

---

---

## ABSTRACT

### Transcriptome analysis of monocytes from patients with Squamous Cell Carcinoma

Monocytes are circulating cells able to migrate inside tissues in response to damage signals and can be recruited to the tumor microenvironment where they locally differentiate in tumor associated macrophages, a diverse population in both phenotype and function. Recruited myeloid cells are known to promote cancer initiation, malignant progression, metastasis, and resistance to therapy in the tumor niche. However, the role of circulating monocytes in human squamous cell carcinoma is poorly understood. Here, we analyzed phenotypically monocyte subsets and their transcriptomes in human squamous cell carcinoma. Our findings demonstrate an expansion of the intermediate monocytes (CD14<sup>++</sup>CD16<sup>+</sup>) in SCC patients. We also establish that monocytes from primary and metastasis cancers are transcriptionally distinct from control monocytes isolated from healthy individuals. Several genes encoding transmembrane receptors, soluble factors, transcription factors, and enzymes were deregulated, including increased expression of transcripts encoding cell migration molecules (CCL2, CCR5, CXCL3), angiogenesis factors, cell communication, and ferroptosis process (AIFM2, GPX4, SLc7a11, SLc39a7). These data suggest that squamous cell carcinoma have a significant impact on circulating monocytes.

**Keywords:** Squamous cell carcinoma, Monocytes, Transcriptome.

---

---