

## CORRIGENDUM

**Identification of novel candidates for replicative senescence by functional proteomics**

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Correction to: *Oncogene* (2002) **21**, 4403–4413. doi: 10.1038/sj.onc.1205525

Since the publication of the above paper, the authors have identified an error in the text. The authors also wish to apologise for an error in table 2. The corrected text and section E of the table are given below.

Spot 883 and 889 (shown in Figure 2) showed a shift in their migration in the tsa cell lines, while they migrated at the same place in gels from the control SV cell lines. Spot 853 also showed a shift in its migration in tsa 4, 8 and 12 cell lines but not in the control SV2 cell line.

**Table 2** Differentially expressed features

<i>ID</i>	<i>MW</i>	<i>pI</i>	<i>tsa4</i>	<i>tsa8</i>	<i>tsa12</i>	<i>tsa29</i>	<i>SV2</i>	<i>SV4</i>
(E) <i>Shift in the migration</i>								
853	34374	6.17	SHIFT	SHIFT	SHIFT	n.c.	n.c.	SHIFT
883	31214	5.72	SHIFT	SHIFT	SHIFT	SHIFT	n.c.	n.c.
889	30933	5.75	SHIFT	SHIFT	SHIFT	SHIFT	n.c.	n.c.

n.c.: no changes