

SUPPLEMENTAL MATERIAL

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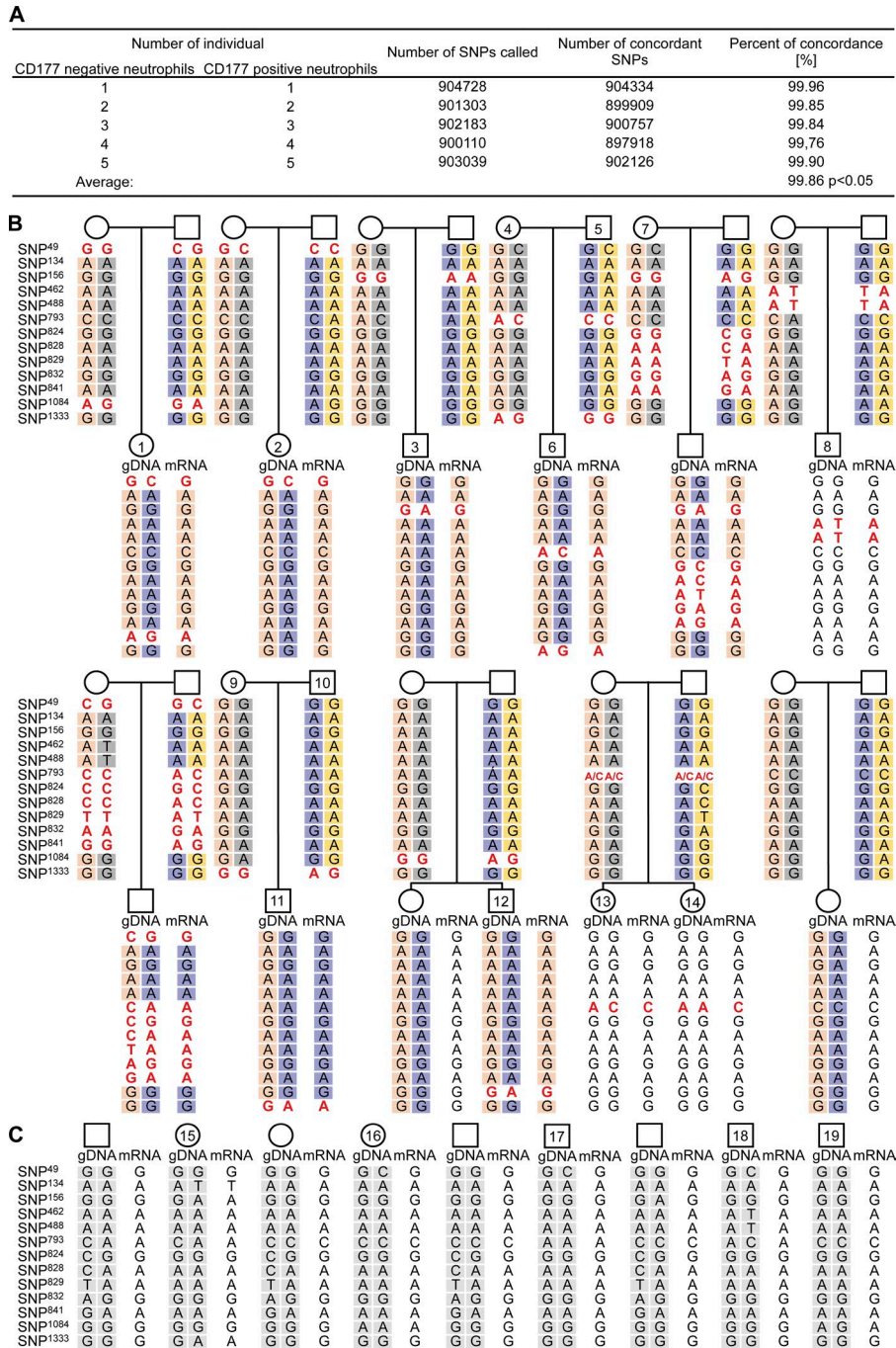


Figure S1. **Genome-wide SNPs analysis of CD177<sup>neg</sup> and CD177<sup>pos</sup> neutrophil subsets and haplotype analysis of the CD177 gene.** (A) Genome-wide SNP analysis using an Affimetrix SNP array 6.0 was performed in the two sorted CD177 neutrophil subsets from five different individuals. 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<sup>829</sup>). Note that these individuals had several informative SNPs indicating monoallelic *CD177* expression (see Discussion).

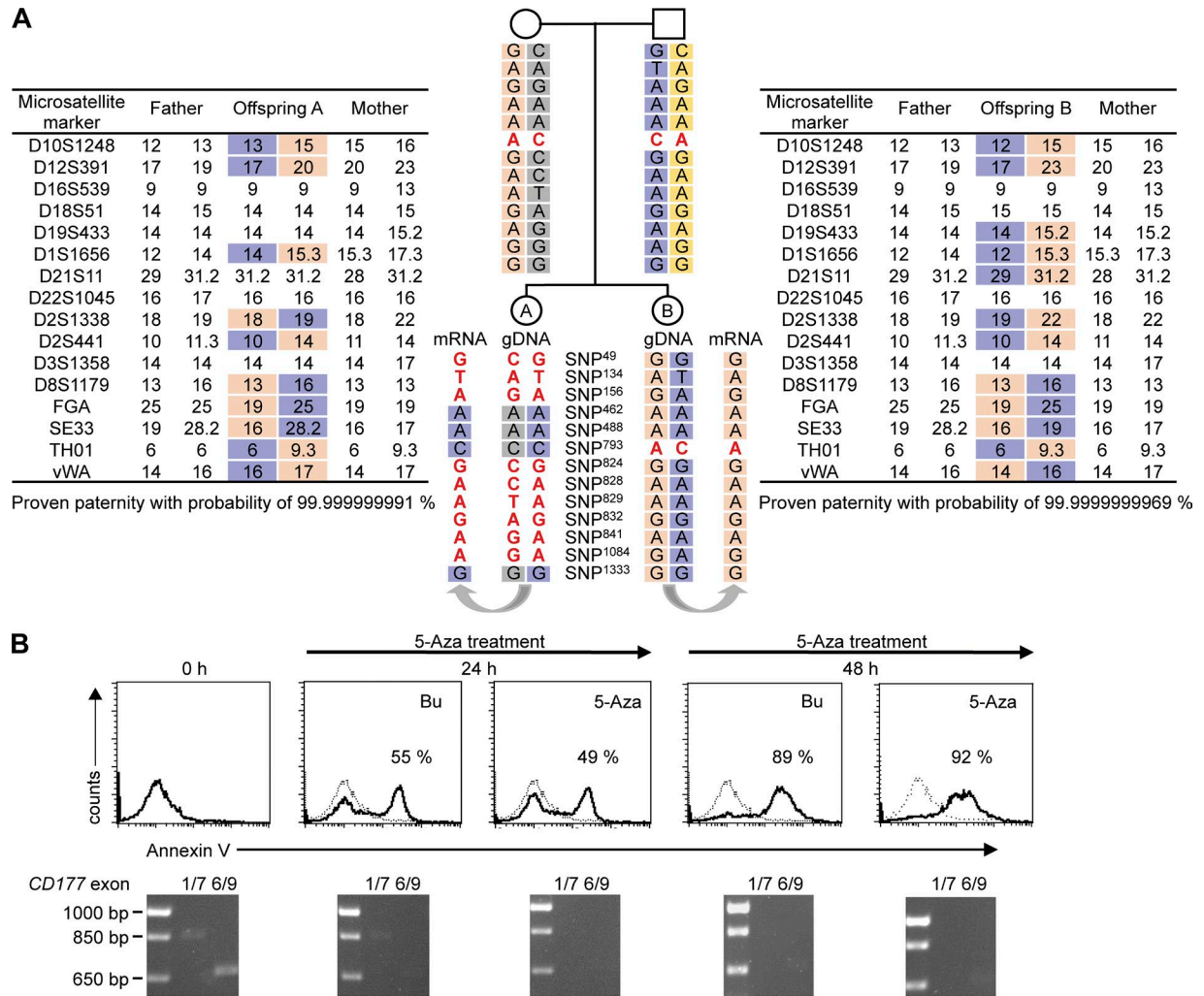


Figure S2. **Haplotype analysis, sibling testing of an informative family with respect to the allelic choice of the *CD177* MAE, and 5-Aza-2-deoxycytidin (5-Aza) treatment of primary human neutrophils.** (A) Haplotype analysis of a family with two siblings. The informative parental haplotype that is 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  $\mu$ M 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 <i>CD177</i> gene | Genomic position on chromosome 19 (hg19) |
|---------------------|---------|-------------|-----------------------------------|--|
| SNP <sup>49</sup>   | G/C     | rs45441892  | exon 1                            | 43.857.873–43.857.873                    |
| SNP <sup>134</sup>  | A/T     | rs45553433  | exon 2                            | 43.858.044–43.858.044                    |
| SNP <sup>156</sup>  | G/A     | rs45571738  | exon 2                            | 43.858.066–43.858.066                    |
| SNP <sup>387</sup>  | C/T     | no          | exon 3                            | 43.858.510–43.858.510                    |
| SNP <sup>462</sup>  | A/T     | no          | exon 4                            | 43.859.853–43.859.853                    |
| SNP <sup>488</sup>  | A/T     | no          | exon 4                            | 43.859.879–43.859.879                    |
| SNP <sup>593</sup>  | T/G     | rs71337594  | exon 5                            | 43.860.192–43.860.192                    |
| SNP <sup>652</sup>  | G/A     | rs199668750 | exon 5                            | 43.860.251–43.860.251                    |
| SNP <sup>656</sup>  | T/G     | rs200662237 | exon 5                            | 43.860.255–43.860.255                    |
| SNP <sup>664</sup>  | T/G     | rs73559882  | exon 6                            | 43.864.419–43.864.419                    |
| SNP <sup>667</sup>  | C/T     | no          | exon 6                            | 43.864.422–43.864.422                    |
| SNP <sup>752</sup>  | T/C     | rs57802244  | exon 6                            | 43.864.507–43.864.507                    |
| SNP <sup>793</sup>  | C/A     | rs10425835  | exon 6                            | 43.864.548–43.864.548                    |
| SNP <sup>798</sup>  | T/C     | no          | exon 6                            | 43.864.553–43.864.553                    |
| SNP <sup>824</sup>  | C/G     | rs200660811 | exon 7                            | 43.865.316–43.865.316                    |
| SNP <sup>828</sup>  | C/A     | rs587670082 | exon 7                            | 43.865.320–43.865.320                    |
| SNP <sup>829</sup>  | T/A     | rs201821720 | exon 7                            | 43.865.321–43.865.321                    |
| SNP <sup>832</sup>  | A/G     | rs200145410 | exon 7                            | 43.865.324–43.865.324                    |
| SNP <sup>841</sup>  | G/A     | rs201266439 | exon 7                            | 43.865.333–43.865.333                    |
| SNP <sup>1084</sup> | G/A     | rs61625631  | exon 8                            | 43.865.692–43.865.692                    |
| SNP <sup>1114</sup> | C/T     | rs61002457  | exon 8                            | 43.865.722–43.865.722                    |
| SNP <sup>1333</sup> | 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 <i>t</i> 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            | <i>CD177</i>  | 43857074          |
| cg15742245 | 2.98E-05 | 14.33                   | 2.80     | 1.07     | 3.3              | 1.73            | <i>CD177</i>  | 43857717          |
| cg12032655 | 3.64E-05 | 13.76                   | -0.49    | -1.58    | 2.1              | 1.09            | <i>CD177</i>  | 43856746          |
| cg05275595 | 4.92E-04 | 8.00                    | 0.38     | -0.21    | 1.5              | 0.59            | <i>CD177</i>  | 43857874          |
| cg11906444 | 4.44E-01 | -0.83                   | 1.57     | 1.64     | 1.0              | -0.07           | <i>CD177</i>  | 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 <i>CD177</i> -102R        | CACTCTGGCAGTGGGAGGATGAA              |
| 5' RACE <i>CD177</i> -265R        | CCTGGAGAGCACCAGGCTCACTT              |
| 5' RACE <i>CD177</i> -616R        | GTGTCCATTGAGCAGGTTGCAAACCT           |
| qRT-PCR human <i>CD177</i> -F     | TTGATGCTCATTGAGAGCGG                 |
| qRT-PCR human <i>CD177</i> -R     | GCCTCCGTGCAAGCCCT                    |
| qRT-PCR human <i>CD177</i> -probe | FAM-CCCCAAGTGAGCCTGGTCTCC-TAMRA      |
| qRT-PCR human <i>18S</i> -F       | ACATCCAAGGAAGCGACGAG                 |
| qRT-PCR human <i>18S</i> -R       | TTTTCGTCACTACCTCCCCG                 |
| qRT-PCR human <i>18S</i> -probe   | FAM-CGCGCAAATTACCCACTCCCGAC-TAMRA    |
| <i>CD177</i> -43.857.788-F        | GCTGGCTGCTTAAGGCTGGTATAA             |
| <i>CD177</i> -43.870.898-R        | CATCCTGTACGGGAAATCAGACTTG            |
| <i>CD177</i> -43.857.825-F        | CTGCTGAAAAGCAGAAAGAGA                |
| <i>CD177</i> -43.858.437-R        | ATCCGGTGCTCAGTGACG                   |
| <i>CD177</i> -43.858.316-F        | AGGCCTGACCTCCATCCT                   |
| <i>CD177</i> -43.859.013-R        | CTGTGTTCAAGCTGTTCCA                  |
| <i>CD177</i> -43.859.487-F        | AACTCCTGACCTCGTATCC                  |
| <i>CD177</i> -43.860.178-R        | GCATCCCTGGACTCTCAGAT                 |
| <i>CD177</i> -43.860.080-F        | CTCTGAGGGTTGGGTGGTC                  |
| <i>CD177</i> -43.860.770-R        | CCACCATGGCTTCTGT                     |
| <i>CD177</i> -43.864.250-F        | TGGGATTCGACTCCCAAGT                  |
| <i>CD177</i> -43.864.943-R        | TGTTTGTTCCTGTTCTCAAGG                |
| <i>CD177</i> -43.864.829-F        | TCAGTGGCTCATACTCTGG                  |
| <i>CD177</i> -43.865.520-R        | GTGTCTGGGCTCATTCTC                   |
| <i>CD177</i> -43.865.418-F        | CCTCGGACCTGTGCAATAGT                 |
| <i>CD177</i> -43.866.126-R        | AGCTCCAGCTCCTCAGACC                  |
| <i>CD177</i> -43.866.021-F        | CTCTGGACTCCTGGGCTGA                  |
| <i>CD177</i> -43.866.676-R        | CCTCTCCATAGGGCAAGTC                  |
| <i>CD177</i> -43.857.862-F        | GGGTCATGAGCGCGGTATTAC                |
| <i>CD177</i> -43.864.453-F        | CACACGAAAATTGGCTCAAGAAC              |
| <i>CD177</i> -43.865.382-R        | GGAGGGGCTGAGTGGATGGTGG               |
| <i>CD177</i> -43.865.688-F        | GGGCGCACTCATTGTTATG                  |
| <i>CD177</i> -43.866.478-R        | ATAGAGTTAGCAGGAAGGGCAAAC             |
| Pyro-SNP49-134-156-F              | AGCCACAGACGGGTCATGAG                 |
| Biotin-Pyro-SNP49-134-156-R       | Biotin-CTGGTGTCTTAGGGTCCATTG         |
| PyroSeq-SNP49-134-156-F           | AGACGGGTCATGAGC                      |
| Pyro-SNP462-488-F                 | AACTCCCTCCCGCTTTGG                   |
| Biotin-Pyro-SNP462-488-R          | Biotin-GGTCCCTTGGGGCAGAT             |
| PyroSeq-SNP462-488-F              | CCAGTCTGTTGTCTATG                    |
| Pyro-SNP793-F                     | GGCAGGTGTGCAGGAGAC                   |
| Biotin-Pyro-SNP793-R              | Biotin-CCAGGGTGTGATGAGTCTAC          |
| PyroSeq-SNP793-F                  | GAGACGCTGCTGCTC                      |
| Biotin-Pyro-SNP1084-F             | Biotin-GCTCCCCGAATGACCT              |
| Pyro-SNP1084-R                    | AGCCACCTCCTGAGAGATGA                 |
| PyroSeq-SNP1084-F                 | CCATCATAACAATGAGTGG                  |
| Luciferase-P1-F                   | TGCGTGGGAATCCGCTTCCCTCTCTGCTTCT      |
| Luciferase-P2-F                   | TGCGTGGGATCCTCCTGGTGGTGGAACTGG       |
| Luciferase-P3-F                   | TGCGTGGGATCCGGGTCAAGATGCCACAGTTT     |
| Luciferase-P4-F                   | TGCGTGGGATCCAAGAAAGGGGGTCCCTGATAG    |
| Luciferase-P5-F                   | TGCGTGGGATCCGGCTGCTTAAGGGCTGGTAT     |
| Luciferase-P6-F                   | TGCGTGGGATCCGTATGAGCGGGTATTACT       |
| Luciferase-R                      | CACGCAGGATCCACAGGGATCAAGGGACTGA      |
| M13-For                           | GTAACACGACGGCCAG                     |
| 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                | CCACCTCTGTACCCAGATG                  |
| ChIP3-43.857.186-F                | ACTGCCITCCAACTACTGG                  |
| ChIP3-43.857.307-R                | AGAAACTGTGGCATCTTGACC                |
| ChIP4-43.857.630-F                | GTCTGGACCTCCATCTG                    |

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  | CTCATCCAAGGATTATCGAGAATA |
| 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.