Reply to "Rare coincident NPM1 and RUNX1 mutations in intermediate risk acute myeloid leukemia display similar patterns to single mutated cases". Haematologica 2014;99(2):e20-21.

We appreciate the efforts of Fasan et al. 1 to further investigate the relationship between NPM1 and RUNX1 mutations in de novo, intermediate-risk acute myeloid leukemia and confirm the rare co-occurrence of these two mutations in their cohort. We would like to clarify that we did not report that all four RUNX1 mutations in the NPM1-mutated cases of our study "were located outside the TAD or RHD domain", as stated by Fasan et al. 1 Rather, we reported that two of the four RUNX1 mutations (those in Patients 1 and 2; see paragraph 2 of our paper) were located in the transactivation domain (TAD).2 Thus, we must emphasize that the RUNX1 mutations in our NPM1mutated cases were in-frame and located outside of the Runt Homology Domain (RHD), not outside of all functional domains of RUNX1. Interestingly, four of the RUNX1 mutations identified by Fasan et al. in their NPM1mutated cases (c.877C>T, c.984C>G, c. 890 C>T, and c. 977T>C) were also in-frame and located outside of the RHD. One caveat is that c.877C>T and c.984C>G result in premature stop codons; a phenomenon we did not see among the RUNX1 mutations in the NPM1-mutated cases of our cohort.

We would also like to clarify that we did not report that all four *RUNX1* mutations in the *NPM1*-mutated cases of our study "were also present in the germline", as stated by Fasan *et al.*¹ in paragraph 1 of their letter. Instead, we reported in paragraph 3 that "germline material was screened in those *RUNX1*-mutated/*NPM1*-mutated patients for whom buccal cells were available (UPN 1-3)". Germline material was not available for Patient 4 of our study and thus germline *RUNX1* mutation status of this patient is unknown.

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