Long non-coding RNA in low-grade glioma

Accumulating evidence demonstrated that Long non-coding RNAs (lncRNAs) involved in the regulation of the immune system and displayed a cell-type-specific pattern in immune cell subsets. Given the vital role of tumor-infiltrating lymphocytes in effective immunotherapy, we explored the tumor-infiltrating immune cell-associated lncRNA (TIIClncRNA) in low-grade glioma (LGG), which has never been uncovered yet. Methods: This study utilized a novel computational framework and 10 machine learning algorithms (101 combinations) to screen out TIIClncRNAs by integratively analyzing the sequencing data of purified immune cells, LGG cell lines, and bulk LGG tissues. Results: The established TIIClnc signature based on the 16 most potent TIIClncRNAs could predict outcomes in public datasets and the Xiangya in-house dataset with decent efficiency and showed better performance when compared with 95 published signatures. The TIIClnc signature was strongly correlated to immune characteristics, including microsatellite instability, tumor mutation burden, and interferon γ, and exhibited a more active immunologic process. Furthermore, the TIIClnc signature predicted superior immunotherapy response in multiple datasets across cancer types. Notably, the positive correlation between the TIIClnc signature and CD8, PD-1, and PD-L1 was verified in the Xiangya in-house dataset. Conclusions: The TIIClnc signature enabled a more precise selection of the LGG population who were potential beneficiaries of immunotherapy [1].

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Zhang N, Zhang H, Wu W, Zhou R, Li S, Wang Z, Dai Z, Zhang L, Liu F, Liu Z, Zhang J, Luo P, Liu Z, Cheng Q. Machine learning-based identification of tumor-infiltrating immune cell-associated lncRNAs for improving outcomes and immunotherapy responses in patients with low-grade glioma. Theranostics. 2022 Aug 8;12(13):5931-5948. doi: 10.7150/thno.74281. PMID: 35966587; PMCID: PMC9373811.