Open access Correction

## Correction: MicroRNA-17 and the prognosis of human carcinomas: a systematic review and meta-analysis

Huang C, Yu M, Yao X. MicroRNA-17 and the prognosis of human carcinomas: a systematic review and meta-analysis. *BMJ Open* 2018;8:e018070. doi:10.1136/bmjopen-2017-018070.

This article was previously published with some errors.

In the table 1, table 2 and figure 1, Robaina *et al.* conducted the study of miR-17 by the method of qRT-PCR instead of ISH as we described in the paper (citation number 38). Secondly, the term Caucasian is not applied in Brazilian for ethnicity classification. The authors would therefore like to use the term non-Asian for describing the studies conducted in the Spain and Brazil. The issue did not affect the main result and the conclusion of the study. Below is the updated table 2 and figure 1.

Table 1 A summary table of the meta-analysis

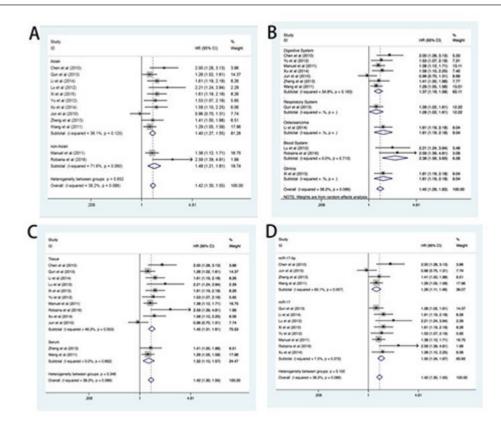
| Study         | Year | Country | Diseases                              | Case<br>Number | Stage   | Sample | Assay   | Cut-off<br>value | HR    | Follow-up<br>(months) | Type of miR-<br>17 detection |
|---------------|------|---------|---------------------------------------|----------------|---------|--------|---------|------------------|-------|-----------------------|------------------------------|
| Chen et al    | 2012 | China   | HCC                                   | 120            | I-IV    | Tissue | qRT-PCR | Median           | RR    | 46                    | miR-17-5p                    |
| Qun et al     | 2013 | China   | Lung Cancer                           | 221            | I-IV    | Tissue | qRT-PCR | Median           | Given | 50                    | miR-17                       |
| Li et al      | 2014 | China   | Osteosarcoma                          | 117            | 1-111   | Tissue | qRT-PCR | Median           | Given | 44                    | miR-17                       |
| Lu et al      | 2012 | China   | Glioma                                | 108            | I-IV    | Tissue | qRT-PCR | Mean             | RR    | 60                    | miR-17                       |
| Xi et al      | 2015 | China   | T-cell lymphoblastic lymphoma         | 57             | III, IV | Tissue | qRT-PCR | Median           | Given | Up to 13<br>years     | miR-17                       |
| Yu et al      | 2012 | China   | Colon Cancer                          | 48             | I-IV    | Tissue | qRT-PCR | Median           | Given | 5-66                  | miR-17                       |
| Manuel et al  | 2011 | Spain   | Gastrointestinal<br>Cancer            | 38             | I-IV    | Tissue | qRT-PCR | Mean             | Given | 38                    | miR-17                       |
| Robaina et al | 2016 | Brazil  | Burkitt lymphoma                      | 41             | I-IV    | Tissue | qRT-PCR | Median           | Given | 69                    | miR-17                       |
| Xu et al      | 2014 | China   | Esophageal Squamous<br>Cell Carcinoma | 105            | I-IV    | Tissue | qRT-PCR | Mean             | Given | 52                    | miR-17                       |
| Jun et al     | 2010 | Japan   | Pancreatic Cancer                     | 80             | I-IV    | Tissue | qRT-PCR | Median           | Given | 60                    | miR-17-5p                    |
| Wang et al    | 2011 | China   | Gastric Cancer                        | 65             | I-IV    | Serum  | qRT-PCR | Median           | Given | 36                    | miR-17-5p                    |
| Zheng et al   | 2013 | China   | HCC                                   | 96             | I-IV    | Serum  | qRT-PCR | Median           | Given | NG                    | miR-17-5p                    |

Revised Table 2 Subgroup analysis.

|                          | Number of | Heterogeneity                 |          | _                  |          |  |
|--------------------------|-----------|-------------------------------|----------|--------------------|----------|--|
| Subgroup                 | studies   | <i>l</i> <sup>2</sup> (95%CI) | P values | pooled HR (95% CI) | P values |  |
| Total                    | 12        | 38.2% (0% to 68.7%)           | 0.086    | 1.42(1.30 to 1.55) | <0.001   |  |
| Ethnic subtotal          |           |                               |          |                    |          |  |
| Non-Asian                | 2         | 71.6% (0% to 93.6%)           | 0.06     | 1.48(1.21 to 1.81) | <0.001   |  |
| Asian                    | 10        | 36.1% (0% to 69.5%)           | 0.12     | 1.40(1.27 to 1.55) | <0.001   |  |
| Disease subtotal         |           |                               |          |                    |          |  |
| Digestive system         | 7         | 34.8% (0% to 72.4%)           | 0.163    | 1.36(1.22 to 1.51) | < 0.001  |  |
| Respiratory system       | 1         | NA                            | NA       | 1.28(1.02 to 1.61) | 0.036    |  |
| Blood system             | 2         | 0                             | 0.713    | 2.38(1.56 to 3.63) | < 0.001  |  |
| Glioma                   | 1         | NA                            | NA       | 1.61(1.19 to 2.18) | 0.002    |  |
| Osteosarcoma             | 1         | NA                            | NA       | 1.61(1.19 to 2.18) | < 0.001  |  |
| Detected Sample subtotal |           |                               |          |                    |          |  |
| Tissue                   | 10        | 46.2% (0% to 74.1%)           | 0.053    | 1.45(1.31 to 1.61) | <0.001   |  |
| Serum                    | 2         | 0                             | 0.662    | 1.32(1.10 to 1.57) | 0.002    |  |
|                          |           |                               |          |                    |          |  |



|                              | Number of | Heterogeneity          |          |                    |          |
|------------------------------|-----------|------------------------|----------|--------------------|----------|
| Subgroup                     | studies   | I <sup>2</sup> (95%CI) | P values | pooled HR (95% CI) | P values |
| Detection of miR-17 subtotal |           |                        |          |                    |          |
| miR-17                       | 8         | 60.1% (13.2% to 81.7%) | 0.057    | 1.29(1.11 to 1.49) | <0.001   |
| miR-17-5p                    | 4         | 7.5% (0% to 43.4%)     | 0.372    | 1.50(1.34 to 1.67) | 0.001    |



In addition, there were some errors in the 'Abstract' section,under the results subheading, the text should read as:

The results indicated that the increased expression of miR-17 played an unfavourable role in overall survival in various human carcinomas with the HR of 1.342 taking into account the publication bias. In subgroup analysis, HR of ethnicity (non-Asian HR=1.48 and Asian HR=1.40), disease (digestive system HR=1.36 and blood system cancer (HR=2.38) were significant with P<0.05.

This was incorrectly published as: The results indicated that the increased expression of miR-17 played an unfavourable role in overall survival in various human carcinomas with the HR of 1.342 taking into account the publication bias. In subgroup analysis, HR of ethnicity (Caucasian HR=1.48 and Asian HR=1.40), disease (digestive system HR=1.36 and blood system cancer (HR=2.38), detection method (quantitative real-time PCR HR=1.40 and in situ hybridization, HR=2.59) and detection sample (tissue HR=1.45 and serum HR=1.32) were significant with P<0.05.

The errors in the Results section, should read as:

A total of 1096 patients with various types of cancers were from People's Republic of China, Japan, Spain and Brazil. Quantitative real-time PCR (qRT-PCR) was used to assess the expression of miR-17 in all studies.

and was incorrectly published as:

A total of 1096 patients with various types of cancers were from People's Republic of China, Japan, Spain and Brazil. Quantitative real-time PCR (qRT-PCR) was used to assess the expression of miR-17 in 12 studies, and one study used the in situ hybridisation (ISH).

The errors in the Discussion section, should read as:

In the subgroup analysis, we found that the potential heterogeneity may have originated from the non-Asian group studies.

and was incorrectly published as:

In the subgroup analysis, we found that the potential heterogeneity may have originated from the Caucasian group in the study conducted by Robaina *et al.* Unlike the commonly used RT-PCR, ISH technique was used to detect miR-17

The errors in the Discussion section, should read as:

However, both studies from Spain and Brazil recruited population of non-Asians decreasing the heterogeneity.

and was incorrectly published as:

However, both studies from Spain and Brazil recruited population of Caucasians decreasing the heterogeneity.

The errors in the Discussion section, should read as:

In subgroup analysis, based on the characteristics of the individual studies, significant HR was found in the non-Asian and Asian groups, and the tissue and serum sample groups.

and was incorrectly published as:

In subgroup analysis, based on the characteristics of the individual studies, significant HR was found in the Caucasian and Asian groups, the qRT-PCR group and the tissue and serum sample groups.

The errors in the Conclusion section, should read as:

However, further multicentre clinical trials with larger sample size and prospective studies including non-Asian and patients representing other ethnicities are needed to confirm the prognostic value of miR-17 and its subsequent application as a prognostic biomarker in the routine clinical guidance of cancers.

and was incorrectly published as:

However, further multicentre clinical trials with larger sample size and prospective studies including Caucasians and patients representing other ethnicities are needed to confirm the prognostic value of miR-17 and its subsequent application as a prognostic biomarker in the routine clinical guidance of cancers.

Revised table 1A summary table of the meta-analysis



| Study         | Year | Country | Diseases                                 | Case<br>Number | Stage   | Sample | Assay   | Cut-off<br>value | HR    | Follow-up<br>(months) | Type of miR-<br>17 detection |
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