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Author Correction: Detection of kinase domain mutations in BCR::ABL1 leukemia by ultra-deep sequencing of genomic DNA

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The original version of this Article contained an error in Figure. 5, where the colors representing "DNA-Deep NGS" and "RNA-Nested NGS" were incorrect. The original Figure. 5 and accompanying legend appear below.

In addition, in the Results section, under the subheading 'Impact of KD mutations in the clinical outcome of the chronic myeloid leukemia patients',

"The mutation was detected in mRNA and gDNA with a corrected VAF of 2.0E−4 and 4.0E−4, respectively."

now reads:

"The mutation was detected in mRNA and gDNA with a corrected VAF of 4.0E−4 and 2.0E−4, respectively."

The original Article has been corrected.

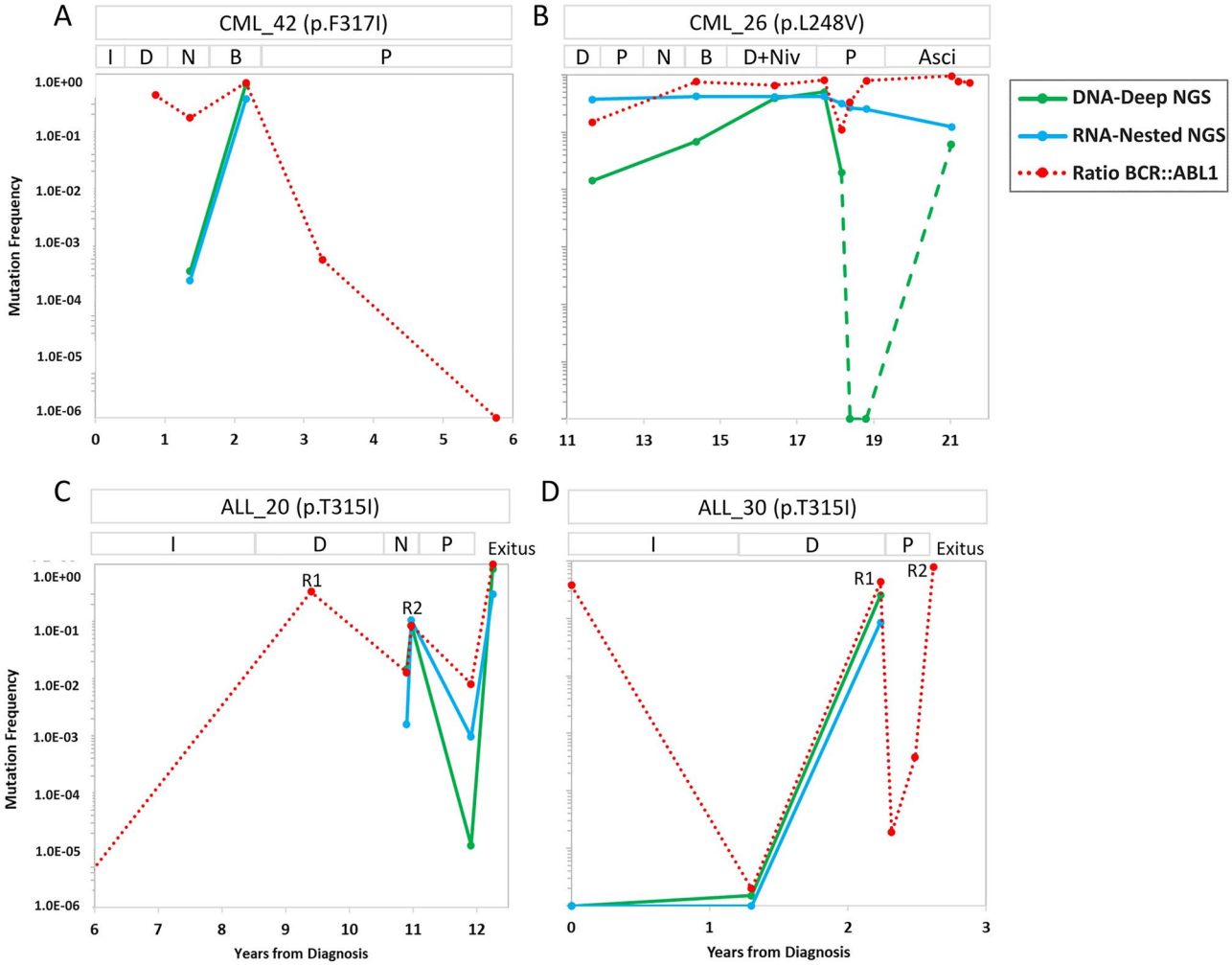

Figure 5. Time course for the mutations measured by DNA-DeepNGS and RNA-NestedNGS, and *BCR::ABL1* levels present in the most clinically relevant patients. Y-axis represents the value of RNA-NestedNGS VAF corrected by the ratio *BCR::ABL1* (green), DNA-DeepNGS VAF (blue) or ratio *BCR::ABL1*/*ABL1* (red). *ALL* acute lymphoblastic leukemia, *Asci* asciminib, *B* bosutinib, *CML* chronic myeloid leukemia, *D* dasatinib, *I* imatinib, *N* nilotinib, *Niv* nivolumab, *P* ponatinib, *R* relapse, *VAF* variant allele frequency.

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