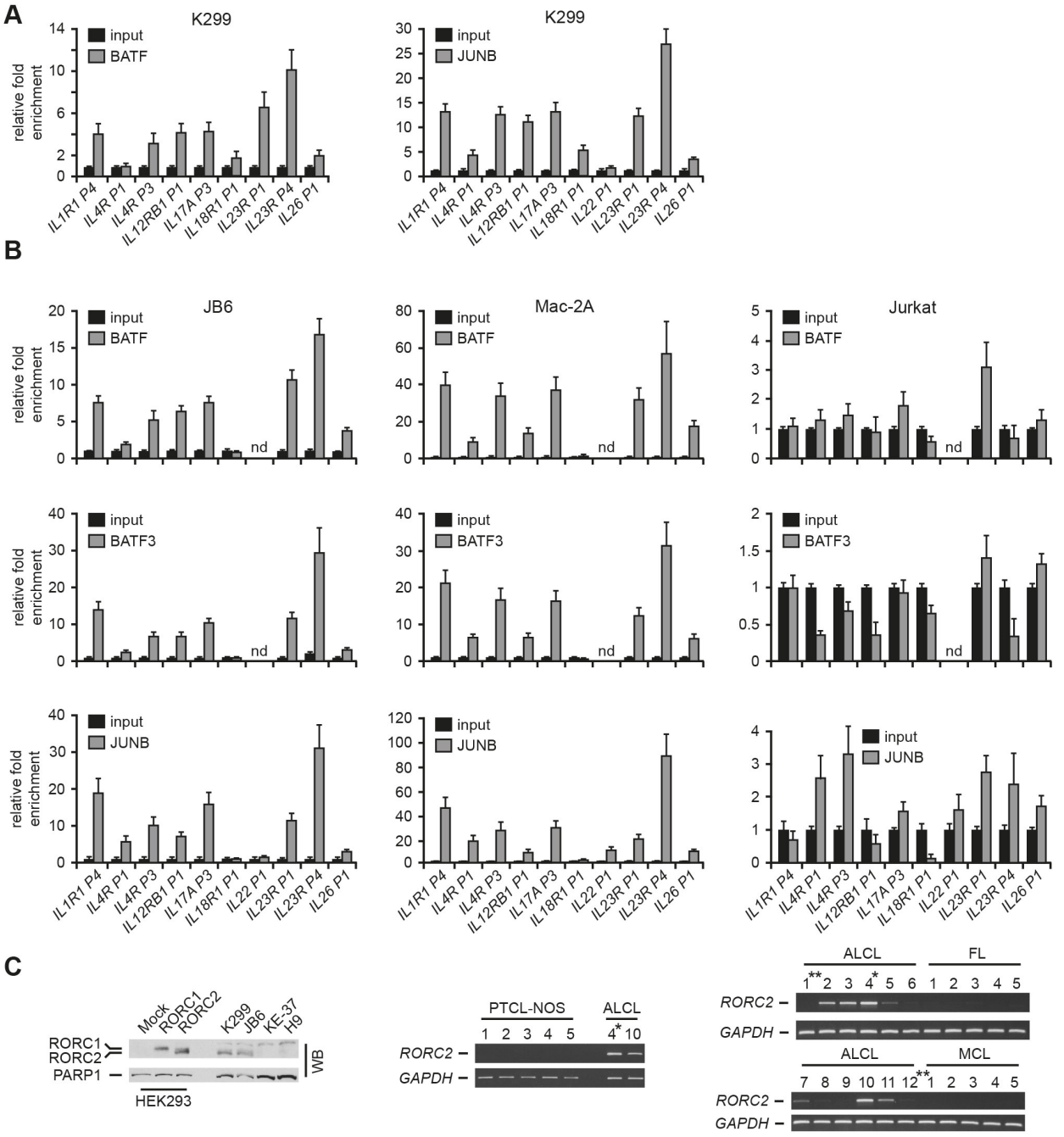
Supplementary Figure 5



Supplementary Figure 5. (**A, B**) BATF, BATF3 and JUNB ChIP analyses. (**A**) BATF (left) and JUNB (right) ChIP of regulatory regions of TH17 / ILC3 genes in K299 cells. Input (analyzed as a control) and precipitated DNA were amplified by qPCR with primers specific to promoter or enhancer regions of the genes indicated underneath. PCRs were performed in triplicates. Data of two biological replicates were combined in a gene study and are shown as mean ± SEM. (**B**) BATF, BATF3 and JUNB ChIP performed as described in (A) in JB6 (left), Mac-2A (center) and Jurkat (right) cells. Data of two biological replicates were combined in a gene study and are shown as mean ± SEM. (**C**) Expression analyses of RORC in ALCL. Left, ALCL cell lines express RORC2. RORC immunoblotting of whole cell extracts of HEK293 cells transfected with empty plasmid (Mock) or plasmids encoding RORC1 or RORC2 as well as nuclear extracts of K299 and JB6 ALCL and KE-37 and H9 non-ALCL cell lines was performed by use of an antibody recognizing RORC1 and RORC2 (Voo KS et al., PNAS, 2009). Positions of RORC1 and RORC2 are indicated. Expression of PARP1 was analyzed as a control. Note, that both ALCL cell lines express RORC2 but not RORC1, and that RORC expression is hardly detectable in KE-37 and H9 cells. Center and right, *RORC2* expression in 12 ALCL (9 ALK$^-$ ALCL; *, ALK$^+$ ALCL; **, ALK status not known), 5 PTCL-NOS, 5 follicular lymphoma (FL) and 5 mantle cell lymphoma (MCL) cases as analyzed by RT-PCR. The *GAPDH* control of center is the same as in Supplementary Figure 4A, right; the *GAPDH* control of right, top is the same as in Supplementary Figure 4A, left; the *GAPDH* control of right, bottom is the same as in Supplementary Figure 4A, center.