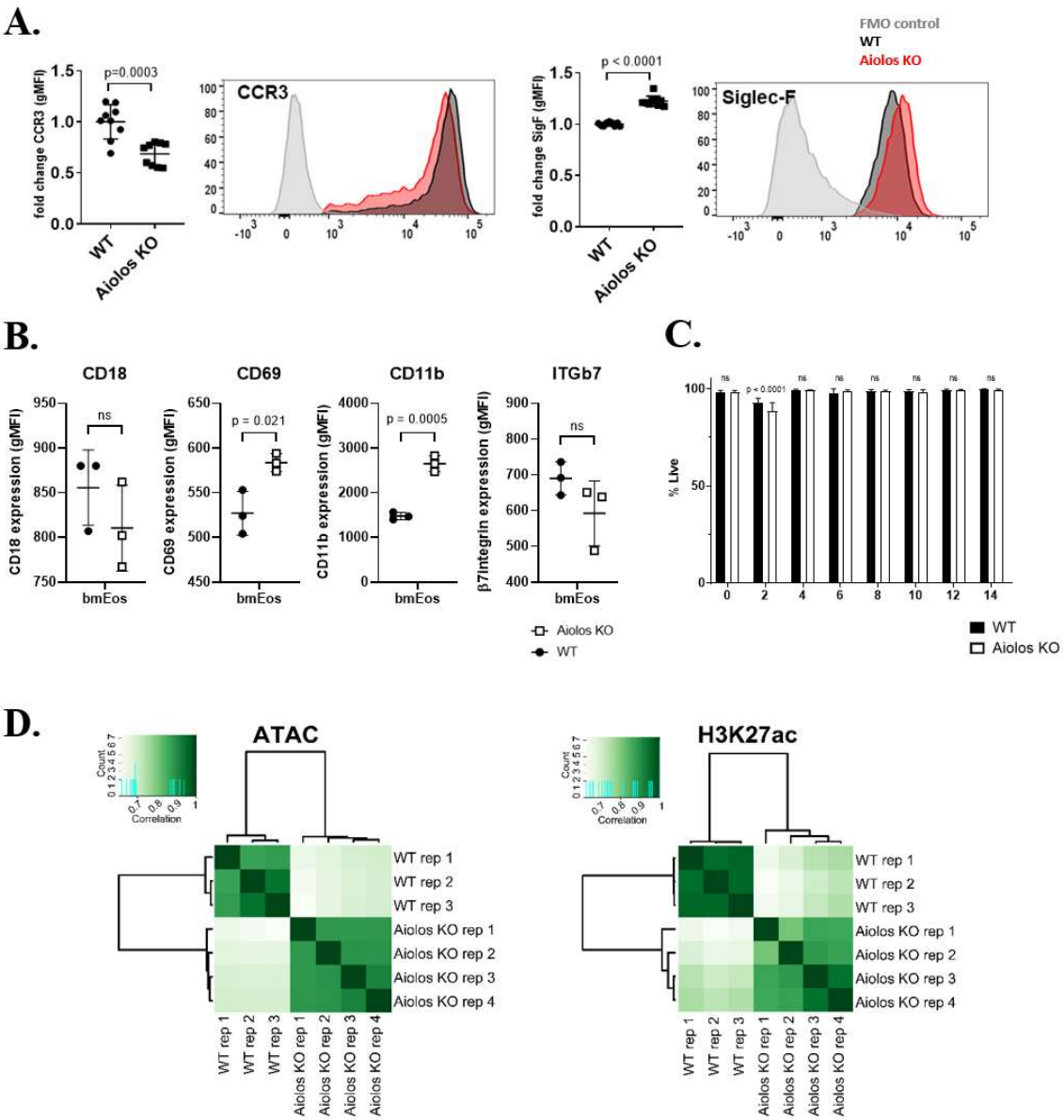
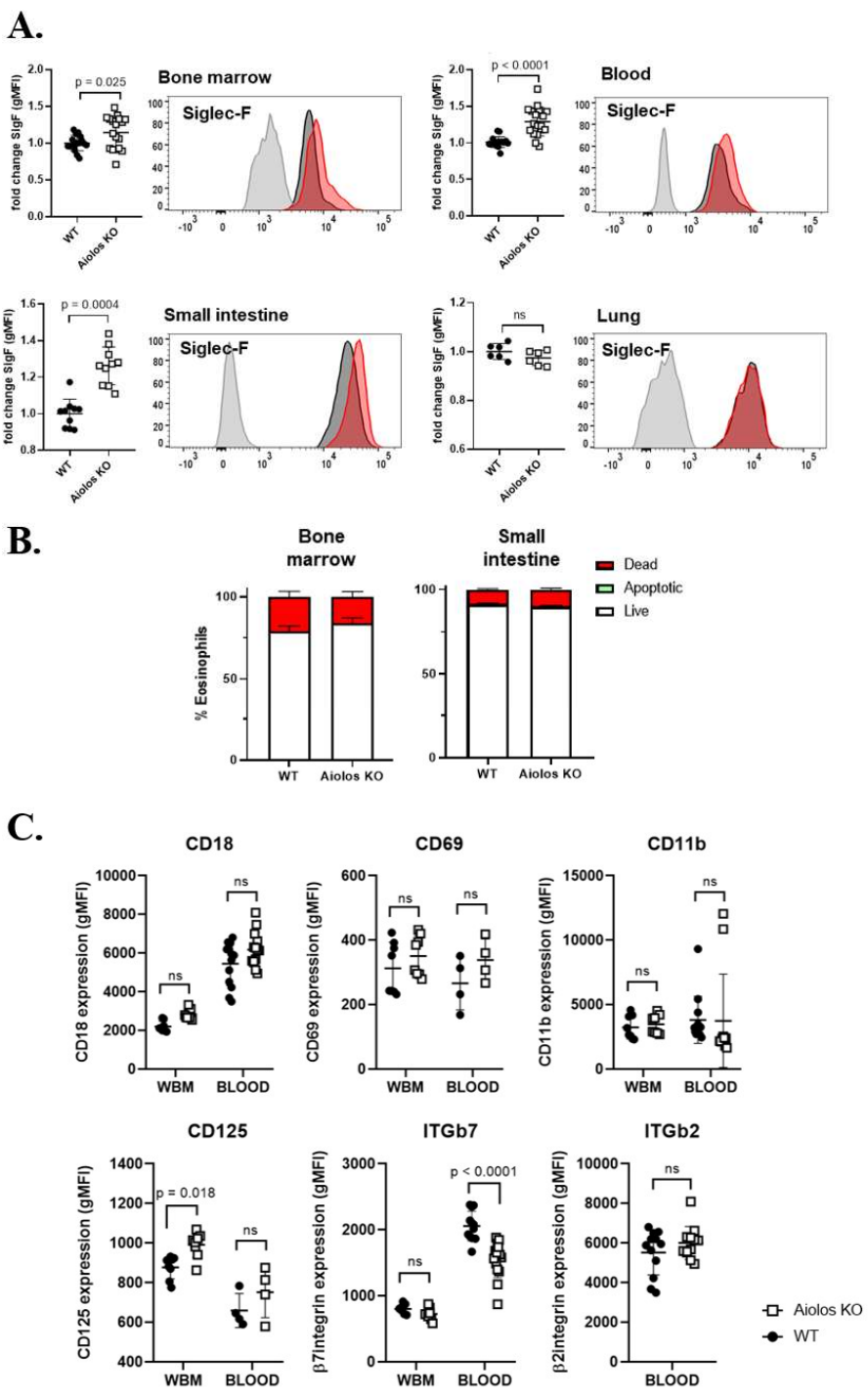
Supplementary Table 1. TaqMan probes for human studies

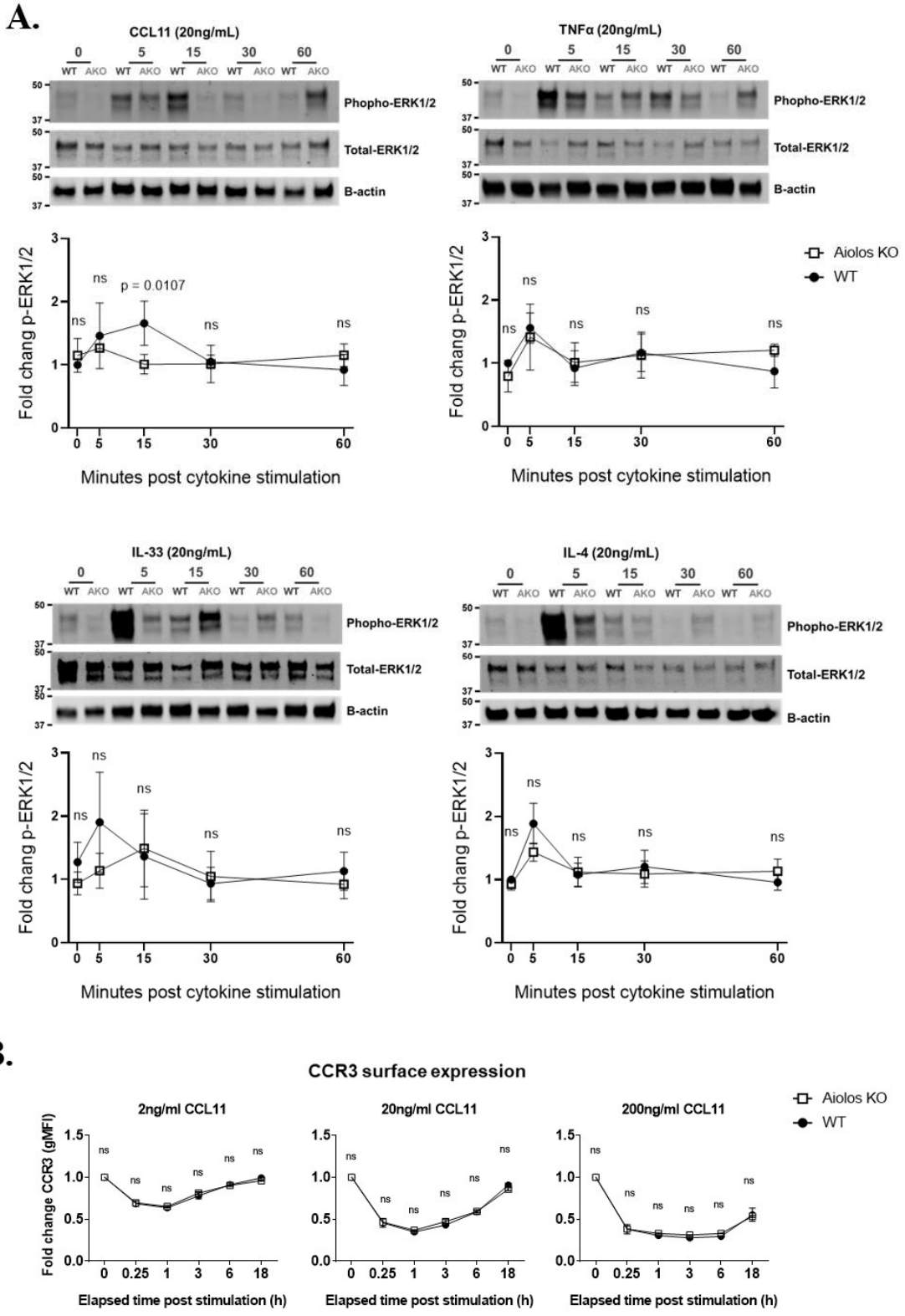
TaqMan probes			
Gene	**TaqMan ID**	**Probes Spans Exons**	**Amplicon Length**
GAPDH	Hs02758991_g1	Yes	93
CSF3R	Hs01114420_m1	Yes	83
IL5RA	Hs00602482_m1	Yes	144
GATA1	Hs0108523_m1	Yes	65
IKZF1	Hs00958474_m1	Yes	73
IKZF2	Hs00212361_m1	Yes	71
IKZF3	Hs00232635_m1	Yes	91



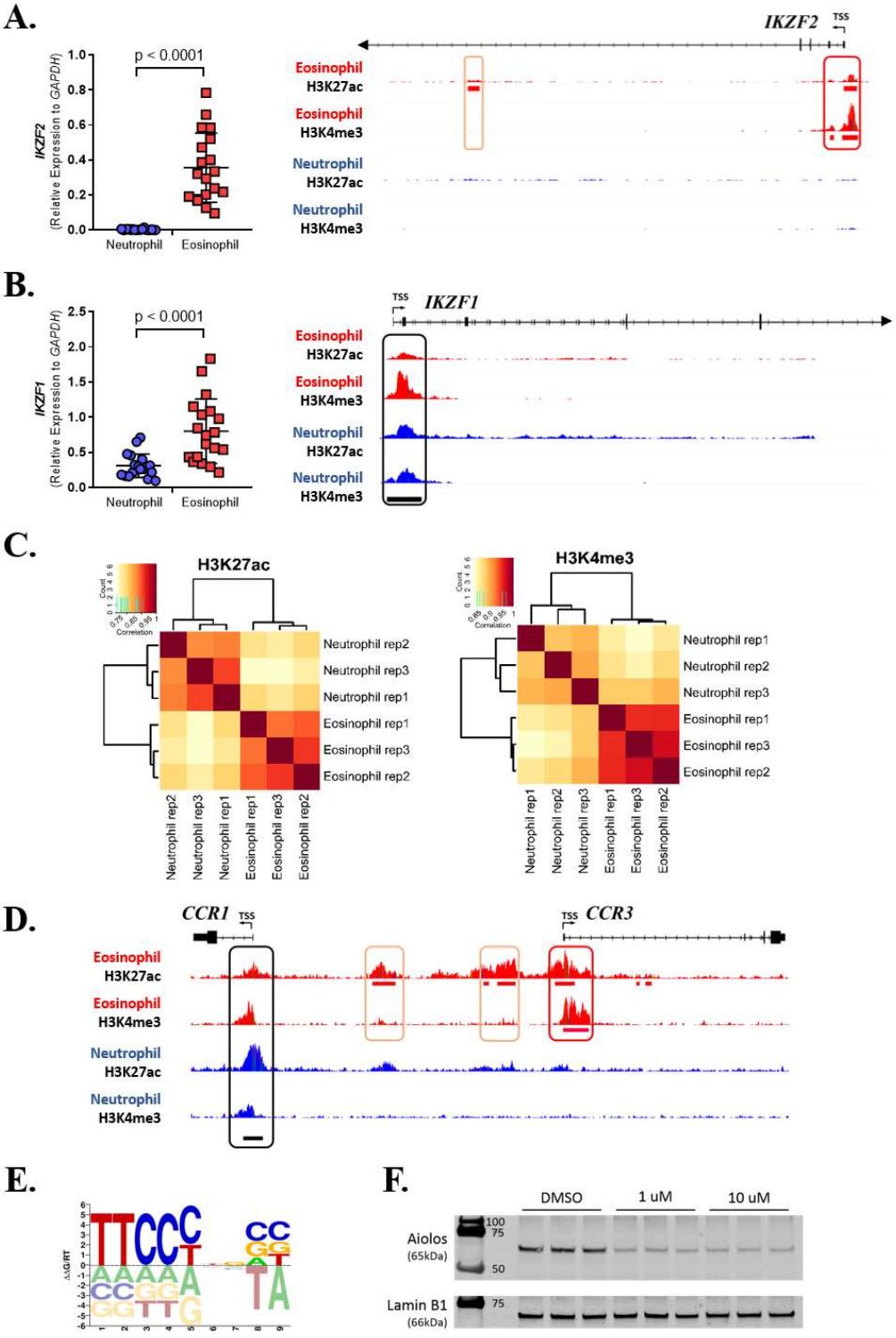
Supplementary Figure 1. bmEos culture supplement (A) Siglec-F surface expression, with representative histograms (geometric mean of fluorescence intensity [gMFI], mean ± SEM) on wildtype (WT, black circles) and Aiolos-deficient (Aiolos KO, white squares) bmEos after 14 days in culture, n = 9/group, 4 independent experiments. (B) CD18, CD69, CD11b and ITGβ7 surface marker expression on WT and Aiolos KO murine bone marrow–cultured eosinophils (bmEos), n = 3/group, 1 independent experiment. (C) Viability of bmEos in culture over 14 days, measured by flow cytometry, n = 9, 4 independent experiments. (D) Heat map showing differential peak binding (DiffPeak) output demonstrating significantly ($p < 0.05$) differentially bound regions present in at least 2 replicates of wildtype (WT) and Aiolos-deficient (Aiolos KO) H3K27ac (left) histone ChIP-seq and ATAC-seq (right) datasets, as expected samples cluster on the basis of chromatin mark and genotype. ns, not significant; SigF+, Siglec-F+



Supplementary Figure 2. In vivo eosinophil supplement. (A) Siglec-F surface expression, with representative histograms, (geometric mean of fluorescence intensity [gMFI], mean ± SEM) on wildtype (WT, black circles) and Aiolos-deficient (Aiolos KO, white squares) eosinophils in the bone marrow (n = 16-18 mice/group, >5 independent experiments), blood (n = 16-18 mice/group, >5 independent experiments), small intestine (n = 10 mice/group, 3 independent experiments) and lung (n = 6 mice/group, 2 independent experiments) during homeostasis is shown. (B) Proportion of live (white), apoptotic (green) and dead (red) primary eosinophils isolated from the bone marrow and small intestine of WT and Aiolos KO mice, n = 3/group, 2 independent experiments. (C) CD18, CD69, CD11b, CD125, ITGβ7 and ITGβ2 surface marker expression on WT (black circle) and Aiolos KO (white box) primary tissue-resident eosinophils isolated from whole bone marrow (WBM) and peripheral blood, n = 4-13/group, >5 independent experiments. ns, not significant; SigF+, Siglec-F+



Supplementary Figure 3. Aiolos KO eosinophils have reduced ERK1/2 phosphorylation in response to eotaxin-1. Representative western blot showing phospho-ERK1/2, total-ERK1/2 and B-actin from cytokine-stimulated murine eosinophils with quantification of fold change (mean ± SEM) in phosphorylated ERK1/2 (pERK1/2) in wildtype (WT, black cirlces) and Aiolos-deficient (Aiolos KO, white squares) eosinophils stimulated with A) eotaxin-1 (CCL11), B) TNFα, C) IL-33 and D) IL-4 (n = 3 mice/group, 3 independent experiments). (B) Fold change in CCR3 surface expression between WT (black circles) and Aiolos KO (white squares) eosinophils after stimulation with increasing doses of CCL11, n = 3/group, 3 independent experiments, mean ± SEM. ns, not significant; AKO, Aiolos KO.



Supplementary Figure 4. Identification of the eosinophil-specific chromatin landscape. Relative human neutrophil and eosinophil gene expression, normalized to *GAPDH* (mean ± SEM, for all groups, with each individual point representing one unique human subject), with chromatin landscape schemas for H3K27ac and H3K4me3 histone marks assessed by ChIP-seq, within (A) *IKZF2* and (B) *IKZF1* genes between human eosinophils (red squares) and neutrophils (blue circles). (C) Heat map showing differential peak binding (DiffPeak) output indicating the correlation and replication of human ChIP-seq datasets; as expected, samples cluster on the basis of histone marks H3K27ac (left)/H3K4me3 (right) and cell type. (D) Chromatin landscape showing H3K27ac and H3K4me3

histone marks surrounding human *CCR1* and *CCR3* genes. The red boxes identifies eosinophil-specific promoters located within 1 kB of the transcriptional start site (TSS). The black box identifies a shared granulocytes-specific promoter present in both eosinophils and neutrophils. The 2 orange boxes identify eosinophil-specific enhancers identified within 20 kB of the *CCR3* gene loci. (E) Aiolos binding motif enriched within eosinophil-specific enhancers. (F) Aiolos expression in EOL-1 cell line following treatment with increasing doses of Lenalidomide (1 μM and 10 μm). ac, acetylation; H, histone; K, lysine; me3, trimethylation; DMSO, dimethylsulfoxide; TSS, transcription start site