Correction

Correction: Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes

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We wish to report some corrections to our study [1], none of which alters the interpretation of the data or the conclusions drawn. After publication, we noticed that one of the microarray hybridizations (on sample NB11) was performed on the same patient’s material as another hybridization (sample NB4; see Table 1; a corrected version of Table 5 [1]). As this error leads to an incorrect subclassification of the patients into the ‘favourable’ and ‘unfavourable’ neuroblastoma subgroups, we would like to exclude this data point from the differential expression analysis of favorable versus unfavorable neuroblastoma given under the heading ‘Differential expression analysis of favorable and unfavorable neuroblastoma’ in the Results section of [1]. Careful reanalysis after exclusion of NB11 did not lead to important changes in the generated gene lists and conclusions; the changes are given in the corrected paragraph and Table 2 (a corrected version of Table 4 [1]), and the Additional data files 1 and 2 (corrected versions of Additional data files 2 and 3 [1]) available online with this article.

We also noticed that sample NB1 is stage 1 instead of stage 4S and that sample NB2 was not localized to the adrenals (see Table 1).

Results

Differential expression analysis of favorable and unfavorable neuroblastoma

So far, most published microarray studies on neuroblastomas mainly compared favorable with unfavorable neuroblastomas in order to identify prognostic markers or pathways that are involved in these clearly different neuroblastoma tumor types. In order to add value to such an analysis, we contrasted similar differentially expressed gene lists with the normal neuroblast expression profile (Additional data file 1). In a first step, we compared the differentially expressed genes between these two tumor types with published prognostic gene lists. We found that 23 of the 193 genes on our list were previously reported, including the well established markers MYCN, NTRK1, and CD44 (see NBGS analysis in Additional data file 2). This overlap demonstrates the validity of the selected neuroblastoma panel and their expression profile. Subsequently, we looked for the corresponding gene expression levels of the differentially expressed genes in the normal counterpart cells, aiming to select neuroblastoma candidate genes. Of the 100 genes that are more highly expressed in favorable tumors (compared to unfavorable) 41 also have a significant differential expression (either higher or lower)
compared to neuroblasts, whereas 43 of the 93 genes that are more highly expressed in unfavorable tumors exhibit differential expression compared to the neuroblasts (Table 2).

From this analysis, a few putative positional tumor suppressor candidates emerge: CDC42 on 1p36, CACNA2D3 on 3p21 and DLK1 on 14q. The latter two genes are of particular interest because they are highly expressed in neuroblasts and favorable neuroblastomas and their expression is significantly lower in unfavorable neuroblastomas. Among the genes that are more highly expressed in unfavorable neuroblastomas than in favorable ones and neuroblasts, the proven oncogenic transcription factor MYCN emerges (and putative downstream genes KIFAP3, OPHN1, RGS7, ASCL1, ODC1, TWIST1 and TYMS, according to NBGS), as well as several other genes that have been identified or studied in the context of neuroblastoma such as ALK and PRAME, and positional candidates on 17q including BIRC5 and RNU2.

### References

1. De Preter K, Vandesompele J, Heimann P, Yigit N, Beckman S, Schramm A, Eggert A, Stallings RL, Benoit Y, Renard M, et al.: Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes. *Genome Biol* 2006, 7:R84.

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**Additional data files**

Additional data files 1 and 2 containing the corrected data available online with this article.

(Continues on the next page)
## Table 2

Genes that are differentially expressed in favorable vs unfavorable neuroblastoma

| Genes that are differentially expressed compared with neuroblasts among the differentially expressed genes in favorable neuroblastoma (NB) vs unfavorable NB, with an indication of the number of neuroblastoma microarray studies in which these genes were found through NBGS analysis. NBGS, Neuroblastoma Gene Server. |
| --- |
| **Favorable NB > unfavorable NB** | NBGS | **Favorable NB < unfavorable NB** | NBGS |
| Neuroblast < favorable NB | Neuroblast < unfavorable NB, neuroblast < unfavorable NB |
| AKAP7 | 6q | - | FABP6 | 5q | - |
| ARL4C | 2q | - | IGLJ3 | 22q | 1 |
| ASPN | 9q | - | NEFL | 8p | - |
| BCL2 | 18q | 1 | NPY | 7p | - |
| CALB1 | 8q | - | - | - | - |
| CAMK2B | 22q | 2 | - | - | - |
| CD24 | 6q | - | - | - | - |
| CDC42 | 1p | 1 | ALK | 2p | - |
| DDAH1 | 1p | - | ASCL1 | 12q | 1 |
| DNaPTP6 | 2q | 1 | BCL1A | 2p | - |
| EP34 | 18p | 1 | BIRC5 | 17q | 3 |
| FAM70A | Xq | - | C3 | 19p | - |
| KIFAP3 | 1q | 1 | CALCB | 11p | - |
| OPHN1 | Xq | - | CCL18 | 17q | - |
| PPAN | 19p | - | CCL2 | 9p | - |
| PRKCB1 | 16p | 1 | CCNB1 | 5q | 1 |
| REEP1 | 2p | - | CD74 | 5q | - |
| RGS7 | 1q | 2 | CRH | 8q | - |
| RNF11 | 1p | - | CSPG2 | 19p | - |
| SCD9 | 4q | 2 | CXCR4 | 2q | 2 |
| SERINC1 | 6q | 1 | DYNCR1 | 7q | - |
| ST6GALNAc5 | 1p | - | F12 | 5q | - |
| SV2C | 5q | - | GPR42 | 8p | - |
| **neuroblast > favorable NB, neuroblast > unfavorable NB** | **neuroblast > favorable NB, neuroblast > unfavorable NB** |
| CACNA2D3 | 3p | - | IGHG3 | 14q | 1 |
| DLK1 | 14q | 2 | IGKC | 2p | 1 |
| HBG1 | 11p | - | IGLC1 | 22q | - |
| HBG2 | 11p | - | IGLC2 | 22q | - |
| **neuroblast > unfavorable NB** | **neuroblast > unfavorable NB** |
| ALDH3A2 | 17p | 1 | LMO3 | 12p | 1 |
| DBH | 9q | 1 | MMP9 | 20q | 1 |
| DGC1 | 8p | - | MYCN | 2p | 9 |
| EYA1 | 8q | - | NEFH | 22q | - |
| GCH1 | 14q | 1 | ODC1 | 2p | 3 |
| HBA1 | 16p | - | ODGHL | 10q | - |
| HBA2 | 16p | - | P2RX5 | 17p | - |
| HTRK1 | 1q | 4 | PRAME | 22q | 1 |
| PTPRD | 9p | - | RPS4Y1 | Yp | 1 |
| PTPRK | 6q | - | SERPINF1 | 17p | - |
| SRPR | 8p | 1 | SIC1 | 2p | - |
| SLC1A7A | 8p | - | SNT2 | 3q | 1 |
| TAP2B | 6p | - | SST | 3q | 1 |
| TNN1 | 15q | 1 | TWIST1 | 7p | 1 |
| **neuroblast > favorable NB** | **neuroblast > favorable NB** |
| RNU2 | 17q | - | XAGE1 | Xp | - |
| **neuroblast > favorable NB, neuroblast > unfavorable NB** | **neuroblast > favorable NB, neuroblast > unfavorable NB** |
| CI Iorf43 | 11p | - | - | - | - |