

CORRECTION

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Correction to: Epigenetic regulation of L1CAM in endometrial carcinoma: comparison to cancer–testis (CT-X) antigens

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Correction

Following publication of the original article [1], we have been alerted to errors in Figs. 2 and 8. In Fig. 2b, the GAPDH loading control for Hec1A cells is shown twice in error (in Fig. 2b and Fig. 2c). In Fig. 8, in testis case 1 (first column) the MAGE-A4 staining panel was repeated and also appears as the NY-ESO-1 staining panel in error. The corrected versions of Fig. 2 and Fig. 8 are shown below. We apologize for this inconvenience.

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Reference

1. Schirmer U, et al. Epigenetic regulation of L1CAM in endometrial carcinoma: comparison to cancer–testis (CT-X) antigens. *BMC Cancer*. 2013;13:156. <https://doi.org/10.1186/1471-2407-13-156>.

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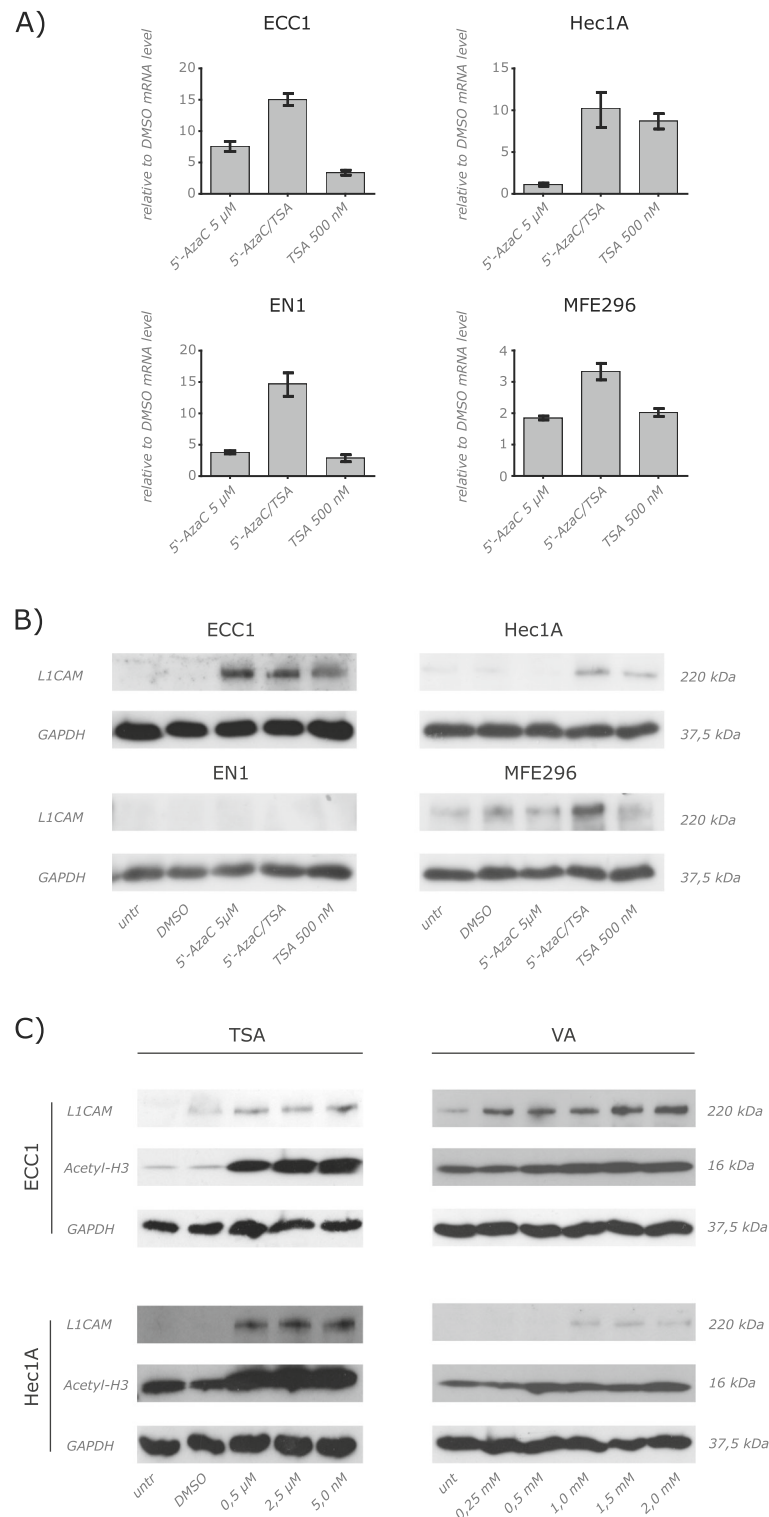


Fig. 2 Regulation of L1CAM expression by epigenetic mechanisms. **(a)** RT-PCR analysis of cells treated for 5 days with the indicated concentration of 5-AzaC, TSA or both compounds. DMSO was used as a mock control. Cells were lysed and mRNA was isolated and transcribed into cDNA. β -actin served as internal standard. **(b)** Cells were treated as described above and cell lysates were prepared for Western blot analysis. Mab L1-11A was used as a primary antibody followed by peroxidase conjugated Goat anti mouse IgG and ECL detection. **(c)** TSA and VA up-regulate L1CAM expression. Cells were treated and analyzed as described in **(b)**

