

# Targeting hyperactive platelet-derived growth factor receptor- $\beta$ signaling in T-cell acute lymphoblastic leukemia and lymphoma

Stien De Coninck,<sup>1,2</sup> Renate De Smedt,<sup>1,2</sup> Béatrice Lintermans,<sup>1,2</sup> Lindy Reunes,<sup>1,2,3</sup> Hansen J. Kosasih,<sup>4,5</sup> Alexandra Reekmans,<sup>1,2</sup> Lauren M. Brown,<sup>4,5</sup> Nadine Van Roy,<sup>2,6,7</sup> Bruno Palhais,<sup>1,2,3</sup> Juliette Roels,<sup>1,2</sup> Malaika Van der Linden,<sup>2,8</sup> Jo Van Dorpe,<sup>2,8</sup> Panagiotis Ntziachristos,<sup>2,3</sup> Frederik W. van Delft,<sup>9</sup> Marc R. Mansour,<sup>10</sup> Tim Pieters,<sup>2,3</sup> Tim Lammens,<sup>2,11,12</sup> Barbara De Moerloose,<sup>2,12</sup> Charles E. de Bock,<sup>4,5#</sup> Steven Goossens<sup>2,13#</sup> and Pieter Van Vlierberghe<sup>1,2#</sup>

<sup>1</sup>Lab of Normal and Malignant Hematopoiesis, Department of Biomolecular Medicine, Ghent University, Ghent, Belgium; <sup>2</sup>Cancer Research Institute Ghent (CRIG), Ghent, Belgium;

<sup>3</sup>Department of Biomolecular Medicine, Ghent University, Ghent, Belgium;

<sup>4</sup>Children's Cancer Institute, Lowy Cancer Research Centre, UNSW Sydney, Kensington, New South Wales, Australia; <sup>5</sup>School of Clinical Medicine, UNSW Medicine and Health, UNSW Sydney, Sydney, New South Wales, Australia; <sup>6</sup>Lab for Translational Oncogenomics and Bioinformatics, Department of Biomolecular Medicine, Ghent University, Ghent, Belgium;

<sup>7</sup>Pediatric Precision Oncology Lab, Department of Biomolecular Medicine, Ghent University, Ghent, Belgium; <sup>8</sup>Department of Pathology, Ghent University and Ghent University Hospital, Ghent, Belgium; <sup>9</sup>Wolfson Childhood Cancer Research Centre, Newcastle University Centre for Cancer, Newcastle upon Tyne, UK; <sup>10</sup>Department of Developmental Biology and Cancer, Institute of Child Health, University College London, London, UK; <sup>11</sup>Department of Internal Medicine and Pediatrics, Ghent University, Ghent, Belgium; <sup>12</sup>Department of Pediatric Hematology-Oncology and Stem Cell Transplantation, Ghent University Hospital, Ghent, Belgium and <sup>13</sup>Unit for Translational Research in Oncology, Department of Diagnostic Sciences, Ghent University, Ghent, Belgium

*#CEdB, SG and PVV contributed equally as senior authors.*

**Correspondence:** S. Goossens  
[steven.goossens@ugent.be](mailto:steven.goossens@ugent.be)

**Received:** August 17, 2023.

**Accepted:** November 2, 2023.

**Early view:** November 9, 2023.

<https://doi.org/10.3324/haematol.2023.283981>

©2024 Ferrata Storti Foundation

Published under a CC BY-NC license



# Targeting hyperactive platelet-derived growth factor receptor- $\beta$ signaling in T-cell acute lymphoblastic leukemia and lymphoma

Stien De Coninck<sup>1,2</sup>, Renate De Smedt<sup>1,2</sup>, Béatrice Lintermans<sup>1,2</sup>, Lindy Reunes<sup>1,2,3</sup>, Hansen J. Kosasih<sup>4,5</sup>, Alexandra Reekmans<sup>1,2</sup>, Lauren M. Brown<sup>4,5</sup>, Nadine Van Roy<sup>2,6,7</sup>, Bruno Palhais<sup>1,2,3</sup>, Juliette Roels<sup>1,2</sup>, Malaika Van der Linden<sup>2,8</sup>, Jo Van Dorpe<sup>2,8</sup>, Panagiotis Ntziachristos<sup>2,3</sup>, Frederik W. van Delft<sup>9</sup>, Marc R. Mansour<sup>10</sup>, Tim Pieters<sup>2,3</sup>, Tim Lammens<sup>2,11,12</sup>, Barbara De Moerloose<sup>2,12</sup>, Charles E. de Bock<sup>4,5,†</sup>, Steven Goossens<sup>2,13,†</sup> ✉, Pieter Van Vlierberghe<sup>1,2,†</sup>

## Supplementary Data

### Targeted Locus Amplification (TLA)

Preparation of the samples for TLA was performed as described (1). In brief, cells were crosslinked using formaldehyde and DNA was digested with NlaIII. The samples were ligated, crosslinks reversed, and the DNA purified. To obtain circular chimeric DNA molecules for PCR amplification, the DNA molecules were trimmed with NspI and ligated at a DNA concentration of 5 ng/ $\mu$ l to promote intramolecular ligation. Importantly, NspI was chosen for its RCATGY recognition sequence that encompasses the CATG recognition sequence of NlaIII. As a consequence, only a subset of NlaIII (CATG) sites were (re-)digested, generating DNA fragments of approximately 2 kb and allowing the amplification of entire restriction fragments. Sequences of the PDGFRB primers are (5 to 3): PDGFRB\_F TGGTGGGCATATAACTCATC and PDGFRB\_R CCCAGCCAATAAAGACATCA. After ligation, the DNA was purified, PCR products were purified and library prepped using the Illumina NexteraXT protocol and sequenced on an Illumina Miseq sequencer. Reads were mapped using BWA-SW, which is a Smith-Waterman alignment tool. This allows partial mapping, which is optimally suited for identifying break-spanning reads. The human genome version hg19 was used for mapping.

### Array Comparative Genomic Hybridization

Patient DNA was profiled on a custom 180K oligonucleotide array platform (Agilent SurePrint G3 Human CGH microarrays, G4449A, design ID: 022060). In brief, genomic DNA from patients and controls were labelled using random prime labelled using random prime labelling with Cy3 and Cy5 dyes (Perkin Elmer, Waltham, MA, USA). Next, hybridization was performed according to the manufacturer's instructions (Agilent Technologies, Santa Clara, CA) and data was analysed using our in-house developed arrayCGHbase tool(2).

### Complete cDNA sequence of MYH9::PDGFRB fusion

```
ATGGCACAGCAAGCTGCCGATAAGTATCTCTATGTGGATAAAAACCTTCATCAACAATCCGCTGGCCCAG
GCCGACTGGGCTGCCAAGAAGCTGGTATGGGTGCCTTCCGACAAGAGTGGCTTTGAGCCAGCCAGCC
TCAAGGAGGAGGTGGGCGAAGAGGCCATCGTGGAGCTGGTGGAGAATGGGAAGAAGGTGAAGGT
GAACAAGGATGACATCCAGAAGATGAACCCGCCAAGTTCTCCAAGGTGGAGGACATGGCAGAGCTC
ACGTGCCTCAACGAAGCCTCGGTGCTGCACAACCTCAAGGAGCGTTACTACTCAGGGCTCATCTACAC
CTATTCAGGCCTGTTCTGTGTGGTCATCAATCCTTACAAGAACCTGCCCATCTACTCTGAAGAGATTGTG
GAAATGTACAAGGGCAAGAAGAGGCACGAGATGCCCCCTCACATCTATGCCATCACAGACACCCGCTA
CAGGAGTATGATGCAAGACCGAGAAGATCAATCCATCTTGTGCACTGGTGAATCTGGAGCTGGCAAGA
CGGAGAACACCAAGAAGGTCATCCAGTATCTGGCGTACGTGGCGTCCTCGCACAAGAGCAAGAAGGA
```

CCAGGGCGAGCTGGAGCGGCAGCTGCTGCAGGCCAACCCCATCCTGGAGGCCTTCGGGAACGCCAA  
GACCGTGAAGAATGACAACCTCCCGCTTCGGCAAATTCATTTCGCATCAACTTTGATGTCAATGGCTA  
CATTGTTGGAGCCAACATTGAGACTTATCTTTTGGAGAAATCTCGTGCTATCCGCCAAGCCAAGGAAG  
AACGGACCTTCCACATCTTCTATTATCTCCTGTCTGGGGCTGGAGAGCACCTGAAGACCGATCTCCTGT  
TGGAGCCGTACAACAATAACCGCTTCTGTCCAATGGACACGTCACCATCCCCGGGCAGCAGGACAAG  
GACATGTTCCAGGAGACCATGGAGGCCATGAGGATTATGGGCATCCCAGAAGAGGAGCAAATGGGCC  
TGCTGCGGGTCATCTCAGGGGTTCTTCAGCTCGGCAACATCGTCTTCAAGAAGGAGCGGAACACTGA  
CCAGGCGTCCATGCCCGACAACACAGCTGCCAAAAGGTGTCCCATCTCTTGGGTATCAATGTGACCG  
ATTTACCAGAGGAATCCTCACCCGCGCATCAAGGTGGGACGGGATTACGTCCAGAAGGCGCAGAC  
TAAAGAGCAGGCTGACTTTGCCATCGAGGCCTTGGCCAAGGCGACCTATGAGCGGATGTTCCGCTGG  
CTGGTGCTGCGCATCAACAAGGCTCTGGACAAGACCAAGAGGCAGGGCGCCTCCTTCATCGGGATCC  
TGGACATTGCCGGCTTCGAGATCTTTGATCTGAACTCGTTTGAGCAGCTGTGCATCAATTACACCAATG  
AGAAGCTGCAGCAGCTCTTCAACCACACCATGTTTCATCCTGGAGCAGGAGGAGTACCAGCGGAGGG  
CATCGAGTGGAATTCATCGACTTTGGCCTCGACCTGCAGCCCTGCATCGACCTCATTGAGAAGCCAG  
CAGGCCCCCGGGCATTCTGGCCCTGCTGGACGAGGAGTGCTGGTTCCCCAAAGCCACCGACAAGA  
GCTTCGTGGAGAAGGTGATGCAGGAGCAGGGCACCCACCCAAGTTCCAGAAGCCCAAGCAGCTGA  
AGGACAAAGCTGATTTCTGCATTATCCACTATGCCGGCAAGGTGGATTACAAAGCTGACGAGTGGCTG  
ATGAAGAACATGGATCCCCTGAATGACAACATCGCCACACTGCTCCACCAGTCTCTGACAAGTTTTGTC  
TCGGAGCTGTGGAAGGATGTGGACCGCATCATCGGCCTGGACCAGGTGGCCGGCATGTCGGAGACC  
GCACTGCCCGGGCCTTCAAGACGCGGAAGGGCATGTTCCGCACTGTGGGGCAGCTTTACAAGGAG  
CAGCTGGCCAAGCTGATGGCTACGCTGAGGAACACGAACCCCAACTTTGTCCGCTGCATCATCCCCAA  
CCACGAGAAGAAGGCCGGCAAGCTGGACCCGCATCTCGTGCTGGACCAGCTGCGCTGCAACGGTGT  
TCTCGAGGGCATCCGTATCTGCCGCCAGGGCTTCCCCAACAGGGTGGTCTTCCAGGAGTTTCGGCAG  
AGATATGAGATCCTGACTCCAAACTCCATTCCCAAGGGTTTCATGGACGGGAAGCAGGCGTGCGTGCT  
CATGATAAAAGCCCTGGAGCTCGACAGCAATCTGTACCGCATTGGCCAGAGCAAAGTCTTCTCCGTG  
CCGGTGTGCTGGCCACCTGGAGGAGGAGCGAGACCTGAAGATCACCGACGTCATCATAGGGTTCCA  
GGCCTGCTGCAGGGGCTACCTGGCCAGGAAAGCATTGCCAAGCGGCAGCAGCAGCTTACCGCCATG  
AAGTCTCCAGCGGAAGTGCCTGCTACCTGAAGCTGCGGAAGTGGCAGTGGTGGCGGCTCTTCA  
CCAAGGTCAAGCCGCTGCTGCAGGTGAGCCGGCAGGAGGAGGAGATGATGGCCAAGGAGGAGGAG  
CTGGTGAAGGTCAGAGAGAAGCAGCTGGCTGCGGAGAACAGGCTCACGGAGATGGAGACGCTGCA  
GTCTCAGCTCATGGCAGAGAAATTGCAGCTGCAGGAGCAGCTCCAGGCAGAAACCGAGCTGTGTGCC  
GAGGCTGAGGAGCTCCGGGCCCGCCTGACCGCCAAGAAGCAGGAATTAGAAGAGATCTGCCATGAC  
CTAGAGGCCAGGGTGGAGGAGGAGGAGGAGCGCTGCCAGCACCTGCAGGCGGAGAAGAAGAAGA  
TGCAGCAGAACATCCAGGAGCTTGAGGAGCAGCTGGAGGAGGAGGAGAGCGCCCGGCAGAAGCTG  
CAGCTGGAGAAGGTGACCACCGAGGCGAAGCTGAAAAGCTGGAGGAGGAGCAGATCATCTGGA  
GGACCAGAAGTCAAGCTGGCCAAGGAAAAGAACTGCTGGAAGACAGAATAGCTGAGTTCACCAC  
CAACCTCACAGAAGAGGAGGAGAAATCTAAGAGCCTCGCCAAGCTCAAGAACAAGCATGAGGCAAT  
GATCACTGACTTGGAAGAGCGCCTCCGCAGGGAGGAGAAGCAGCGACAGGAGCTGGAGAAGACCC  
GCCGGAAGCTGGAGGGAGACTCCACAGACCTCAGCGACCAGATCGCCGAGCTCCAGGCCAGATCG  
CGGAGCTCAAGATGCAGCTGGCCAAGAAAGAGGAGGAGCTCCAGGCCGCCCTGGCCAGGTGTCAC  
GTGAGCTGCCGCCACGCTGCTGGGGAACAGTTCGAAGAGGAGAGCCAGCTGGAGACTAACGTGA  
CGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAACACTGCGTCTGCAGCACGTGGATCGGC  
CACTGTGCGGTGCGCTGCACGCTGCGCAACGCTGTGGGCCAGGACACGCAGGAGGTCATCGTGGTGC  
CACACTCCTTGCCCTTAAGGTGGTGGTGTATCTCAGCCATCCTGGCCCTGGTGGTGTCTACCATCATCT  
CCCTTATCATCTCATCATGCTTTGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGT  
CTGTGAGCTCTGACGGCCATGAGTACATCTACGTGGACCCCATGCAGCTGCCCTATGACTCCACGTGGG  
AGCTGCCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTGG

AGGCCACGGCTCATGGCCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATGCTTAAATCC  
ACAGCCCCGAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATGAGTCACCTTGGGCCCC  
ACCTGAACGTGGTCAACCTGTTGGGGGCCTGCACCAAAGGAGGACCCATCTATATCATCACTGAGTAC  
TGCCGCTACGGAGACCTGGTGGACTACCTGCACCCGCAACAAACACACCTTCTGCAGCACCCTCCGA  
CAAGCGCCGCCGCCAGCGCGGAGCTCTACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCAGC  
CATGTGTCCTTGACCGGGGAGAGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGAC  
TATGTGCCCATGCTGGACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACACTACATGGCC  
CCTTACGATAACTACGTTCCCTCTGCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGAGTCTCCA  
GTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCATGGAGTTTCTGGCCTC  
CAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCATCTGTGAAGGCAAGCTGGTCAAG  
ATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGACTCGAATTACATCTCCAAGGCAGCACCTTT  
TTGCCTTTAAAGTGGATGGCTCCGGAGAGCATCTTCAACAGCCTCTACACCACCTGAGCGACGTGTG  
GTCCTTCGGGATCCTGCTCTGGGAGATCTTACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGA  
ACGAGCAGTTCTACAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCATGCCTCCGACGAG  
ATCTATGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTGAGATTCGGCCCCCTTCTCCAGCTGGT  
GCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAGAAGTACCAGCAGGTGGATGAGGAGTT  
TCTGAGGAGTGACCACCCAGCCATCCTTCGGTCCCAGGCCCGCTTGCCTGGGTTCCATGGCCTCCGAT  
CTCCCTGGACACCAGCTCCGTCTCTATACTGCCGTGCAGCCCAATGAGGGTGACAACGACTATATCA  
TCCCCCTGCCTGACCCCAAACCCGAGGTTGCTGACGAGGGCCCACTGGAGGGTTCCCCCAGCCTAGC  
CAGCTCCACCCTGAATGAAGTCAACACCTCTCAACCATCTCCTGTGACAGCCCCCTGGAGCCCCAGG  
ACGAACCAGAGCCAGAGCCCCAGCTTGAGCTCCAGGTGGAGCCGGAGCCAGAGCTGGAACAGTTGC  
CGGATTCGGGGTGCCCTGCGCCTCGGGCGGAAGCAGAGGATAGCTTCTCTGTAG

### **MYH9-PDGFRB cloning**

A custom made hPGK-backbone containing the full length MYH9-PDGFRB fusion was made by VectorBuilder (Chicago, IL, USA). The fusion was re-amplified with Q5 High Fidelity 2x Master Mix (NEB, Ipswich, MA, USA) and primers 1 and 2 using a touchdown PCR method for cloning into pMIGII-IRES-GFP (MSCV) backbone. The PCR product was purified using Isolate II PCR & Gel Kit (Bioline, London, UK) and digested with EcoRI (NEB, Ipswich, MA, USA). MSCV backbone was also digested with EcoRI and dephosphorylated with quick CIP (NEB, Ipswich, MA, USA). After the final round of purification using Isolate II PCR & Gel Kit, the eluates were ligated using T4 DNA Ligase (NEB, Ipswich, MA, USA) at 4°C overnight. The ligation product was transformed into NEB® Stable Competent *E. coli* (NEB, Ipswich, MA, USA). Colonies were assessed by colony PCR using MyTaq Red Mix (Bioline, London, UK). Plasmid DNA was obtained from positive colonies using ZymoPUREII Plasmid Midiprep Kit (Zymo Research, Irvine, USA). DNA was Sanger Sequenced to confirm the sequence of the *MYH9-PDGFRB* fusion.

Cloning primers	
Primer 1	CCCGAATTCGCCACCATGGCACAGCAAG
Primer 2	CCCGAATTCGCTGGGTCTACAGGAAGCTA
Colony PCR primers	
Primer 3	CCTCGATCCTCCCTTTATCC
Primer 4	GAGCCCTGAGTAGTAACGCT

### **Clinical information MYH9::PDGFRB T-LBL patient**

A 7 year old boy was referred to the department of pediatric hematology-oncology because of palpable supraclavicular lymph nodes and mild tiredness. Chest X-ray and CT-scan showed a mediastinal mass. A supraclavicular lymph node biopsy was performed and T-cell lymphoblastic lymphoma diagnosed. Cerebrospinal fluid was initially negative and 12% lymphoblasts were found in bone marrow, resulting in a diagnosis of stage 4 T-cell lymphoblastic lymphoma with CD2+, CD45+, CD8+, CD4+, sCD3 weak+ and cyCD3+ immunophenotype. Karyotyping (46,XY,add(22)(q12)[2]/46,XY[20]) and FISH (Kreatech) diagnostics were performed on the bone marrow sample which showed a TCR beta (7q35) rearrangement with absence of t(9;22), 11q23 and TAL1 rearrangements. Treatment according to EORTC-58951-CLG (3) was initiated. In the first weeks of treatment a clinical deterioration and disease progression was seen as the patient developed skin rash, pleural effusion and ascites. Lymphoblasts were found in the pleural effusion and in the cerebrospinal fluid on day 13, and the patient developed hyperleukocytosis. The patient was assigned to the very high risk group due to poor corticosteroid response at the end of prephase and absence of remission at the end of induction treatment (M2 marrow). Treatment continued with an intensified Berlin-Frankfurt-Münster based consolidation 1 (3), and continued consolidation with high dose chemotherapy (VANDA course and HR-1 block) until hematopoietic stem cell transplantation (HSCT) with his HLA-matched sibling brother. Four months after transplantation a relapse was detected in the left orbit and local irradiation, 20 Gy, was administered with positive effect. Seven months after HSCT the patient developed a testicular relapse and palliative care was started. The patient died one month later.

### **Immunohistochemistry**

Tissue was cut (3  $\mu\text{m}$ ) and mounted on TOMO<sup>®</sup> slides (Matsunami, Bellingham, WA, USA). Slides were stained with primary antibodies directed against human PDGFRB. Slides were stained with the Benchmark Ultra platform, Roche Diagnostics (Ventana Medical Systems, Inc, Tucson, AZ, USA) according to manufacturer`s protocols. Staining conditions were as follows: PDGFRB (clone 28E1, rabbit/monoclonal, Cell Signaling Technology, Danvers, Massachusetts, USA) 1:50, 32 min incubation, OptiView kit, pretreatment CC1 (32min). Specimens were analyzed by light microscopy (Olympus BX50, Tokyo, Japan) and scanned images (Nano Zoomer 2.0 -RS Virtual Slide Light microscope scanner and NDP View Software, version NDP.view2, both Hamamatsu Photonics K.K., Hamamatsu City, Japan). Staining intensities were compared to positive controls.

### **Retroviral transduction**

Viral supernatant was produced by transfecting  $4 \times 10^6$  HEK293T cells plated overnight in T75 flasks with lipofectamine<sup>™</sup> 2000 Transfection Reagent (ThermoFisher), containing 10  $\mu\text{g}$  purified plasmid DNA and 10  $\mu\text{g}$  EcoPac. Viral supernatant was collected and filtered through a 0.45  $\mu\text{m}$  filter.  $1 \times 10^6$  Ba/F3 cells were loaded onto Nunc<sup>™</sup> Non-Treated Multidishes (150239, ThermoScientific). Viral supernatant was loaded onto Ba/F3 cells with 8  $\mu\text{g}/\text{mL}$  polybrene (28728-5-4, Sigma Aldrich) and spun for 90 min at 2500 rpm 30°C.

### **Western blotting**

Cells were lysed with radioimmunoprecipitation assay (RIPA) buffer supplemented with phosphatase inhibitors (PhosSTOP<sup>™</sup>, Roche) and proteinase inhibitor (AA Blocks). Protein concentration was measured with the Pierce BCA Protein Assay Kit (Thermo Fisher Scientific).

Denatured protein was loaded on a 4-12% Bolt Bis-Tris Plus gel (ThermoFisher), proteins were separated by electrophoresis for 1hr then transferred onto PVDF membrane using iBlot 2 (Invitrogen). Antibodies used are: pPDGFRB (#3161, Cell Signaling Technology), PDGFRB (#3169, Cell Signaling Technology),  $\beta$ -actin (A1978, Sigma-Aldrich), pSTAT3 (#9131S, Bioké BV), pSTAT5 (#9351S, Bioké BV), pGSK3B (#5558S, Bioké BV), pAKT (4060S, Bioké BV).

### **Phospho-STAT5 flow cytometry**

Cells were treated for 1h with 1 $\mu$ M CP-673451 in 10% RPMI, washed and fixed with PFA (Life Technologies). Cells were permeabilised with ice cold 90% methanol (Sigma-Aldrich) and stored overnight. Samples were stained for 1h with pSTAT5 (612599, BD Biosciences) and isotype control (557783, BD Biosciences). After washing away excess antibody, cells were analyzed by flow cytometry (LSRFortessa, BD Biosciences) and data analysis was performed using FlowJo software.

### **PDGFRB stimulation**

HEK293T-PDGFRB<sup>wt</sup> were a kind gift from Prof. Paul Ekert. Cells were serum starved for 6 hours prior to 1 hour 1  $\mu$ M CP-673451 treatment or DMSO followed by 8 minute stimulation with 20 ng/mL PDGF-BB (100-14B-10UG, PreproTech).

### **Ex vivo culture transduced HSPCs (BMT)**

Transduced HSPCs were cultured in RPMI 1640 medium supplemented with 20% fetal bovine serum (FBS) and 100  $\mu$ g/ml Primocin (Jomar Life Research, Australia) at 37°C with 5% CO<sub>2</sub>.

### **Immunophenotyping organs (BMT)**

Organs were made into single cell suspension. Cells were stained with CD4-V450 (75-0042-U100, Cytek Biosciences), CD8-APC-Cy7 (25-0081-U100, Cytek Biosciences), CD11b-PE (50-0112-U100, Cytek Biosciences), Gr1-APC (20-5931-U100, Cytek Biosciences).

### **Patient information**

In Figure 3D, samples from two different patients cohorts were used. Samples labelled T-ALL1, 2, 3, 4, 5, and T-LBL1 were sourced from patients recruited at Ghent University Hospital. The samples T-ALL6, 7, 8, 9, 10, 11 are part of the Pediatric Preclinical Testing Consortium (including patients from St Jude Children's Research Hospital) with IDs T-ALL6 = ETP1, T-ALL7 = ETP3, T-ALL8 = SJTALL056732\_D1, T-ALL9 = ETP6, T-ALL10 = SJTALL187\_D1, T-ALL11 = SJTALL009\_D1.

### **References**

1. Paula J P de Vree EdW, Mehmet Yilmaz, Monique van de Heijning, Petra Klous, Marjon J A M Verstegen, Yi Wan, Hans Teunissen, Peter H L Krijger, Geert Geeven, Paul P Eijk, Daoud Sie, Bauke Ylstra, Lorette O M Hulsman, Marieke F van Dooren, Laura J C M van Zutven, Ans van den Ouweland, Sjef Verbeek, Ko Willems van Dijk, Marion Cornelissen, Atze T Das, Ben Berkhout, Birgit Sikkema-Raddatz, Eva van den Berg, Pieter van der Vlies, Desiree Weening, Johan T den Dunnen, Magdalena Matusiak, Mohamed Lamkanfi, Marjolijn J L Ligtenberg, Petra ter Brugge, Jos Jonkers, John A Foekens, John W Martens, Rob van der Luijt, Hans Kristian Ploos van Amstel, Max van Min, Erik Splinter, Wouter de Laat. Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. *Nature Biotechnology*. 2014;32(10):1019-1025.

2. Björn Menten FP, Katleen De Preter, Piet Robbrecht, Evi Michels, Karen Buysse, Geert Mortier, Anne De Paepe, Steven van Vooren, Joris Vermeesch, Yves Moreau, Bart De Moor, Stefan Vermeulen, Frank Speleman and Jo Vandesompele. arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. *BMC Bioinformatics*. 2005;6(1):124.

3. Carine Domenech SS, Barbara De Moerloose, Françoise Mazingue, Geneviève Plat, Alina Ferster, Anne Uyttebroeck, Nicolas Sirvent, Patrick Lutz, Karima Yakouben, Martine Munzer, Pierre Röhrlich, Dominique Plantaz, Frederic Millot, Pierre Philippet, Nicole Dastugue, Sandrine Girard, Hélène Cavé, Yves Benoit, Yves Bertrandfor; Children's Leukemia Group (CLG) of European Organisation for Research and Treatment of Cancer (EORTC). Dexamethasone (6 mg/m<sup>2</sup>/day) and prednisolone (60 mg/m<sup>2</sup>/day) were equally effective as induction therapy for childhood acute lymphoblastic leukemia in the EORTC CLG 58951 randomized trial. *Haematologica*. 2014;99(7):1220-1227.

Supplementary Table 1: Immunophenotypes of mice that received MYH9::PDGFRB in the bone marrow transplant model.

		<b>Organ</b>			
	<b>EFS</b>	<b>Peripheral Blood</b>	<b>Spleen</b>	<b>Bone Marrow</b>	<b>Thymus</b>
<b>Mouse 1</b>	119 days	22.3 % GFP Major GFP+ Clone (22.3%): CD8+	27.7% GFP Major GFP+ Clone (27.7%): CD8+	3.41% GFP Major GFP+ Clone (3.41%): CD8+	80.2% GFP Major GFP+ Clone (80.2%): CD8+/CD4+CD8+
<b>Mouse 2</b>	86 days (non leukemic event)	10.4% GFP Major GFP+ Clone (10.4%): CD8+	17.7% GFP Major GFP+ Clone (17.7%): CD8+	7.11% GFP Major GFP+ Clone (7.11%): Gr1+ CD11b+	23.7% GFP Major GFP+ Clone (23.7%): CD8+
<b>Mouse 3</b>	126 days	64.5% GFP Major GFP+ Clone (64.5%): CD8+	41.6% GFP Major GFP+ Clone (27%): CD8+ Minor GFP+ Clone (14.6%): Gr1+ CD11b+	54.1% GFP Major GFP+ Clone (44.96%): Gr1+ CD11b+ Minor GFP+ Clone (9.14%): CD8+	91.2% GFP Major GFP+ Clone (91.2%): CD8+/CD4+CD8+
<b>Mouse 4</b>	72 days	65.3% GFP Major GFP+ Clone (45%): Gr1+ CD11b+ Minor GFP+ Clone (20.3%): CD8+	42% GFP Major GFP+ Clone (28%): Gr1+ CD11b+ Minor GFP+ Clone (14%): CD8+	55.8% GFP Major GFP+ Clone (35%): Gr1+ CD11b+ Minor GFP+ Clone (20.8%): CD8+	54.4% GFP Major GFP+ Clone (54.4%): CD8+/CD4+CD8+
<b>Mouse 5</b>	101 days	33.8% GFP Major GFP+ Clone (33.8%): Gr1+ CD11b+	33.6% GFP Major GFP+ Clone (33.6 %): Gr1+ CD11b+	17.6% GFP Major GFP+ Clone (10.72%): Gr1+ CD11b+ Minor GFP+ Clone (6.88%): CD8+	12.5% GFP Major GFP+ Clone (12.5%): CD8+
<b>Mouse 6</b>	56 days	73.3% GFP Major GFP+ Clone (73.3%): Gr1+ CD11b+	98.7% GFP Major GFP+ Clone (80.1%): Gr1+ CD11b+ Minor GFP+ Clone (18.6%): CD8+	99.8% GFP Major GFP+ Clone (99.8%):	N/A

Supplementary Table 2: Immunophenotypes of mice that received EBF1::PDGFRB in the bone marrow transplant model.

	EFS	Organ			
		Peripheral Blood	Spleen	Bone Marrow	Thymus
<b>Mouse 1</b>	45 days (non leukemic event)	8.96% GFP (no staining performed)	9.2% GFP Major GFP+ Clone (9.2%): Gr1+CD11b+	0.88% GFP	N/A
<b>Mouse 2</b>	112 days (non leukemic event)	13.4% GFP Major GFP+ Clone (13.4%): CD8+	15.8% GFP Major GFP+ Clone (15.8%): CD8+	16.7% GFP Major GFP+ Clone (16.7%): CD8+	N/A
<b>Mouse 3</b>	Still alive at >150 days post transplant	N/A	N/A	N/A	N/A
<b>Mouse 4</b>	62 days (non leukemic event)	11.1% GFP Major GFP+ Clone (11.1%): CD8+	25.2% GFP Major GFP+ Clone (25.2%): CD8+	27.2% GFP Major GFP+ Clone (27.2%): Gr1+ CD11b+	69.2% GFP Major GFP+ Clone (69.2%): CD8+/CD4+CD8+
<b>Mouse 5</b>	83 days (non leukemic event)	27% GFP Major GFP+ Clone (27%): Gr1+CD11b+	58.5% GFP Major GFP+ Clone (58.5%): Gr1+ CD11b+	36.5% GFP Major GFP+ Clone (36.5%): CD8+	N/A
<b>Mouse 6</b>	100 days (non leukemic event)	9.66% GFP Major GFP+ Clone (%):	20.6% GFP Major GFP+ Clone (20.6%): Gr1+ CD11b+	20.5% GFP Major GFP+ Clone (20.5%): Gr1+ CD11b+	0.63% GFP

## Supplementary Figure Legends

### Figure S1

- (A) Array CHG of the t(5;22) MYH9::PDGFRB T-LBL patient. Red bars depict losses whereas blue bars are gains.
- (B) TLA of a T-LBL case with PDGFRB (chromosome 5) as viewpoint. Additional reads were detected at chromosome 22 suggesting the presence of a (5;22) translocation.

### Figure S2

- (C) (p)PDGFRB (Tyr751) Western blot analysis of Ba/F3 transduced cells with MYH::PDGFRB, EBF1::PDGFRB (positive control[1]), NRAS(G12D) (negative control, no PDGFRB) and JAK3(M511I) (negative control, no PDGFRB)
- (D) (p)PDGFRB (Tyr751) Western blot analysis on PDGFRB<sup>wt</sup> stably transduced HEK293T cells. Cells were pre-treated for 1 hour with 1 $\mu$ M CP-673451 or DMSO followed by 8 minutes of stimulation with 20 ng/mL PDGF-BB.

### Figure S3

- (A) Flow cytometric analysis of murine stem cells harvested from C57BL/6JausB mice transduced with *MYH9::PDGFRB-GFP* construct. Cells were cultured without cytokines (IL-3, IL-6 and SCF) and were analyzed at days 0, 5, 7 and 14.
- (B) White Blood Cell count and % GFP of peripheral blood from MYH9::PDGFRB mice (n=6). Mice were bled weekly.
- (C) Gating strategy for immunophenotyping of peripheral blood, spleen, BM and thymus from MYH9::PDGFRB/EBF1::PDGFRB mice.

### Figure S4

- (A) (p)PDGFRB (Tyr751) Western blot analysis of PDX samples treated *ex vivo* for 1 hour with 0 or 1  $\mu$ M CP-673451.
- (B) pSTAT5 (Y694) flow cytometry analysis of CTV-1 and T-ALL1 treated with DMSO vehicle control or 1  $\mu$ M CP-673451 for 1 hour.

### Figure S5

- (A) Body weight changes in both control (90% PEG300, 10% N-methyl pyrrolidone) and treated (CP-673451) NSG-SGM3 mice during the course of the experiment

### Figure S6

- (A) Schematic overview of a conditional PDGFRB gain-of-function mouse model generated as previously described [2]. After CD2-iCre induced recombination of loxP sites, *Pdgfrb* is being overexpressed from the *ROSA26* promoter.
- (B) *Pdgfrb* mRNA expression in thymi from wild type (WT) versus *CD2-iCre<sup>tg/+</sup> R26-Pdgfrb<sup>tg/tg</sup>* mice (PDGFRB) (p<0.0001)
- (C) PDGFRB Western blot analysis of thymi from wild type (WT) versus *CD2-iCre<sup>tg/+</sup> R26-Pdgfrb<sup>tg/tg</sup>* (PDGFRB) mice

- (D) Aging cohort of *Lck-Cre<sup>tg/+</sup> Pten<sup>fl/fl</sup>* (n=12, median survival 94 days) and *Lck-Cre<sup>tg/+</sup> Pten<sup>fl/fl</sup> R26-Pdgfrb<sup>tg/tg</sup>* (n=13, median survival 91 days) mice
- (E) (p)PDGFRB (Tyr751) Western blot analysis of thymi from *Lck-Cre<sup>tg/+</sup> Pten<sup>fl/fl</sup> R26-Pdgfrb<sup>tg/tg</sup>* mice

### Supplementary References

1. S J Welsh, M.L.C., M Togni, C G Mullighan & J Hagman *Deregulation of kinase signaling and lymphoid development in EBF1-PDGFRB ALL leukemogenesis*. *Leukemia*, 2017. **34**: p. 38-48.
2. Tim Pieters, S.T.S., Lisa Demoen, André Almeida, Lieven Haenebalcke, Filip Matthijssens, Kelly Lemeire, Jinke D'Hont, Frederique Van Rockeghem, Tino Hochepped, Beatrice Lintermans, Lindy Reunes, Tim Lammens, Geert Berx, Jody J. Haigh, Steven Goossens & Pieter Van Vlierberghe, *Novel strategy for rapid functional in vivo validation of oncogenic drivers in haematological malignancies*. *Scientific Reports*, 2019. **9**: p. 10577.

Figure S1











