ERRATA

List of papers (p. i):

Should be

III. Delsing Malmberg E., J. Alm S., Nicklasson M., **Lazarevic V**., Ståhlman S., Samuelsson T., Lenhoff S., Asp J., Ehinger M., Palmqvist L., Brune M., and Fogelstrand L. Minimal residual disease assessed with deep sequencing **of *NPM1* mutations** predicts relapse after allogeneic stem cell transplant in AML.
Leukemia & Lymphoma 2019 Feb;60(2):409-417.

Sammanfattning:

Skall vara

Prognosen är oftast dålig, där femårs-överlevnaden för vuxna som insjuknar i medianåldern (72år) är cirka **10%**.

1.2.1 AML epidemiology (p. 6):

Should be

At this age, the 5-year overall survival (OS) was **10%** for patients fit for intense treatment.

4.4. Results (p.51)

Should be

Children treated with the NOPHO-DBH AML-2012 protocol since **2013** were offered participation in the "Early detection of relapse study".

Paper I (p. 2):

Should be

Reverse transcription followed by quantitative polymerase chain reaction (RT-qPCR) can be used to quantify leukemic burden with a higher sensitivity than MFC-MRD in AML with fusion genes such as *RUNX1-RUNX1T1*, *CBFB-MYH11*, or ***KMT2A-MLLT3*** (previously *MLL-AF9*), that is, in approximately 50% of children, 30% of adults 15-60 yr old, and 10% of adults >60 yr old with AML.

Paper II (p. 158):

Should be

The limit of quantification was higher in the BM samples analyzed with *KMT2A-MLLT10* assay (median of diagnostic level, 2×10^{-3}; range of diagnostic level, 1×10^{-3} to 5×10^{-3}) than with the *RUNX1-RUNX1T1* assay (**median of diagnostic level**, 1.9×10^{-5}; range of diagnostic level, 8×10^{-6} to 6.1×10^{-5}; P = 0.006).

Paper III (p. 3, Table 1, Patient and disease characteristics):

Should be

Female/male (n) 22/7 in row gender.

Paper IV (p. 9, Figure 1E):

Should be

Time from first MRD **measurement**.