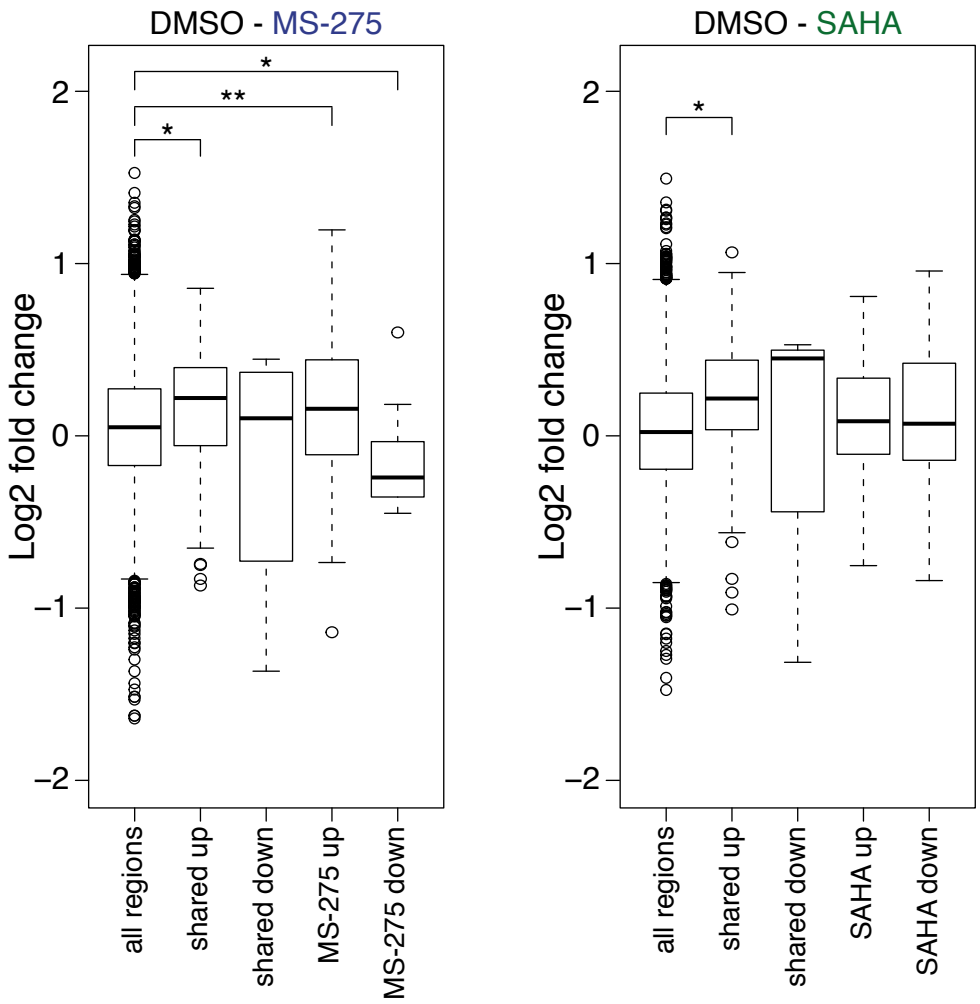
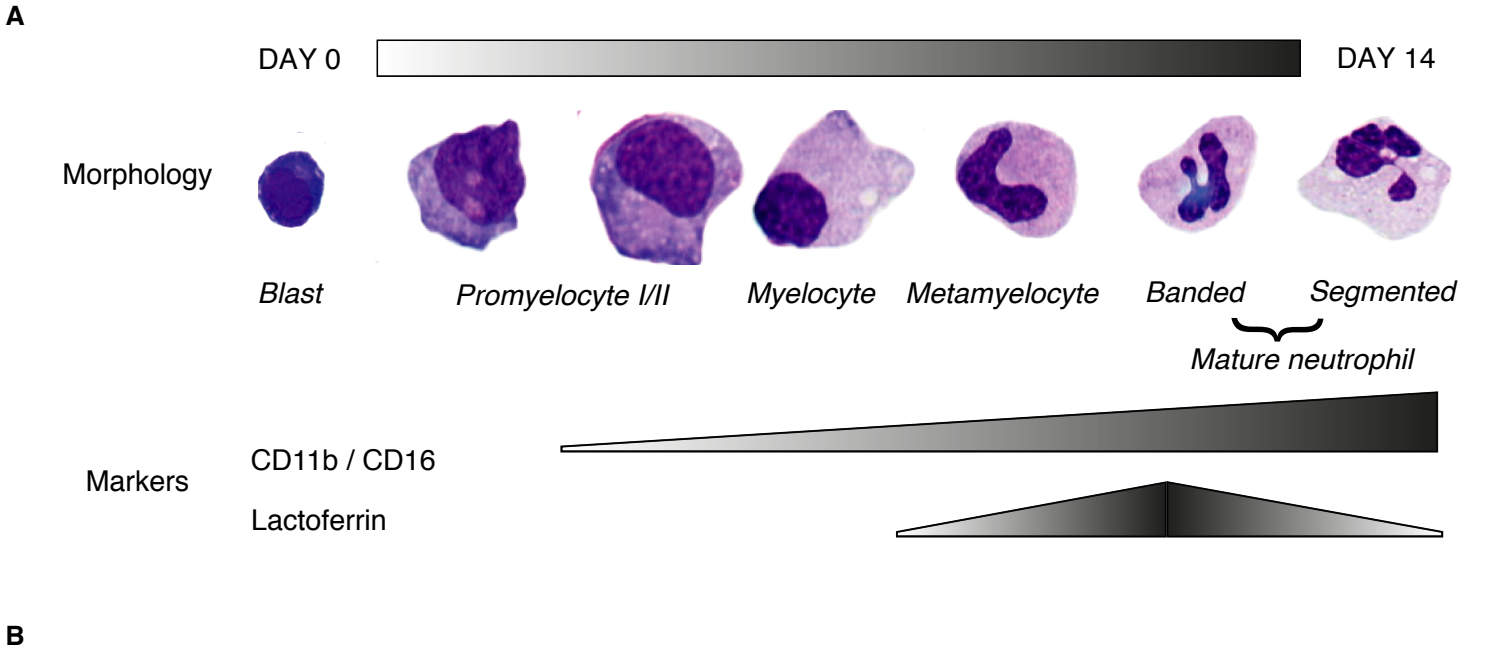
Supplemental Figure 1

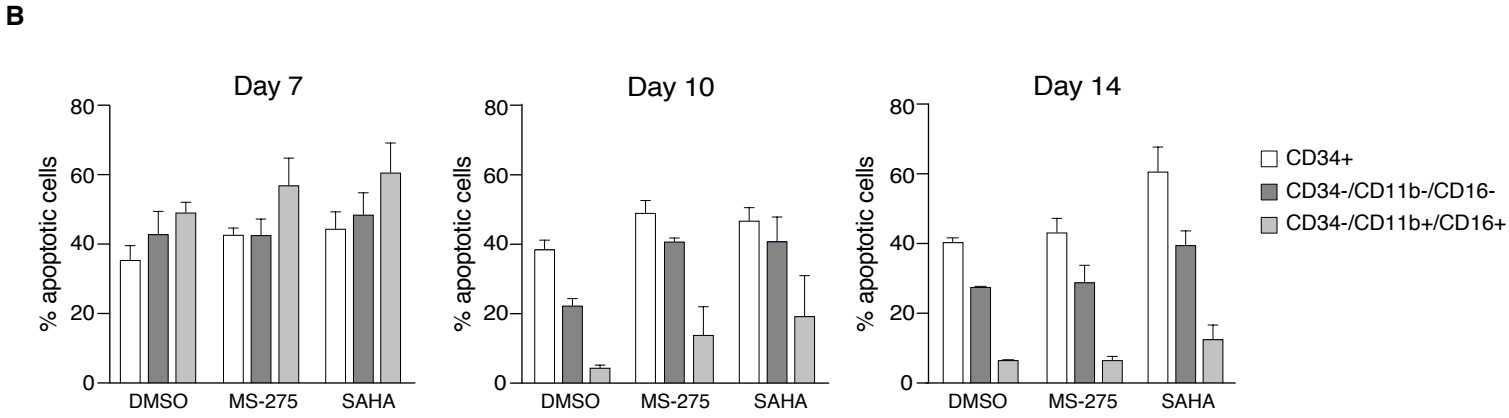


Supplemental Figure 1. Log2 fold changes in H3K27ac enrichment after treatment with histone deacetylase inhibitors MS-275 and SAHA.

Boxplots of log2 fold changes of RPKM values of H3K27acetylated closest distal regulatory elements of commonly regulated genes, MS-275 specific and SAHA specific differentially expressed genes upon treatment with either 100nM MS-275 (left) or 100nM SAHA (right). Significance is calculated against all H3K27ac enriched regions, Wilcoxon rank-sum test, **p<0.01, *p < 0.05.

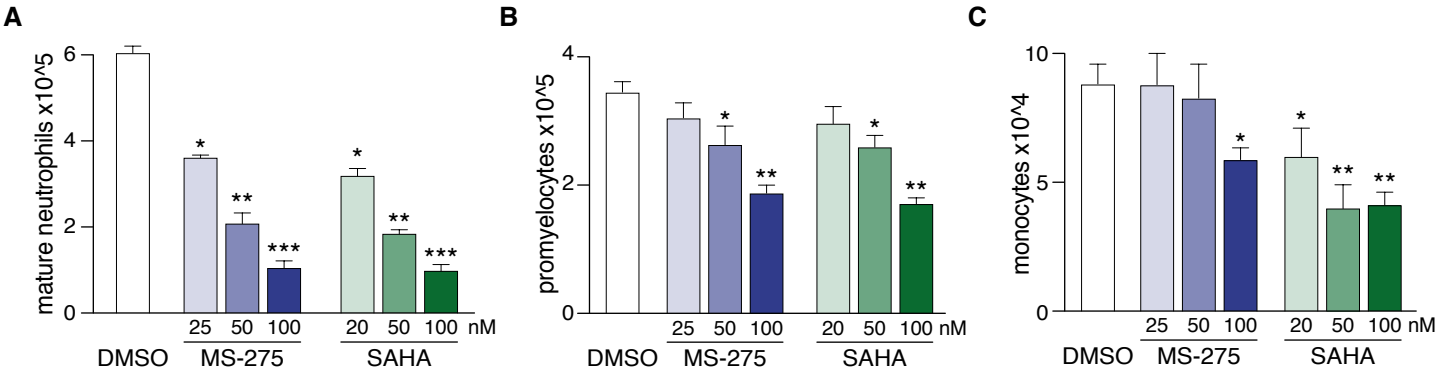
Supplemental Figure 2





Supplemental Figure 2. Effects of HDACi on neutrophil differentiation.
(A) Schematic overview of the developmental stages of maturation during human neutrophil differentiation. **(B)** Percentage of apoptotic cells (annexin-V / propidium iodide-positive cells analyzed by FACS) of cells treated with DMSO, 100nM MS-275 or 100nM SAHA at days 7, 10 and 14 of neutrophil differentiation in specific cell populations; i.e. CD34+ cells, including HSC and early progenitor cells; CD34-/CD16-/CD11b- cells, including immature neutrophils (promyelocytes, myelocytes, metamyelocytes; and CD34-/CD16+/CD11b+ cells, including mature neutrophils (banded and segmented). Error bars represent SEM from three independent replicates.

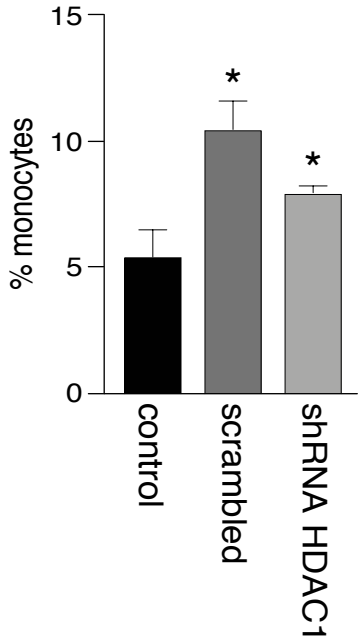
Supplemental Figure 3



Supplemental Figure 3. MS-275 and SAHA differentially modulate neutrophil differentiation

(A-C) Absolute numbers of morphologically mature neutrophils (either banded or segmented nuclei) (A), promyelocytes (B) and monocytes (C) at day 14 of HDACi treatment. Cells were counted using cytospin analysis as described in the Materials and Methods. Error bars represent SEM from three independent replicates, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$,

Supplemental Figure 4



Supplemental Figure 4. HDAC1 knockdown in myeloid precursor cells.
Percentages of monocytes after 14 days of neutrophil differentiation, after shRNA knockdown of HDACi in progenitor cells. Monocytes were counted using cytospin analysis as described in the methods section. Error bars represent SEM from three independent replicates, * $p<0.05$.