Corrigenda for *IARC Biennial Report 2018–2019*				
Page, location	**Details of Corrigendum**	**First published in PDF format**	**Correction made to PDF format?**	**Correction made to print format?**
Page 10, column 1, paragraph 3	The text of the first sentence in the third paragraph was modified, as follows: Original text: "Expanding regional partnerships have led to six new IARC GICR Collaborating Centres: one in Africa (Morocco), five in Asia (China, Islamic Republic of Iran, Japan, Republic of Korea, and Thailand), and one in the Caribbean (Martinique)." Revised text: "Expanding regional partnerships have led to **seven** new IARC GICR Collaborating Centres: one in Africa (Morocco), five in Asia (China, Islamic Republic of Iran, Japan, Republic of Korea, and Thailand), and one in the Caribbean (Martinique)."	13 December 2019	Yes, 30 March 2020	No
Page 28, Figure 3 legend	The text for panels (e), (f), and (g) in the legend for Figure 3 was modified, as follows: Original text: "(e) Density plot of the distribution of methylation values along the D-loop region. (f) Relative ND6 messenger RNA (mRNA) expression normalized to mtDNA amount compared with methylation index across the light strand promoter (LSP). High LSP methylation is associated with low ND6 expression. (g) Comparative box plot indicating significant ($P < 0.001$) difference of mean methylation across gene-encoding regions of normal versus cancer cells in each strand." Revised text: "(e) Methylation index (MI) across tRNA-encoding regions in breast cancer versus normal cells. Each horizontal segment compares the MI within tRNAs that have been grouped according to the amino acid they carry (acidic, basic, aromatic, or hydrophobic). The left panel indicates MI across the H-strand, and the right panel indicates MI across the L-strand. (f) Comparative box plot indicating significant ($P < 0.001$) difference of mean methylation across gene-encoding regions of normal versus cancer cells in each strand. (g) Density plot of the distribution of methylation values along the D-loop region."	13 December 2019	Yes, 30 March 2020	No

Corrigenda for *IARC Biennial Report 2018–2019*					
Page, location	**Details of Corrigendum**	**First published in PDF format**	**Correction made to PDF format?**	**Correction made to print format?**
Page 37, Figure 4 legend	The text of the last sentence in the legend for Figure 4 was modified, as follows: Original text: "Reprinted Clifford et al. (2019), Copyright 2019, with permission from Elsevier." Revised text: "Reprinted **from** Clifford et al. (2019), Copyright 2019, with permission from Elsevier."	13 December 2019	Yes, 30 March 2020	No
Page 55, column 3	The text of the last sentence was modified, as follows: Original text: "Penalized approaches can yield more accurate estimates by properly accounting for specific structures of large-dimension data, and were shown to be particularly useful in identifying and evaluating heterogeneity in multigroup analyses, under graphical models (Ballout and Viallon, 2019), or under conditional and multinomial logistic regression models." Revised text: "Penalized approaches can yield more accurate estimates by properly accounting for specific structures of large-dimension data, and were shown to be particularly useful in identifying and evaluating heterogeneity in **subgroup** analyses, under graphical models (Ballout and Viallon, 2019), or under conditional and multinomial logistic regression models."	13 December 2019	Yes, 30 March 2020	No
Page 64, Table 1	The text of the second footnote of Table 1 was modified, as follows: Original text: "[b] Cases with [3] HSIL not associated with HPV 16/18, HPV 16, or HPV 18 excluded. Genotyping based on GP5/GP6." Revised text: "[b] Cases with $\geq$ **HSIL** not associated with HPV 16/18, HPV 16, or HPV 18 excluded. Genotyping based on GP5/GP6."	13 December 2019	Yes, 30 March 2020	No