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# Correction: A positive feedback loop regulation between NOTCH1 and USP11 in T-cell leukemia

Igor Fijalkowski, Jin Wang, Qi Jin, Jolien Van Laere, Valentina Serafin, John D. Crispino  and Panagiotis Ntziachristos 

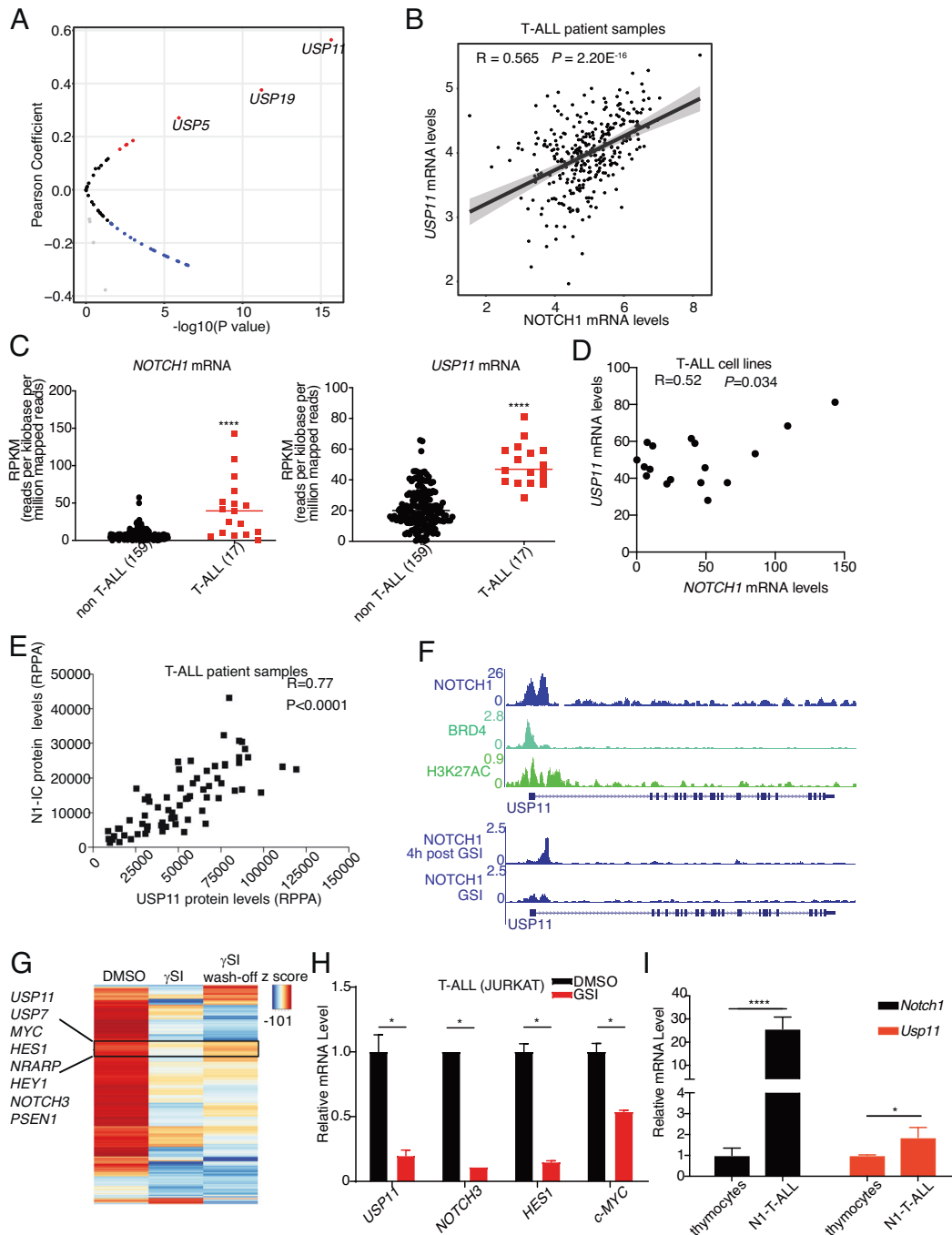
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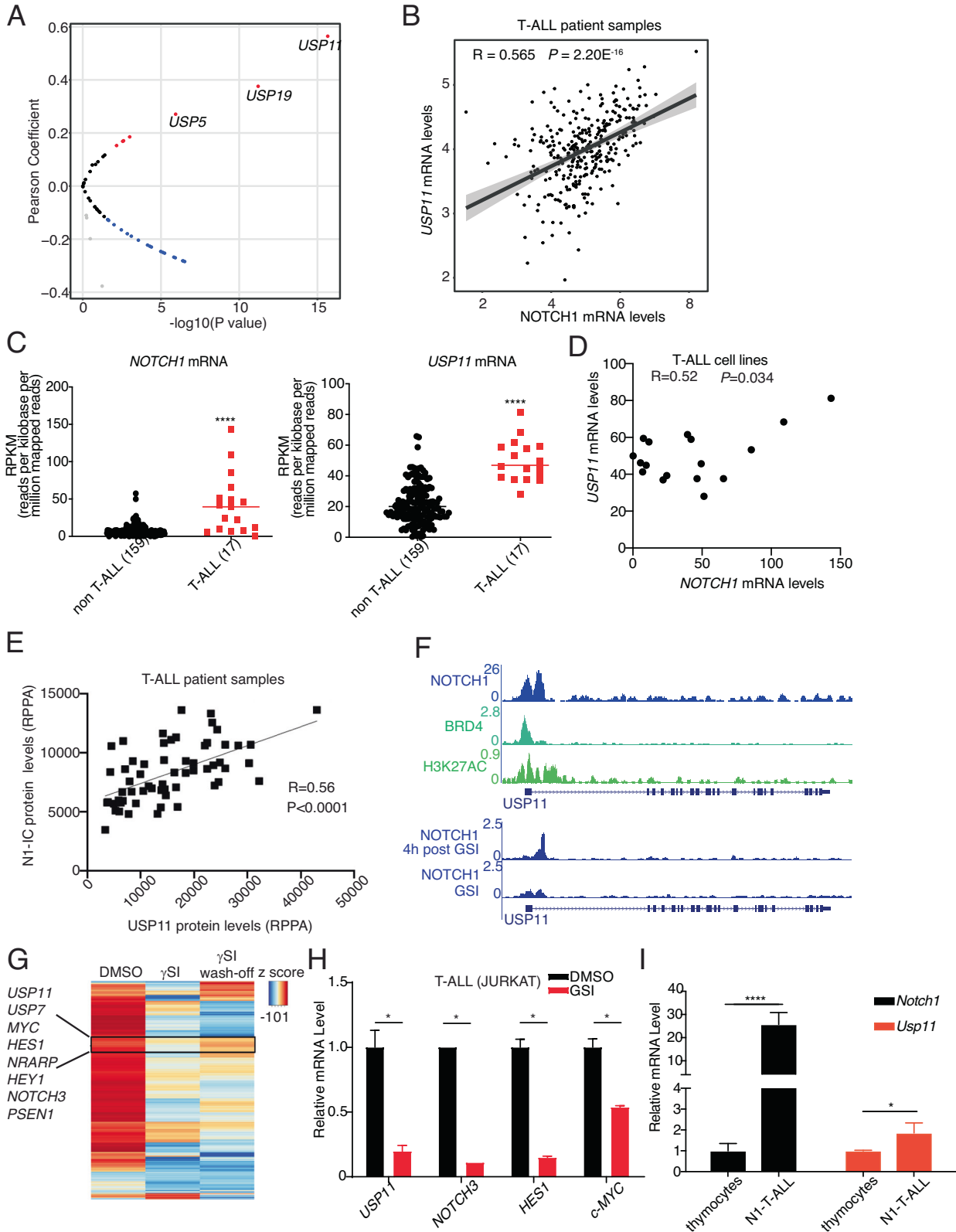
In this article, the wrong figure and legend appeared as Fig. 1E:



**Fig. 1 NOTCH1 and USP11 expression levels are positively correlated in T-ALL.** **A** Volcano plot showing Pearson correlation between 52 *USPs* and *NOTCH1* mRNA levels in T-ALL patient samples analyzed from the Pediatric Cancer Genome Project data portal (PeCan, St. Jude, Memphis). **B** Pearson correlation between *NOTCH1* and *USP11* mRNA levels in T-ALL patient samples (source: PeCan). **C** RPKM values for *NOTCH1* and *USP11* in 176 blood cancer cell lines were obtained from <https://software.broadinstitute.org/morpheus/>, using the CCLE RNA sequencing data. These include 17 T-ALL cell lines, and all other cell lines were analyzed against these T-ALL cell lines. A two-tailed unpaired *t*-test was conducted using the RPKM values ( $****P < 0.0001$ ). **D** Pearson correlation between *NOTCH1* and *USP11* mRNA levels in 17 T-ALL cell lines analyzed from CCLE RNA sequencing data. **E** Reverse-phase protein array (RPPA)

for *USP11* and intracellular *NOTCH1* (N1IC) protein levels ( $n = 64$ ). **F** Tracks showing *NOTCH1*, *BRD4*, and the activating histone marks *H3K27Ac* ChIP-Seq signal enrichment in T-ALL cells (CUTLL1) at the *USP11* locus. **G** Heatmap representation of significant gene expression changes upon treatment of CUTLL1 cells with gamma-secretase inhibitor ( $\gamma$ SI) followed by drug wash-off for 320' (*wash-off*) [7]. Classical *NOTCH1* targets (e.g., *HES1*, *MYC*, *NRARP*) and the deubiquitinases *USP7* and *USP11* follow the intracellular *NOTCH1* levels. **H** JURKAT T-ALL cells were treated with  $\gamma$ SI (1  $\mu$ M) for 24 h. RT-qPCR analysis of *USP11* and other *NOTCH1* targets was shown ( $*P < 0.05$ ). **I** RT-qPCR analysis of *Usp11* and *Notch1* in normal mouse thymocytes and spleen cells isolated from N1 $\Delta$ E induced mouse T-ALL model ( $*P < 0.05$ ,  $****P < 0.00001$ ).

The figure and legend should have appeared as shown below:



**Fig. 1 NOTCH1 and USP11 expression levels are positively correlated in T-ALL.** **A** Volcano plot showing Pearson correlation between 52 *USPs* and *NOTCH1* mRNA levels in T-ALL patient samples analyzed from the Pediatric Cancer Genome Project data portal (PeCan, St. Jude, Memphis). **B** Pearson correlation between *NOTCH1* and *USP11* mRNA levels in T-ALL patient samples (source: PeCan). **C** RPKM values for *NOTCH1* and *USP11* in 176 blood cancer cell lines were obtained from <https://software.broadinstitute.org/morpheus/>, using the CCLE RNA sequencing data. These include 17 T-ALL cell lines, and all other cell lines were analyzed against these T-ALL cell lines. A two-tailed unpaired *t*-test was conducted using the RPKM values (\*\*\*\* $P < 0.0001$ ). **D** Pearson correlation between *NOTCH1* and *USP11* mRNA levels in 17 T-ALL cell lines analyzed from CCLE RNA sequencing data. **E** Reverse-phase protein array (RPPA) for *USP11* and intracellular *NOTCH1* (N1IC) protein levels ( $n = 61$ ). **F** Tracks showing *NOTCH1*, *BRD4*, and the activating histone marks H3K27Ac ChIP-Seq signal enrichment in T-ALL cells (CUTLL1) at the *USP11* locus. **G** Heatmap representation of significant gene expression changes upon treatment of CUTLL1 cells with gamma-secretase inhibitor ( $\gamma$ SI) followed by drug wash-off for 320' (*wash-off*) [7]. Classical *NOTCH1* targets (e.g., *HES1*, *MYC*, *NRAPR*) and the deubiquitinases *USP7* and *USP11* follow the intracellular *NOTCH1* levels. **H** JURKAT T-ALL cells were

treated with  $\gamma$ SI (1  $\mu$ M) for 24 h. RT-qPCR analysis of *USP11* and other *NOTCH1* targets was shown (\* $P < 0.05$ ). **I** RT-qPCR analysis of *Usp11* and *Notch1* in normal mouse thymocytes and spleen cells isolated from N1 $\Delta$ E induced mouse T-ALL model (\* $P < 0.05$ , \*\*\*\* $P < 0.00001$ ).

The original article has been corrected.



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