Author's response to reviews

Title: Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia

Authors:

Domenica Ronchetti (domenica.ronchetti@unimi.it)
Laura Mosca (laura.mosca@unimi.it)
Giovanna Cutrona (giovanna.cutrona@istge.it)
Giacomo Tuana (giacomo.tuana@gmail.com)
Massimo Gentile (massimogentile@virgilio.it)
Sonia Fabris (sonia.fabris@quest.unimi.it)
Luca Agnelli (luca.agnelli@gmail.com)
Gabriella Ciceri (gabriella.ciceri@unimi.it)
Serena Matis (serena.matis@istge.it)
Carlotta Massucco (carlotta.massucco@istge.it)
Monica Colombo (monica.colombo@istge.it)
Daniele Reverberi (daniele.reverberi@istge.it)
Anna Grazia Recchia (annarecchia@libero.it)
Sabrina Bossio (sabrinabossio@libero.it)
Massimo Negrini (massimo.negrini@unife.it)
Pierfrancesco Tassone (tassone@unicz.it)
Fortunato Morabito (fortunato_morabito@tin.it)
Manlio Ferrarini (manlio.ferrarini@istge.it)
Antonino Neri (antonino.neri@unimi.it)

Version: 2 Date: 30 July 2013

Author's response to reviews:

Dear Editor,

I am sending the revised version of the manuscript “Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia” by Ronchetti D.et al., which I would like to submit for publication in BMC Medical Genomics as a Research Article.

Different investigators have recently introduced updated probe set definitions to more accurately annotate probes to the current human genome build release GRCh37/hg19. This is particularly important for the correct identification of sno/scaRNAs molecules, and it becomes fundamental to discriminate transcripts within family of snoRNAs present in multiple copies that may differ only for a single nucleotide.

Such an issue emerged in our previous study investigating sno/scaRNAs expression in multiple myeloma, in which the deregulation of SNORD 115 and -116 family members could be correctly assessed thanks to the BrainArray CDF annotations, instead of the original Affymetrix probe set definitions. The
correctness of the annotation procedures was confirmed by qRT-PCR validation (Ronchetti D et al, BCJ 2013). For this reason, we assumed that the use of custom BrainArray CDF could be considered a better choice than the manufacturer’s one to detect sno/scaRNAs expression.

According with the request of a clearer description of the mapping annotation procedure, we added in the Material and Methods section –(Gene Expression Profiling pag 8) - a brief description of the methodological principles, also indicating the references addressing this issue in details. In addition, we specified the human genome build release GRCh37/hg19 in the first paragraph of Results section (sno/scaRNA expression profile of CLL cells compared to normal B-cell populations).

Looking forward to hearing from you in due course.

Yours sincerely

Antonino Neri, MD