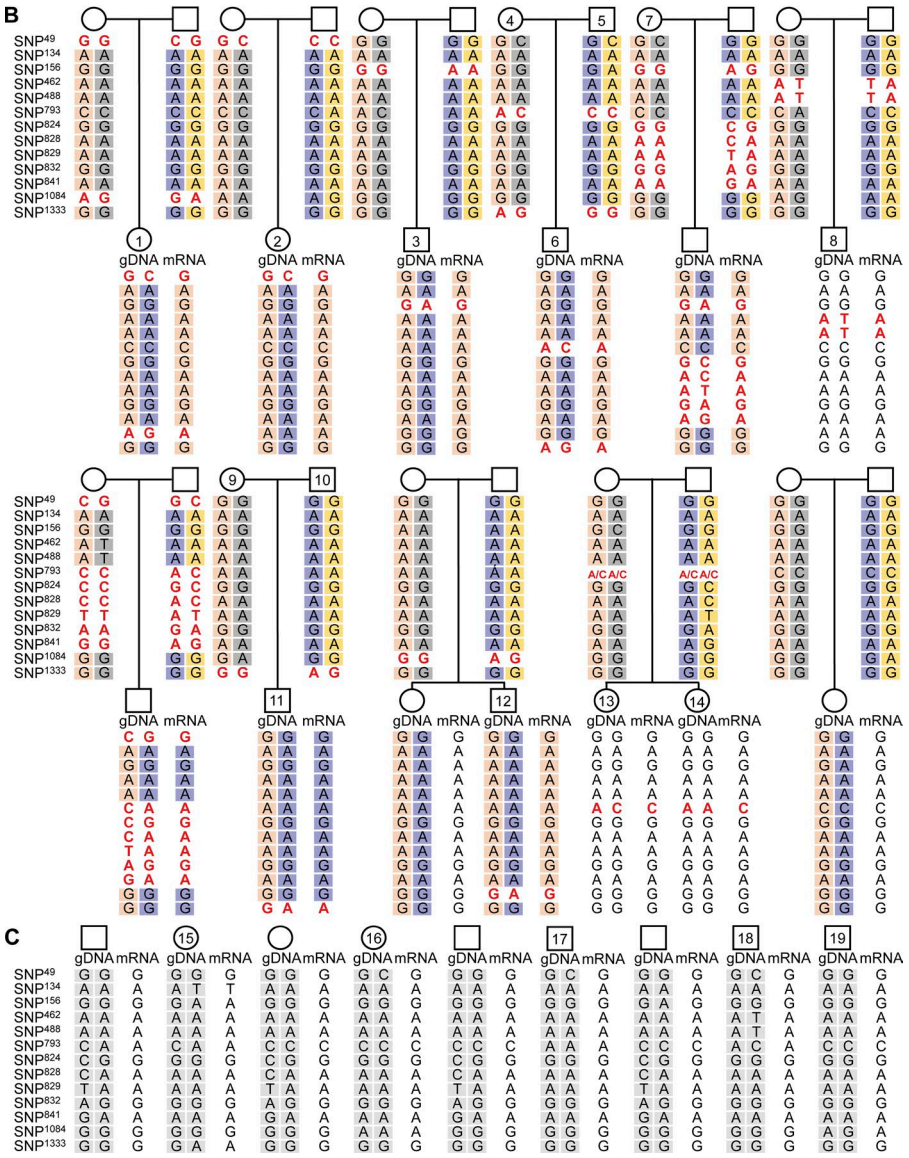

Figure S1. **Genome-wide SNPs analysis of CD177^{neg} and CD177^{pos} neutrophil subsets and haplotype analysis of the *CD177* gene.** (A) Genome-wide SNP analysis using an Affimetrix SNP array 6.0 was performed in the two sorted CD177 neutrophil subsets from five different individuals. Shown are the number of SNPs called and the number of concordant SNPs between the two subsets in a given individual (five biological replicates, 99.9% concordance by Fisher's exact test). (B) Haplotype analysis of the *CD177* gene. Analyses were performed in 12 families with 17 offspring, and (C) 9 additional individuals. 13 SNPs are depicted in the haplotype analysis that were selected because they were informative with respect to the allelic choice in at least one trio. The informative parental haplotype that is inherited by the offspring is boxed in light orange (maternal) and blue (paternal), and the SNP positions are indicated. SNPs that were informative for the allelic choice in a given trio are marked in red. Individuals numbered 1–19 are homozygous for g7497A (SNP^{829}). Note that these individuals had several informative SNPs indicating monoallelic *CD177* expression (see Discussion).

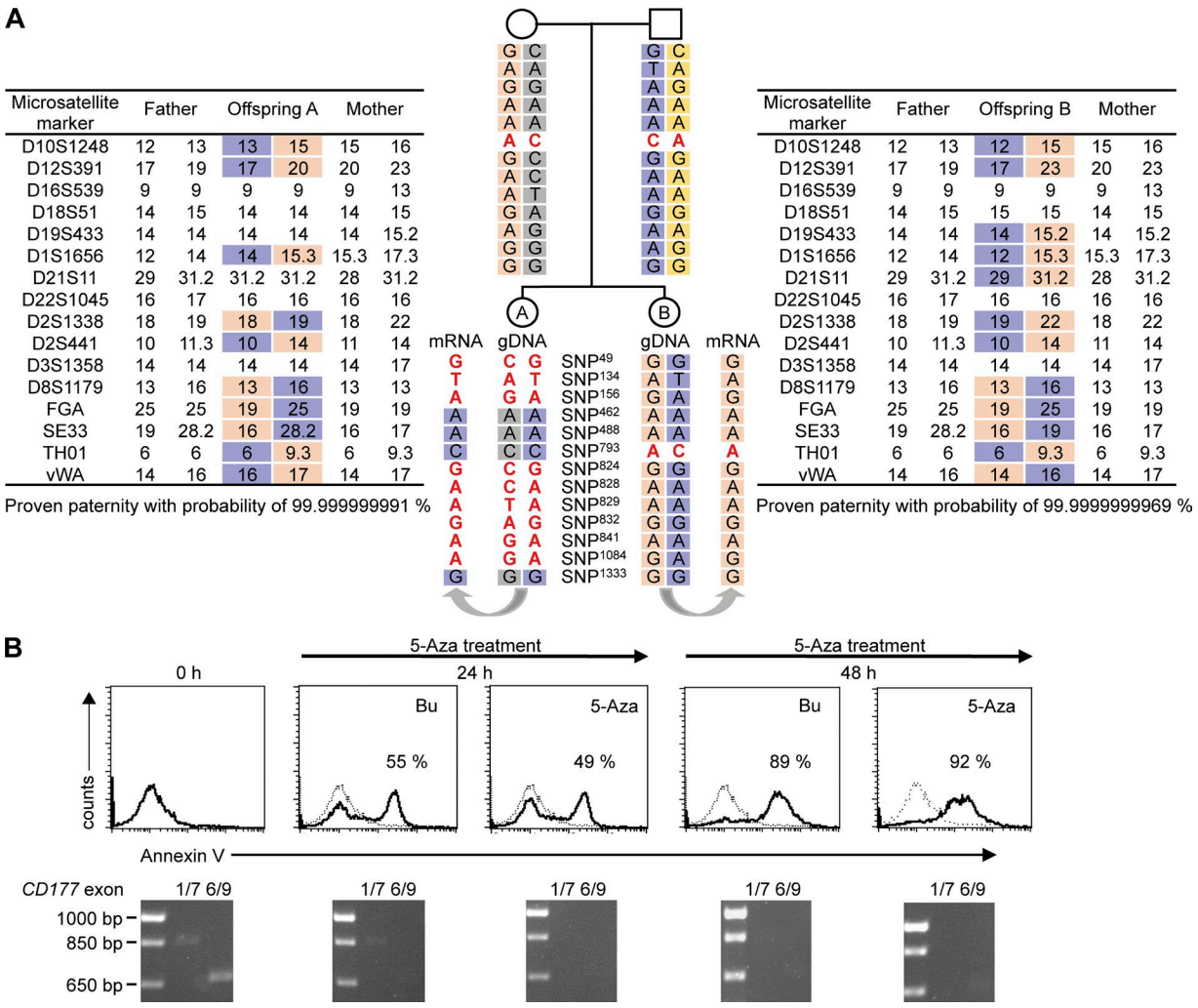

Figure S2. **Haplotype analysis, sibling testing of an informative family with respect to the allelic choice of the *CD177* MAE, and 5-Aza-2-deoxycytidin (5-Aza) treatment of primary human neutrophils.** (A) Haplotype analysis of a family with two siblings. The informative parental haplotype that is inherited by the offspring is boxed in light orange (maternal) and blue (paternal). SNPs that were informative for the allelic choice are marked in red. One offspring showed MAE of the paternal (left) and one of the maternal allele (right). The corresponding tables show the microsatellite markers obtained by Power Plex ESX-17 for both offspring establishing full-sibling status. Red and blue color-coding as described above. (B) Primary human neutrophils were treated with buffer (Bu) or 10 µM 5-Aza-2-deoxycytidin (5-Aza) for 24 h and 48 h, respectively. The percentage of Annexin V–positive apoptotic neutrophils was assessed by flow cytometry, and histograms are depicted. mRNA was purified and subjected to *CD177* PCR. Freshly isolated cells, but not 5-Aza–treated cells, showed a PCR product. One of two representative experiments is given.

Table S1. **SNPs identified in the *CD177* exons by sequencing**

SNP position	Allele	SNP-ID no.	Location in the *CD177* gene	Genomic position on chromosome 19 (hg19)
SNP[49]	**G/C**	**rs45441892**	**exon 1**	**43.857.873-43.857.873**
SNP[134]	**A/T**	**rs45553433**	**exon 2**	**43.858.044-43.858.044**
SNP[156]	**G/A**	**rs45571738**	**exon 2**	**43.858.066-43.858.066**
SNP[387]	C/T	no	exon 3	43.858.510-43.858.510
SNP[462]	**A/T**	**no**	**exon 4**	**43.859.853-43.859.853**
SNP[488]	**A/T**	**no**	**exon 4**	**43.859.879-43.859.879**
SNP[593]	T/G	rs71337594	exon 5	43.860.192-43.860.192
SNP[652]	G/A	rs199668750	exon 5	43.860.251-43.860.251
SNP[656]	T/G	rs200662237	exon 5	43.860.255-43.860.255
SNP[664]	T/G	rs73559882	exon 6	43.864.419-43.864.419
SNP[667]	C/T	no	exon 6	43.864.422-43.864.422
SNP[752]	T/C	rs57802244	exon 6	43.864.507-43.864.507
SNP[793]	**C/A**	**rs10425835**	**exon 6**	**43.864.548-43.864.548**
SNP[798]	T/C	no	exon 6	43.864.553-43.864.553
SNP[824]	C/G	rs200660811	exon 7	43.865.316-43.865.316
SNP[828]	C/A	rs587670082	exon 7	43.865.320-43.865.320
SNP[829]	T/A	rs201821720	exon 7	43.865.321-43.865.321
SNP[832]	A/G	rs200145410	exon 7	43.865.324-43.865.324
SNP[841]	G/A	rs201266439	exon 7	43.865.333-43.865.333
SNP[1084]	G/A	rs61625631	exon 8	43.865.692-43.865.692
SNP[1114]	C/T	rs61002457	exon 8	43.865.722-43.865.722
SNP[1333]	A/C/G/T	rs78718189	exon 9	43.866.449-43.866.449

SNP-ID is SNP identification number. SNP used for haplotype analysis are shown in bold.

Table S2. **Probes in the *CD177* promoter and gene body that are covered by the Illumina Infinium HumanMethylation450 BeadChips used for genome-wide DNA methylation**

Probe name	P-value	Student's *t* test	Mean (N)	Mean (P)	Mean ratio (N/P)	Mean diff (N-P)	UCSC ref gene	hg19 (bps) chr.19
cg22537604	7.10E-07	30.51	0.94	-0.80	3.3	1.74	*CD177*	43857074
cg15742245	2.98E-05	14.33	2.80	1.07	3.3	1.73	*CD177*	43857717
cg12032655	3.64E-05	13.76	-0.49	-1.58	2.1	1.09	*CD177*	43856746
cg05275595	4.92E-04	8.00	0.38	-0.21	1.5	0.59	*CD177*	43857874
cg11906444	4.44E-01	-0.83	1.57	1.64	1.0	-0.07	*CD177*	43858174

cg means CpG cluster number.

Table S3. **Oligonucleotides for PCR assays**

Name	5′–3′ sequence
RACE Abridged Anchor Primer	GGCCACGCGTCGACTAGTACGGGIIGGGIIGGGIIG
Abridged Universal Primer	GGCCACGCGTCGACTAGTAC
Universal Amplification Primer	CUACUACUACUAGGCCACGCGTCGACTAGTAC
5′ RACE *CD177*-102R	CACTCCTGGCAGTGGGAGGATGAA
5′ RACE *CD177*-265R	CCTTGGAGAGCACCAGGCTCACTT
5′ RACE *CD177*-616R	GTGTCCCATTGAGCAGGTTGCAAACT
qRT-PCR human *CD177*-F	TTGATGCTCATTGAGAGCGG
qRT-PCR human *CD177*-R	GCCTCCGTGCAGCCCT
qRT-PCR human *CD177*-probe	FAM-CCCCAAGTGAGCCTGGTGCTCTCC-TAMRA
qRT-PCR human *18S*-F	ACATCCAAGGAAGGCAGCAG
qRT-PCR human *18S*-R	TTTTCGTCACTACCTCCCCG
qRT-PCR human *18S*-probe	FAM-CGCGCAAATTACCCACTCCCGAC-TAMRA
CD177-43.857.788-F	GCTGGCTGCTTAAGGGCTGGTATAA
CD177-43.870.898-R	CATCCTGTACGGGGAAATCAGACTTG
CD177-43.857.825-F	CTGCTGAAAAAGCAGAAAGAGA
CD177-43.858.437-R	ATCCGGTGCTCAGTGACG
CD177-43.858.316-F	AGGCCTGACCTCCATCCT
CD177-43.859.013-R	CTGTGTTCACAAGCTGTTCCA
CD177-43.859.487-F	AACTCCTGACCTCGTGATCC
CD177-43.860.178-R	GCATCCCTGGACTCTCAGAT
CD177-43.860.080-F	CTCTGAGGGTTGGGTGGTC
CD177-43.860.770-R	CCACCATGGCTTCCTGTT
CD177-43.864.250-F	TGGGATTTCGACTCCCAAGT
CD177-43.864.943-R	TGTTTGTTTCCTGTTTCTCAAGG
CD177-43.864.829-F	TCAGTGGCTTCATACATTCTGG
CD177-43.865.520-R	GTGTCTGGGCCTCATTTCTC
CD177-43.865.418-F	CCTCGGACCTGTGCAATAGT
CD177-43.866.126-R	AGCTCCAGCTCCTCAGACC
CD177-43.866.021-F	CTCTGGACTCCTGGGTCTGA
CD177-43.866.676-R	CCTCTCCCATAGGGCAAGTC
CD177-43.857.862-F	GGGTCATGAGCGCGGTATTAC
CD177-43.864.453-F	CACACGGAAACTTGGCTCAAGAAC
CD177-43.865.382-R	GGAGGGGCTGAGTGGATGGTGG
CD177-43.865.688-F	GGGCGCCACTCATTGTTATG
CD177-43.866.478-R	ATAGAGTTAGCAGGAAGGGCAAAC
Pyro-SNP49-134-156-F	AGCCACAGACGGGTCATGAG
Biotin-Pyro-SNP49-134-156-R	Biotin-CTGGTGTTCTTAGGGGTCCATTG
PyroSeq-SNP49-134-156-F	AGACGGGTCATGAGC
Pyro-SNP462-488-F	AACTCCCTCCCGCTTTGG
Biotin-Pyro-SNP462-488-R	Biotin-GGTCCCCTTGGGGCAGAT
PyroSeq-SNP462-488-F	CCAGTCTGCTTGTCTATG
Pyro-SNP793-F	GGCAGGTGTGTCAGGAGAC
Biotin-Pyro-SNP793-R	Biotin-CCAGGGTTGATGTGAGTCCTAC
PyroSeq-SNP793-F	GAGACGCTGCTGCTC
Biotin-Pyro-SNP1084-F	Biotin-GCTCCCCCCGAATGACCT
Pyro-SNP1084-R	AGCCCACCTCCTGAGAGATGA
PyroSeq-SNP1084-F	CCATCATAACAATGAGTGG
Luciferase-P1-F	TGCGTGGGAATCCGCCTTCCCTCTTCTGCTTCT
Luciferase-P2-F	TGCGTGGGATCCTCCTGGTGGTAGGAAACTGG
Luciferase-P3-F	TGCGTGGGATCCGGGTCAAGATGCCACAGTTT
Luciferase-P4-F	TGCGTGGGATCCAAGAAAGGGGGTCCCTGATAG
Luciferase-P5-F	TGCGTGGGATCCGGCTGCTTAAGGGCTGGTAT
Luciferase-P6-F	TGCGTGGGATCCGTCATGAGCGCGGTATTACT
Luciferase-R	CACGCAGGATCCCACAGGGATCAAGGGACTGA
M13-For	GTAAAACGACGGCCAG
M13-Rev	CAGGAAACAGCTATGAC
ChIP1–43.856.451-F	TTGCAAGTCACATTCATTTCTCT
ChIP1–43.856.582-R	AGGAAGGAACCTGGGGTATCT
ChIP2–43.857.044-F	GGGAAGACAGTGGAGGGTAGA
ChIP2–43.857.159-R	CCACCTCTGTACCCCAGATG
ChIP3–43.857.186-F	ACTGCCTTCCCAAACTACTGG
ChIP3–43.857.307-R	AGAAACTGTGGCATCTTGACC
ChIP4–43.857.630-F	GTCCTGGACCCTCCATCTG

Table S3. **Oligonucleotides for PCR assays** *(Continued)*

Name	5′–3′ sequence
ChIP4–43.857.720-R	GCCGCAGTGGCCTATCAG
ChIP5–43.857.792-F	GCTGCTTAAGGGCTGGTATAAA
ChIP5–43.857.896-R	CAGGAGGGCCAGCAGTAATA
ChIP6–43.857.862-F	GGGTCATGAGCGCGGTATTAC
ChIP6–43.858.070-R	GGGCAGGTCGGACACCTT
Ctrl-43.870.329-F	CTCATCCAGGAGTTATCGAGAATA
Ctrl-43.870.406-R	GAAATGAACCACAGCACTTCC
hACTgProm-H3K4-F	ACCGGCAGAGAAACGCGA
hACTgProm-H3K4-R	CGGAAAGATCGCCATATATGGAC
hALDOA-H3K4-F	TCCTGGCAAGATAAGGAGTTGAC
hALDOA-H3K4-R	ACACACGATAGCCCTAGCAGTTC

ACT is actin and ALDOA aldolase A.