

Description of Additional Supplementary Files

Supplementary Data 1

Differential Gene Expression Analysis between Scissor1 (Aneuploid Cells) and Scissor0 (Diploid Cells) using Seurat's FindAllMarkers Function

Supplementary Data 2

Differential Gene Expression Analysis between CD276 Antibody Treatment Resistant and Sensitive Groups using Seurat's FindAllMarkers Function

Supplementary Data 3

SCENIC analysis to investigate the potential mechanism by which ITGB6 mediates CX3CL1 expression. The analysis identified 22 downregulated inferred transcription factors in cells with altered ITGB6 expression.

Supplementary Data 4

Predicted transcription factors at the promoter region of the Cx3cl1 gene, identified using tools from the UCSC Genome Bioinformatics Site (<http://genome.ucsc.edu/>). The transcription factors listed have a score greater than 10 and a relative score greater than 0.95.

Supplementary Data 5

The distinct gene signature of PF4+ macrophages identified to delineate their functional implications in tumorigenesis. The gene signature was derived using single-cell RNA sequencing data.

Supplementary Data 6

Comprehensive demographic, pathological, and clinical metadata for a cohort of 81 HNSCC cases from the First Affiliated Hospital of Sun Yat-sen University (FAH-SYSU). The dataset includes detailed patient information used for subsequent verification of

the study findings.

Supplementary Data 7

The results of CXCR6 correlation analyses with cytotoxic and suppressive markers in Dario AA Vignali et al. human HNSCC cohort. The analysis aimed to explore the association of CXCR6 with both cytotoxic and suppressive profiles within CXCR6+ CD8+ T cells.

Supplementary Data 8

The results of CXCR6 correlation analyses with cytotoxic and suppressive markers in Robert L. Ferris et al. human HNSCC cohort. The analysis aimed to explore the association of CXCR6 with both cytotoxic and suppressive profiles within CXCR6+ CD8+ T cells.

Supplementary Data 9

The results of CXCR6 correlation analyses with cytotoxic and suppressive markers in TCGA HNSCC dataset. The analysis aimed to explore the association of CXCR6 with both cytotoxic and suppressive profiles within CXCR6+ CD8+ T cells.

Supplementary Data 10

The results of SCENIC analysis, which identified 18 putative transcription factors that were downregulated in the analyzed cells.

Supplementary Data 11

The predicted transcription factors at the promoter region of the Cx3cl1 gene, identified using tools from the UCSC Genome Bioinformatics Site (<http://genome.ucsc.edu/>). The transcription factors listed have a score greater than 10 and a relative score greater than 0.95.

Supplementary Data 12

list of primers used for this manuscript.

Supplementary Data 13

MRI parameters in detail.