Correction: Long non-coding RNA SNHG17 is an unfavourable prognostic factor and promotes cell proliferation by epigenetically silencing P57 in colorectal cancer

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The authors regret that incorrect flow cytometry images were inadvertently used for Fig. 3 in the original article. The corrected Fig. 3 is included herein.

Fig. 3  SNHG17 downregulation promotes cell cycle arrest and apoptosis in CRC cells in vitro. (A and B) The bar chart represents the percentage of cells in G0/G1, S, or G2/M phase, as indicated. (C and D) The percentage of apoptotic cells was determined by flow-cytometric analysis. The data represent the mean ± SD from three independent experiments. *P < 0.05 and **P < 0.01.

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The authors regret that the siRNA labels in the two graphs in Fig. 5A of the original article are incorrect. The labels si-SNHG17 2# and si-SNHG17 3# in the original article should read si-SNHG17 1# and si-SNHG17 2#, respectively. The corrected Fig. 5 is included herein.

The authors would also like to add a clearer citation to the CRC gene expression data from the Gene Expression Omnibus (GEO) dataset GSE21510 used in the study (ref. 1). These data were cited in the original article using the link https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21510.

Finally, the authors would like to draw attention to the fact that the analysis presented in Fig. 1A in the original manuscript is the same as that presented in Fig. 1a of ref. 2. In each case the data were used to select the candidate gene to study.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

References