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Corrigendum

An E2F7-dependent transcriptional program modulates DNA damage repair and genomic stability

Jone Mitxelena[1,†], Aintzane Apraiz[2,†], Jon Vallejo-Rodríguez[1,†], Iraia García-Santisteban[1], Asier Fullaondo[1], Mónica Alvarez-Fernández[3], Marcos Malumbres[3] and Ana M. Zubiaga[1,*]

[1]Department of Genetics, Physical Anthropology and Animal Physiology, University of the Basque Country UPV/EHU, 48080 Bilbao, Spain, [2]Department of Cell Biology and Histology, University of the Basque Country UPV/EHU, 48080 Bilbao, Spain and [3]Cell Division and Cancer Group, Spanish National Cancer Research Centre (CNIO), 28029 Madrid, Spain

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The Authors wish to make the following corrections to their article.

Analysis of FANCD2 foci quantification in Figure 5B was not performed with the Definiens Tissue Phenomics analysis software as stated in Materials and Methods, but with a similar software. A new Figure 5B, obtained with the Definiens Tissue Phenomics analysis software is provided below. The Figure in the published article has been updated. This correction does not affect the results of conclusion of the article.

*To whom correspondence should be addressed. Ana M. Zubiaga. Tel: +34 94 601 2603; Fax: +34 94 601 3143; Email: ana.zubiaga@ehu.es
†The authors wish it to be known that, in their opinion, the first three authors should be regarded as joint First Authors.

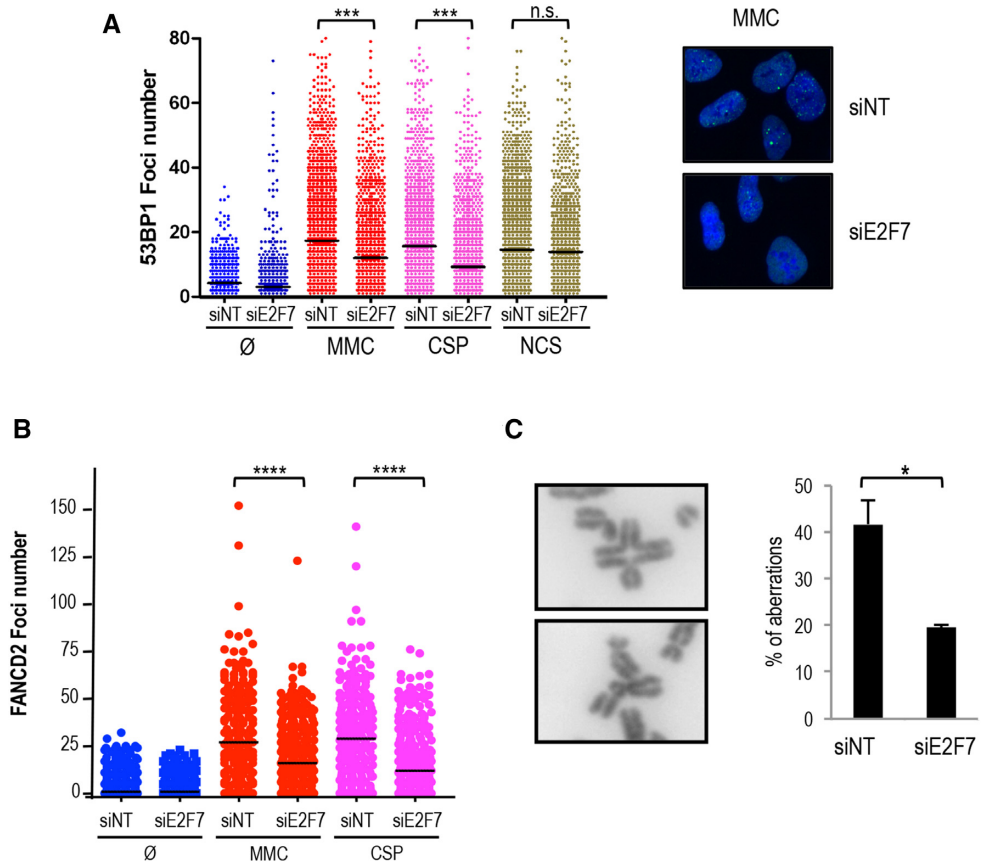

Figure 5. E2F7 knockdown results in reduced foci and chromosome break number after ICL induction. (A) siNT and siE2F7 transfected U2OS cells were treated with MMC, CSP and NCS and fixed 24 h later. Cells were stained for 53BP1 with a FITC-conjugated specific antibody. Nuclear DNA was stained with DAPI. The number of 53BP1 foci was scored by HTM. Data are representative of three independent analyses. Horizontal lines indicate mean vales. (B) siNT and siE2F7 transfected U2OS cells were treated with 250nM MMC or with 4 μM CSP. Twenty fours hours later, samples were fixed and stained for FANCD2. The number of FANCD2 foci was scored on fluorescence microscope images. Continuous horizontal lines indicate mean values. Data are representative of three independent analyses. (C) siNT and siE2F7 transfected U2OS cells were treated with 250 nM MMC for 48 h and scored for chromosomal aberrations by analyzing metaphase spreads. Representative images of a radial chromosome and a chromatid break are shown. Chromosomal aberrations are expressed as the average breaks and radial chromosomes found per metaphase (n = 50 cells) in three independent experiments. (*, $P < 0.05$; ***, $P < 0.001$), Ø, untreated, n.s. not significant.