



The role of CD4+T cell expression profiles in colorectal cancer development

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WCE

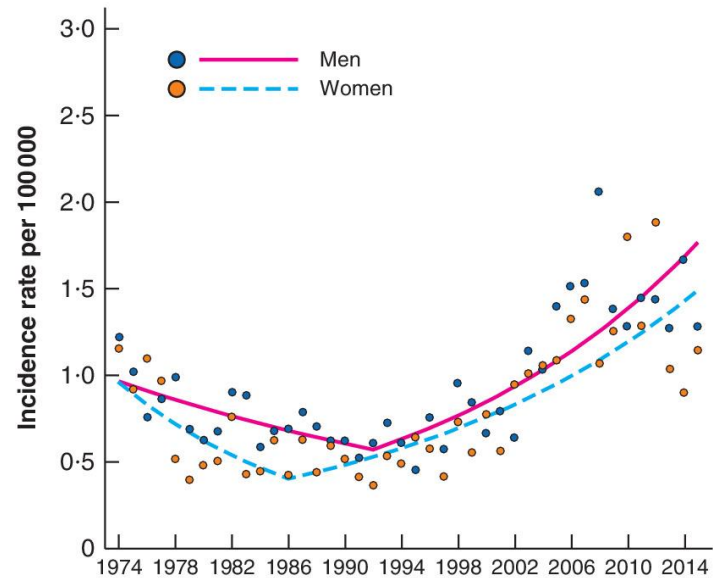
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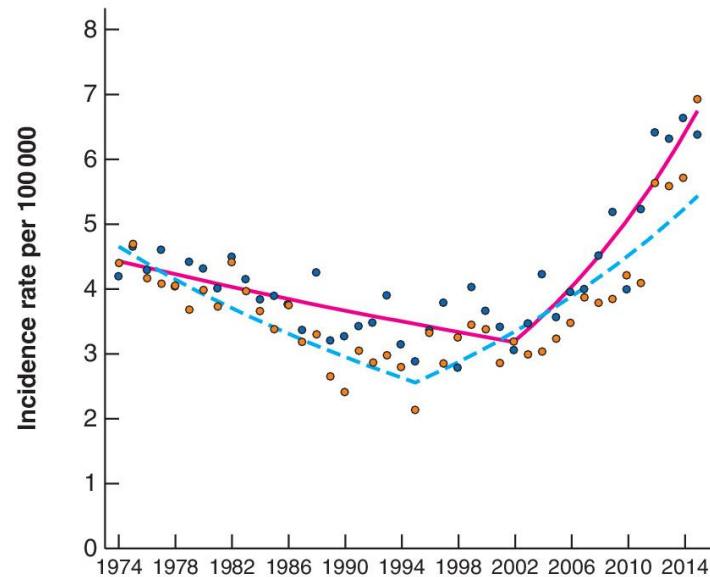
Colorectal cancer

- Colorectal cancer (CRC) is the **4th most common** cancer in the UK
- 54% cases are estimated to be **preventable**

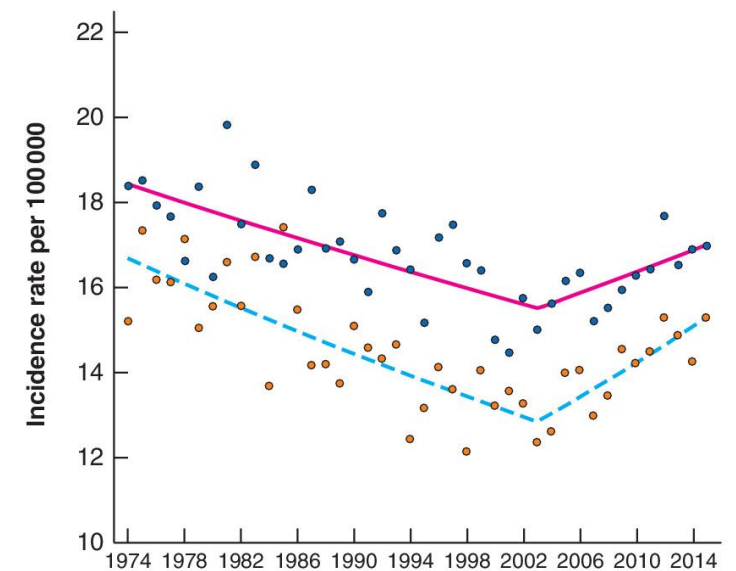
a 20–29 years



b 30–39 years




c 40–49 years




Chambers et al. (2020)

Circulating white blood cell traits and colorectal cancer risk: A Mendelian randomisation study

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Immune disease risk variants regulate gene expression dynamics during CD4⁺ T cell activation

[Blagoje Soskic](#), [Eddie Cano-Gamez](#), [Deborah J. Smyth](#), [Kirsty Ambridge](#), [Ziying Ke](#), [Julie C. Matte](#), [Lara Bossini-Castillo](#), [Joanna Kaplanis](#), [Lucia Ramirez-Navarro](#), [Anna Lorenc](#), [Nikolina Nakic](#), [Jorge Esparza-Gordillo](#), [Wendy Rowan](#), [David Wille](#), [David F. Tough](#), [Paola G. Bronson](#) & [Gosia Trynka](#) 

[Nature Genetics](#) **54**, 817–826 (2022) | [Cite this article](#)

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**Aim: to investigate the role of CD4+T cell
expression profiles on colorectal cancer
development.**

Methods

Mendelian randomisation (MR)

Identification of
genetic
instruments



Outcome
dataset
selection



Two-sample MR
analysis

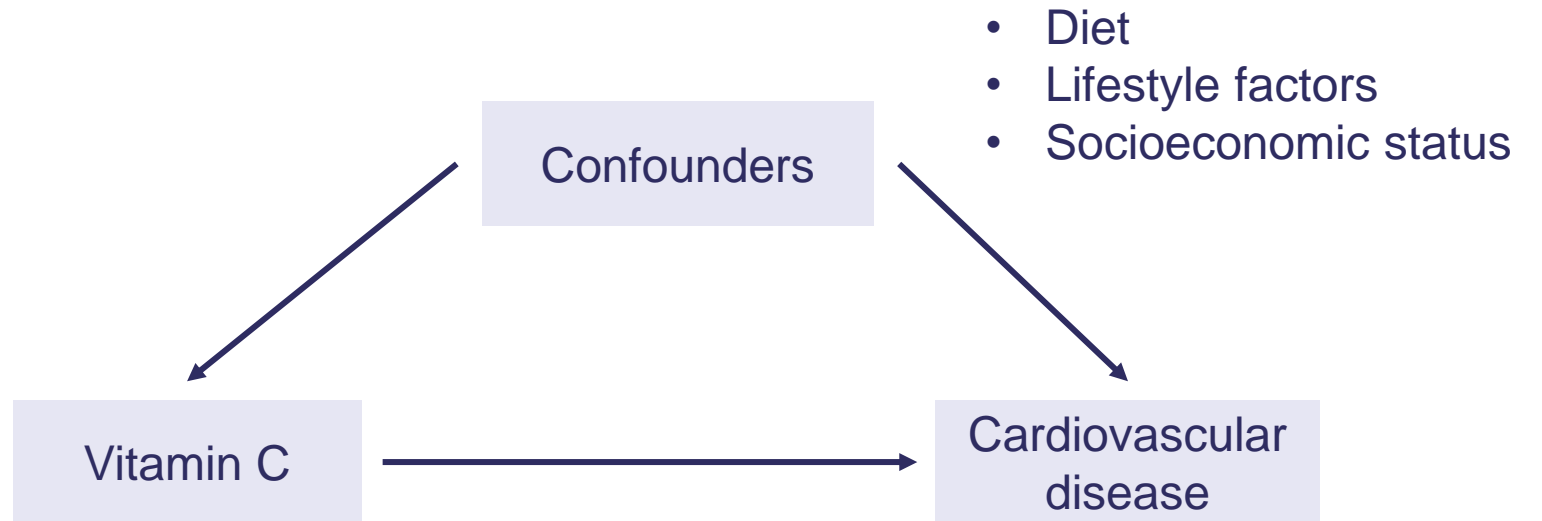


Sensitivity
analyses

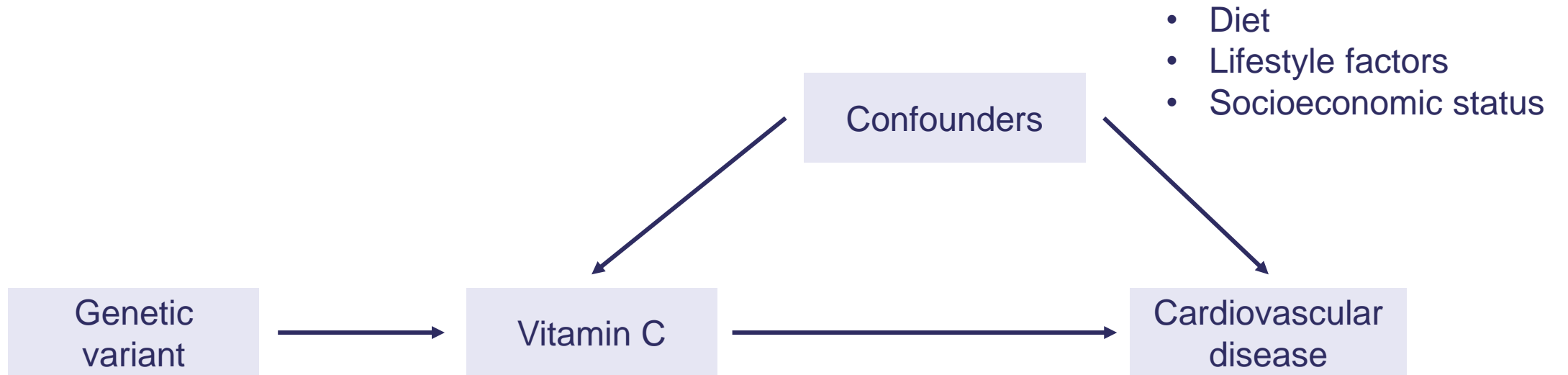
Mendelian randomisation



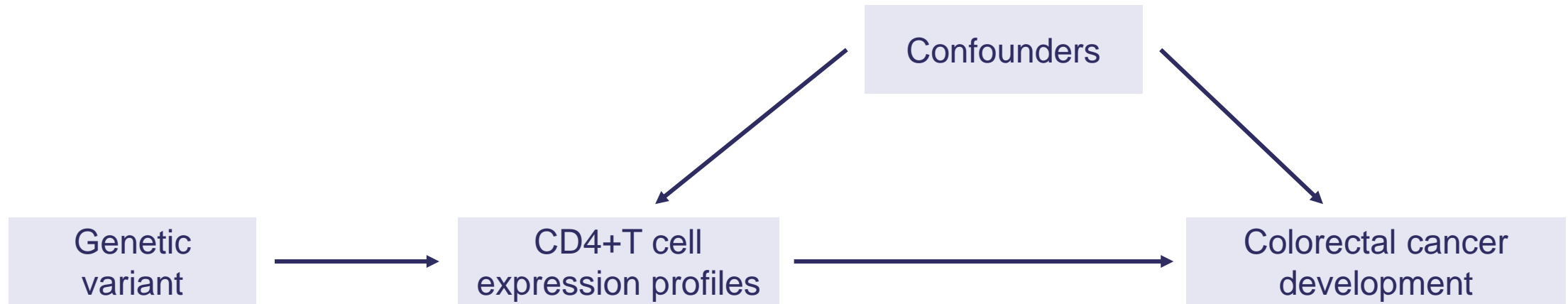
Mendelian randomisation



Mendelian randomisation



Mendelian randomisation



Instrument selection

- Summary-level dynamic eQTL data extracted from Soskic et al. (2022)
- 119 healthy individuals of British ancestry
- Rest and four activation states
- *cis*-eQTLs (+-500kb) strongly associated with gene expression ($P < 5 \times 10^{-8}$), independent ($r^2 < 0.001$) and *F*-statistic > 10

eQTL = expression quantitative trait loci

Outcome data selection

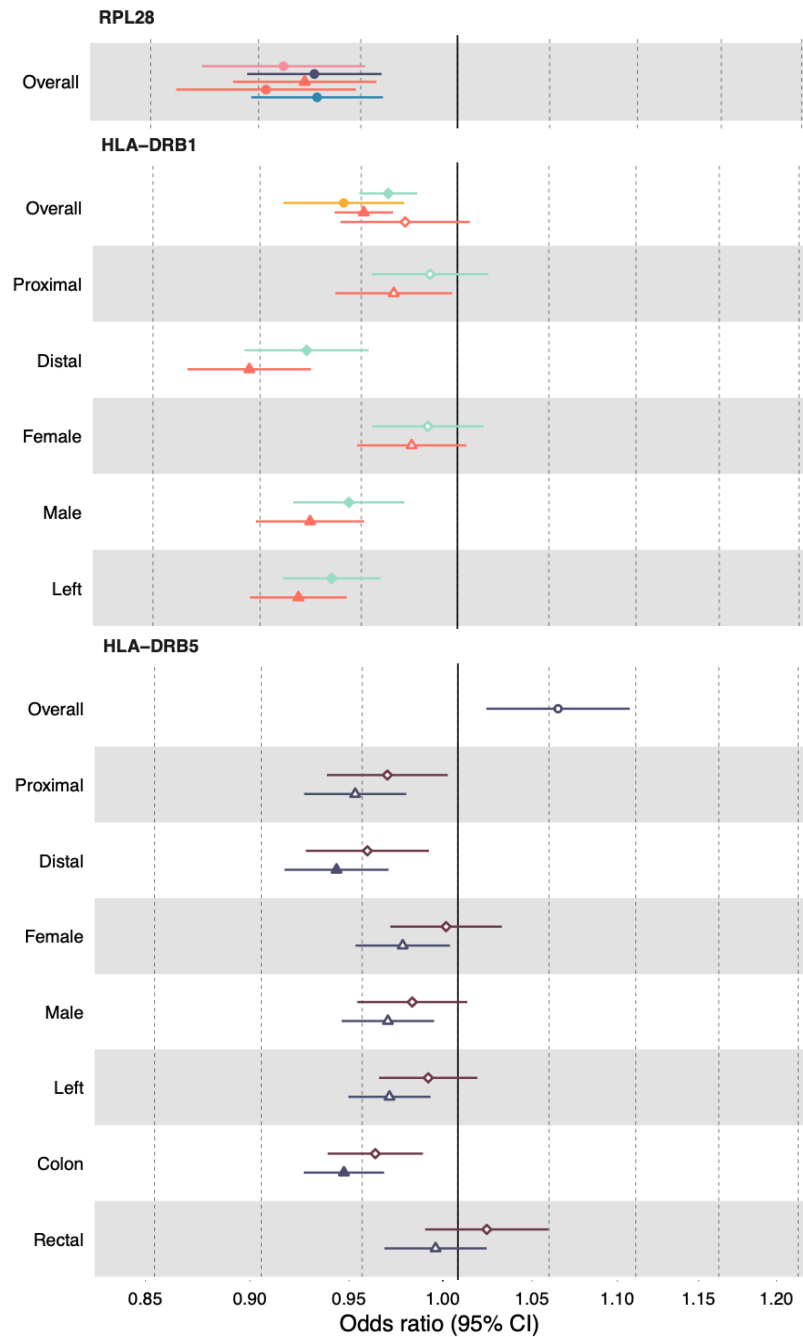
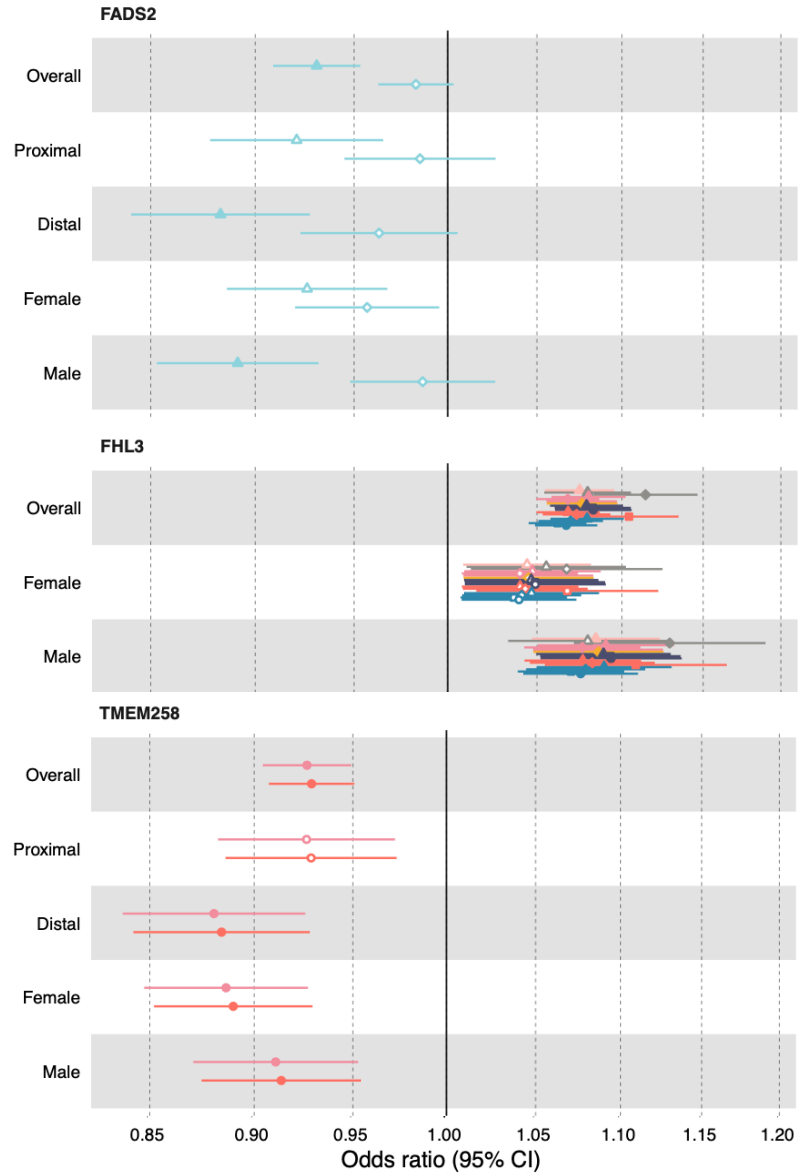
1

Fernandez-Rozadilla et al. (2023)
78,473 CRC cases and 107,143
controls

2

Huyghe et al. (2021) (GECCO)
Site- and sex-specific CRC cases
Proximal, distal, rectal, left-sided,
colon, female, male

Results



timepoint

- ▲ 5d
- ◆ 40h
- 16h
- ▼ Lowly active
- 0h

exposure

- TN_IFN
- TN_HSP
- TN_cycling
- TN
- TM_ER-stress
- TEMRA
- TEM
- TCM
- CD4_Naive
- CD4_Memory

FDR-P

- < 0.05
- > 0.05

Results are given for every SD increase in expression of a gene in activated CD4+T cells at a specific activation timepoint.

TMEM258

- Located in endoplasmic reticulum (ER)
- Part of the OST complex
- Involved in N-linked glycosylation

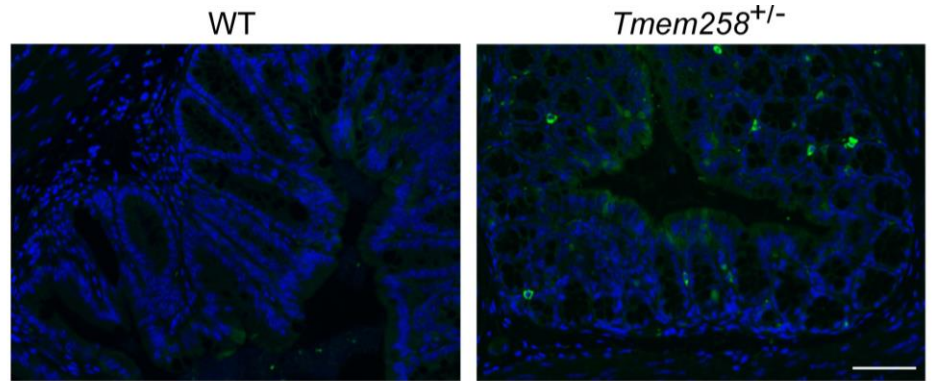
OST = oligosaccharyltransferase

TMEM258

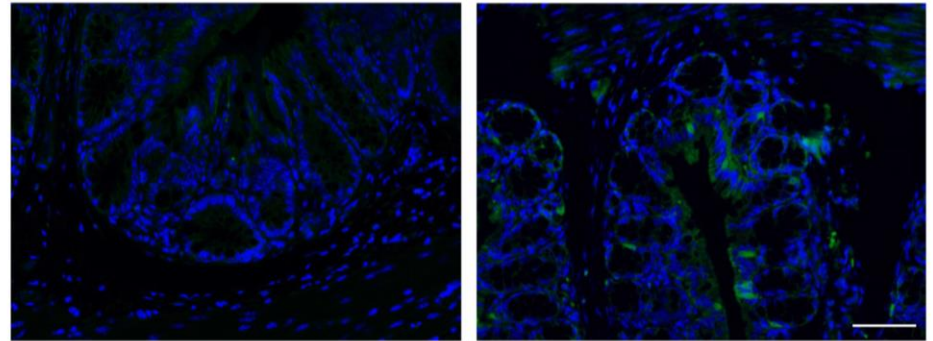
- Located in endoplasmic reticulum (ER)
 - Part of the OST complex
 - Involved in N-linked glycosylation
-
- Increased *TMEM258* expression in inflammatory bowel disease
 - Mouse model: *TMEM258*^{+/-} greater intestinal inflammation
 - Hypothesis: differential *TMEM258* expression may alter OST complex stoichiometry and impair its catalytic assembly / activity

Graham et al. (2016)

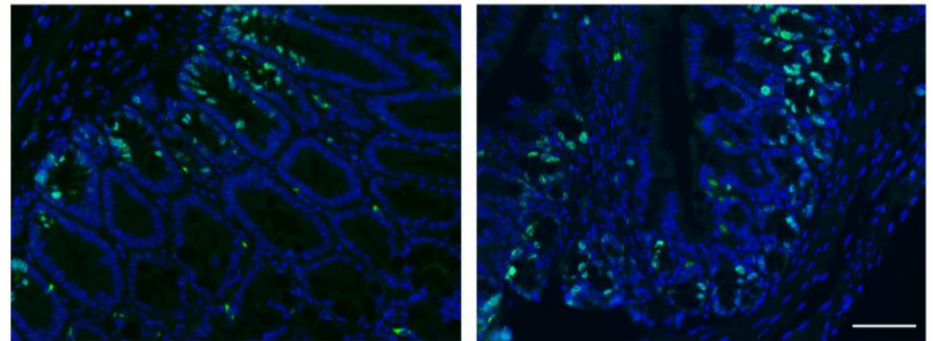
OST = oligosaccharyltransferase



ER stress: BiP, DAPI



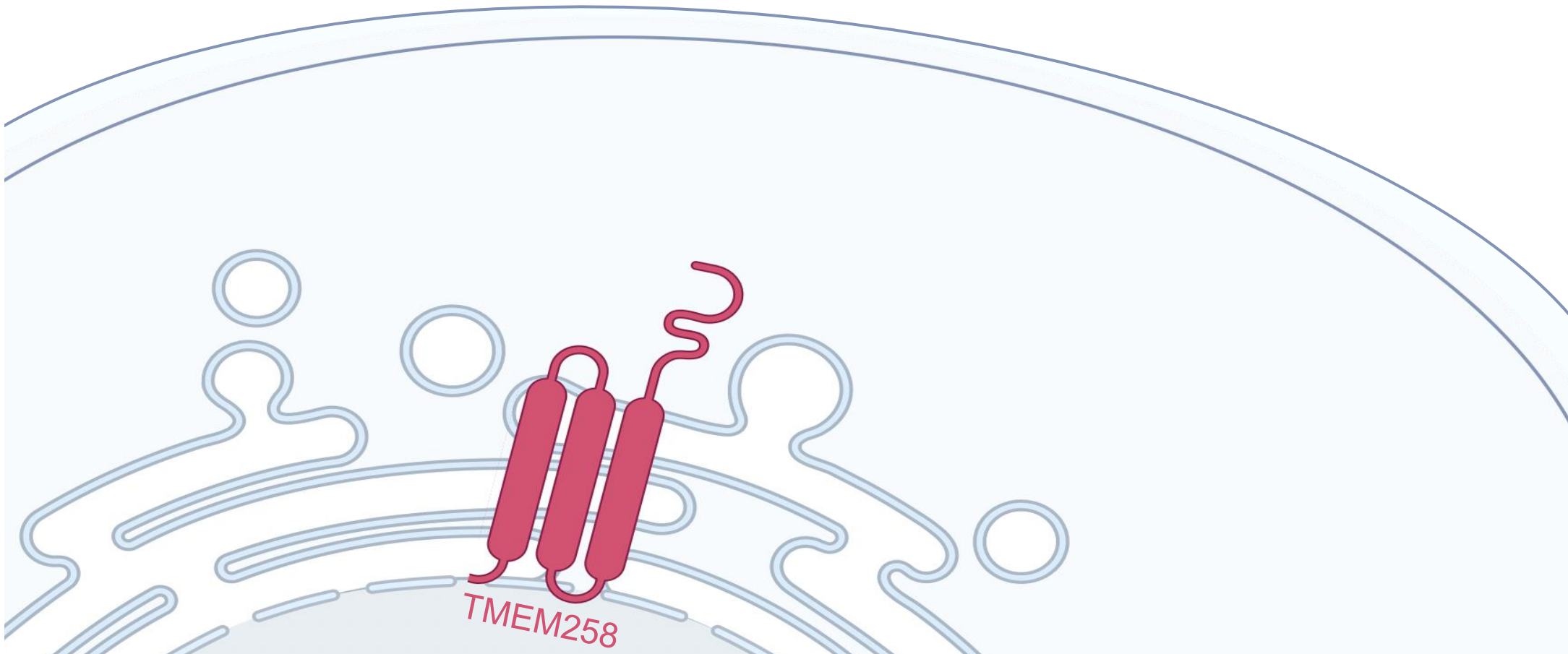
Apoptosis: active caspase 3, DAPI



Proliferation: Ki67, DAPI

***TMEM258* - ?**

Results: increased *TMEM258* expression in CD4 naïve cells at 0h is protective of CRC development



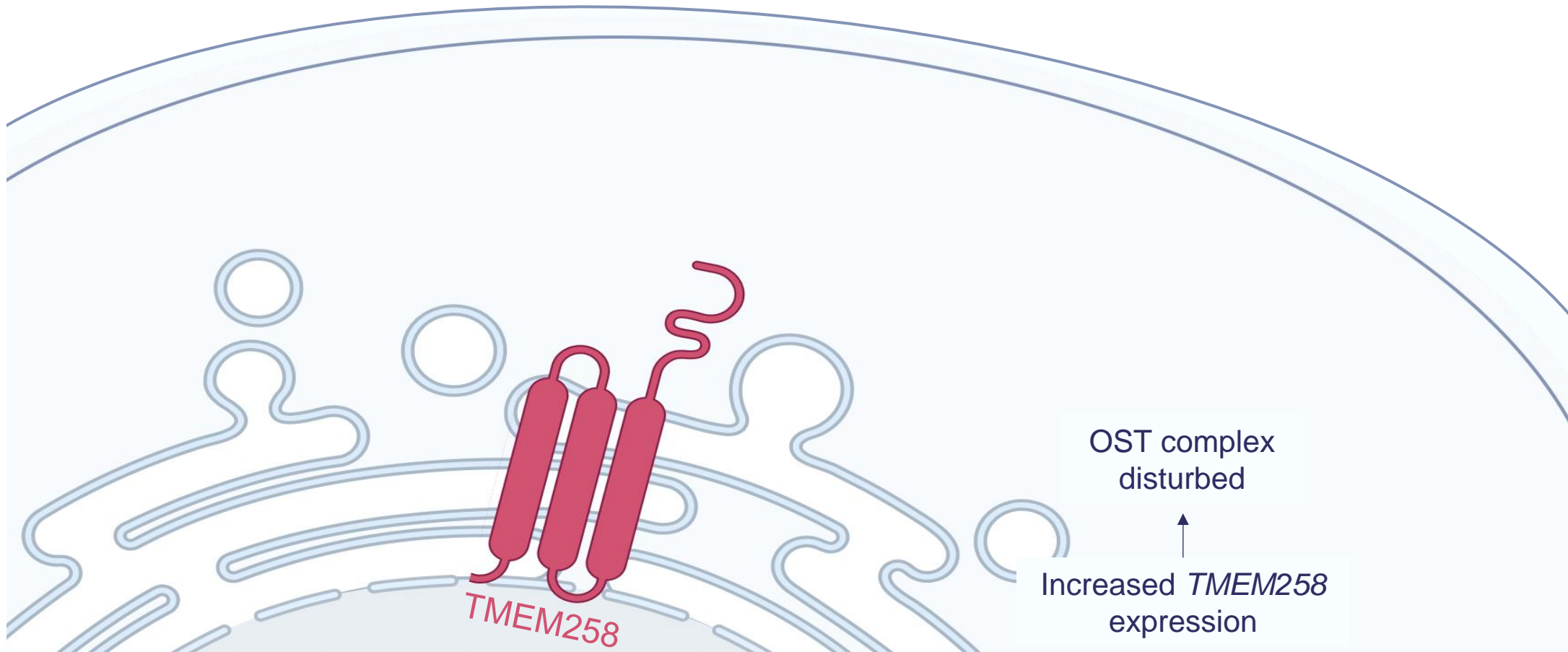
TMEM258 - ?

Results: increased *TMEM258* expression in CD4 naïve cells at 0h is protective of CRC development



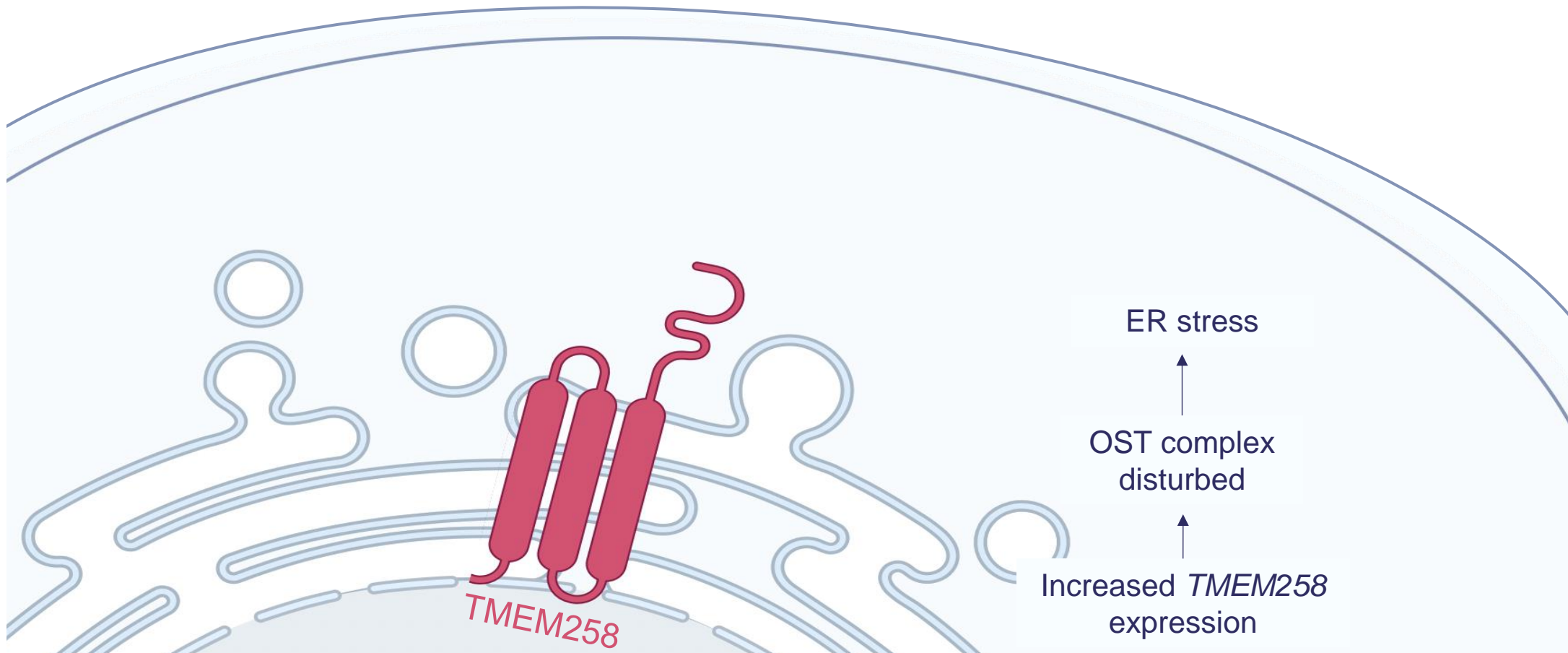
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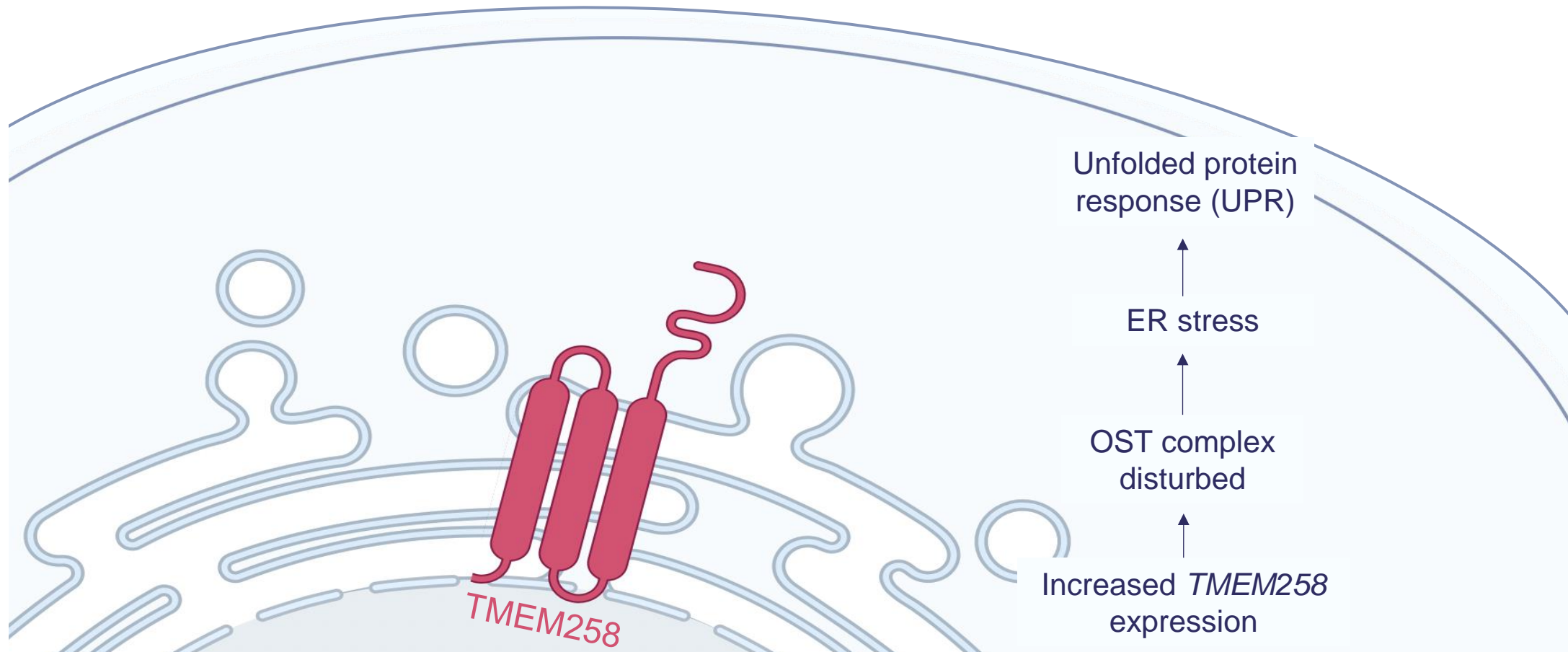
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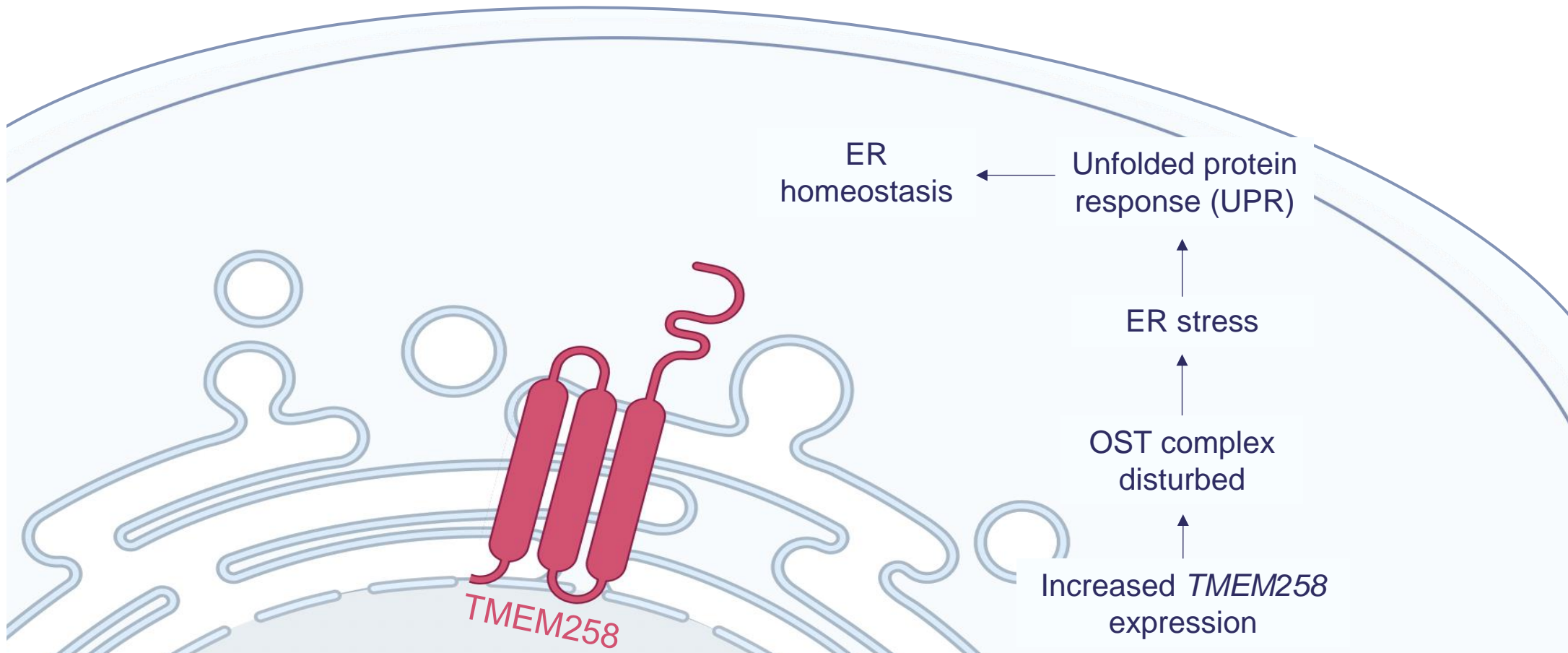
TMEM258 - ?

Results: increased *TMEM258* expression in CD4 naïve cells at 0h is protective of CRC development



TMEM258 - ?

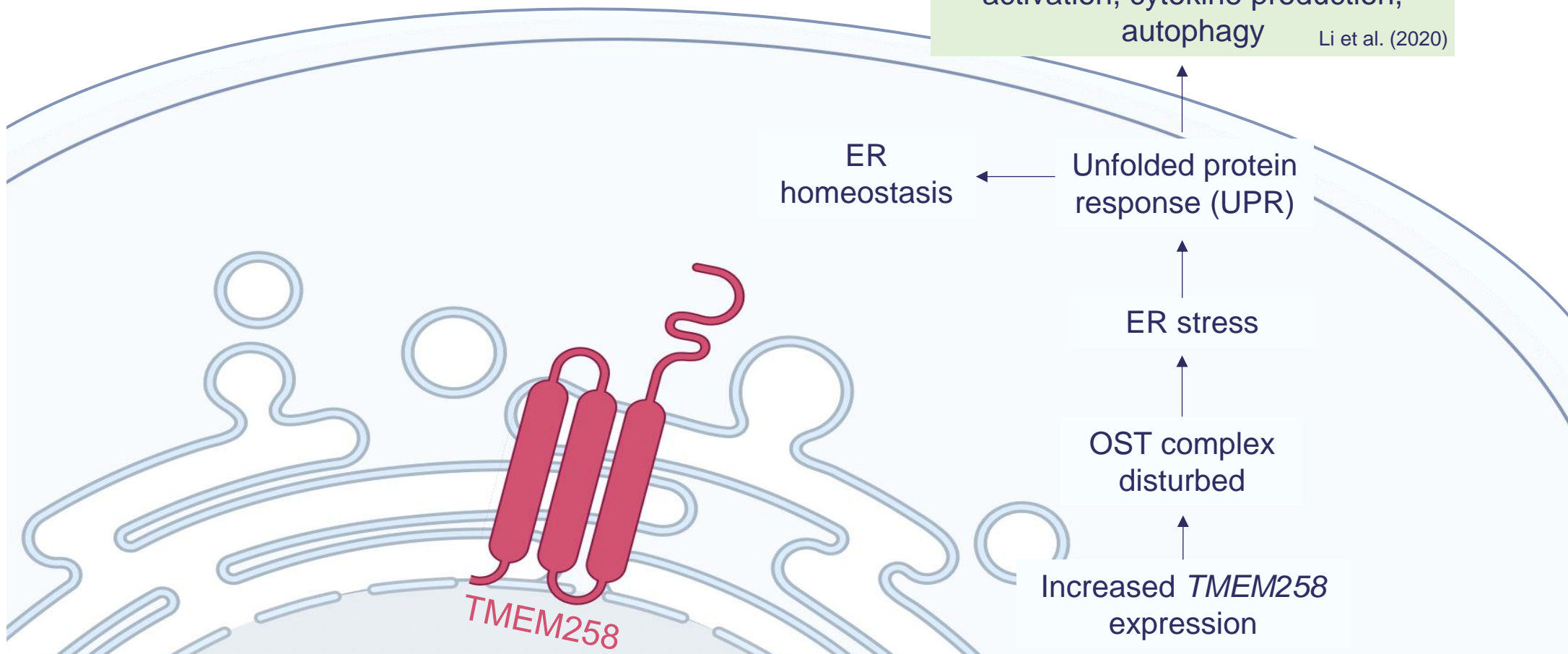
Results: increased *TMEM258* expression in CD4 naïve cells at 0h is protective of CRC development



TMEM258 - ?

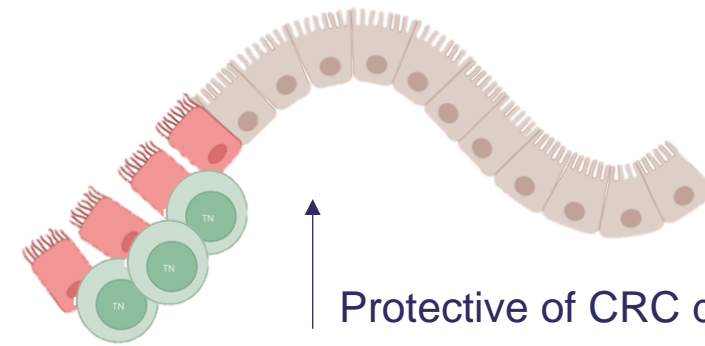
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Naïve CD4+T cells: differentiation, activation, cytokine production, autophagy Li et al. (2020)

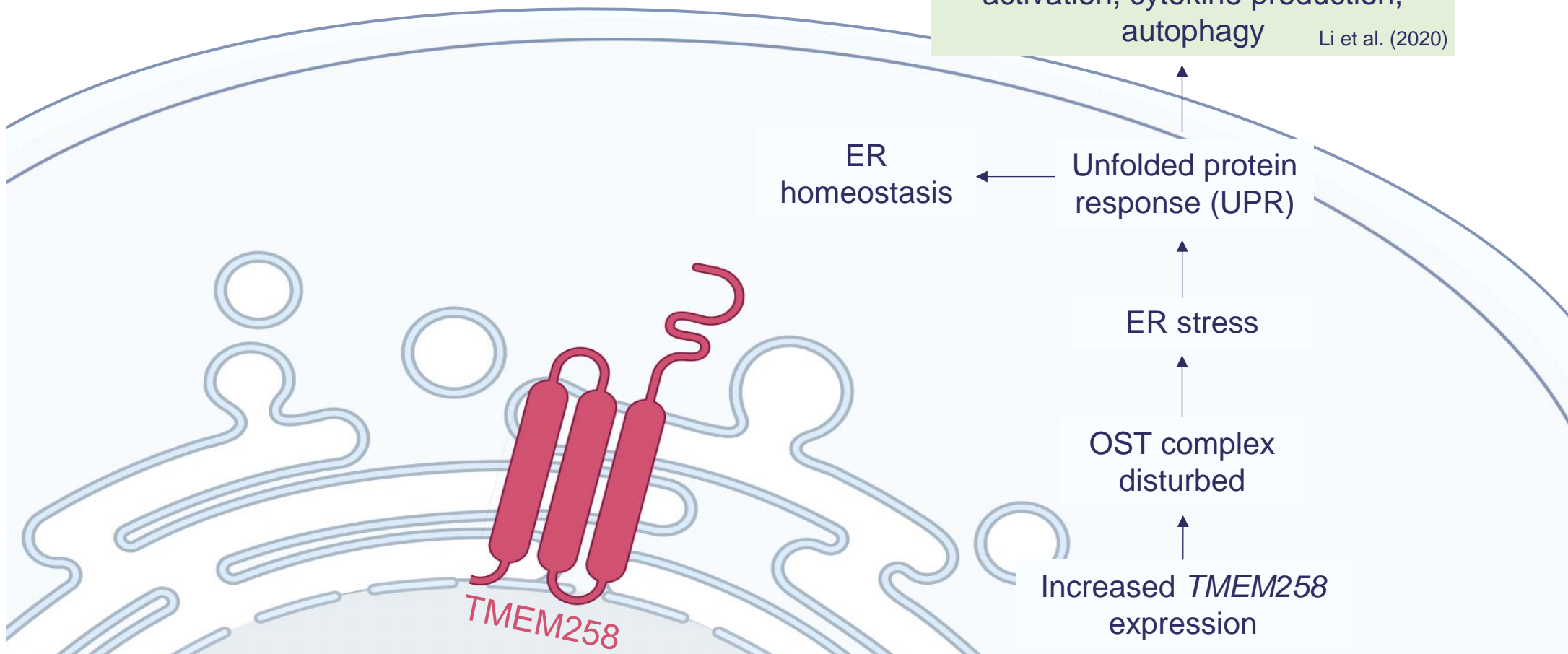


TMEM258 - ?

Results: increased *TMEM258* expression in CD4 naïve cells at 0h is protective of CRC development



Naïve CD4+T cells: differentiation, activation, cytokine production, autophagy
Li et al. (2020)



Summary

- **6 genes** with strong evidence with a potential causal role in CRC development.
- Observed differences across different CD4+T cell subtypes, activation timepoints, CRC subsites and sex.
- Demonstrate importance of capturing the **dynamic nature** of CD4+T cells in understanding CRC risk and prevention.

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MRC Integrative
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Unit

