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Erratum

Integrated Analyses Identify a Master MicroRNA Regulatory Network for the Mesenchymal Subtype in Serous Ovarian Cancer

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We regret that we failed to acknowledge the unpublished data provided by Bagnoli et al. in our paper. The case material first reported by Bagnoli et al. (Oncotarget, 2012) was part of Table 1. The unpublished clinical follow-up data was generously provided by the authors and used for the curve shown in Figure 6E in our paper. The correct text on page 193 of the original article should be as follows:

"To further confirm miR-506's association with good prognosis in ovarian cancer, we obtained two miRNAs microarray data sets from GEO and ArrayExpress (Bentink Data set and Bagnoli Data set, Table 1) with 129 and 55 OvCa cases, respectively. In both data sets, miR-506 expression is significantly associated with longer progression-free survival (Bagnoli et al., personal communication) (log-rank p = 0.02 and 0.0006 for Bentink and Bagnoli Data sets, respectively, Figures 6D and 6E)."

We would like to apologize for this oversight and sincerely thank the authors for providing this unpublished data to our study.