Supplementary Information



Fig. S1 Cell death and CD11b mRNA expression in MBVPs incubated with indicated mixed NET-formed medium for 24 h. Control (normal culture medium), 2% (NET-formed medium:normal medium, 1:49), 10% (NET-formed medium:normal medium, 1:9), 25% (NET-formed medium:normal medium, 1:3), 50% (NET-formed medium:normal medium, 1:1), 100% (NET-formed medium replaces normal medium). NET formation and pericyte dysfunction post-TBI. A RT-PCR analysis of relative expression of CD11b in indicated groups. **B** FACS analysis of apoptotic MBVPs (Annexin-V-positive). Data are shown as the mean \pm SEM of 3 individual experiments. **C** Percentage of CD11b⁺ pericytes in brain tissue from TBI mice at different time points. Mean \pm SEM of 5 individual samples; ***P* <0.01, **P* <0.05, Sham *vs* target groups, ANOVA..



Fig. S2: Heatmap and plot of pericyte RNA-seq and neutrophil medium proteomics. A Full view of differential mRNAs in specific brain pericyte subpopulations (n = 3 per group; red, up-regulation; blue, down-regulated). B Scatter plots of detected mRNAs in A. C Quantified protein expression of control

(Neu) and NET-formed (PMA) medium. **D** Molecular weight distribution of identified proteins in neutrophil medium proteomics. **E** Full view of heatmap from neutrophil medium proteomics [blue, NET-formed (PMA) medium; orange, control (Neu) medium].



Fig. S3 Heatmap, plots, and bioinformatics analysis of neutrophil medium metabolomics. **A** Full view of differential metabolites in indicated groups (n = 7 per group; 3 samples of control groups were also tested as quality control; red, up-regulated; blue, down-regulated). **B** Distribution of detected metabolite intensity in neutrophil medium metabolomics. **C** Volcano plot of differential metabolites in PMA groups compared with control. **D** KEGG pathway enrichment bubble plot of the differential expression in neutrophil medium (X-axis, enrichment factor; Y-axis, pathways).



Fig. S4 Relative expression of CD11b in MBVPs stimulated under indicated conditions for 24 h. A–C RT-PCR analysis of relative expression of CD11b in MBVPs treated with gradient concentrations of Lactoferrin (A), L-cysteine (B), and Isoleucine (C). Data are presented as the mean \pm SEM; NS, no statistically significant difference by ANOVA.



Fig. S5 Expression of lectin-related receptors in the CNS and pericytes. **A** Relative expression of the lectin receptor family in various human tissues. Online data from the Human-protein Atlas (www.proteinatlas.org) were searched and revealed 6 types of lectin receptor: Dectin-1, Dectin-2, MINCLE, DNGR-1, DC-SIGN, and CLEC2D. Yellow bars represent the CNS. **B** Amino-acid sequences of CLEC7A (Dectin-1) and CLEC2D from human and mouse (yellow, binding zones. **C** Possible binding residues in different murine histone subtypes, including lysine (K), arginine (R), and histidine (H), highlighted in grey. Data for Q9UHP7, Q91V08, Q6QLQ4, Q9BXN2, P84228, P62806, P10922, Q6GSS7, and P70696 were analyzed on Uniprot (www.uniprot.org).



Fig. S6: Promoter gene sequences of the CD11b promoter region and CHIP-related primers. **A** Promoter region of mouse CD11b (yellow, putative binding sites of c-Jun). **B** Truncated sequence of mouse the CD11b promoter gene containing only one binding site (yellow). **C** Promoter sequence of the mouse CD11b promoter gene with a mutated putative c-Jun binding site (yellow). Muted bases are marked with red.

Table S1 Patient data of TBI cases.

Table S2 Antibodies used in this study.

Table S3 Specific primers for qRT-PCR analysis.

 Table S4 CHIP primers for promoter sequences.