In silico analysis of microRNA-510 as a potential oncomir in human breast cancer

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In a recent issue of Breast Cancer Research, Guo and colleagues provided mechanistic evidence supporting the role for microRNA (miR)-510 as a novel oncomir playing a pivotal role in human breast cancer via regulation of expression of peroxiredoxin 1 [1]. Their study follows the original observation of elevated miR-510 expression in human breast tumor samples described by Findlay and colleagues in 2008 [2].

To acquire a deeper insight into the potential role of miR-510 in human breast cancer, we carried out an in silico analysis of the miR-510 abundance in clinical breast cancer samples using three independent publicly available datasets (described in Additional file 1). Conspicuously, we have found that expression of miR-510 was virtually nonexistent in clinical sample sets (Dataset 1 [3] and Dataset 2 [4]). Only seven out of 473 clinical breast cancer specimens altogether demonstrated the miR-510 miRNA-Seq reads (Figure 1A,B, left), all of which could be attributed to a very low spectrum of the whole expression range of all miRNAs expressed in the respective datasets (Figure 1A,B, right). Analysis of the same kind carried out in 11 normal tissue samples (included in Dataset 2 [4]) revealed one sample expressing a low level of the miR-510 gene (Figure 1C). Similarly, one out of six breast cancer cell lines (included in Dataset 2) showed detectable expression of miR-510 (Figure 1D).

Analysis of an independent dataset (Dataset 3 [5]) showed expression of miR-510 in a substantial number of cases studied. One should, however, consider that, similar to the previously mentioned miRNA-Seq experiments, the expression of miR-510 in Dataset 3 could be attributed to the very low spectrum of the expression range (Figure 2A), and consider that microarray results are by their nature characterized by a very modest signal-to-noise separation, resulting in a low estimation confidence for the low readouts. Nevertheless, we did attempt to assess whether stratification of Dataset 3 by the median expression signal of miR-510 would correlate with the disease-free survival time (Figure 2B). Results of the analysis revealed that, although the higher strata of miR-510 expression showed a tendency to correlate with slightly worse disease-free survival times (Figure 2B), the correlation did not reach statistical significance ($P = 1.88 \times 10^{-1}$).

Considering our observations and acknowledging the high clarity of mechanistic observations by Guo and colleagues [1], we assume that miR-510 ought to be further evaluated in human cancer types other than breast cancer, especially those in which peroxiredoxin 1 seems to play a role.
Figure 1 (See legend on next page.)
Additional file

Additional file 1: Is the supplemental methods.

Abbreviations
miR: microRNA.

Competing interests
The authors declare that they have no competing interests.

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References
1. Guo QJ, Mills JN, Bandurraga SG, Nogueira LM, Mason NJ, Camp ER, Larue AC, Turner DP, Findlay VJ. MicroRNA-510 promotes cell and tumor growth by targeting peroxiredoxin1 in breast cancer. Breast Cancer Res 2013, 15:R70.
2. Findlay VJ, Turner DP, Moussa O, Watson DK. MicroRNA-mediated inhibition of prostate-derived Ets factor messenger RNA translation affects prostate-derived Ets factor regulatory networks in human breast cancer. Cancer Res 2008, 68:9499-9506.
3. The Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumours. Nature 2012, 490:61-70.
4. Farazi TA, Horlings HM, Ten HJ, Mihailovic A, Halfwerk H, Morozov P, Brown M, Hafner M, Reyal F, van Kouwenhove M, Kreike B, Sie D, Hovestadt V, Wessels L, van de Vijver MJ, Tuschl T. MicroRNA sequence and expression analysis in breast tumors by deep sequencing. Cancer Res 2011, 71:4443-4453.
5. Enerly E, Steinfeld I, Kleivi K, Leivonen S-K, Aare MR, Russnes HG, Rønneberg JA, Johnsen H, Navon R, Rødland E, Mäkelä R, Naume B, Perälä M, Kallioniemi O, Kristensen VN, Yakhini Z, Barreze-Dale A-L. miRNA-mRNA integrated analysis reveals roles for miRNAs in primary breast tumors. PLoS One 2011, 6:e19695.

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