

Author Correction: *TAp63* suppresses metastasis through coordinate regulation of *Dicer* and miRNAs

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 Check for updates

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In the original version of this article, the number of mice per cohort in Fig. 1d, f, g, j, k and Supplementary Table 1 was erroneously stated as 30 per group. The error has been corrected in Supplementary Table 1 with $n = 40$ in all cohorts and $n = 50$ in the *TAp63*^{-/-} cohort. The authors confirm that all experiments were performed following the approved guidelines of the IACUC at the University of Texas MD Anderson Cancer Center with proper monitoring of animal welfare. The amended caption to Fig. 1 can be seen below, and the corrected Supplementary Table 1 is included as Supplementary information with this notice.

Fig. 1 | *TAp63*^{-/-} mice develop metastatic tumours. a, b, Metastatic mammary adenocarcinoma in lung (LU; **a**) and brain (BR; **b**). **c**, Tumour-free survival curves; $n = 30$ and $P \leq 0.05$. WT, wild type. **d**, Tumour spectra of the indicated mice genotypes; $n = 40$ for *TAp63*^{+/-} and $n = 50$ for *TAp63*^{-/-}. **e**, LOH analysis of *TAp63* in sarcomas (S) and carcinomas (C) from the indicated genotypes. **f, g**, Percentage of metastatic sarcomas and carcinomas (**f**) and multiple malignancies (**g**); $n = 40$ for *TAp63*^{+/-} and $n = 50$ for *TAp63*^{-/-}. **h, i**, Metastatic squamous cell carcinoma (SCC) on skin (**h**) and in lung (LU; **i**). **j, k**, Tumour spectrum (**j**) and metastases (**k**) of the indicated mice genotypes; $n = 40$. Asterisk, statistical difference between *TAp63/p53* mutant and *p53*^{+/-} or *p53*^{-/-} mice; two asterisks, statistical difference between two double-mutant genotypes; $P \leq 0.05$. **l, m**, PCR analysis for LOH of *TAp63* (**l**) or *p53* (**m**) in carcinomas (C) and sarcomas (S) of the indicated genotypes.

Supplementary information is available in the online version of this Amendment.

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