Reviewer's report

Title: Specific Gene Expression Profiles and Unique Chromosomal Abnormalities are Associated with Regressing Tumors Among Infants with Dissiminated Neuroblastoma.

Version: 2 Date: 2 October 2008

Reviewer: PAOLA SCARUFFI

Reviewer's report:

I have reviewed the resubmission for this manuscript and I feel that the Authors have addressed my major concerns appropriately. This reviewer is delighted that Authors followed suggestions and modified both title and conclusions in order to avoid drawing definitive assertions. Actually, the manuscript is a description of chromosomal alterations and gene expression profiles, without identification of any specific gene-signature associated with infant NB outcome, as Authors themselves state in the report to my previous comments.

There are still some points that need the Authors’ attention.

1. Authors should be careful in reporting the exact number of annotated sequences identified by gene expression analyses. In the response to my comments, Authors correctly indicate the number of selected probes sets (Table 2A: 233 probe sets, Table 2B: 224 sets, Table 2C: 107 sets) and of annotated sequences (Table 2A: 231 sequences, Table 2B: 220 sequences, Table 2C: 107 sequences). On the contrary, in the manuscripts they still report wrong numbers of differentially expressed genes in Results (page 9, row 20; page 10, row 13; page 12, row 1), Legends of Supplementary Table 2A, Table 2B and Table 2C, Legends of Figure 1, Supplementary Figure 1A and Supplementary Figure 2B.

2. Similarly, Authors should not use indiscriminately terms “genes” and “probe sets” in sentence “The number of genes common between…..on gene expression profiles.” at Results section at page 11, rows 7-10 and in Supplementary Figure 2.

3. Since data size is limited, I would recommend to remove percentages of alterations also in the Abstract and Results (“Allelic and MYCN analysis” paragraph, pages 8-9)

4. As regarding microarray platform (Affymetrix U95), it is true that results obtained using such outdated chip have recently been reported by leader groups involved in NB investigation, but they specified that those data were partially the ones reported on earlier (i.e.: Fujita et al in JNCI 2008 and Mosse et al in Genes, Chromosomes and Cancer 2007 refer to Wang Q et al, Cancer Res 66, 2006; Schramm et al in CCR 2007 refer to Schramm A et al, Oncogene 24, 2005). Similarly, it would be important that Authors give information about the fact of having partially presented in this manuscript gene expression profiles that have
been already reported (i.e. in Alaminos M et al., Genome-wide analysis of gene expression associated with MYCN in human neuroblastoma, Cancer Res. 63(15):4538-46, 2003). This will not preclude publication of the manuscript, rather it would represent an added value because in future further information could be drawn putting together all the molecular data collected on the same subset of patients (and publicly available) by using different technologies.

**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Acceptable

**Statistical review:** No, the manuscript does not need to be seen by a statistician.

**Declaration of competing interests:**

I declare that I have no competing interests