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A potential new biomarker in lip cancer: Metastasis suppressor protein 1 (MTSS1)

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ABSTRACT

Objective: Metastasis suppressor protein 1 (MTSS1) has been investigated as a marker of tumor aggressiveness across various tumor entities but remains poorly studied in head and neck squamous cell carcinoma. Its role in lip squamous cell carcinoma has not yet been investigated. Given the higher risk of lymphatic metastasis in lip squamous cell carcinoma compared with cutaneous squamous cell carcinoma, identifying associated immunohistochemical markers may provide clinically relevant insights into tumor progression.
Design: The tumour marker MTSS1 was examined immunohistochemically on FFPE sections from (n = 49) patients using MTSS1 expression and MTSS1 intensity analysis. The results were then correlated with clinical-pathological characteristics and follow-up outcome parameters.
Results: There was a correlation between MTSS1 expression (%) and ASA-score (surrogate of patient frailty) (p = 0.0139), the risk of local recurrence (p = 0.0125) and pV status (p = 0.0347).
Conclusion: MTSS1 correlates with local tumor aggressiveness factors, local recurrence during-follow up and, given the small cohort size, should be investigated further in follow-up studies. This hypothesis-generating study may provide a basis for future investigations.

1. Introduction

In cutaneous squamous cell carcinoma (cSCC), the lip (LSCC) is a high-risk localization with an increased risk of lymph node metastasis (LNM) (Alam & Ratner, 2001). Immunohistochemically tumour markers on formalin-fixed paraffin-embedded (FFPE) tissue samples from high-risk sites of cSCC can be used to assess tumour aggressiveness, progression and prognosis. In addition, they could potentially be used for diagnostic subclassification to facilitate therapeutic and diagnostic decisions (Klein et al., 2021, 2023a; Valea et al., 2025). One other tumour marker with such potential is metastasis suppressor protein 1 (MTSS1). Klein et al. showed in head and neck squamous cell carcinoma (HNSCC) that MTSS1 intensity in particular, but also MTSS1 expression frequency, could be used for risk assessment and that reliable and reproducible results can be obtained with the evaluation methods. The authors also showed a correlation between MTSS1 intensity with the increased risk of lymph node metastases and an increased risk of extracapsular growth of LNM (Klein et al., 2024). Additional studies have also focused on MTSS1 in HNSCC (Dawson et al., 2012; Guo et al., 2020, 2015). MTSS1 has also been investigated in other tumour entities

Abbreviations: ASA, American Association of Anesthesiologists; DM, distant metastasis; FFPE, formalin-fixed paraffin-embedded; HNSCC, head and neck squamous cell carcinoma; LNM, lymph node metastasis; LSCC, lip squamous cell carcinoma; MTSS1, metastasis suppressor protein 1; UICC, Union for International Cancer Control.

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for example: Bladder cancer, acute myeloid leukemia, breast cancer, pancreatic cancer and colo-rectal cancer (Lee et al., 2002; Schemionek et al., 2015; Parr & Jiang, 2009; Wang et al., 2011; Zhou et al., 2016). In contrast, MTSS1 has not yet been investigated in LSCC.

The aim of this study was to evaluate the prognostic potential of MTSS1 in FFPE tissue samples of LSCC in relation to prognosis and clinical outcome. In addition, it should be investigated whether MTSS1 expression (%) or MTSS1 intensity is beneficial for outcome progression evaluation. Interestingly, MTSS1 expression was also able to predict tumour aggressiveness and thus prognosis in LSCC in our cohort.

2. Material and methods

2.1. Ethics statement

This study was approved by the local ethics committee (Ethical Committee of the University RWTH Aachen, EK 22–373) and was conducted in accordance with the Guidelines for Good Clinical Practice and in compliance with the Declaration of Helsinki. All patients gave their written informed consent to participate in the study design.

2.2. Patients and clinical data

Patients (>18 years) with histologically proven LSCC were included in our analysis. The initial diagnosis of the patients was between 2008 and 2023. We excluded patients with unavailable histologic specimens or incomplete datasets from the study. The tumour characteristics and follow-up data were collected retrospectively from the hospital information system database. A preoperative staging was performed (at least Sonography, computed tomography or magnet resonance tomography of the head and neck, if necessary, chest X-ray, abdominal sonography). Furthermore, patients with history of other malignancies, recurrence or a second HNSCC were also included. The Department of Pathology at RWTH-University in Aachen, Germany performed the histological diagnoses of primary tumor LSCC and all nodal metastases by histological examination. To harmonize the tumour data, LSCC patients classified before 2017 with 7th TNM UICC classification were reclassified according to the current 8th TNM UICC Classification. The date of first diagnosis or age at first diagnosis was taken as the start of the analyses. The last recording in the electronic hospital system has been used to assess the duration of the follow-up. We analysed the statistical correlation between MTSS1 expression (%) and MTSS1 intensity (see below), tumour characteristics and disease progression (recurrence, lymph node or distant metastases). For evaluation of patients constitution und frailty analysis the American Association of Anesthesiologists (ASA) score was used. In addition the immunosuppression status (weak, strong immunosuppression) was documented. Weak immunosuppression was defined as low immunosuppressive disease or medication. Strong immunosuppression was defined as e.g. organ transplantation or similar.

2.3. Tissue samples and immunohistochemistry of MTSS1

The immunohistochemical MTSS1 analyses has been performed using formalin-fixed and paraffin-embedded (FFPE) tissue blocks. The primary antibody used for MTSS1 was the ((D2H4L) XP Rabbit mAb #93065 (1:400) rabbit monoclonal anti human/rat antibody, Cell Signaling, Frankfurt am Main, Germany), the detection system "Vector polymer Kit 7451 goat anti rabbit" (Vector, California, United States) and diaminobenzidine. In the establishment phase, HNSCC tissue was used as a positive control and as an internal control of no MTSS1 expression in striated muscles and nerves on individual slices as a negative control. Overall, the methodological approach was based on Klein et al (Klein et al., 2024). The microscope Olympus BX51 (Hamburg, Germany) was used for histological evaluation. Slides (Fig. 1.) were digitised using Aperio AT2 whole-slide scanner with a 20x objective (Leica Biosystems, Wetzlar, Germany). Scale bar equals 250µm.

2.4. MTSS1 analyzing methods: MTSS expression % and MTSS1 intensity

Evaluation of immunohistochemical expression on tumour tissue was carried out in a blinded fashion by two investigators (MK and CC) in a consensus analysis. We performed a consensus analysis, because Klein et al. previously showed a high kappa value and thus high reproducibility for the MTSS1 expression analysis and the MTSS1 intensity analysis in a previous study (Klein et al., 2024). First, MTSS1 expression (%) was defined in each tumour slide with a 4 × magnification and then semi-quantitatively in %. MTSS1 expression (%) was defined as the expression of positive tumour cells/total tumour cells in the whole section in %. The MTSS1 intensity expression (no intensity = 0, weak intensity = 1, distinct intensity = 2 and strong intensity = 3) evaluation was performed in a hot spot analysis (magnification 10 ×) of the highest expression intensity in the tumour slide. After that, we recorded the hot spot with the highest intensity, rated as cytoplasmic positivity (Fig. 1 left side low expression (MTSS1 expression 5%; MTSS1 intensity 1); Fig. 1 right side Mtss1 expression: 100%; MTSS1 intensity 3).

2.5. Statistical analysis

Statistical analyses were performed using the statistical program R.

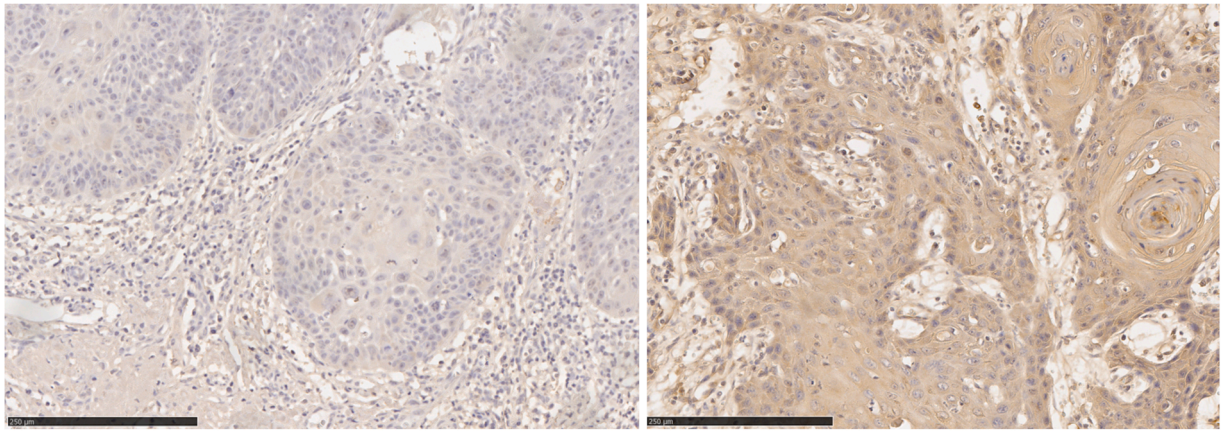


Fig. 1. Histological staining of LSCC with low and strong MTSS1 expression. (left side) Shown is a slice with an MTSS1 expression of 5% and an MTSS1 intensity of 1 (weak staining; magnification 10 ×). (Right side) Shown is a slice with an MTSS1 expression of 100% and an MTSS1 intensity of 3 (strong staining; magnification 10 ×).

Continuous variables were tested for normality using the Shapiro-Wilk test. As the data were not normally distributed, non-parametric tests were applied for group comparisons. For comparisons between two independent groups, the Mann-Whitney *U* test was employed. For comparisons involving more than two independent groups, the Kruskal-Wallis test was used to determine whether there were statistically significant differences among the groups. In cases where the Kruskal-Wallis test yielded significant results ($p < 0.05$), post hoc pairwise comparisons were conducted using Dunn's test with Bonferroni correction to control for multiple comparisons. All statistical tests were two-tailed, and a significance level of $\alpha = 0.05$ was applied. Descriptive statistics were reported as median and interquartile range (IQR). The results were visualized using box plots where appropriate. Kaplan–Meier curves were generated to assess recurrence-free survival, the occurrence of lymph node and distant metastases during follow-up (excluding metastases present at initial diagnosis), and overall survival.

3. Results

3.1. Patient characteristics of study cohort and patients constitution

A total of n = 49 patients (31 male, 18 female) were included. The mean age at first diagnosis 70.2 years [range 24–92 years]). The average follow-up time was 23.6 months (range 0–152 months). Three patients (6.1%) showed an ASA score of 1, and 23 (46.9%) had an ASA score of 2. 21 patients (42.9%) had an ASA score of 3, and 2 (4.1%) had an ASA score of 4. 9 Patients had an immunosuppression and 39 had no immunosuppression. Of these, 5 patients had weak immunosuppression and 4 patients had strong immunosuppression.

3.2. Clinical cohort data

Two patients had an upper lip carcinoma and the remaining 47 patients had a lower lip carcinoma. In 30 patients the tumour was located bilateral and in 19 patients unilateral. The cohort showed the following clinicopathological parameters: pT1 n = 27 (55.1%); rpT1 n = 1 (2%); pT2 n = 11 (22.4%); pT3 n = 9 (18.4%); pT4 n = 1 (2%); cN + n = 8; pNX n = 18 (36.7%); pN0 n = 24 (49%); pN1 n = 4 (8.2%); pN2 n = 2 (4.1%); pN3 n = 1 (2%); extranodal growth n = 1; G1 n = 7 (14.3%); G2 n = 33 (67.3%); G3 n = 9 (18.4%); V0 n = 47 (95.9%); V1 n = 2 (4.1%); Pn0 n = 39 (79.6%); Pn1 n = 10 (20.4%); L0 49 (100%); L1 n = 0 (0%); R0 n = 48 (98%); R1 n = 1 (2%). The follow-up showed: n = 2 local recurrences, n = 2 LNM and n = 1 DM. Tumour progression (n = 5) was assessed as the presence of one or more factors (local recurrence during follow-up, LNM during follow-up and DM during follow-up).

3.3. MTSS1 expression (%) shows significant differences in regards to patient frailty (ASA-score), local recurrence and pV status

There was a significant difference between MTSS1 expression (%) and the ASA score (p = 0.0139; Fig. 2). A significant difference was also found for local recurrence (p = 0.0125; Fig. 3) and venous infiltration (V) status (p = 0.0347; Fig. 4). MTSS1-Expression (%) showed, on the other and no statistic significant association with these parameter: extranodal expansion, Grading, perineural invasion (Pn) status, immunosuppression, lymph node (pN) status, LNM (yes/no) status, gender, tumor size (pT), clinical lymph node (cN) status. In addition, it showed a tendency between MTSS1 expression (%) and tumour progression (p = 0.0674).

3.4. The MTSS1 intensity appears to be less suitable as an aggressive, prognostic and progression marker in LSCC

We found non-significant correlations between MTSS1 intensity and these clinical-pathological parameters: age, ASA, pN, Grading, cN status, gender, pT, V status, extranodal expanding of LNM, Pn status, Lymph node count and immunosuppression. Nevertheless, a tendency between MTSS1 intensity with infiltration depth (p = 0.0882) and tumour size (p = 0.0694) was observed.

3.5. High MTSS1 expression was associated with a shorter recurrence-free interval

Kaplan–Meier analysis demonstrated a statistically significant association between MTSS1 expression and recurrence, with a significant difference in recurrence-free survival between patients with high and low MTSS1 expression (Log-rank: p = 0.026; Fig. 5**A**). In contrast, no

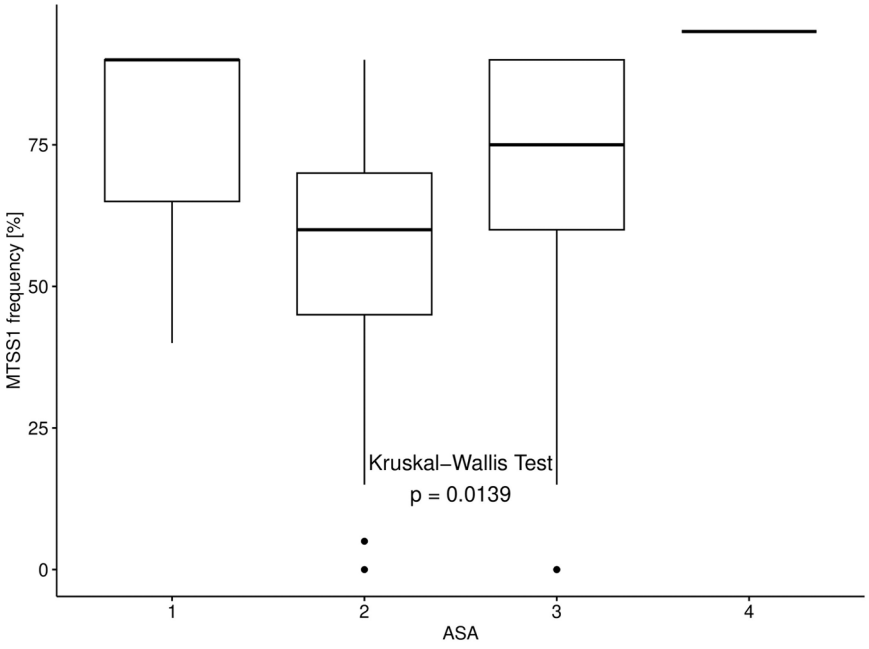


Fig. 2. MTSS1 expression is differs with patient frailty. Shown is that MTSS1 expression % is different (p = 0.0139) across ASA-scores (American Association of Anesthesiologists score). It seems that MTSS1 is associated with patients frailty.

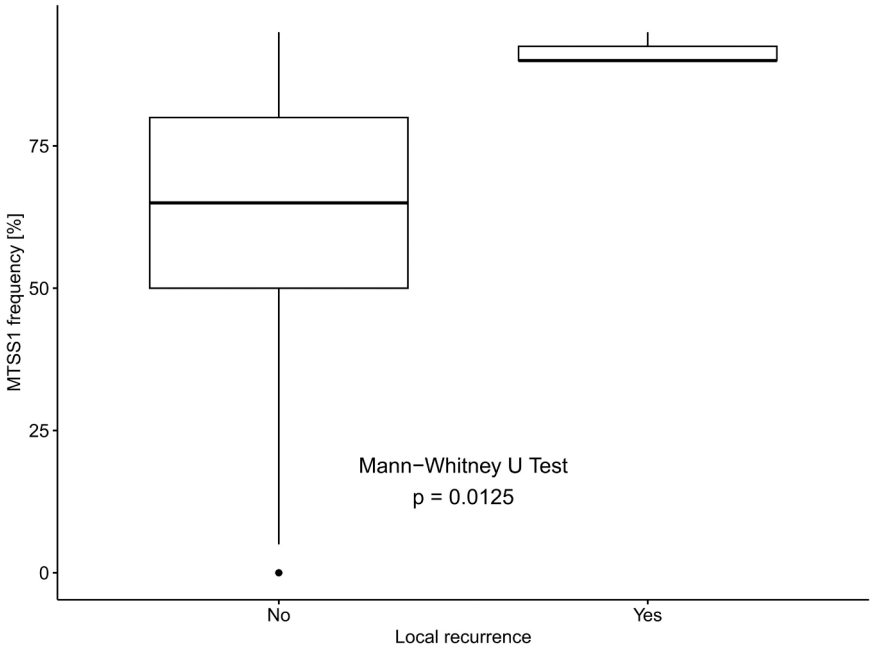


Fig. 3. Higher MTSS1 expression (%) is ass with risk of local recurrence in follow-up. Shown is that a higher MTSS1 expression (%) is correlated with the risk of local recurrence ($p = 0.0125$).). It seems that MTSS1 could be associated with risk for local recurrence in follow-up.

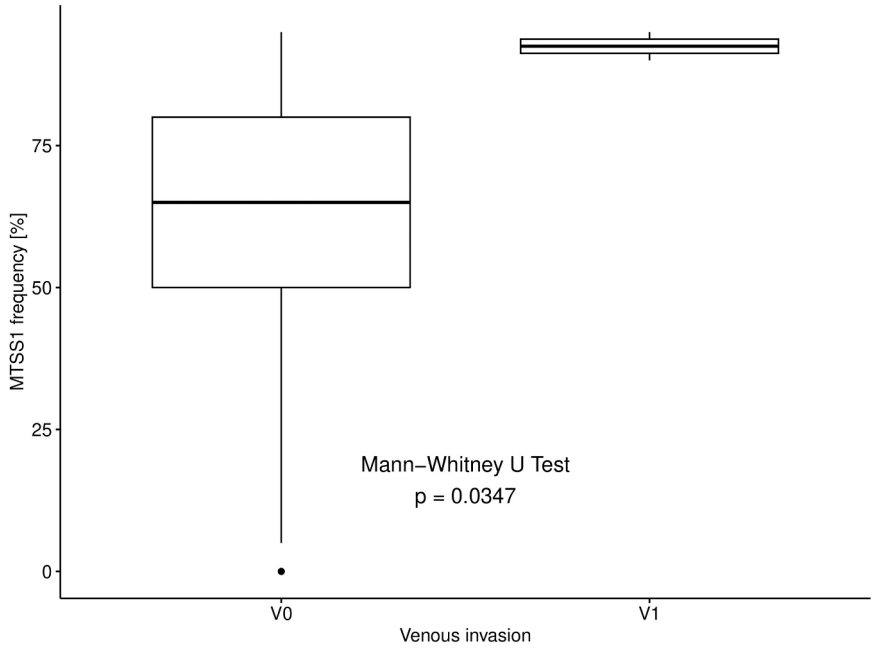


Fig. 4. High MTSS1 expression (%) is associated with increased risk of venous invasion. Shown is that a higher MTSS1 expression (%) is associated with the risk of V status ($p = 0.0347$). It appears that MTSS1 is involved in local tumour aggressiveness.

statistically significant differences were observed in the occurrence of lymph node metastases during follow-up, distant metastases during follow-up or overall survival between the high- and low-MTSS1-expression groups (Fig. 5**B, C, D**).

4. Discussion

4.1. Strengths and weaknesses of the study

The aim of this study was to generate initial insights into the potential role of MTSS1 in LSCC and to serve as a hypothesis-generating study that may provide a basis for future investigations. The weakness of the study is its retrospective design and the relatively small number of cases ($n = 49$). Nevertheless, it must be kept in mind that lip carcinoma and especially advanced tumour stages are relatively rare and it is therefore difficult to establish large tumour collectives. In the future, additional emphasis should be placed on the preservation of LSCC tissue in biobanks for future biomarker studies. To our best knowledge, this is the first study to investigate MTSS1 in LSCC. However, there are few studies that have dealt with MTSS1 expression analysis in head and neck tumours (Dawson et al., 2012; Guo et al., 2020, 2015; Klein et al., 2024). The MTSS1 analysis is a standardized analysis method, which has an

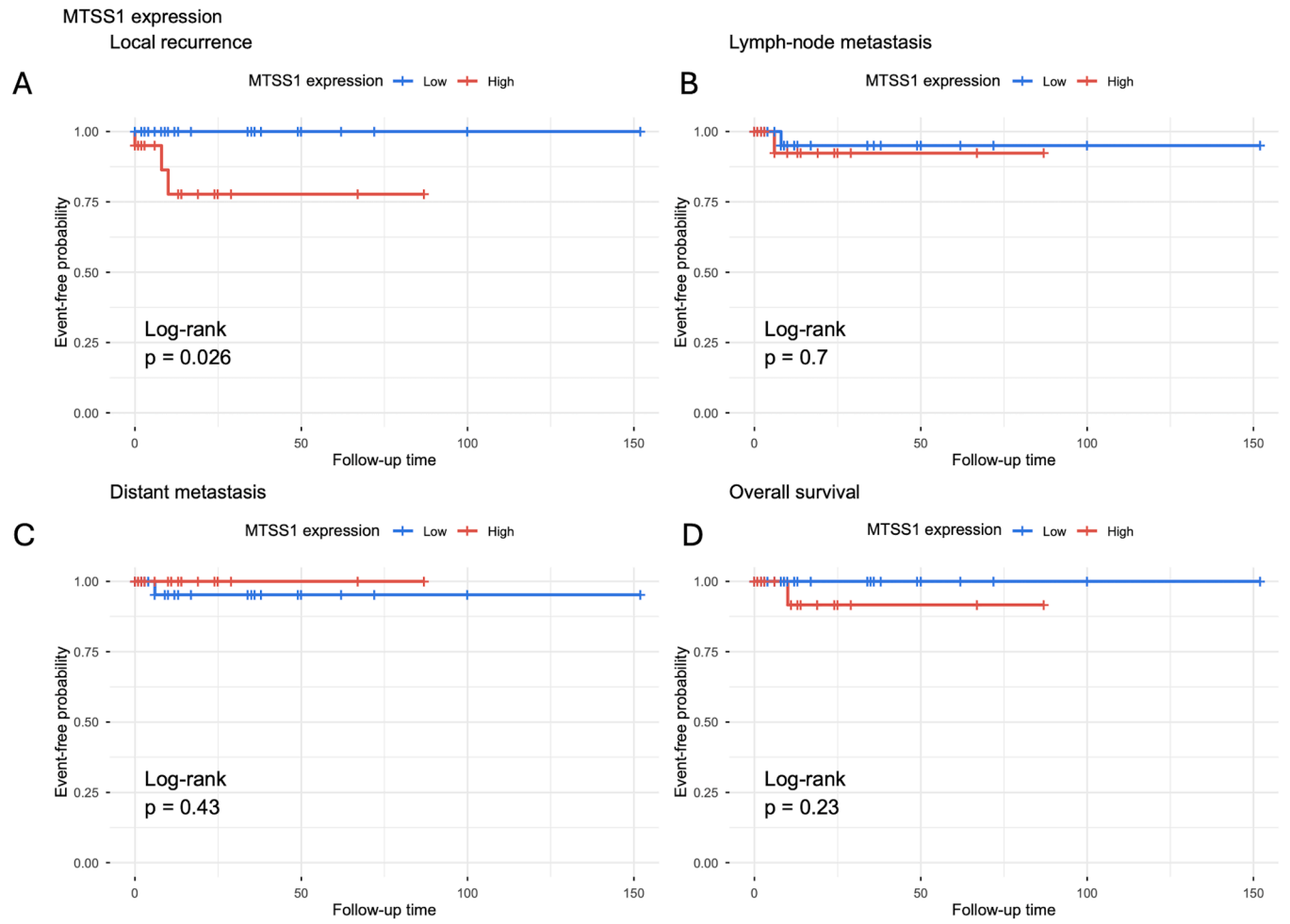


Fig. 5. High MTSS1 expression was significantly associated with a shorter recurrence-free interval (A; p = 0.026). No significant associations were observed with lymph node metastases during follow-uo, distant metastases during follow-up, or overall survival (B, C, D).

investigator independency for the MTSS1 expression analysis and MTSS1 intensity analysis (Klein et al., 2024). This study also showed that the prognostic significance may depend on the MTSS1 analysis method used (MTSS1 expression vs. MTSS1 intensity). It should also be noted that the small cohort size and the limited number of events (recurrence, lymph node metastasis, and distant metastasis during follow-up) limit the strength of the conclusions that can be drawn. Nevertheless, comparable cohort sizes have been reported in the literature (Klein et al., 2023a, 2023b; Leypold et al., 2025; Valea et al., 2025) In addition, the study does not include an independent validation cohort, multivariable adjustment, or mechanistic evidence.

4.2. MTSS1 appears to be associated with patient frailty similar to HNSCC

A correlation between MTSS1 and the ASA score can also be found in the literature for the HNSCC (Klein et al., 2024). There is currently no explanation for this phenomenon. However, it still seems scientifically exciting, as this new observation could suggest an unknown causal relationship between MTSS1 and patient frailty or tumour resilience, as a correlation has already been found in a second tumour entity. In contrast, unlike cases of HNSCC, LSCC cases showed no correlation with immunosuppression (Klein et al., 2024).

4.3. MTSS1 appears to be useful for local tumour aggressiveness evaluation in LSCC

It appears that MTSS1 could be useful as a predictive marker for local recurrence in follow-up prediction. Of particular interest is the fact that this anatomical region of the lip is highly vascularized and these data also show a further correlation with local tumor aggressiveness, as MTSS1 correlates significantly with V status (vascular-invasive). Nevertheless, the data require verification in larger collectives.

4.4. MTSS1 Expression and Recurrence in LSCC: Lack of Mechanistic Evidence

Furthermore, increased MTSS1 expression was associated with a higher risk of local recurrence during follow-up. Although a mechanistic link between MTSS1 expression and local recurrence has not yet been established in LSCC, previous studies in other tumor entities have suggested several potential mechanisms through which MTSS1 may influence tumor progression and aggressiveness. MTSS1 has been implicated in the modulation of cell–cell contacts and cellular differentiation, as well as in lipid metabolism and vesicle formation. In addition, MTSS1 may function as a scaffolding protein for several E3 ubiquitin ligases, thereby potentially affecting the stability and activity of proteins involved in tumor-related signaling pathways (Matskova et al., 2024). These findings provide a potential biological rationale for the association observed in our cohort; however, whether these mechanisms contribute to local recurrence in LSCC remains to be elucidated.

MTSS1 exhibits a context-dependent dual role in tumor metastasis. While MTSS1 suppresses migration, invasion and epithelial-mesenchymal transition in several tumor entities, e.g. gastric cancer via the PTEN/PI3K/AKT pathway, it can promote metastasis in melanoma through Rho-GTPase/cofilin-dependent regulation of actin dynamics (Mertz et al., 2014; Wang et al., 2019). Similarly, the p63/MTSS1 axis has been linked to increased migration and invasion in breast cancer. Thus, the metastatic function of MTSS1 appears to be strongly dependent on tumor type and cellular context (Giacobbe et al., 2016). This may also explain the heterogeneous findings regarding clinical outcomes in oral squamous cell carcinoma in relation to MTSS1 expression (Klein et al., 2024).

4.5. Besides the prognostic and diagnostic use, there is therapeutic potential

Klein et al. emphasised the high translational therapeutic potential of the tumour marker (Klein et al., 2024). In breast cancer Carrara et al. showed that low MTSS1 expression was correlated with an better response to neoadjuvant chemotherapy (Carrara et al., 2021). MTSS1 plays an important role in cytoskeletal regulation (Xie, 2011). MTSS11 also has an influence on signal transduction. For example MTSS1 probably has an influence on EGFR in HNSCC (Dawson et al., 2012).

In addition to this connection, there also appears to be an interesting link with the immune system. MTSS1 also appears to be in contact with the PD-L1 pathway in other tumour entities. In adenocarcinomas of the lung, for example, it was shown that EGFR-KRAS signalling suppresses MTSS1 and PD-L1 upregulation (Wang et al., 2023). Perhaps this could be a key in adjuvant therapy to PD-1 or EGFR inhibitors in advanced or distant metastatic LSCC. The pretherapeutic analysis of MTSS1 for immunotherapies thus appears interesting for future studies (Wang et al., 2023).

5. Conclusion

MTSS1 expression (%) analysis is easy to perform. Choosing the right analysis method (MTSS1 expression % vs. MTSS1 intensity) is critical in terms of the local aggressiveness evaluation of LSCC. It seem that MTSS1 evaluation and especially MTSS1 expression (%) appear to be more suitable for assessing local tumour aggressiveness in LSCC, which could lead to better evaluating of treatment modalities. Nevertheless, the limited sample size and the low number of events warrant validation in follow-up studies.

Authors' contributions

MK analysed the histology, performed data acquisition, contributed to study conception, interpreted data, conducted the literature search, and drafted and wrote the manuscript. JR analysed data and revised the manuscript. SL, KW MK, NG, DJ, FH gave important intellectual input and critically revised the manuscript. CC analysed the histology, contributed to study conception and revised the manuscript. All authors read and approved the final manuscript.

CRediT authorship contribution statement

M. Klein: Writing – original draft, Visualization, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **J. Riese:** Writing – review & editing, Visualization, Software, Methodology, Formal analysis. **S. Leypold:** Writing – review & editing. **K. Wermker:** Writing – review & editing. **M. Katz:** Writing – review & editing. **N. Garrelfs:** Writing – review & editing. **D. Jonigk:** Writing – review & editing, Supervision, Resources. **F. Hölzle:** Writing – review & editing, Supervision, Resources. **C. Cacchi:** Writing – review & editing, Validation, Methodology, Investigation, Formal analysis, Data curation, Conceptualization.

Ethics declaration

Written informed consent to take part in the study and to publish the article has been obtained from all participants or their legal representatives. The privacy rights of participants have been observed.

This study included organ or tissue donors. This study includes human biological material and consent was obtained by donors, or their next of kin or legal representatives, for use in this study and for publication of the article. The samples used in this research were not sourced from executed prisoners or prisoners of conscience.

This study was performed in compliance with relevant laws, regulatory frameworks and guidelines where the research took place. This study was approved by the Ethical Committee of the University RWTH Aachen Germany. (Approval No. EK 22–373)

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

Alam, M., & Ratner, D. (2001). Cutaneous squamous-cell carcinoma. *The New England Journal of Medicine, 344*, 975–983.

Carrara, G. F. A., et al. (2021). Analysis of RPL37A, MTSS1, and HTRA1 expression as potential markers for pathologic complete response and survival. *Breast Cancer, 28*, 307–320.

Dawson, J. C., Timpson, P., Kalna, G., & Machesky, L. M. (2012). Mtss1 regulates epidermal growth factor signaling in head and neck squamous carcinoma cells. *Oncogene, 31*, 1781–1793.

Giacobbe, A., et al. (2016). p63 controls cell migration and invasion by transcriptional regulation of MTSS1. *Oncogene, 35*, 1602–1608.

Guo, Y., Qiao, X., Zhu, L., & Song, R. (2020). MicroRNA-182-5p modulates oral squamous cell carcinoma migration and invasion via targeting MTSS1 Gene. *Pathology and Oncology Research, 26*, 1007–1013.

Guo, Y., Ren, M.-S., Shang, C., Zhu, L., & Zhong, M. (2015). MTSS1 gene regulated by miR-96 inhibits cell proliferation and metastasis in tongue squamous cellular carcinoma Tca8113 cell line. *International Journal of Clinical and Experimental Medicine, 8*, 15441–15449.

Klein, M., et al. (2021). Immune checkpoint analysis in lip cancer. *The Journal of Cranio-Maxillofacial Surgery is the official publication of the European Association for Cranio-Maxillo-Facial Surgery, 49*, 950–958.

Klein, M., et al. (2023a). IMP3 expression as a potential tumour marker in high-risk localisations of cutaneous squamous cell Carcinoma: IMP3 in Metastatic cSCC. *Cancers, 15*, 4087.

Klein, M., et al. (2023b). Immune checkpoint analysis in ear cancer. *Head & Face Medicine, 19*, 48.

Klein, M., et al. (2024). A potential new biomarker in HNSCC: metastasis suppressor protein 1 (MTSS1). *Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology, 137*, 391–401.

Lee, Y.-G., Macoska, J. A., Korenchuk, S., & Pienta, K. J. (2002). MIM, a potential metastasis suppressor gene in bladder cancer. *Neoplasia, 4*, 291–294.

Leypold, S., et al. (2025). Tumor budding predicts lymph node metastasis in squamous cell carcinoma of the lip. *Head & Face Medicine, 21*, 74.

Matskova, L., Zheng, S., Kashuba, E., Ernberg, I., & Aspenström, P. (2024). MTSS1: beyond the integration of actin and membrane dynamics. *Cellular and Molecular Life Sciences, 81*, 472.

Mertz, K. D., et al. (2014). MTSS1 is a metastasis driver in a subset of human melanomas. *Nature Communications, 5*, 3465.

Parr, C., & Jiang, W. G. (2009). Metastasis suppressor 1 (MTSS1) demonstrates prognostic value and anti-metastatic properties in breast cancer. *European Journal of Cancer, 45*, 1673–1683.

Schemionek, M., et al. (2015). Identification of the adapter molecule MTSS1 as a potential oncogene-specific tumor suppressor in acute myeloid leukemia. *PLOS ONE, 10*, Article e0125783.
Valea, C.-V., et al. (2025). EZH2: An analysis of a potential new tumor marker in high-risk localization of cutaneous squamous cell carcinomas. *Frontiers in Oncology, 14*, Article 1438021.
Wang, D., Xu, M., Wang, T., Li, T., & Zhu, J. (2011). wei. MTSS1 overexpression correlates with poor prognosis in colorectal cancer. *Journal of Gastrointestinal Surgery, 15*, 1205–1212.
Wang, H., et al. (2019). Metastasis suppressor protein 1 regulated by PTEN suppresses invasion, migration, and EMT of gastric carcinoma by inactivating PI3K/AKT signaling. *Journal of Cellular Biochemistry, 120*, 3447–3454.
Wang, Y., et al. (2023). MTSS1 curtails lung adenocarcinoma immune evasion by promoting AIP4-mediated PD-L1 monoubiquitination and lysosomal degradation. *Cell Discovery, 9*, 20.
Xie, F. (2011). MTSS1 a multifunctional protein and its role in cancer invasion and metastasis. *Frontiers in Bioscience, S3*, 621–631.
Zhou, L., et al. (2016). Expression and significances of MTSS1 in pancreatic cancer. *Pathology and Oncology Research, 22*, 7–14.