Group	Lesion location	Lesion type
Normal tissue	Gingival mucosa	Normal tissue
OPMD with *Candida albicans* infection	Buccal mucosa	Squamous hyperplasia
OSCC without *Candida albicans* infection	Buccal mucosa	Squamous cell carcinoma
OSCC with *Candida albicans* infection	Gingival mucosa	Squamous cell carcinoma

Table S1: Lesion locations and types of patient specimens.

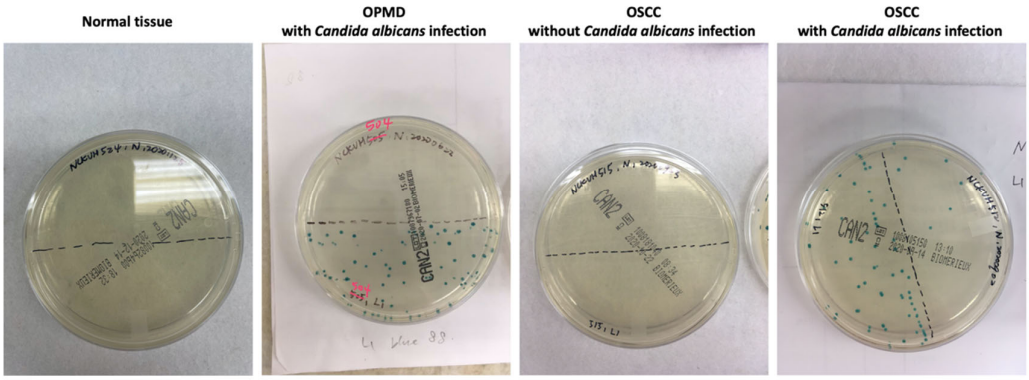
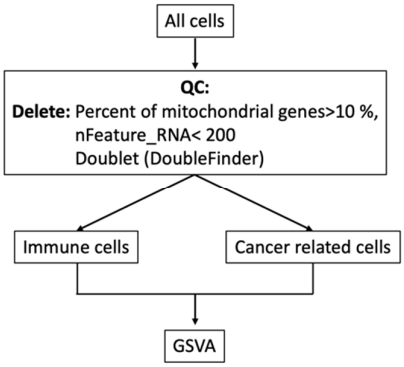


Figure S1: Candidiasis detection. CHROMagar Candida was used to detect whether patients were infected with *Candida albicans*. Green colony formation was recorded as a *C. albicans*-positive case.



Groups	Cell-ranger output cell number-Preset parameters	Cell-ranger output cell number-Forced output of 10,000 cells
Normal tissue	7477	-
OPMD with *Candida albicans* infection	10045	-
OSCC without *Candida albicans* infection	3016	10000
OSCC with *Candida albicans* infection	2089	10000

Groups	Normal tissue	OPMD with *Candida albicans* infection	OSCC without *Candida albicans* infection	OSCC with *Candida albicans* infection
Raw data	7477	10045	10000	10000
Percent.mt< 10 %, nFeature> 200	6345	7363	4837	2791
After Doublet Finder	5947	5819	4195	2472

Figure S2: Flow of quality control. Cells with >10% mitochondrial genes, <200 nFeature_RNA, and doublets were excluded.

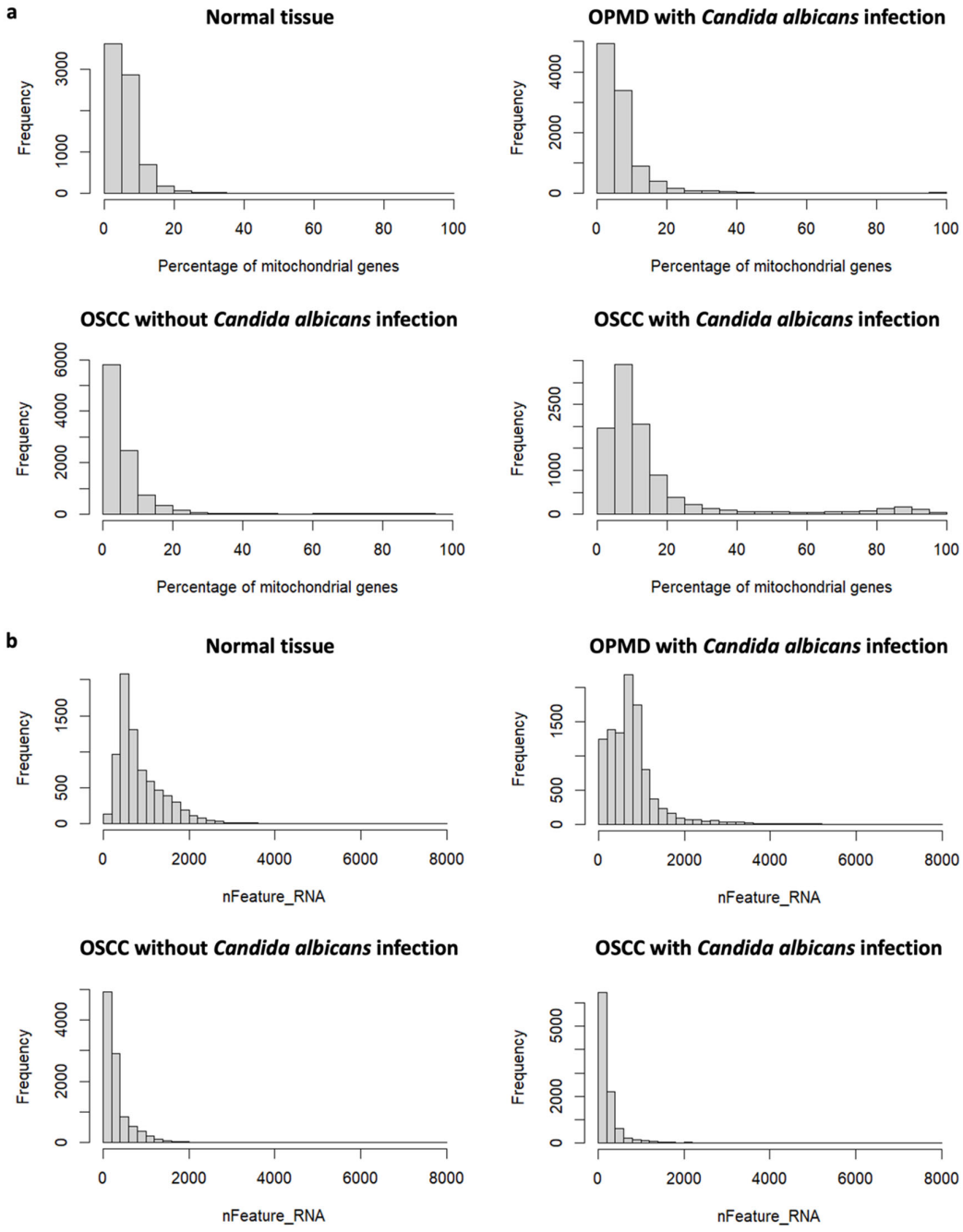


Figure S3: Performance of each group after quality control: (**a**) percentage of mitochondrial genes and (**b**) gene number in the cells.

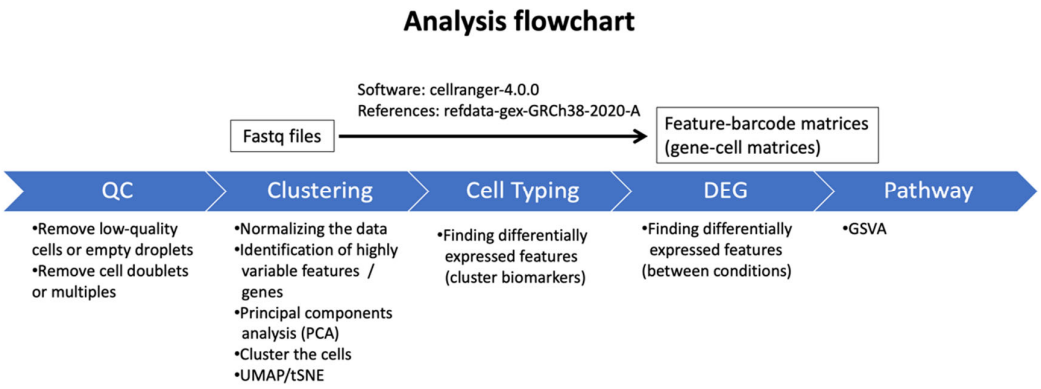


Figure S4: Analysis flow after next-generation sequencing.

Cluster	0	1	2	3	4	5	6	7	8	9	10	11	12
Cell type	Fibroblast	Fibroblast	Fibroblast	Fibroblast	Epithelial	Fibroblast	Endothelial	Fibroblast	Endothelial	Epithelial	Others	Endothelial	Epithelial
Normal tissue	29 %	21 %	0 %	20 %	2 %	11 %	5 %	5 %	0 %	1 %	4 %	2 %	0 %
OPMD with *Candida albicans* infection	0 %	2 %	1 %	0 %	1 %	32 %	8 %	16 %	31 %	1 %	9 %	0 %	0 %
OSCC without *Candida albicans* infection	0 %	0 %	59 %	0 %	0 %	0 %	11 %	9 %	15 %	0 %	1 %	3 %	0 %
OSCC with *Candida albicans* infection	0 %	0 %	5 %	0 %	42 %	0 %	8 %	0 %	3 %	20 %	3 %	7 %	11 %

Cluster	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Cell type	T-Cell	T-Cell	T-Cell	B-cell	T-Cell	Macrophage	B-cell	Others	Macrophage	T-cell	Macrophage	Neutrophils	Mast cell	Others	Others
Normal tissue	41 %	17 %	8 %	13 %	1 %	0 %	8 %	6 %	2 %	2 %	0 %	0 %	3 %	0 %	0 %
OPMD with *Candida albicans* infection	26 %	27 %	19 %	13 %	1 %	1 %	9 %	1 %	0 %	2 %	0 %	0 %	0 %	0 %	0 %
OSCC without *Candida albicans* infection	13 %	17 %	9 %	3 %	33 %	2 %	1 %	9 %	8 %	0 %	0 %	0 %	0 %	3 %	0 %
OSCC with *Candida albicans* infection	2 %	2 %	4 %	2 %	2 %	57 %	2 %	5 %	1 %	0 %	9 %	9 %	0 %	0 %	5 %

Table S2. Cell ratios of the clusters within the four groups.

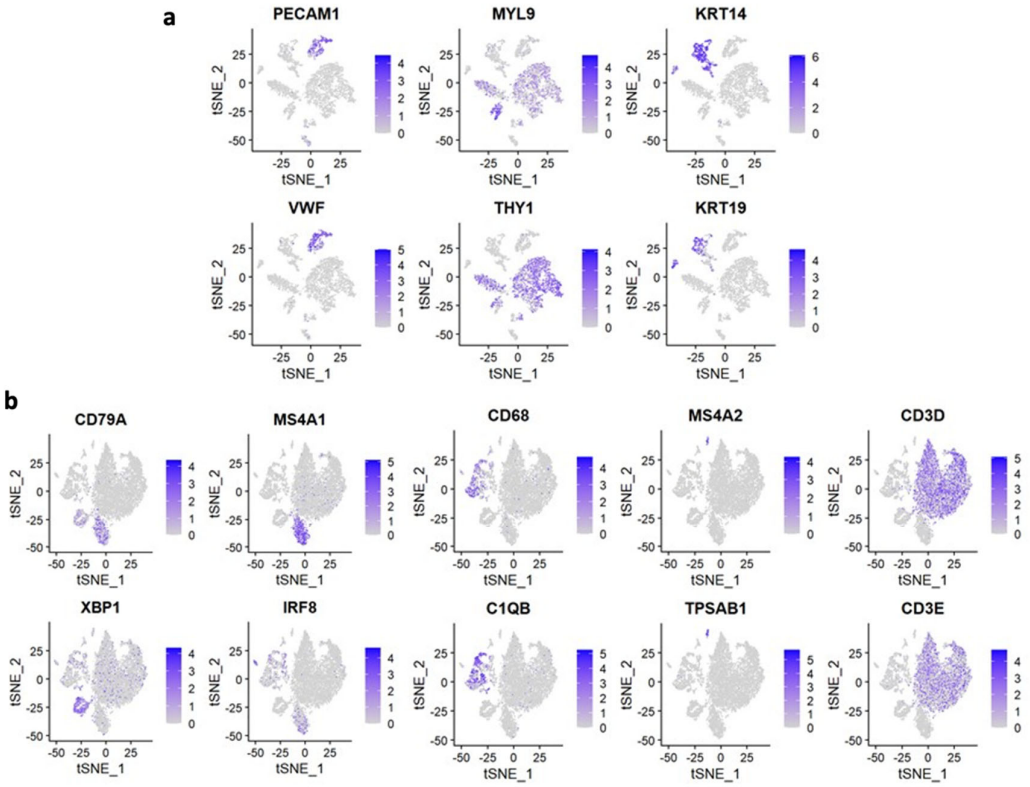


Figure S5: t-SNE for specific biomarkers distribution in the clusters. (a) PECAM1 and VWF are the specific biomarkers of endothelial cells, MYL9 and THY1 are those of fibroblast cells, and KRT14 and KRT19 are those of epithelial cells. (**b**) CD79A, XBP1, MS4A1, and IRF8 are the specific biomarkers of B cells; CD68 and C1QB are those of macrophages; MS4A2 and TPSAB1 are those of mast cells; and CD3D and CD3E are those of T cells.

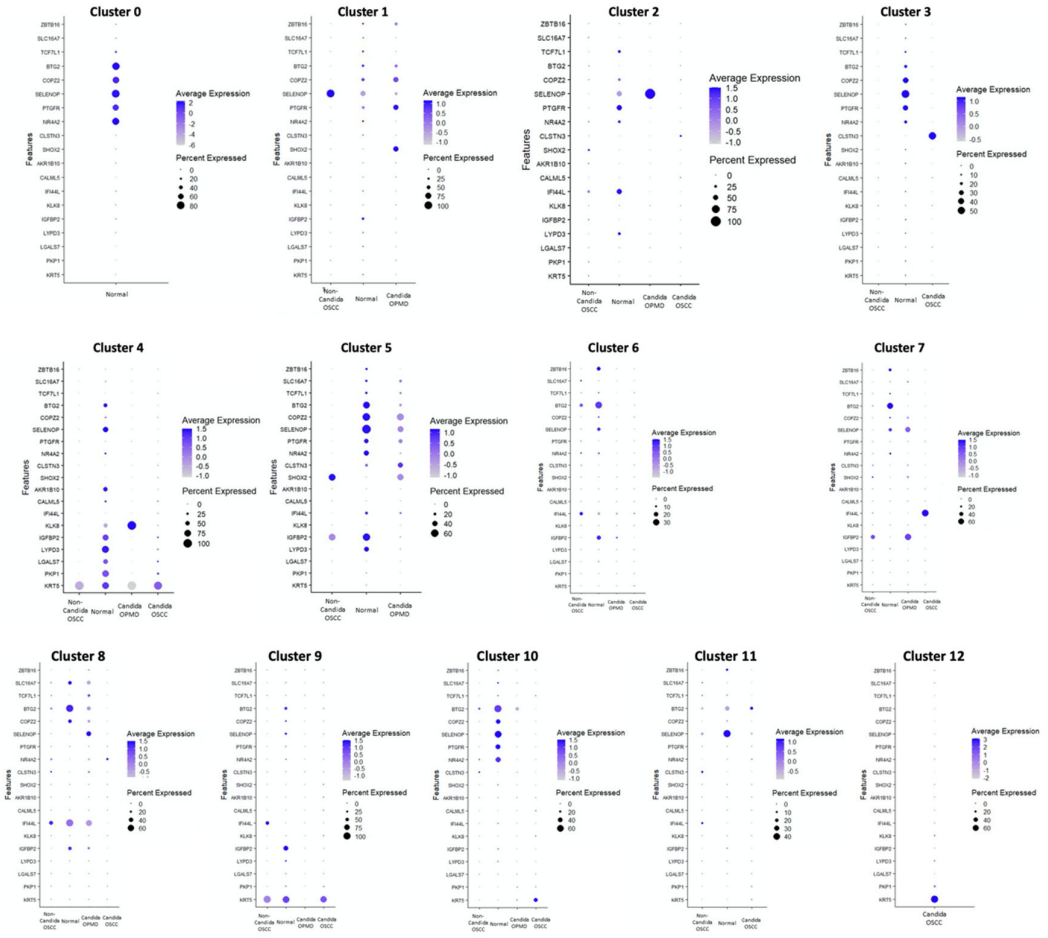


Figure S6: Dot diagrams presenting genes involved in KRAS_SIGNALING_DN. Expression of genes involved in the KRAS signaling pathway in 13 clusters within the four groups is illustrated. The average gene expression levels and percentages of cells in the four groups are indicated using different colors and sizes of the dots.

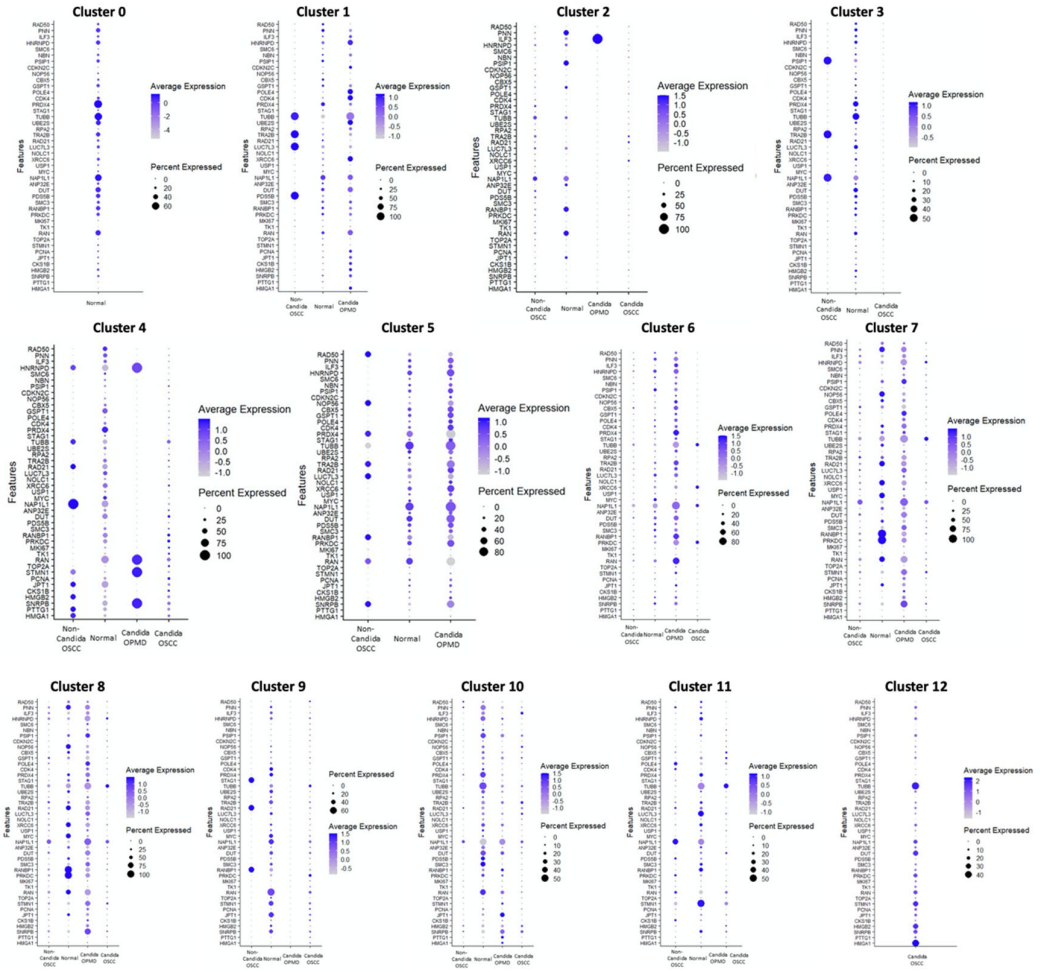


Figure S7: Dot diagrams presenting genes involved in the E2F_TARGETS. Expression of E2F target genes in 13 clusters within the four groups are illustrated. The average gene expression levels and percentages of cells in the four groups are indicated using different colors and sizes of the dots.

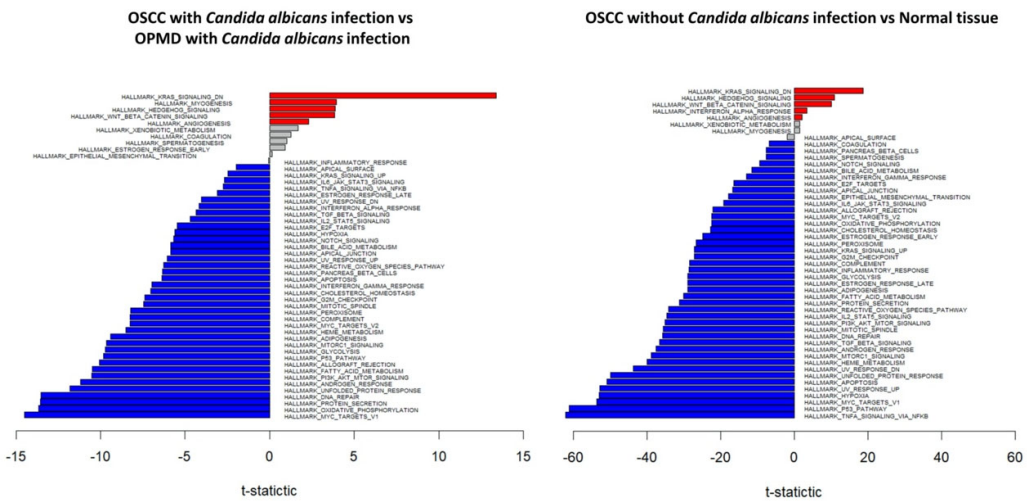


Figure S8: GSVA of regulatory pathways in (**a**) OSCC tissue with *Candida albicans* infection and OPMD with *Candida albicans* infection. Red and blue bars indicate that gene expression was significantly increased in OSCC tissue with *C. albicans* infection compared with OPMD lesion with *Candida albicans* infection and OPMD lesion with *Candida albicans* infection compared with OSCC tissue with *C. albicans* infection. (**b**) OSCC tissue without *Candida albicans* infection and normal tissue. Red and blue bars indicate that gene expression was significantly increased in OSCC tissue without *C. albicans* infection compared with normal tissue and normal tissue compared with OSCC tissue without *C. albicans* infection