Gene expression profiling of oesophageal adenocarcinoma

Comparative analysis of oesophageal adenocarcinoma with and without Barrett's metaplasia

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1 Background

- Chronic inflammation caused by stomach acid reflux on the oesophagus can lead to metaplasia of the oesophagus called Barrett's metaplasia of the oesophagus or Barrett's metaplasia in short.
- Barrett's metaplasia can progress and advance to develop oesophageal adenocarcinoma.
- Oesophageal adenocarcinomas do not always arise in a background of Barrett's metaplasia.
- A study[1] argued that oesophageal adenocarcinomas with and without Barrett's metaplasia were two different cancers and they had distinct clinical and molecular characteristics.
- The study concluded that oesophageal adenocarcinomas that did not arise in a background of Barrett's metaplasia had less common mononuclear cell infiltration and were more invasive than those did arise from Barrett's metaplasia.

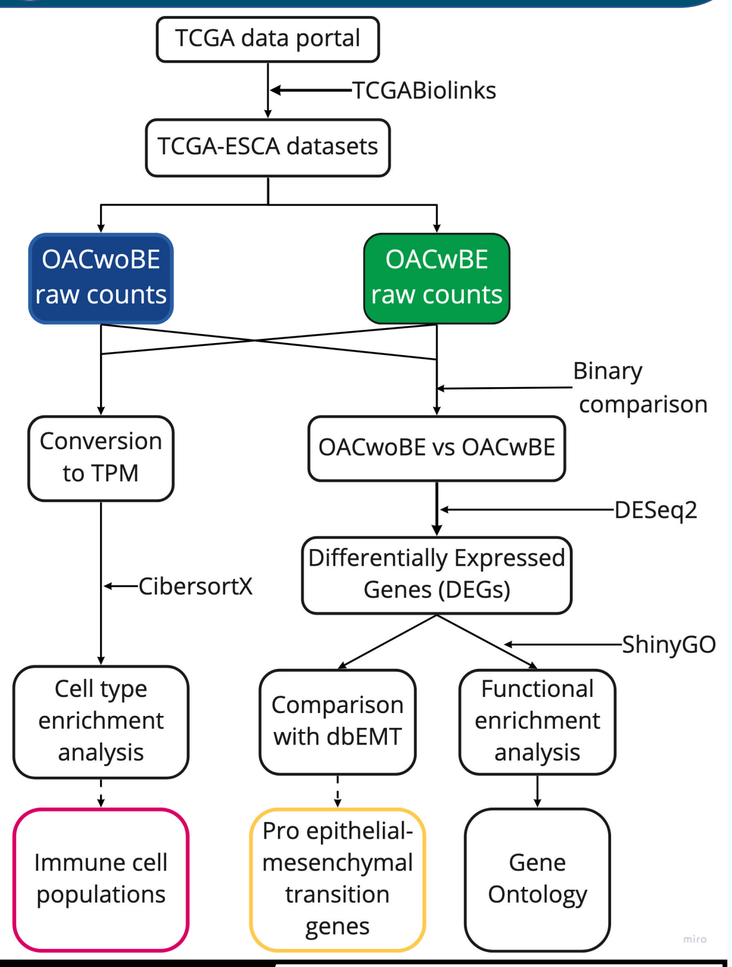
2 Aim & Objectives

Aim: To understand differences in the immune response and epithelial mesenchymal plasticity of oesophageal adenocarcinoma that arise in a background of Barrett's metaplasia of the oesophagus with those that do not.

Objectives:

1. To investigate immune response characteristics between oesophageal adenocarcinoma with and without Barrett's metaplasia.
2. To investigate gene expression differences that suggest invasive behaviour between oesophageal adenocarcinoma with and without Barret's metaplasia.

3 Methods



Abbreviations

OACwoBE: Oesophageal adenocarcinoma without Barrett's metaplasia

OACwBE: Oesophageal adenocarcinoma with Barrett's metaplasia

4 Results

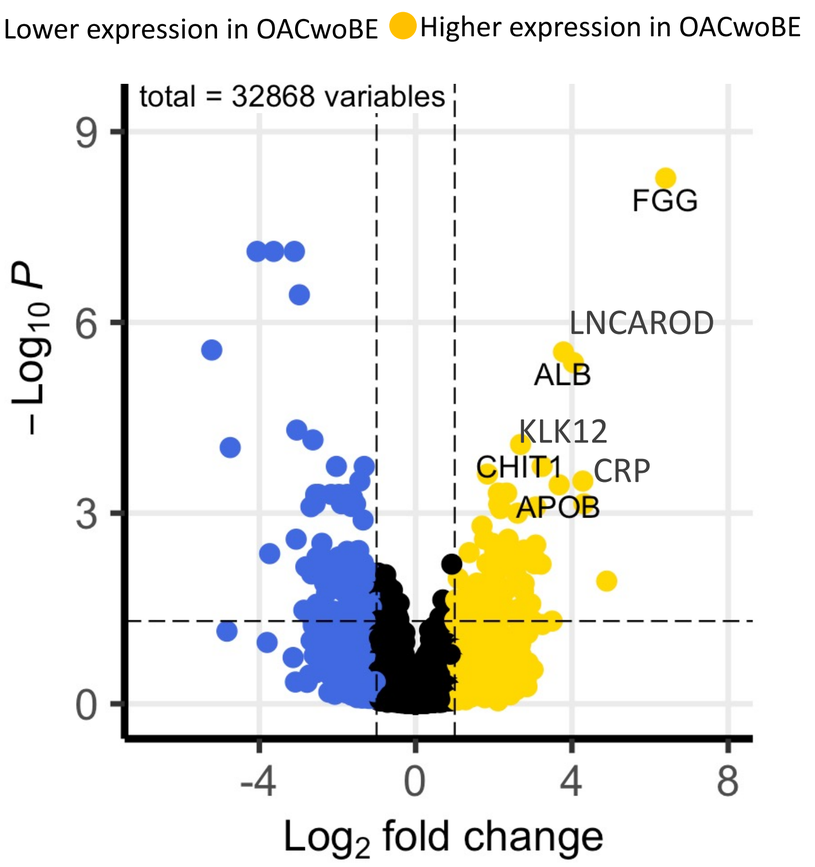


Figure 1. Gene expression comparison between OACwoBE and OACwBE. Out of 32868 genes, approximately 0.7% genes are significantly different between OACwoBE and OACwBE. Most significant seven genes expressed higher in OACwoBE are shown.

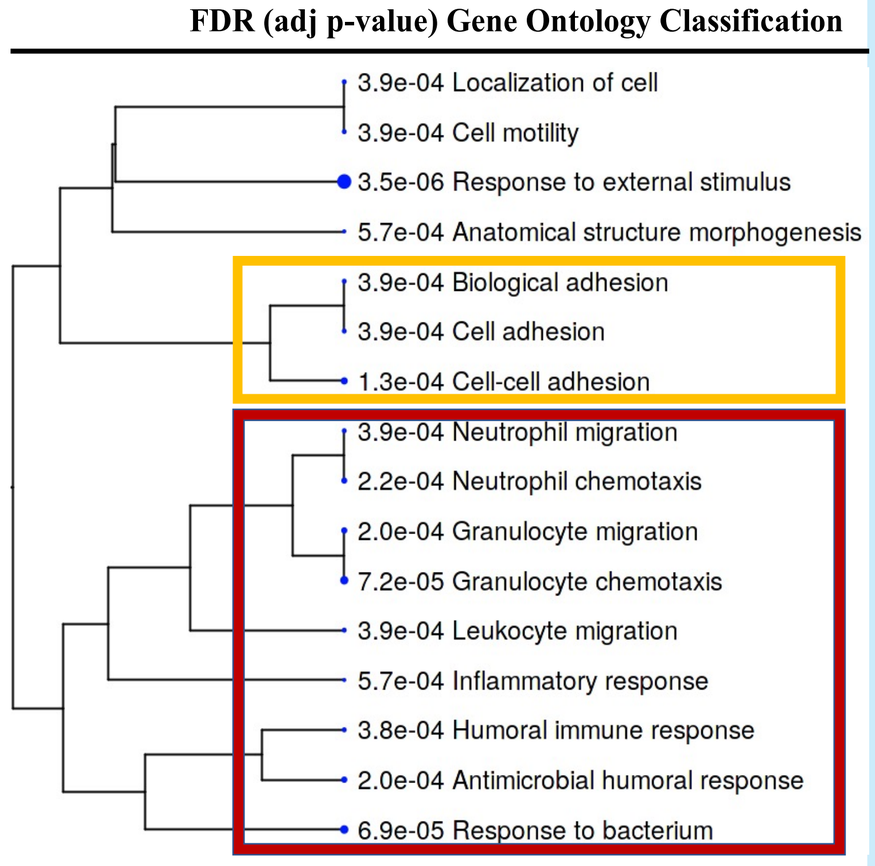


Figure 2. Gene ontology of genes expressed higher in OACwoBE reveals functional groups involve in invasive behaviour (yellow box) and immune responses (red box).

Immune response differences

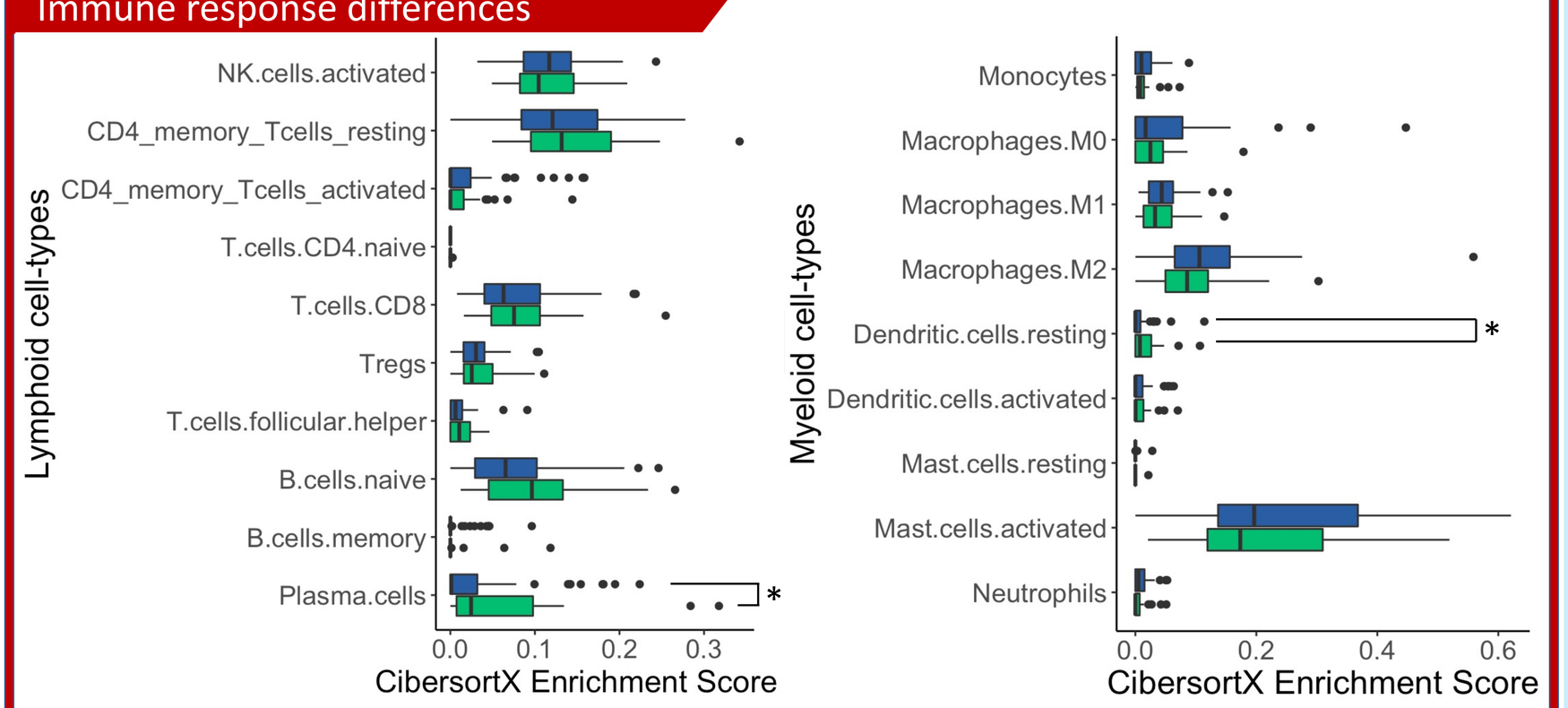


Figure 3. Immune cell populations comparison between oesophageal adenocarcinoma with and without Barrett's metaplasia predicted by CIbersortX. Plasma and resting dendritic cells populations are more numerous in oesophageal adenocarcinoma with Barrett's metaplasia (p = 0.024; p = 0.046, Mann-Whitney U test).

Invasive behaviour differences

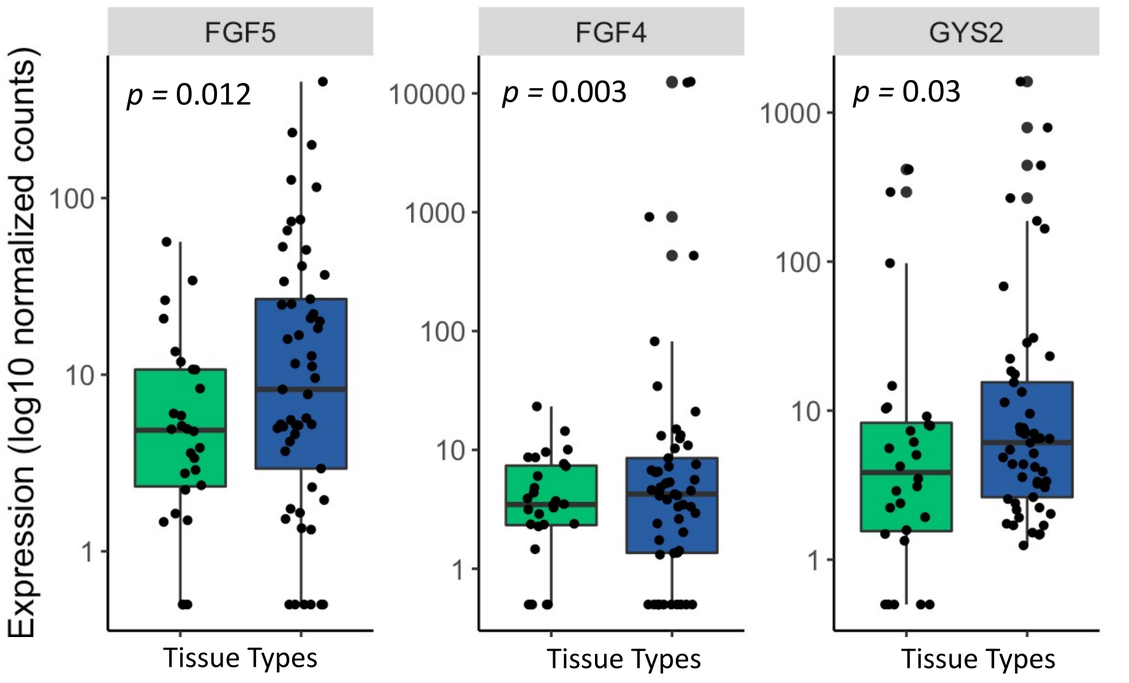


Figure 4. Three pro epithelial-mesenchymal transition genes are expressed significantly higher in oesophageal adenocarcinoma without Barrett's metaplasia. In contrast, there is no pro-epithelial mesenchymal transition gene expressed higher in oesophageal adenocarcinoma with Barrett's metaplasia.

Legends

Oesophageal adenocarcinoma with Barrett's metaplasia

Oesophageal adenocarcinoma without Barrett's metaplasia

5 Conclusion

- Two subsets of mononuclear cells are significantly more numerous in oesophageal adenocarcinomas that are associated with Barrett's metaplasia, confirming results from the previous study.
- Oesophageal adenocarcinomas that do not rise in a background of Barrett's metaplasia have more pro epithelial-mesenchymal transition genes that may be the driver of their invasive behaviour.

References

1. Lasanudin J, May F, Madhavan A. Intra-tumour and Inter-tumour Heterogeneity in Oesophageal Adenocarcinoma [Postgraduate]. Newcastle University; 2020.

Acknowledgements

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