

CORRECTION

Open Access



Correction: A network-based approach to overcome BCR::ABL1-independent resistance in chronic myeloid leukemia

Valeria Bica^{1†}, Veronica Venafrà^{1,3†}, Giorgia Massacci², Simone Graziosi¹, Sara Gualdi³, Gessica Minnella^{4,5}, Federica Sorà^{4,5}, Patrizia Chiusolo^{4,5}, Maria Elsa Brunetti⁶, Gennaro Napolitano^{6,7,8}, Massimo Breccia⁹, Dimitrios Mougiakakos^{10,11}, Martin Böttcher^{10,11}, Thomas Fischer^{10,11}, Livia Perfetto^{3*} and Francesca Sacco^{2,6*}

Correction: *Cell Commun Signal* 23, 179 (2025)
<https://doi.org/10.1186/s12964-025-02185-0>

The correct order of figures and figure legends are given below:

Following publication of the original article [1], the authors identified a typesetting error, whereby the figures and figure legends were mistakenly misaligned.

[†]Valeria Bica and Veronica Venafrà contributed equally to this work.

The original article can be found online at <https://doi.org/10.1186/s12964-025-02185-0>.

*Correspondence:

Livia Perfetto

livia.perfetto@uniroma1.it

Francesca Sacco

francesca.sacco@uniroma2.it

¹Ph.D. Program in Cellular and Molecular Biology, Department of Biology, University of Rome 'Tor Vergata', Rome, Italy

²Department of Biology, University of Rome Tor Vergata, Rome, Italy

³Department of Biology and Biotechnologies "C. Darwin", University of Rome La Sapienza, Rome, Italy

⁴Sezione di Ematologia, Dipartimento di Scienze Radiologiche ed Ematologiche, Università Cattolica del Sacro Cuore, Roma, Italy

⁵Dipartimento di Scienze di laboratorio ed Ematologiche, Fondazione Policlinico A. Gemelli IRCCS, Roma, Italy

⁶Telethon Institute of Genetics and Medicine (TIGEM), Naples, Italy

⁷Department of Medical and Translational Science, Federico II University, Naples, Italy

⁸Scuola Superiore Meridionale (SSM), School for Advanced Studies, Genomics and Experimental Medicine program, Naples, Italy

⁹Department of Translational and Precision Medicine, Azienda Policlinico Umberto I, Sapienza University of Rome, Rome, Italy

¹⁰Health campus for Inflammation, Immunity and Infection (GCI3), University of Magdeburg, Magdeburg, Germany

¹¹Department of Hematology, Oncology and Cell Therapy, University of Magdeburg, Magdeburg, Germany



© The Author(s) 2025. **Open Access** This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by-nc-nd/4.0/>.

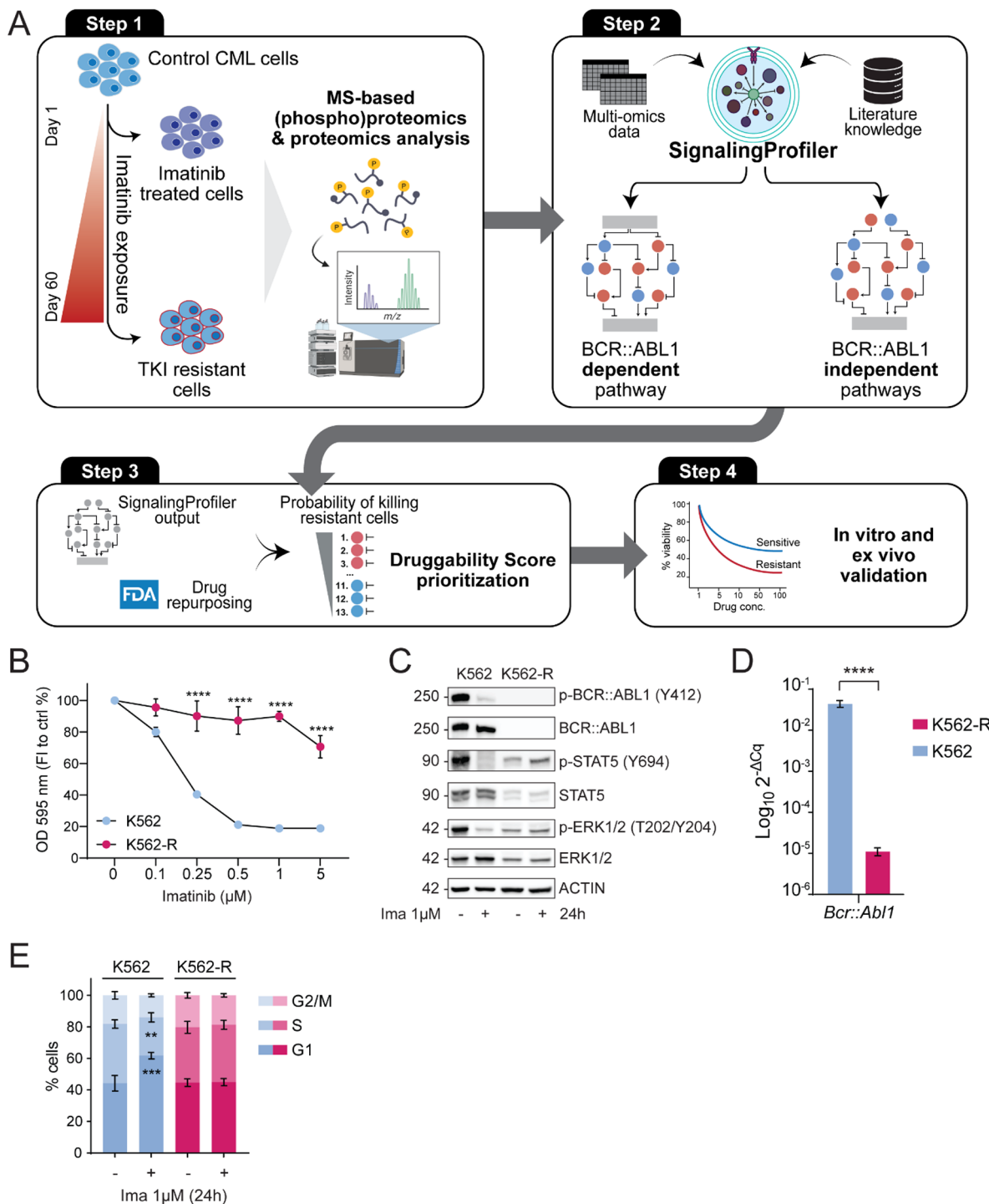


Fig. 1 Experimental strategy and in vitro resistant model characterization. **A**. Schematic representation of the multi-step strategy. **B**. MTT viability assay. Sensitive cells (blue) and resistant cells (red) were exposed to increasing concentration of imatinib (0.1 μM , 0.25 μM , 0.5 μM , 1 μM and 5 μM) for 72 h. The graph shows the percentage of absorbance at 595 nm normalized on control condition. **C**. Representative western blots of BCR::ABL1 activity status (Y412), MAPK and JAK/STAT canonical downstream pathways (p-STAT5 (Y694), p-ERK1/2 (T202/Y204)) in K562 and K562-R cells upon 24 h of 1 μM imatinib treatment. **D**. Real Time quantitative PCR was performed to measure BCR::ABL1 transcript levels in K562 and K562-R cells. Bar graph shows quantification of the BCR::ABL1 mRNA levels as $\text{Log}_{10} 2^{-\Delta\text{Cq}}$. **E**. Flow cytometry analysis of cell cycle progression of K562 and K562-R cells upon 24 h exposure to imatinib 1 μM . The bar graph shows the percentage of cells in a specific cell cycle phase measured using DAPI staining

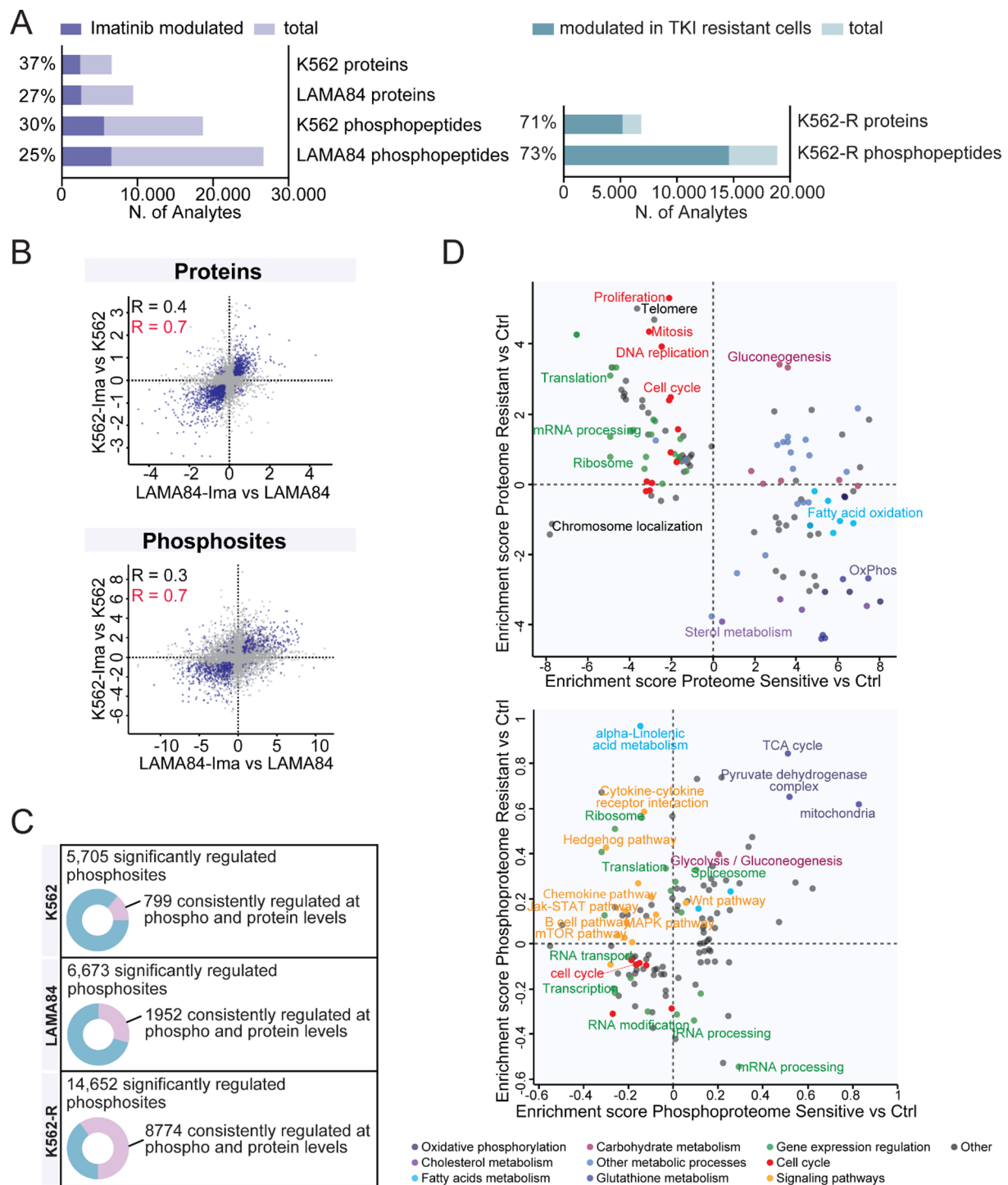


Fig. 2 Phosphoproteomics analysis and functional characterization of sensitive and resistant CML models upon imatinib exposure. **A.** Quantification coverage of phosphopeptides and proteins. For K562 and LAMA84 cells perturbed by 24 h of imatinib 1 μ M treatment, significantly modulated analytes (t test, $S_0 = 0.1$, $FDR < 0.05$) are reported in violet (left panel). For K562-R cells compared to K562 cells, significantly modulated analytes (t test, $S_0 = 0.1$, $FDR < 0.05$) are reported in green (right panel). **B.** Scatterplots showing the Pearson correlation coefficients between the imatinib-dependent changes at the phosphoproteome and proteome levels of K562 cells as compared to LAMA84 cells. Proteins/phosphosites significantly modulated by imatinib, in both K562 and LAMA84 cell lines, are represented in blue. R indicates Pearson correlation considering all proteins/phosphosites (black) or only proteins/phosphosites significantly modulated in both cell lines (red). **C.** Pie charts showing the proportion of phosphopeptides consistently modulated by imatinib (upper panels) or in K562-R cells at their phosphorylation and protein levels. **D.** Scatterplots representing gene ontology enrichment analysis comparing sensitive cells (K562 and LAMA84) upon imatinib treatment with resistant cells (K562-R), at the proteome (upper panel) and phosphoproteome (lower panel) levels

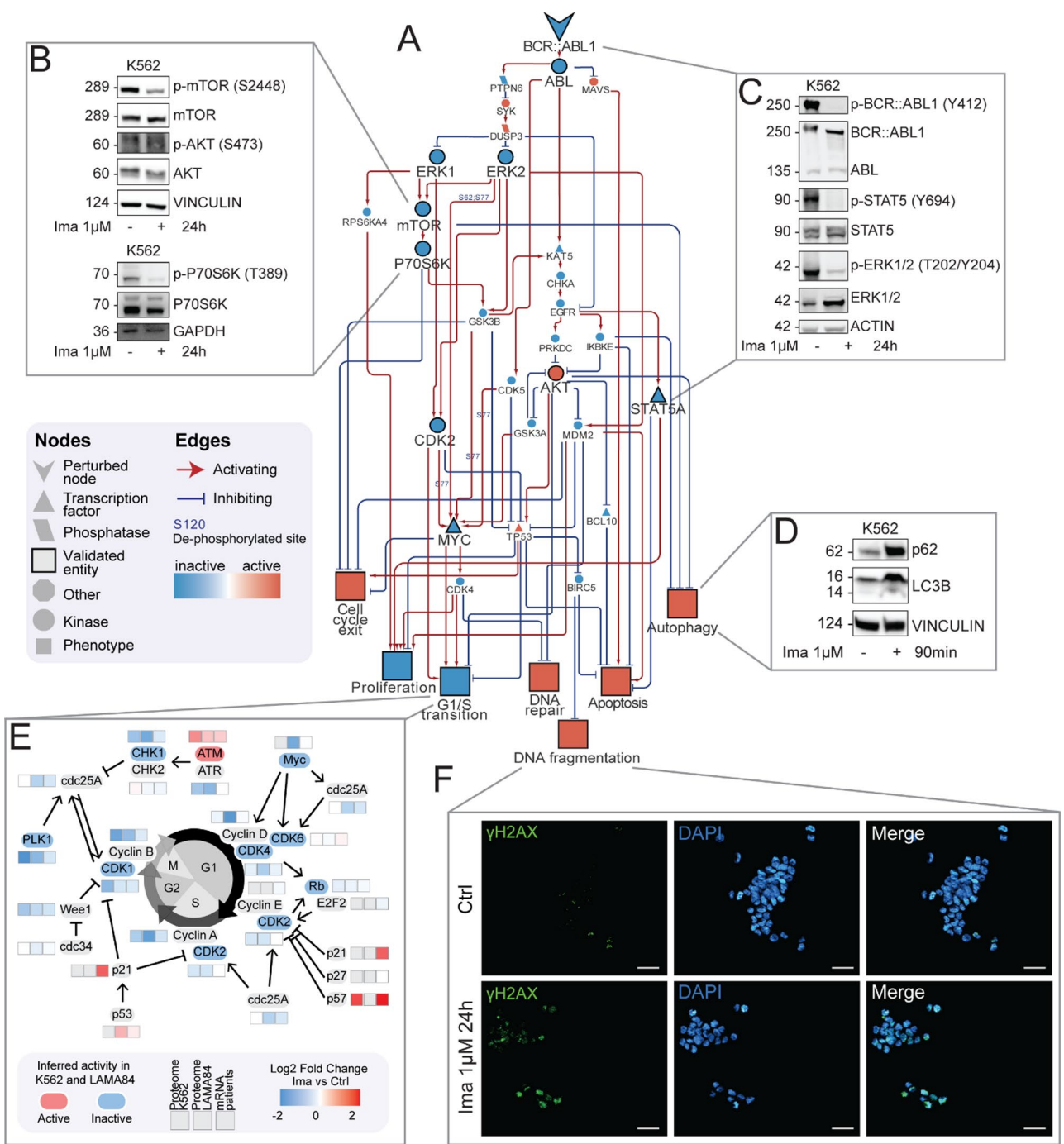


Fig. 3 Characterization of BCR::ABL1-dependent mechanisms in sensitive cells. **A**. Functional submodel extracted from SignalingProfiler 2.0 output linking BCR::ABL1 to cellular phenotypes modulated upon imatinib treatment. **B**. Representative western blots of PI3K/AKT/mTOR axis activity upon 24 h of 1μM imatinib treatment. **C**. Representative western blots of BCR::ABL1 activity status, MAPK and JAK/STAT canonical downstream pathways upon 24 h of 1μM imatinib treatment. **D**. Representative western blots showing expression levels of key autophagy regulators, such as p62 and LC3B perturbed by 90 min of imatinib 1μM treatment. **E**. Illustration showing cell cycle-related proteins modulation by imatinib at mRNA, protein, and activation level. **F**. Representative images of γH2AX staining in K562 cells perturbed with imatinib for 24 h. Scale bars represent 50 μm

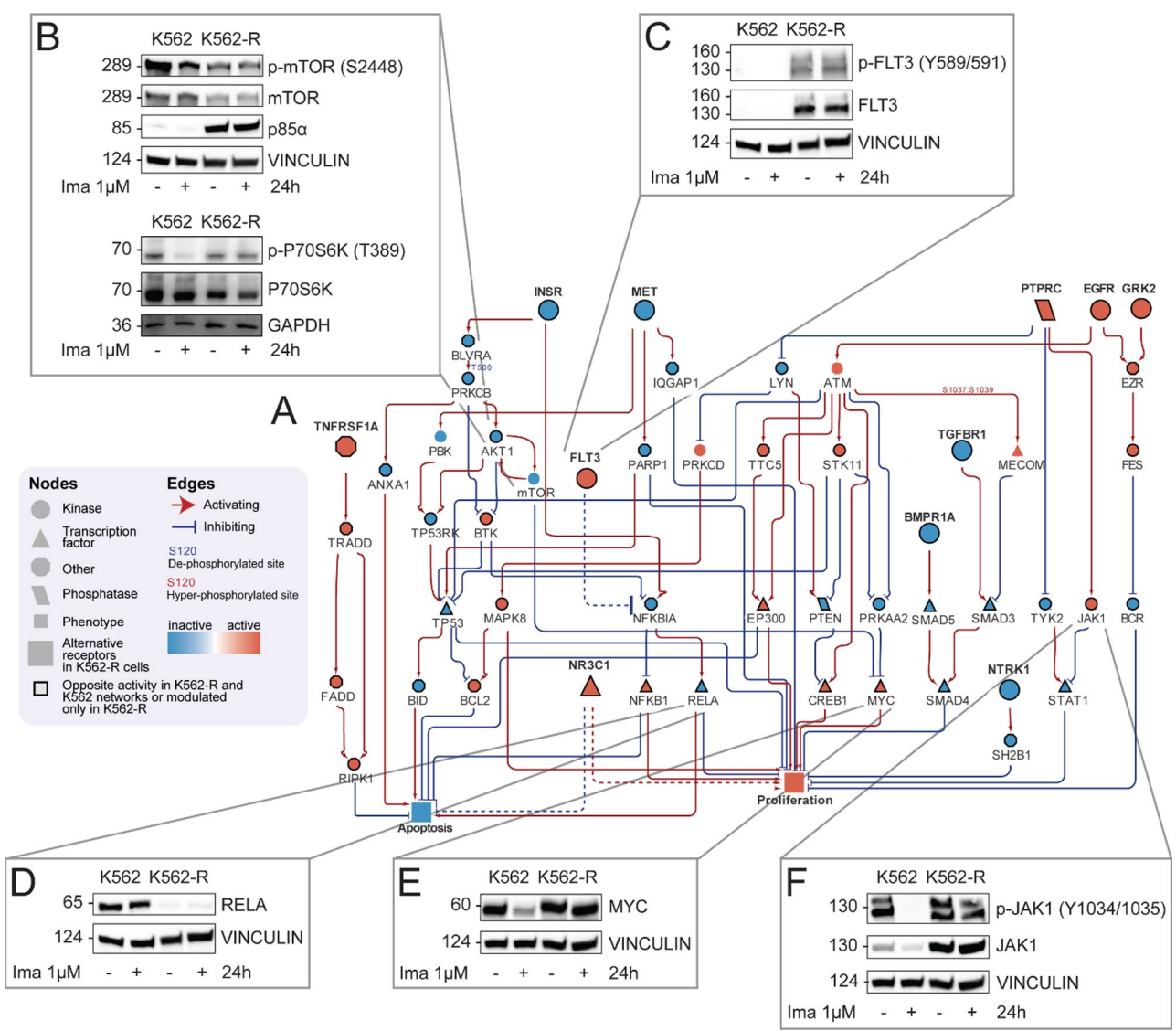


Fig. 4 Characterization of BCR::ABL1-independent mechanisms in resistant cells. **A.** Functional submodel extracted from BCR::ABL1 independent-specific subnetwork reporting paths going from 10 alternative receptors oppositely modulated in imatinib K562-R and K562 cells exposed to imatinib to apoptosis and proliferation phenotypes. **B.** Representative western blots of PI3K/AKT/mTOR axis activity upon 24 h of 1μM imatinib treatment in control cells and K562-R cells. **C-D.** Representative western blot of control cells and K562-R cells showing phosphorylation status and protein abundance of FLT3 receptor **C.** and RELA protein **D.** upon imatinib treatment. Both panels were obtained from the same gel and divided for aesthetic purposes of the figure. **E-F.** Representative western blot of control cells and K562-R cells showing phosphorylation status and protein abundance of MYC transcription factor **E.** and JAK1 kinase **F.** upon imatinib treatment. Both panels were obtained from the same gel and divided for aesthetic purposes of the figure

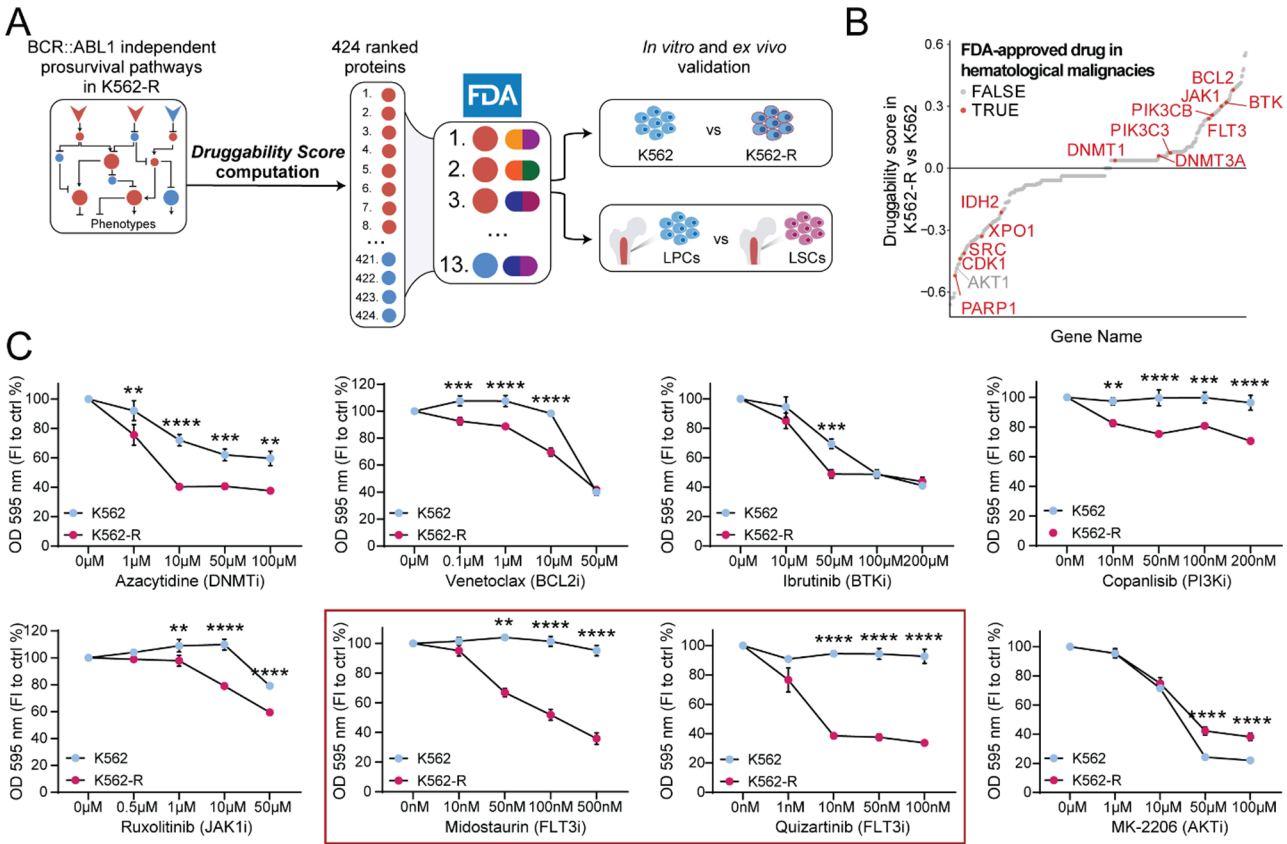


Fig. 5 Identification of new druggable targets and repurposing of FDA-approved drugs. **A**. Druggable targets prioritization strategy. **B**. Scatterplot showing drug targets ranked according to the Druggability Score. **C**. MTT assay on K562 and K562-R cells exposed for 24 h at different concentrations of FDA-approved inhibitors of prioritized targets. MK-2206 (AKTi) was used as a negative control. The graphs show the percentage of absorbance at 595 nm normalized on control condition. The reported statistical significance is between K562 and K562-R cells at the same experimental condition

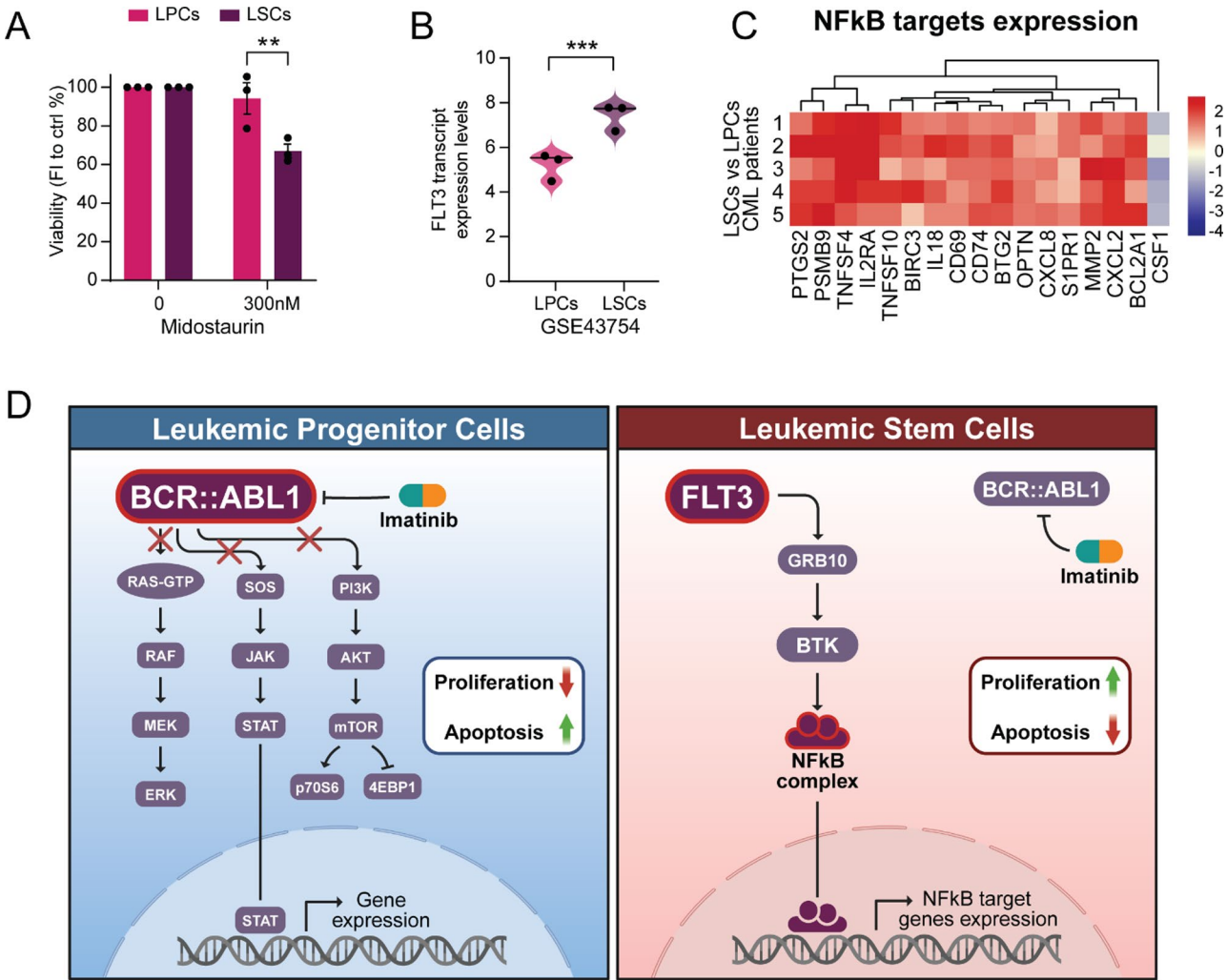


Fig. 6 LSCs rely on FLT3-NFkB axis for proliferation and survival. **A.** LPCs (CD38+) and LSCs (CD26+) were sorted and exposed to midostaurin for 24 h. Viability assay was performed by trypan blue exclusion. **B.** Quantification of FLT3 in LPCs and LSCs from RNAseq analysis obtained from GEO dataset (GSE43754). **C.** Heatmap showing transcript levels of NFkB targets in LSCs compared to LPCs from RNAseq analysis obtained from GEO dataset (GSE43754). **D.** Graphic representation of how LSCs rely on the FLT3-NFkB signaling axis for proliferation and survival

The original article [1] has been corrected.

Publisher's note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Published online: 28 April 2025

References

1. Bica V, Venafrà V, Massacci G, et al. A network-based approach to overcome BCR::ABL1-independent resistance in chronic myeloid leukemia. *Cell Commun Signal*. 2025;23:179. <https://doi.org/10.1186/s12964-025-02185-0>.