

CORRECTION

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Correction to: Identification and validation of the high expression of pseudogene TCAM1P in cervical cancer via integrated bioinformatics analysis

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In this article [1], there was an error in naming the Table 4. In the paragraph, Results of "Correlation between TCAM1P and clinicopathological characteristics in patients with CC", the sentence "Result showed

that TCAM1P expression is higher in patients with Lymph node metastasis than in non-metastasis while the difference was not statistically significant in the remaining groups (Table 1)". This should be Table 4. Also, in Fig. 4B, it is not "Hela" but "Caski".

Table 4 and corrected Fig. 4 are given in this erratum.

The original article can be found online at <https://doi.org/10.1186/s12935-021-02440-7>.

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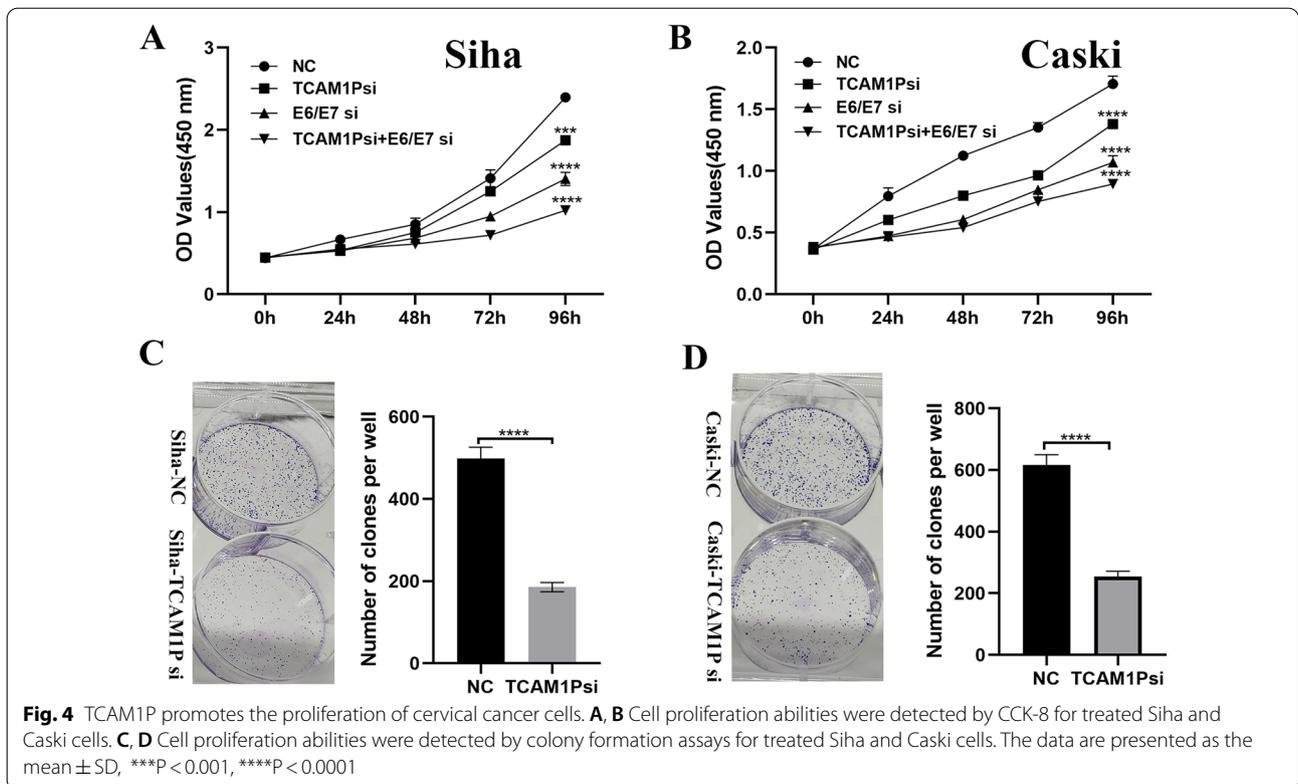


Table 4 Analysis of the relationship between the expression of TCAM1P and the clinicopathological characteristics of cervical cancer patients based on the TCGA database

Characteristics	Number	TCAM1 expression	t value	P value
Age (years)			0.927	0.355
< 40	84	8.37 \pm 2.77		
\geq 40	220	8.01 \pm 3.04		
FIGO stage			-0.667	0.505
I-II	231	8.05 \pm 3.00		
III-IV	66	8.32 \pm 2.87		
TNM stage			0.084	0.933
T1-T2	212	8.08 \pm 3.01		
T3-T4	30	8.03 \pm 3.12		
Histological type			1.012	0.316
Squamous cell carcinoma	252	8.23 \pm 2.81		
Adenocarcinoma	48	7.69 \pm 3.51		
Lymph nodes metastasis			-2.896	0.004
Yes	60	8.94 \pm 2.08		
No	133	7.82 \pm 3.16		
Distant metastasis			0.951	0.343
Yes	10	6.91 \pm 4.32		
No	116	7.92 \pm 3.13		
TP53 mutation			2.612	0.016
Mutation	22	5.97 \pm 3.95		
Wild type	287	8.21 \pm 2.88		

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