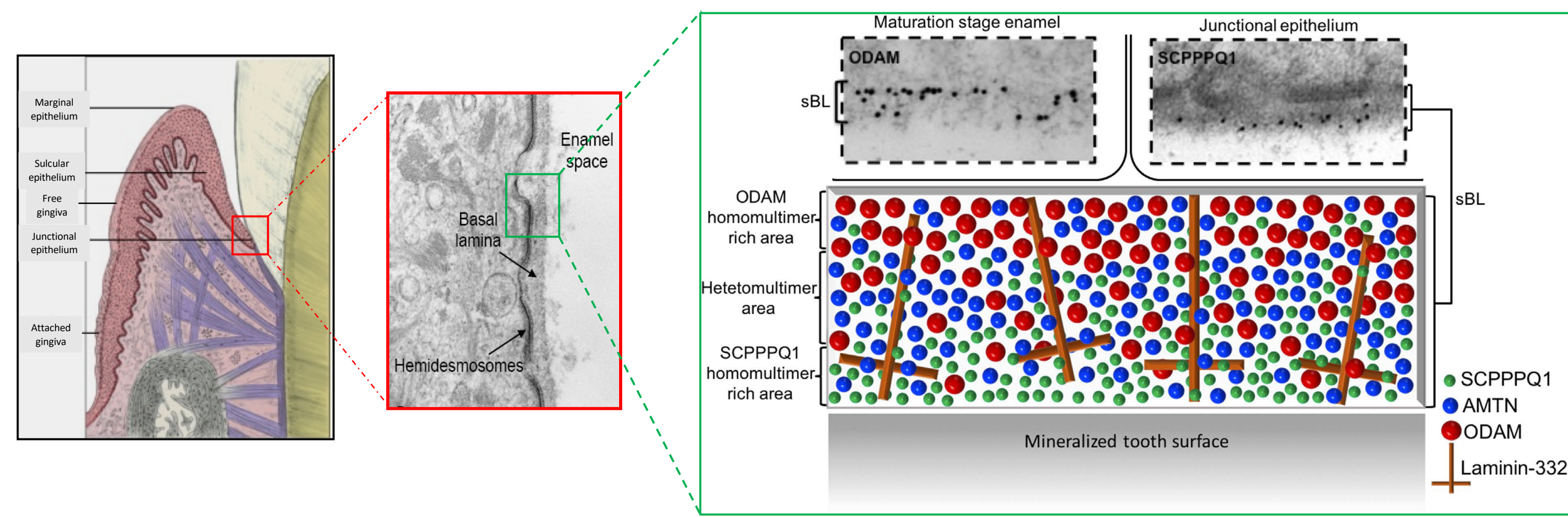


The junctional epithelium protein *Odontogenic ameloblast-associated* affects cell behavior

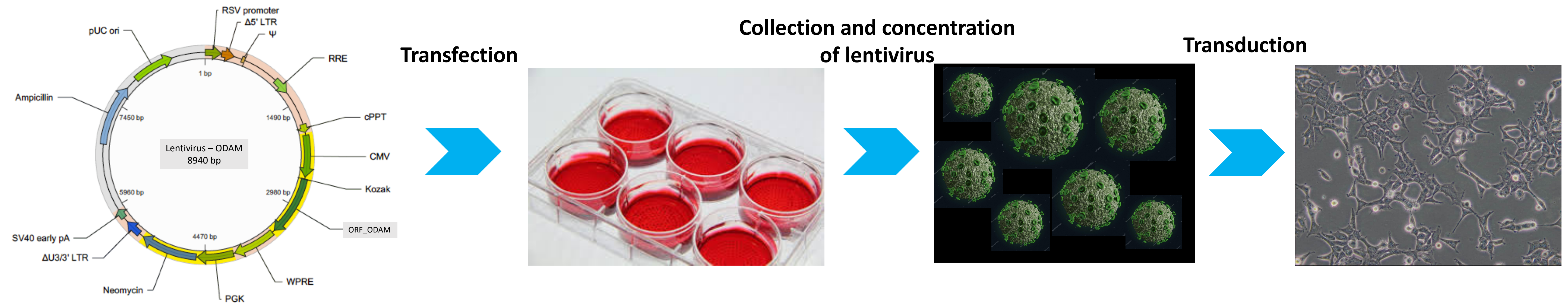
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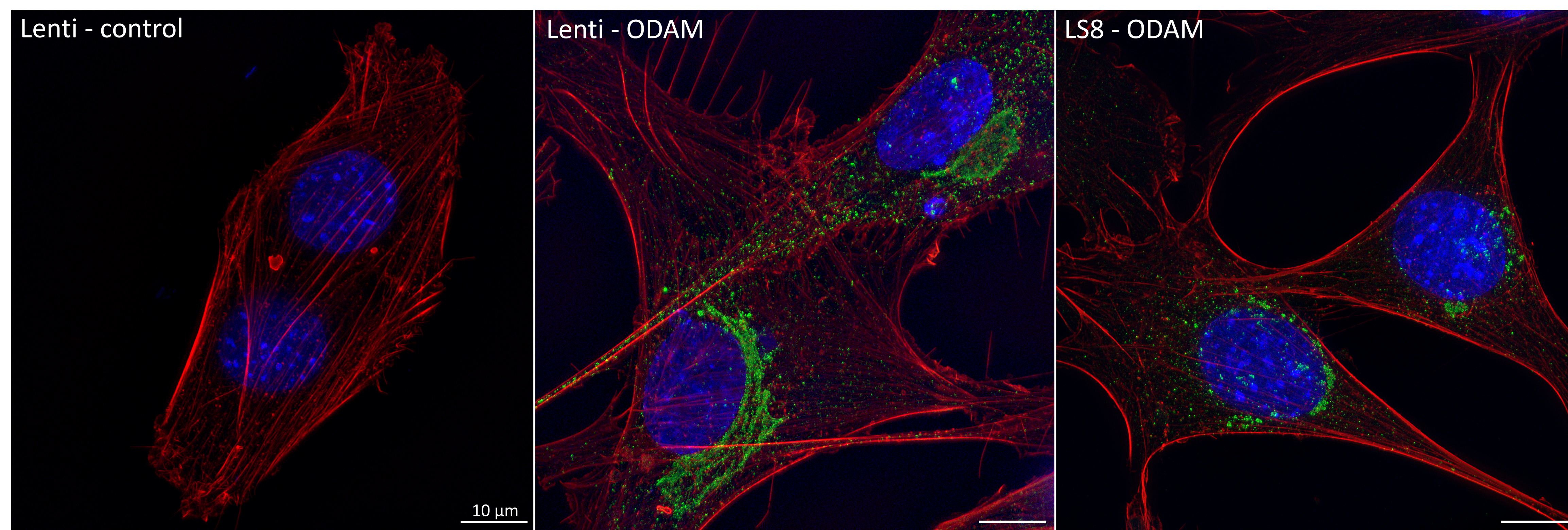
The junctional epithelium (JE), which initially derives from the enamel organ, produces a specialized basal lamina (sBL) that mediates its attachment to the tooth. This adhesive matrix is composed of four proteins. One of them, **Odontogenic ameloblast-associated** (ODAM), stands out by being also continuously present among cells of the JE. However, the expression of ODA is reduced in patients suffering from periodontal diseases (PD). This unique protein is also highly upregulated in epithelial neoplasia but is not found in healthy cells. The expression of ODA in the incompletely differentiated cells of the JE and in dedifferentiated neoplastic cells has led to the hypothesis that ODA influences cell status and behavior.



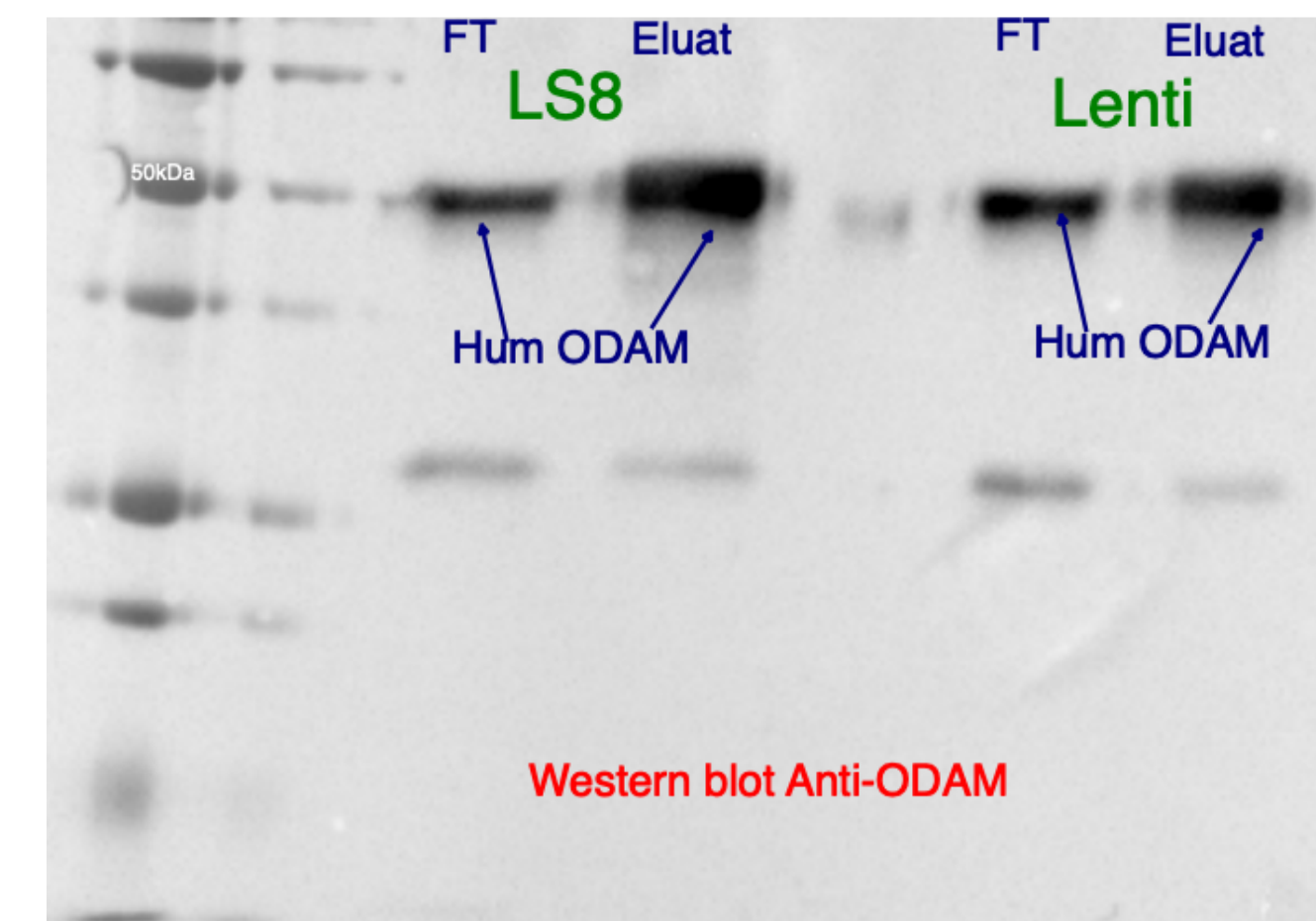
To test this hypothesis, we have expressed ODA in lentiviral transduced HEK (lenti) and in LS8 ameloblast-related cells, and investigated its influence on cellular behavior by combining molecular and microscopic approaches.



Evaluation of protein production (Nucleus, ODA, Actin)



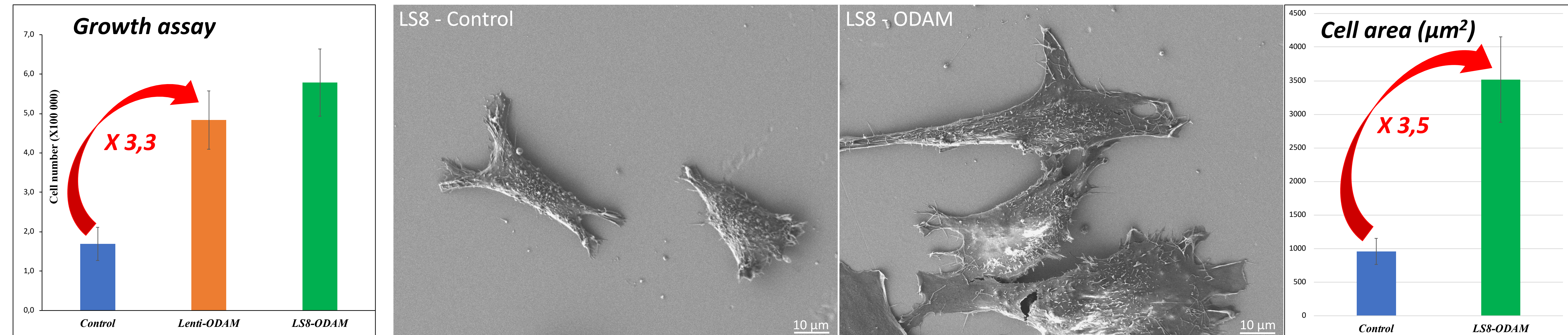
Western blot analysis to detect ODA in LS8 or Lenti cells



3D movie of the immunolabeling of ODA

Western blot analysis and Immunofluorescence confirmed the successful integration of the transgene and production of the protein in both cell types. Immunofluorescence additionally showed the localization of ODA in the Golgi region. As assessed by cell counts, cells expressing ODA divided ~3 times faster than control cells (non-infected and GFP-transduced). Both fluorescence and scanning electron microscopy revealed that cells were larger and generally more spread.

Evaluation of the behaviour of ODA producing cell



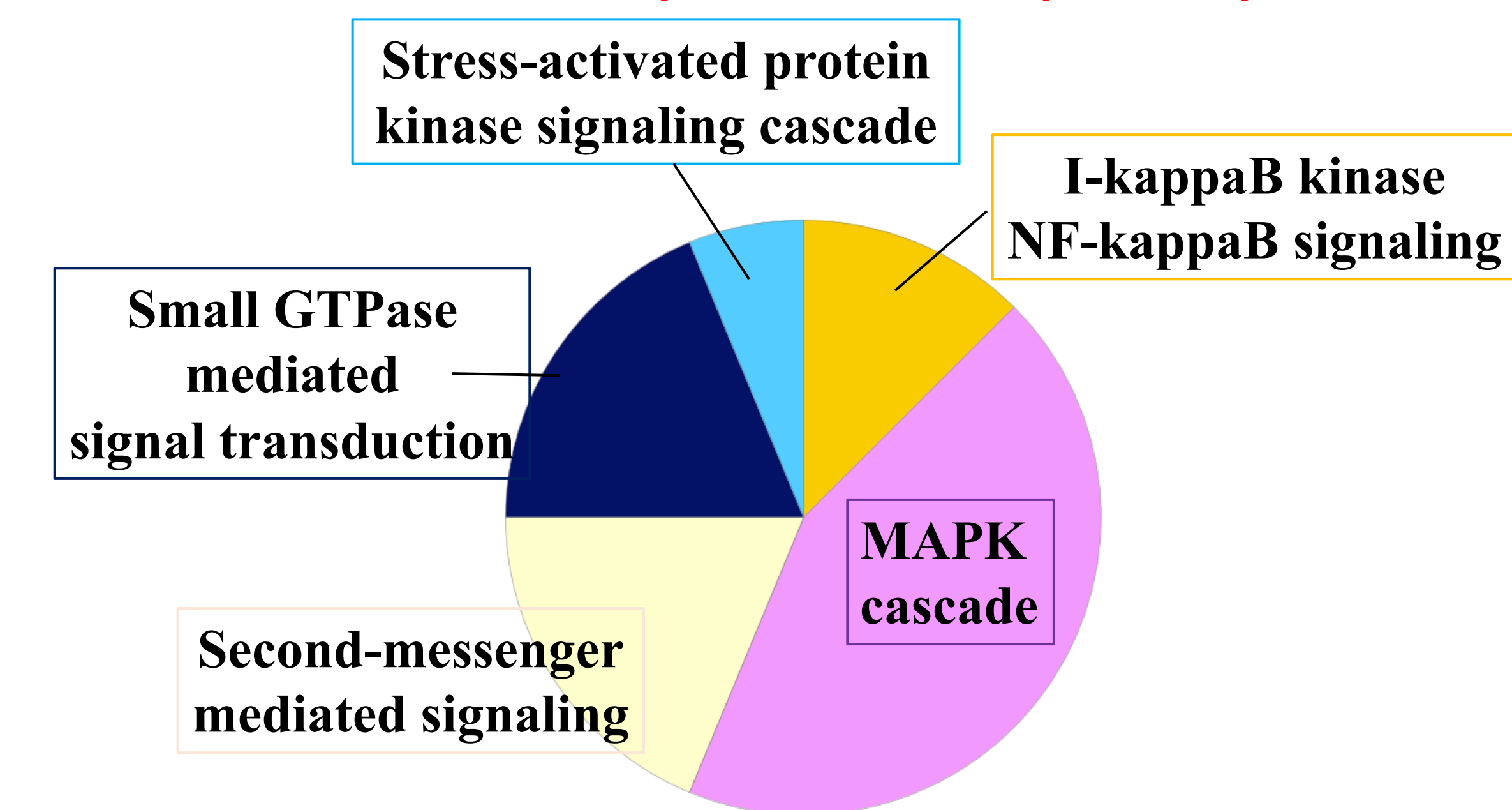
RNA-Sequencing confirmed this cell behavior by highlighting the upregulation of genes implicated in **cell proliferation and differentiation pathways** (e.g. *JAK/STAT3*, *MAPK*). Some genes related to **inflammation** were also upregulated (e.g. *NF-kB signaling*).

RNA Seq data treatment
LS8 vs LS8-ODA

55338 genes
153 upregulated
1331 downregulated

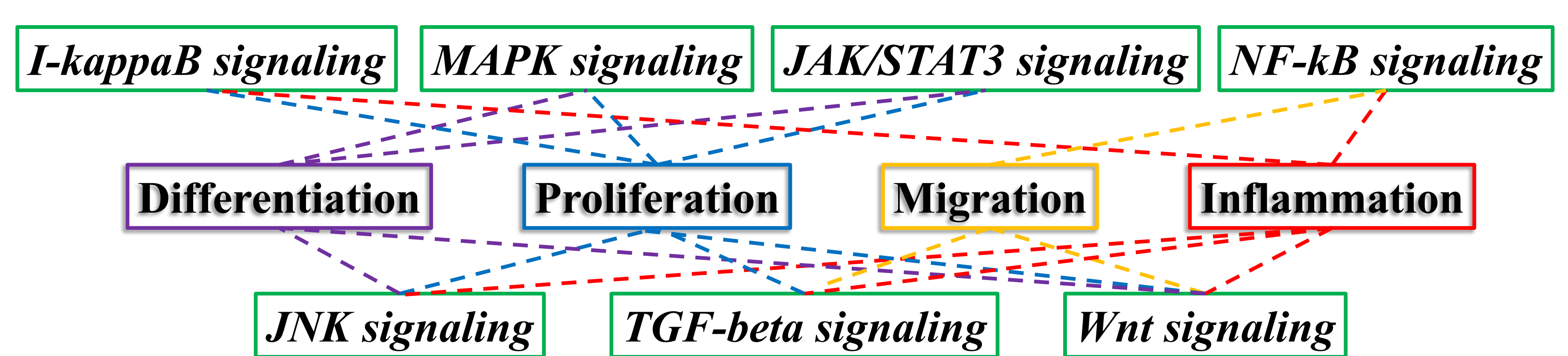
	log2FoldChange	pvalue	Gene
ENSRNOG0000023372-NM	10.1388511551037	5.08144633147113e-28	<i>Odam-rat</i>
ENSMUSG00000027656.7	2.93787094872597	8.25732612649346e-16	<i>Ccn5</i>
ENSMUSG00000006143.12	3.03959625101626	0.00446950574939687	<i>Upk3bl</i>
ENSMUSG00000018570.17	3.05295708561872	0.000326338972201319	<i>2810408A11Rik</i>
ENSMUSG00000033510.14	3.26141964427908	4.86402072650233e-06	<i>Otud7a</i>
ENSMUSG00000023039.17	3.50246251234712	5.53707288540622e-06	<i>Krt7</i>

PantherDB (data analysis – Pathways analysis)



GeneOntology (Data analysis)

Major pathways activated



These data support the concept that :

- ODA plays a key role in JE specialization.
- The increase in cell number is consistent with the higher rate of cell division of the JE compared to the slower dividing adjacent gingival keratinocytes that do not express ODA.
- The upregulation of inflammation-related genes makes a parallel with the perpetually inflamed state of the JE.

A better understanding of the role of ODA may provide clues on how to revert the changes of JE during PD and on how it promotes epithelial neoplastic transformation.