CORRECTIONS & AMENDMENTS

CORRIGENDUM

doi:10.1038/nature25161

Corrigendum: Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution

Christopher Abbosh, Nicolai J. Birkbak, Gareth A. Wilson, Mariam Jamal-Hanjani, Tudor Constantin, Raheleh Salari, John Le Quesne, David A. Moore, Selvaraju Veeriah, Rachel Rosenthal, Teresa Marafioti, Eser Kirkizlar, Thomas B. K. Watkins, Nicholas McGranahan, Sophia Ward, Luke Martinson, Joan Riley, Francesco Fraioli, Maise Al Bakir, Eva Grönroos, Francisco Zambrana, Raymondo Endozo, Wenya Linda Bi, Fiona M. Fennessy, Nicole Sponer, Diana Johnson, Joanne Laycock, Seema Shafi, Justyna Czyzewska-Khan, Andrew Rowan, Tim Chambers, Nik Matthews, Samra Turajlic, Crispin Hiley, Siow Ming Lee, Martin D. Forster, Tanya Ahmad, Mary Falzon, Elaine Borg, David Lawrence, Martin Hayward, Shyam Kolvekar, Nikolaos Panagiotopoulos, Sam M. Janes, Ricky Thakrar, Asia Ahmed, Fiona Blackhall, Yvonne Summers, Dina Hafez, Ashwini Naik, Apratim Ganguly, Stephanie Kareht, Rajesh Shah, Leena Joseph, Anne Marie Quinn, Phil A. Crosbie, Babu Naidu, Gary Middleton, Gerald Langman, Simon Trotter, Marianne Nicolson, Hardy Remmen, Keith Kerr, Mahendran Chetty, Lesley Gomersall, Dean A. Fennell, Apostolos Nakas, Sridhar Rathinam, Girija Anand, Sajid Khan, Peter Russell, Veni Ezhil, Babikir Ismail, Melanie Irvin-Sellers, Vineet Prakash, Jason F. Lester, Malgorzata Kornaszewska, Richard Attanoos, Haydn Adams, Helen Davies, Dahmane Oukrif, Ayse U. Akarca, John A. Hartley, Helen L. Lowe, Sara Lock, Natasha Iles, Harriet Bell, Yenting Ngai, Greg Elgar, Zoltan Szallasi, Roland F. Schwarz, Javier Herrero, Aengus Stewart, Sergio A. Quezada, Karl S. Peggs, Peter Van Loo, Caroline Dive, C. Jimmy Lin, Matthew Rabinowitz, Hugo J. W. L. Aerts, Allan Hackshaw, Jacqui A. Shaw, Bernhard G. Zimmermann, The TRACERx consortium, The PEACE consortium & Charles Swanton

Nature 545, 446-451 (2017); doi:10.1038/nature22364

For 6 of the 96 patients included in this Article (patients CRUK0014, CRUK0030, CRUK0048, CRUK0059, CRUK0096 and CRUK0097) incorrect tumour volumetric data and positron emission tomography (PET) tumour background ratio (TBR) data were analysed. This error occurred because of the incorrect assignment of patient identifiers during the anonymization mandated by the independent review board of pre-operative computed tomography (CT) scans belonging to these patients. Data relating to this error were presented in Figs 2a and 3a and b, Extended Data Figs 3d and 4c-f, Extended Data Table 2b and Supplementary Table 1. The reanalysis of correctly anonymized scans does not influence the conclusions of this Article and correlation coefficients improve following inclusion of the corrected data. These

errors have been corrected online in the original Article. The authors apologize for any confusion these errors may have caused.

Quartiles for the heat map in Fig. 2a have been redefined after including the correct data to reflect changes in quartiles for 3 (of 92) PET TBR values and 7 (of 95) volume parameters. The Source Data file supplied for Fig. 2 was not uploaded on publication; the corrected Source Data file for Fig. 2 is now available in the HTML version of the original Article.

The plot and legend for Fig. 3a have been corrected to reflect updated volumetric data for the two patients affected by the correction who were analysed in this figure (CRUK0096 and CRUK0097). CRUK0096 was excluded from the updated volumetric analysis based on a criterion applied to our original analysis (large cavity within primary tumour). Consequently, the sentence in the legend to Fig. 3a "n=38, grey vertical lines represent range of clonal VAF, red shading indicates 95% confidence intervals (CIs)" has been updated to read "n=37" and in the Methods section 'Statistical data analysis' the line "8 out of 46 patients were not included in the analysis: CRUK0036 had no preoperative CT scan available; CRUK0087 had a large cavity inside the primary" has been updated to read "9 out of 46 patients were not included in the analysis: CRUK0036 had no preoperative CT scan available; CRUK0087 and CRUK0096 had a large cavity inside the primary cancer".

In Fig. 3b and the main text, the variant allele frequency (VAF) prediction values (based on tumour volume), confidence intervals and estimated malignant cell number contributing to a VAF of 0.1% have been updated. In the section 'Determinants of ctDNA detection in NSCLC', confidence intervals in the sentence "a primary tumour burden of 10 cm³ would result in a mean clonal plasma VAF of 0.1% (95% confidence interval, 0.05-0.17%)" have been altered to read "a primary tumour burden of 10 cm³ would result in a mean clonal VAF of 0.1% (95% confidence interval, 0.06-0.18%)" and the sentence "a plasma VAF of 0.1% would correspond to a primary NSCLC malignant burden of 326 million tumour cells" has been altered to read "a plasma VAF of 0.1% would correspond to a primary NSCLC malignant burden of 302 million tumour cells". In the 'Discussion' section the sentence "on the basis of the relationship between tumour volume and ctDNA plasma VAF observed in this study, a tumour volume of $0.034\,\mathrm{cm^3}$ would equate to a plasma VAF of $1.4\times10^{-4}\%$ (95% confidence interval, 6.4×10^{-6} –0.0031%)", has been altered to read "on the basis of the relationship between tumour volume and ctDNA plasma VAF observed in this study, a tumour volume of 0.034 cm³ would equate to a VAF of 1.8×10^{-4} % (95% confidence interval, $9.8 \times 10^{-6} - 0.0033\%$)".

Further figure corrections pertaining to the six affected patients in Extended Data Figs 3d and 4c–f, Extended Data Table 2b and Supplementary Table 1 of the original Article are described and corrected in the Supplementary Information of this Corrigendum, which also shows the original, wrong Figs 2a and 3a and b. The Supplementary Data (containing Supplementary Table 1) of the original Article has been corrected.

Supplementary Information is available in the online version of this Corrigendum.