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# A short overview of gut microbiome studies in SCAPIS enabled by the Bianca compute cluster

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# Human microbiome

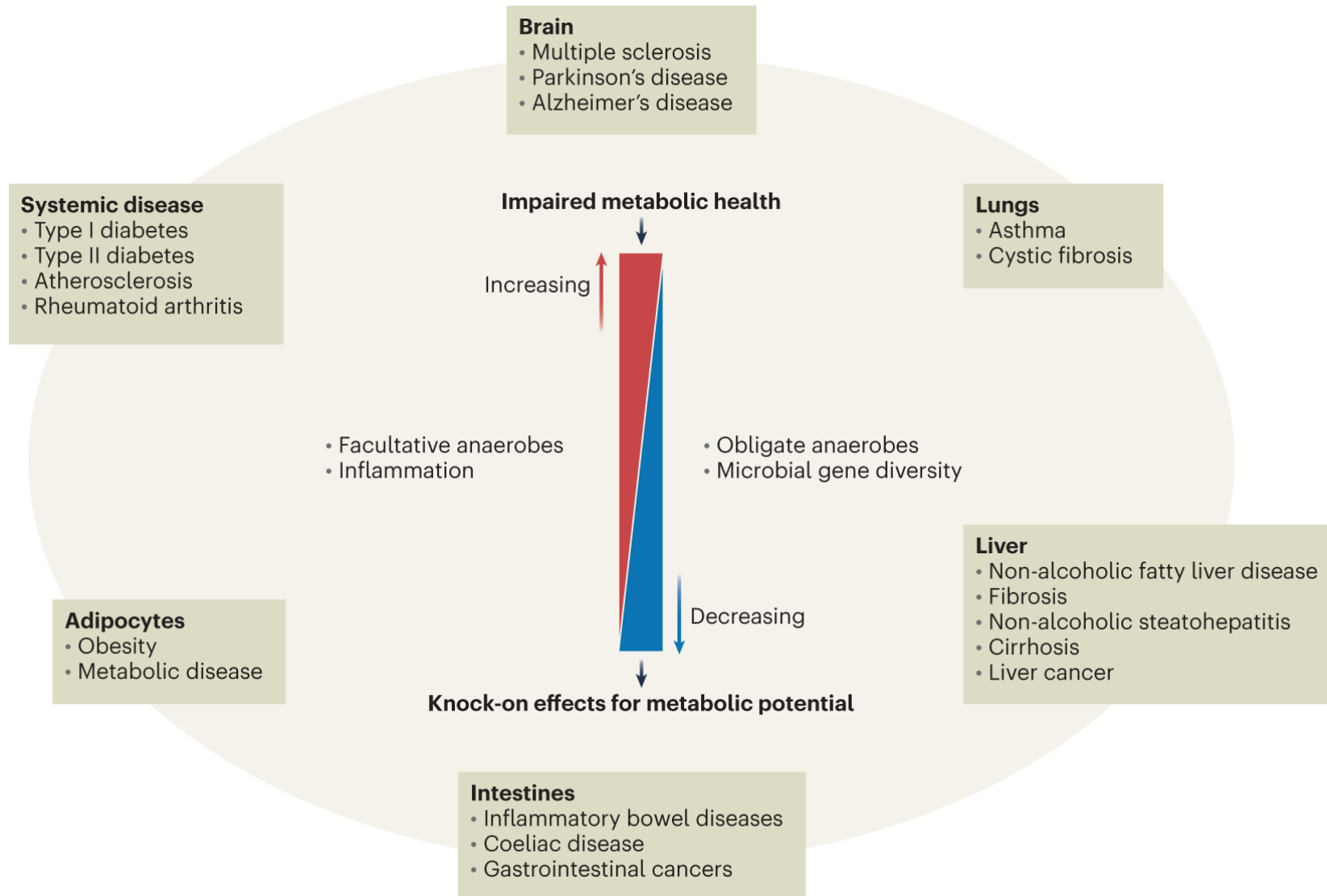
- Human microbiota: microbes that live on or inside the human body
- Human microbiome: the collection of genomes and genes of human microbiota
- Most human microbiota live in the gut



# Gut microbiome

- digesting food
- regulating gut endocrine function and neurological signaling
- modifying drug action and metabolism
- eliminating toxins
- training of host immunity
- producing numerous other compounds that influence the host





# The GUTSY Atlas

Associations between gut microbiota and plasma metabolites in the SCAPIS study



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# Gut microbiome

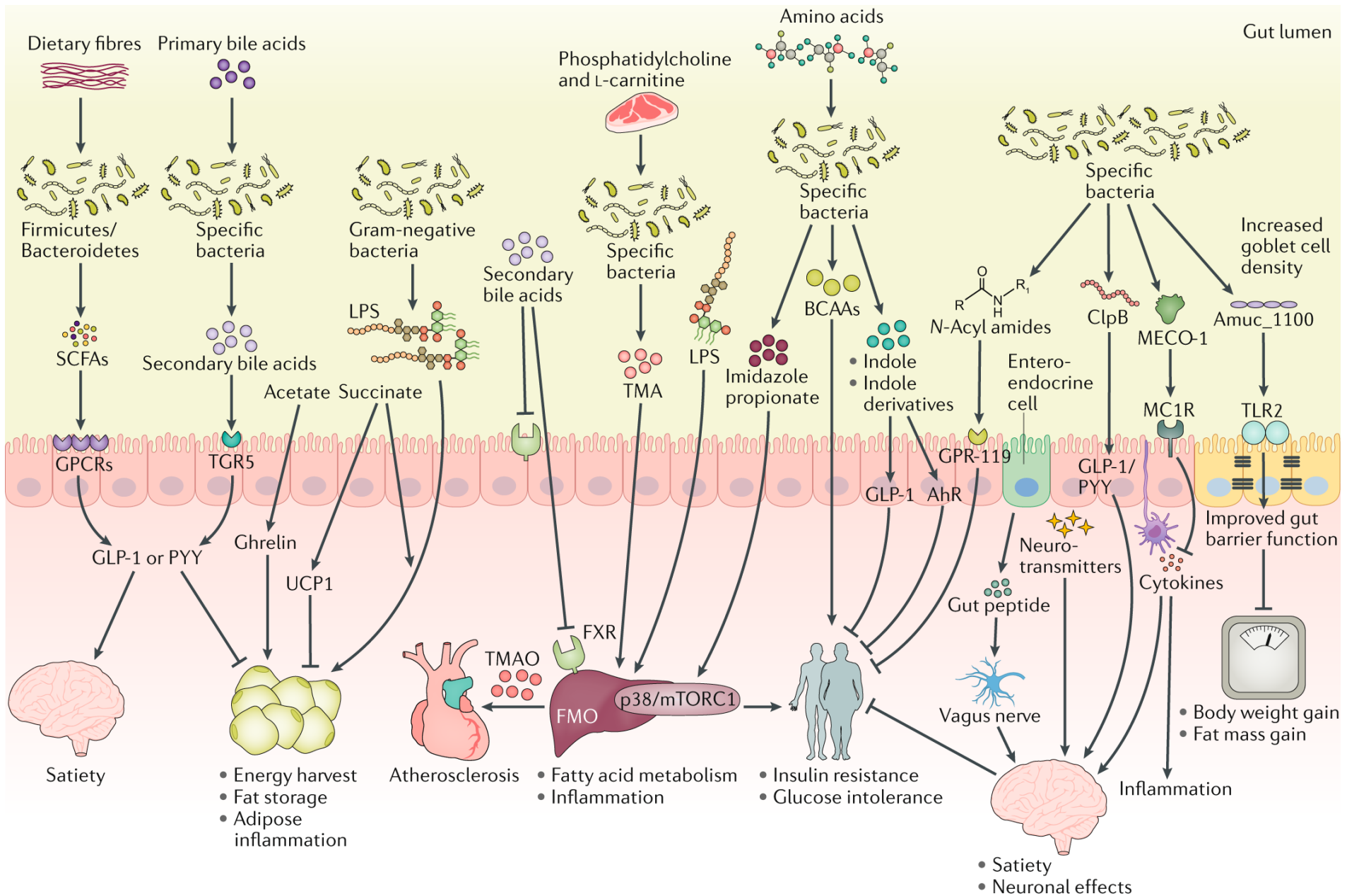
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**metabolites**



# Gut microbiota and metabolites

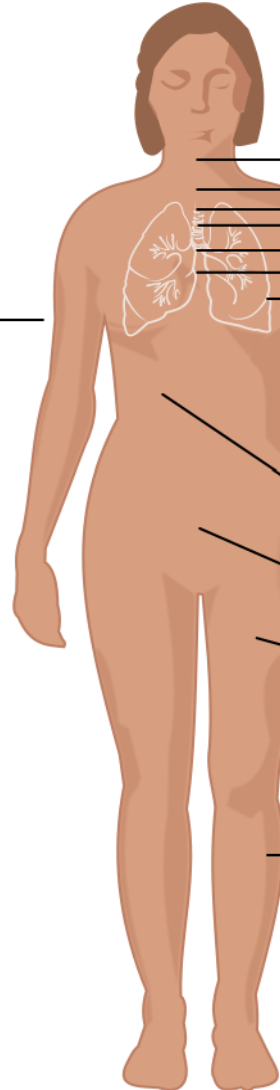




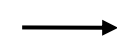


# SCAPIS

n = 30,154



- Carotid arteries (Ultrasound, MRI)
- Ascending aorta (CCTA)
- Epicardial fat (CT)
- Coronary artery calcification score (CT)
- Coronary plaques (CCTA)
- ECG
- Lungs (CT, spirometry)
- Blood pressure
- Liver steatosis (CT)
- Fat depots, subcutaneous/visceral (CT)
- Intra-muscular fat (CT)
- Ankle brachial index
- Questionnaires
- Blood chemistry (lipid profile, HbA1c, plasma glucose, hsCRP, creatine)
- Biobanking
- Site-specific investigations



Genetics  
Proteomics  
Metabolomics  
etc.



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Umeå **Uppsala** Stockholm Gothenburg Linköping **Malmö**

- 8583 men and women (50 – 64 years)

- Gut microbiome
  - 1528 species

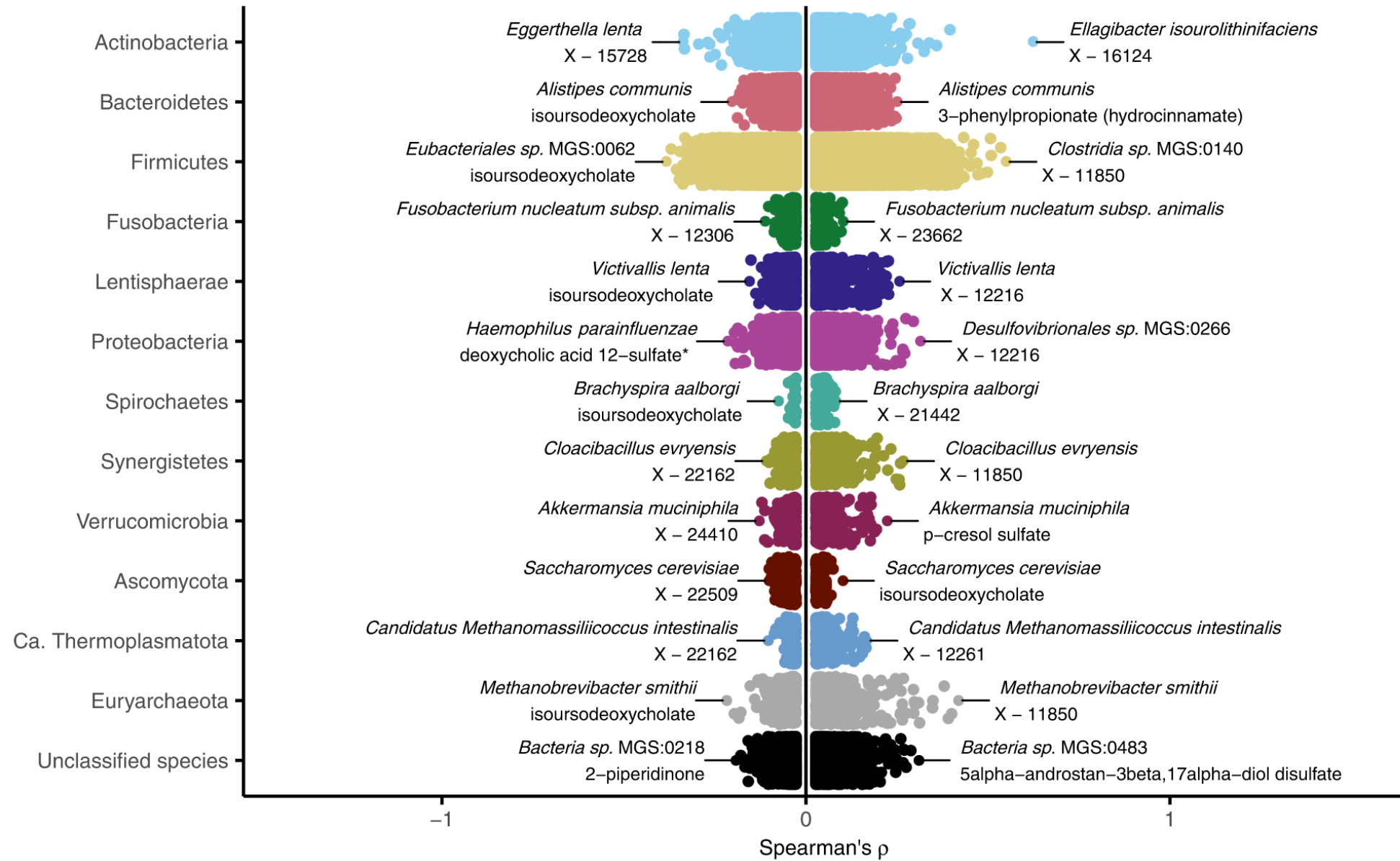


- Plasma metabolomics
  - 1321 metabolites



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# 546,819 associations between gut microbiota and plasma metabolites



<https://gutsyatlas.serve.scilifelab.se/>



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This page contains summary statistics for an individual metagenomic species or metabolite. A metagenomic species or metabolite is first selected from the drop down menu. Metabolites follow the last metagenomic species *Weissella confusa* MGS:1557 in the drop down menu. Various tables are generated. The search function will become activated once a metagenomic species or metabolite has been selected.

Depending on whether you choose a metabolite or a metagenomic species, the table for annotations for one or the other appears.

metformin

Show 10 entries

Search:

Supplementary Table 6. Associations between gut microbial species and plasma metabolites. Partial Spearman's rank correlations were calculated for 1,528 species and 1,321 metabolites, adjusting for age, sex, place of birth, study site, microbial DNA extraction plate and metabolomics delivery batch. Shown are the significant associations after adjusting for multiple testing using the Benjamini-Hochberg method at 5% FDR (q-value < 0.05). Columns with "+Shannon" are additionally adjusted for Shannon diversity index. Each species name is followed by an internal species identifier (MGS). Specific considerations: \* and \*\* denotes metabolites annotated without an internal standard.

Metagenomic species	Metabolite	Spearman's rho	t	p-value	q-value	Spearman's rho (+Shannon)	t (+Shannon)	p-value (+Shannon)	n
<i>Romboutsia timonensis</i> MGS:0053	metformin	-0.19	-17.3	1.07e-65	4.54e-63	-0.18	-16.5	1.98e-60	8583
<i>Escherichia marmotae</i> MGS:1282	metformin	0.17	15.6	4.57e-54	1.33e-51	0.16	15.2	9.05e-52	8583
<i>Escherichia coli</i> MGS:0195	metformin	0.16	14.6	2.09e-47	4.79e-45	0.15	14.3	6.73e-46	8583
<i>Intestinibacter</i> sp. MGS:0194	metformin	-0.12	-11.5	1.73e-30	1.90e-28	-0.11	-10.6	5.51e-26	8583
<i>Intestinibacter bartlettii</i> MGS:0115	metformin	-0.12	-11	4.77e-28	4.54e-26	-0.12	-11.3	1.89e-29	8583
<i>Clostridiaceae</i> sp. MGS:0238	metformin	-0.12	-10.8	4.63e-27	4.16e-25	-0.1	-9.2	4.09e-20	8583
<i>Peptostreptococcaceae</i> sp. MGS:0200	metformin	-0.11	-10.3	1.07e-24	8.36e-23	-0.1	-9	2.94e-19	8583
<i>Enterocloster clostridioformis</i> MGS:0686	metformin	0.1	9.4	6.57e-21	3.95e-19	0.08	7	3.08e-12	8583
<i>Clostridium disporicum</i> MGS:0222	metformin	-0.1	-9.1	8.24e-20	4.55e-18	-0.09	-8.1	6.50e-16	8583
<i>Enterocloster citroniae</i> MGS:0285	metformin	0.09	8.7	2.83e-18	1.38e-16	0.07	6.3	2.64e-10	8583

Showing 1 to 10 of 1,528 entries



Does your DNA affect what species  
live in your gut?

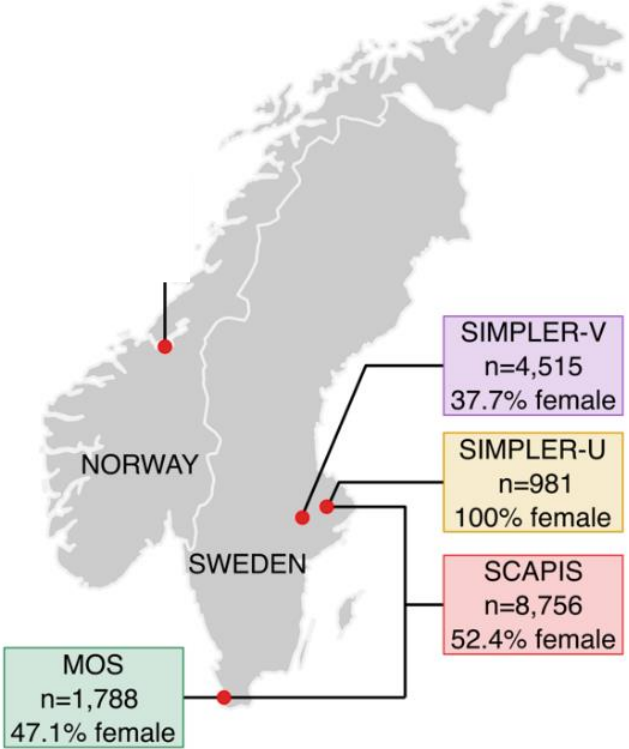
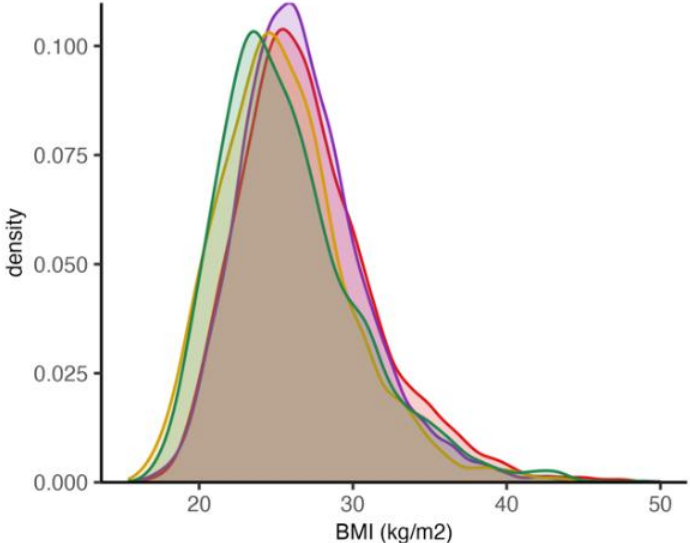
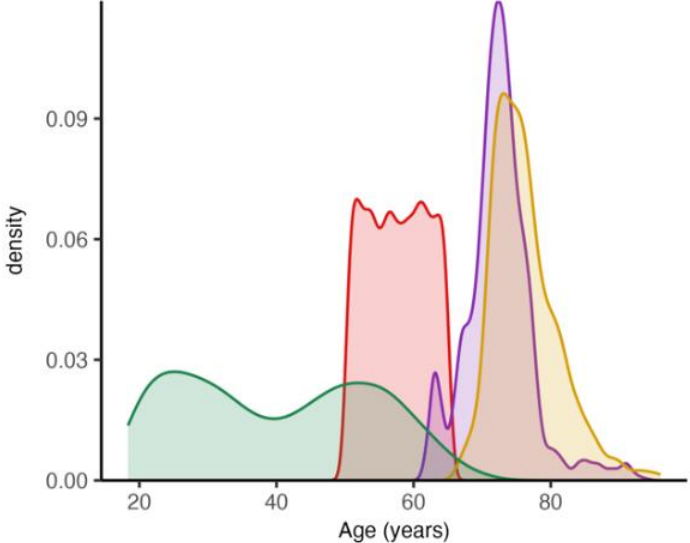


# Why?

- Previous studies only discovered two locations on the human genome
  - *LCT* locus – lactose intolerance
  - *ABO* locus – blood group A, B, AB, O
- Need for larger studies or meta-analysis of harmonized studies with high-resolution data

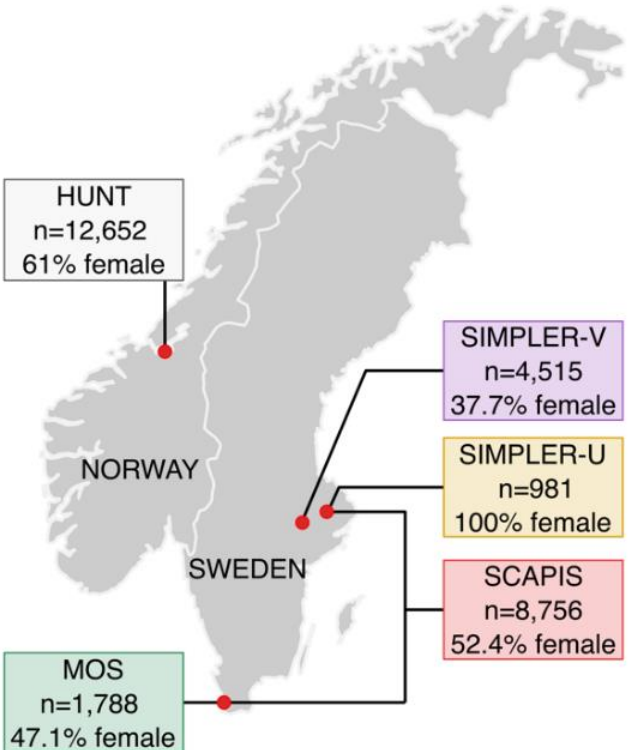
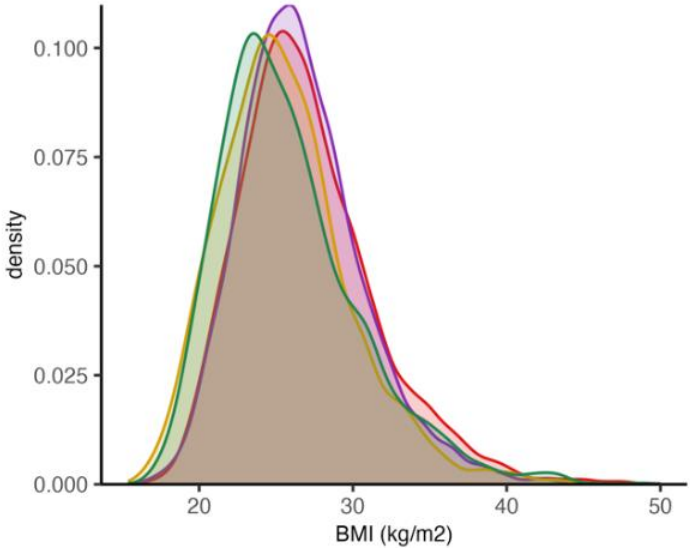
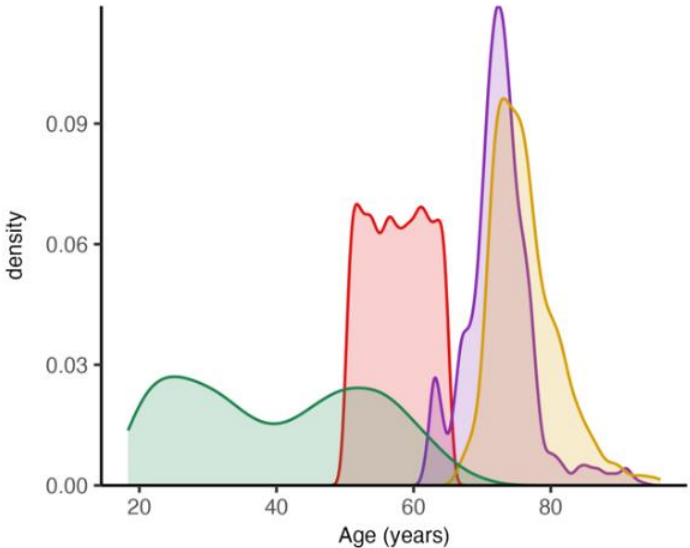


# 16,040 Swedish discovery samples





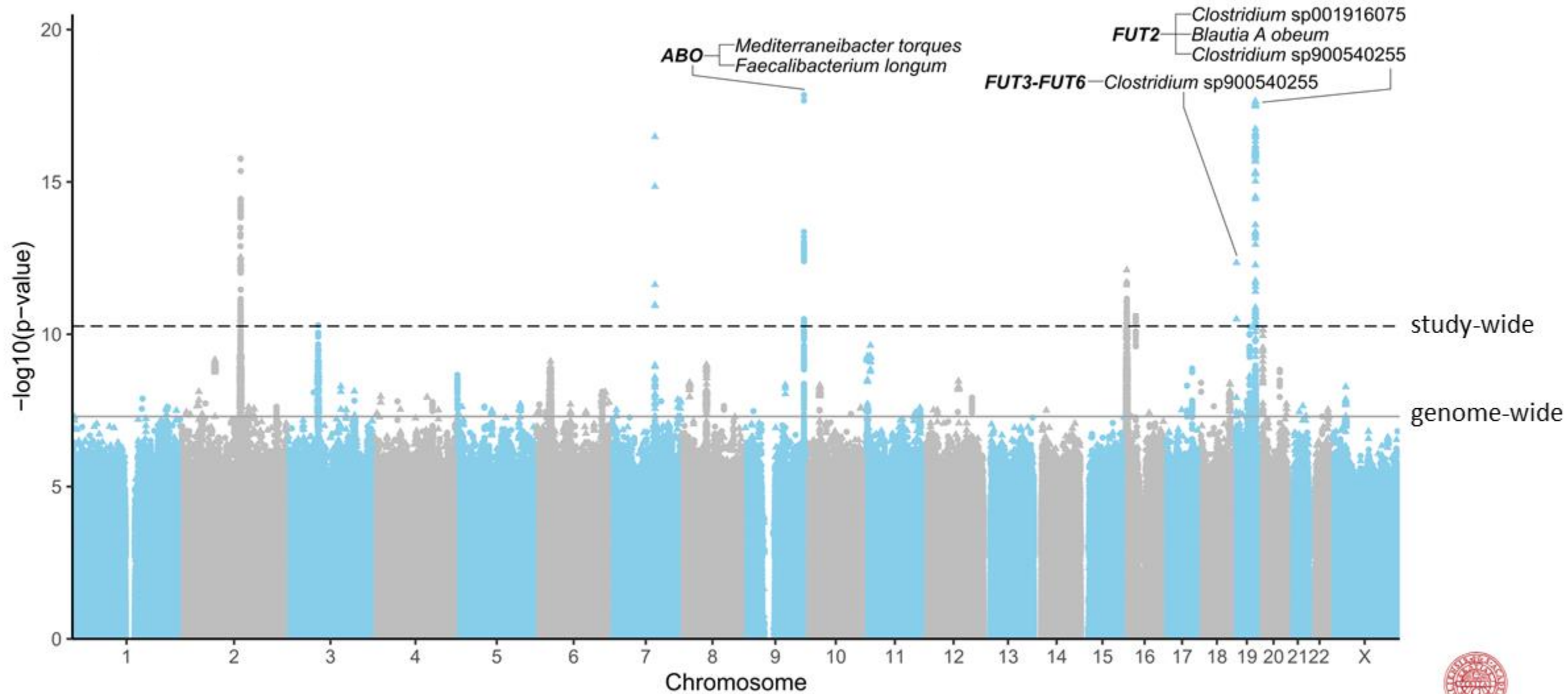
# 12,652 Norwegian replication samples



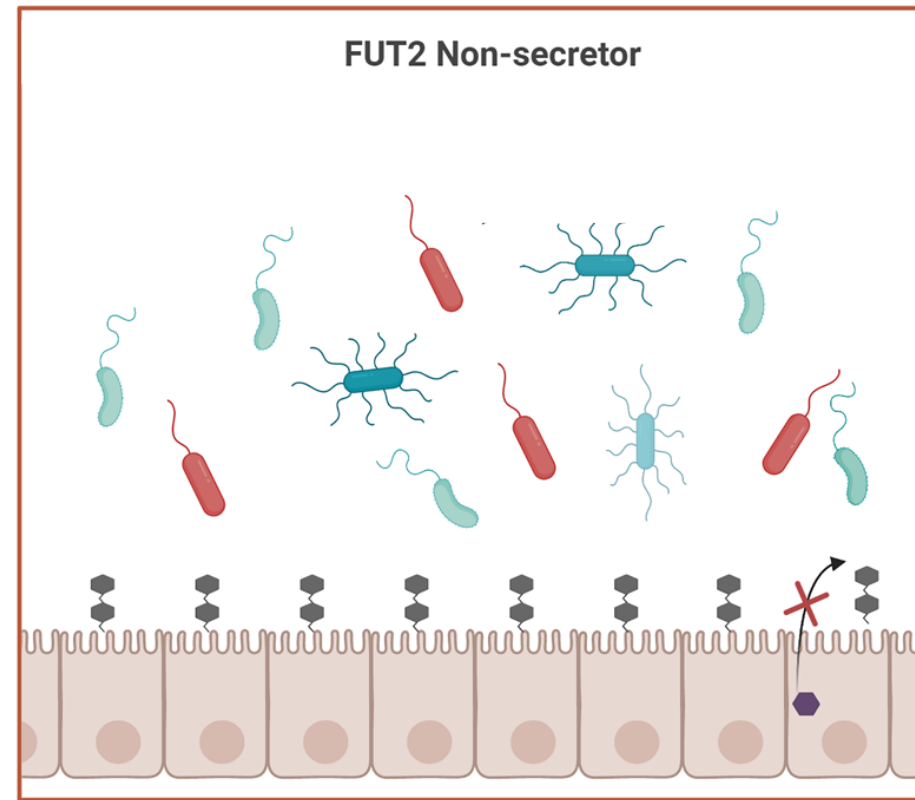
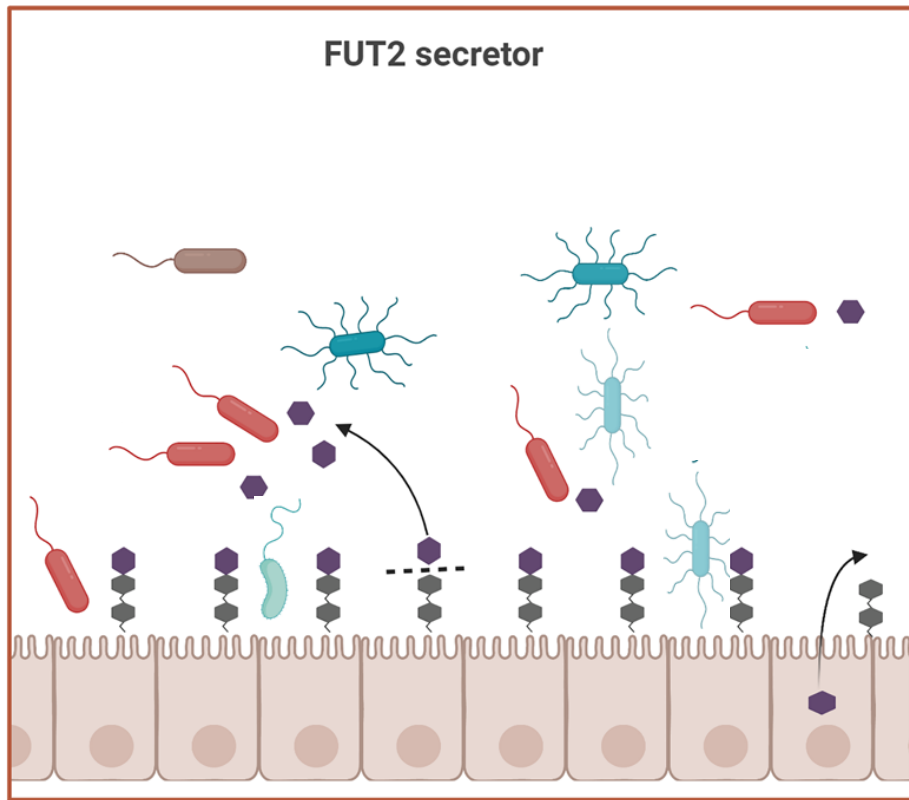
# Your DNA affects what species live in your gut

- 921 microbial species
  - >5 million locations on the human genome
- 14 species affected by your DNA
- 8 genomic locations, including *LCT* and *ABO*

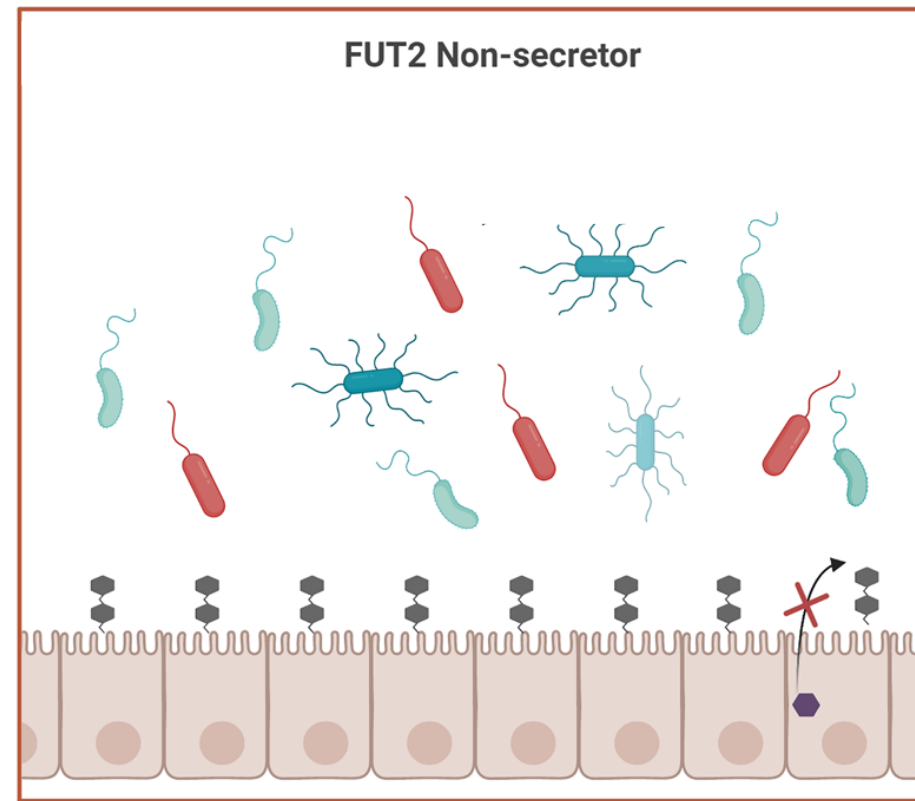
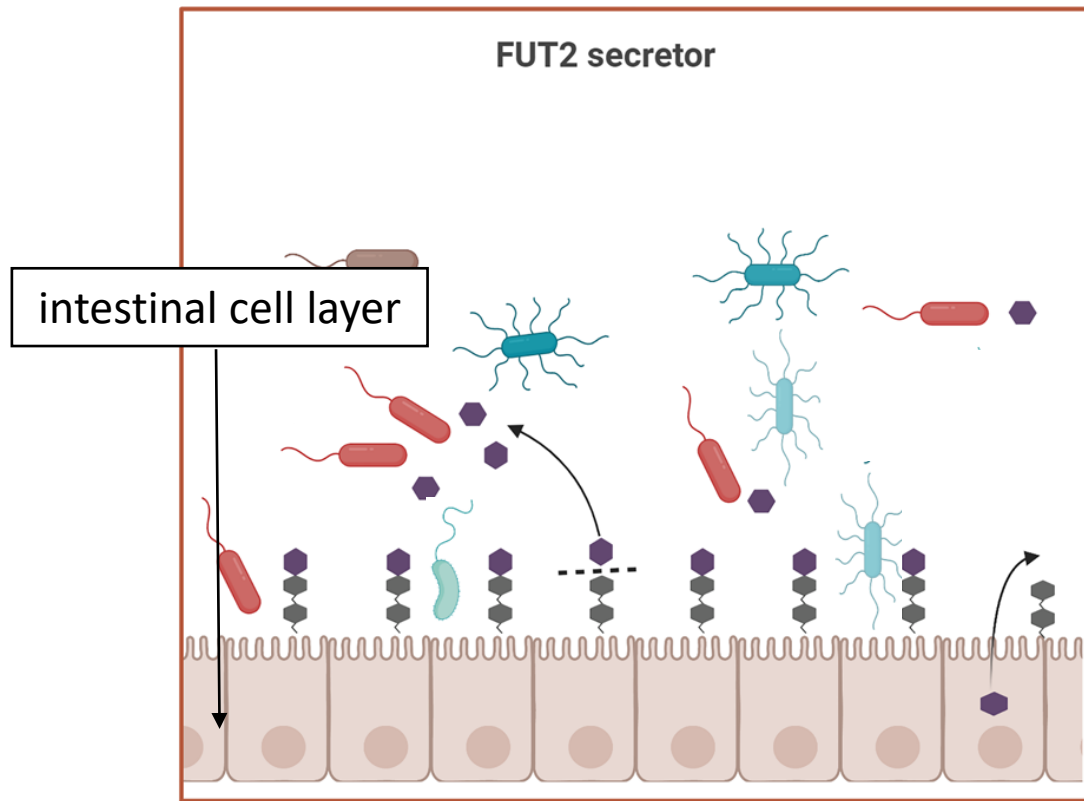




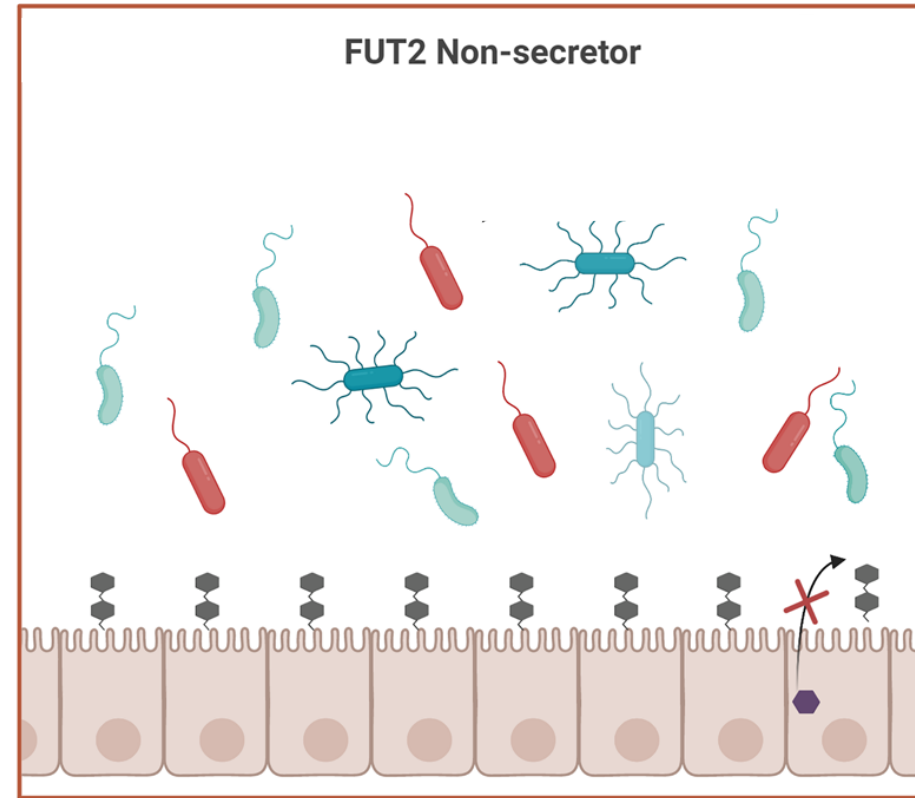
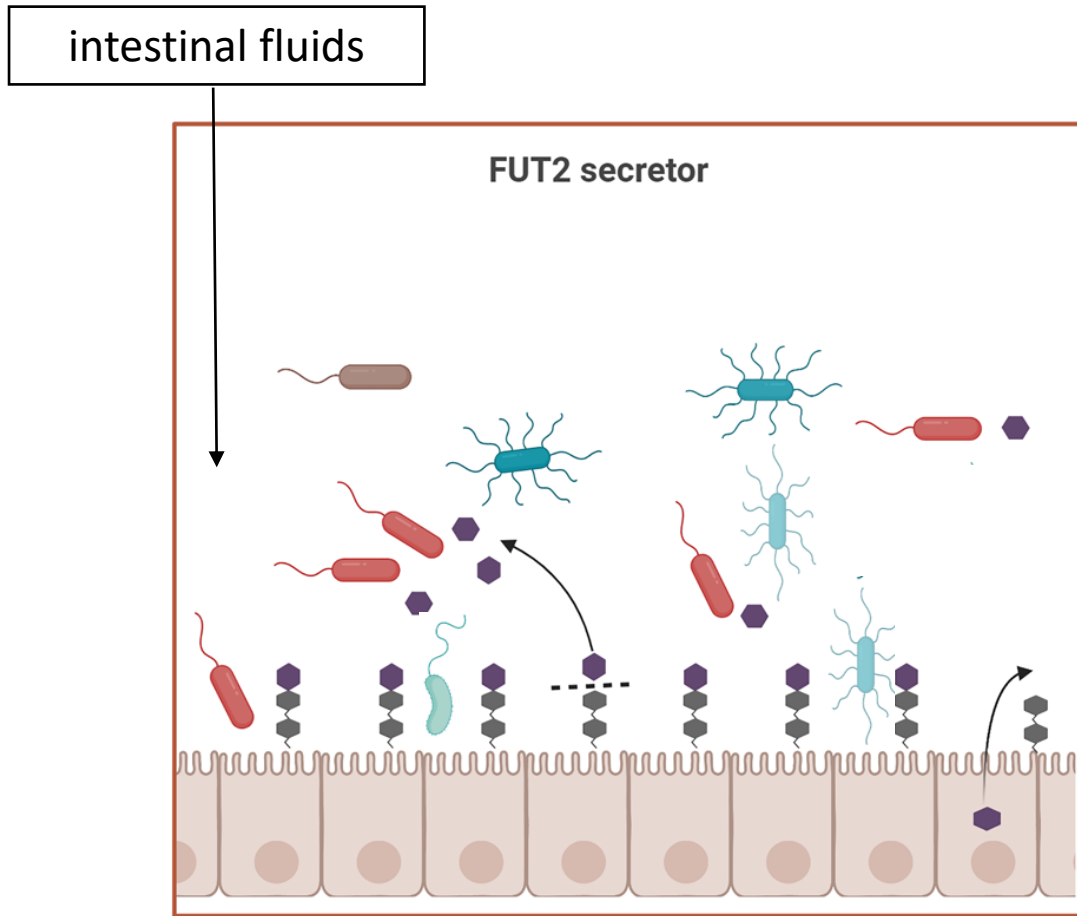
# ABO and *FUT2*



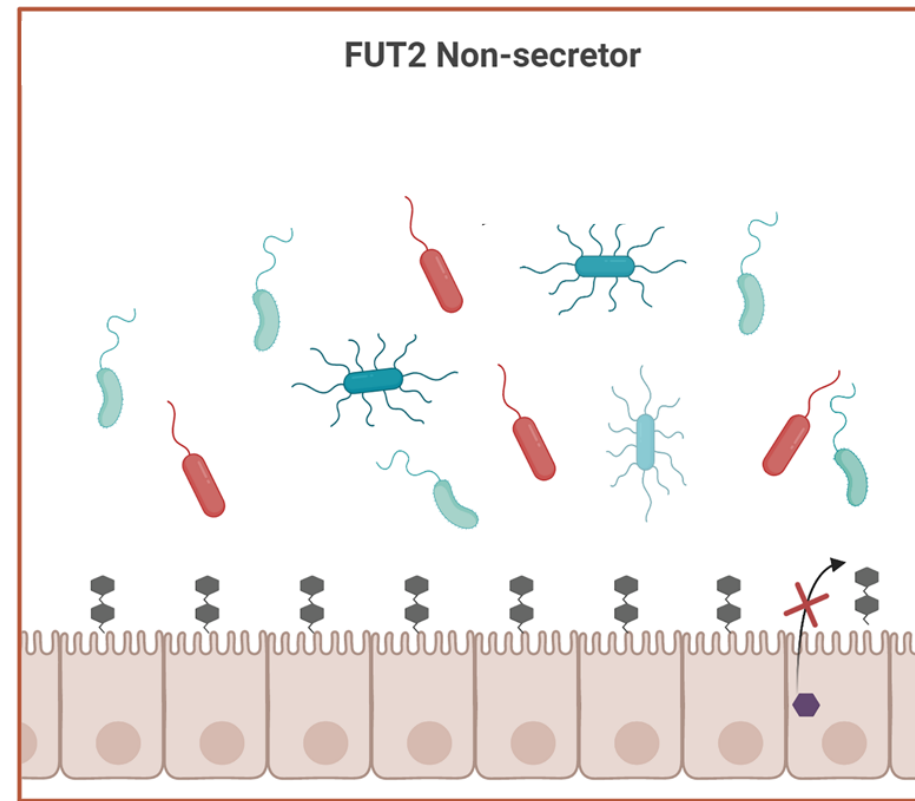
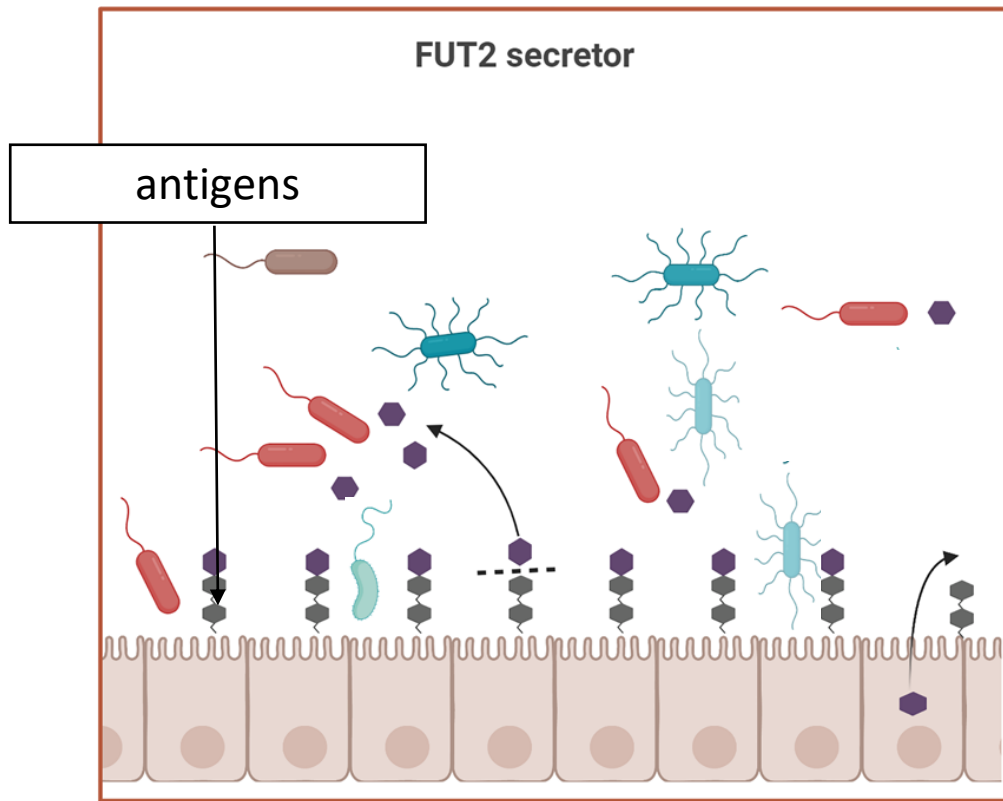
# ABO and *FUT2*



# ABO and *FUT2*

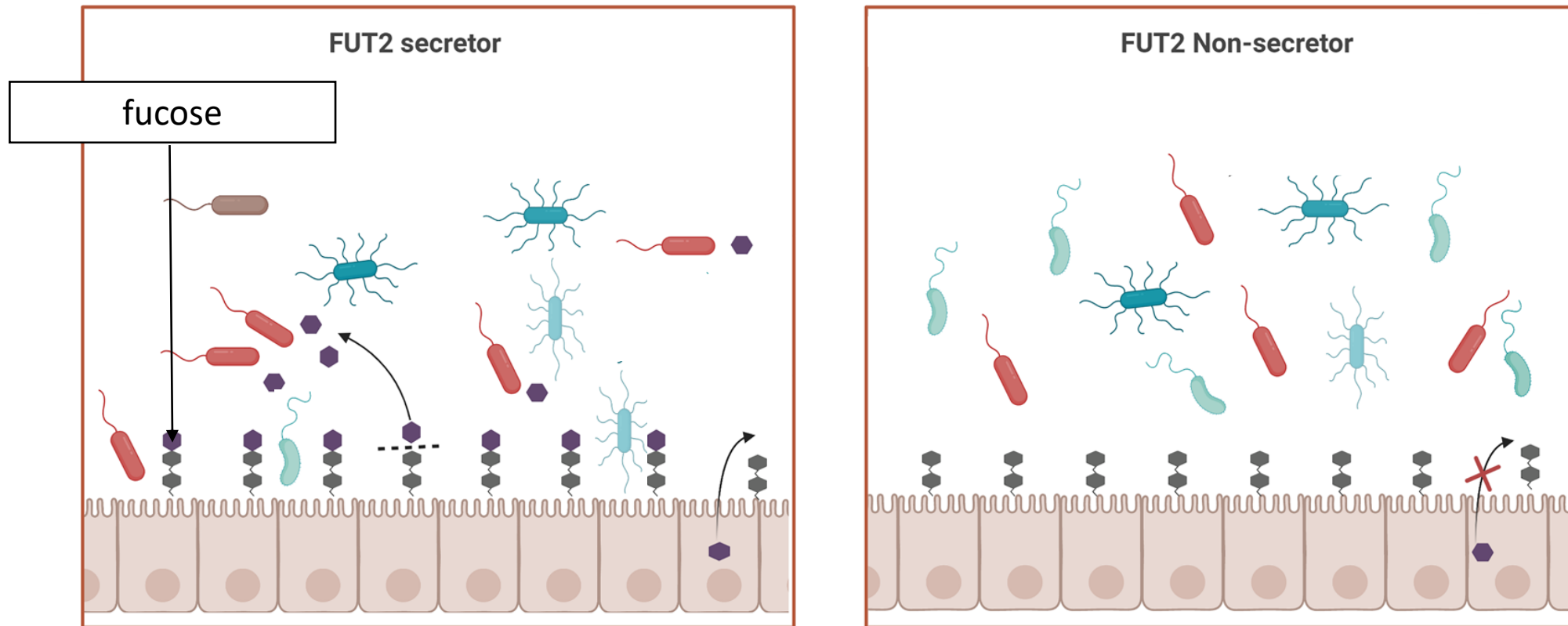


# ABO and *FUT2*



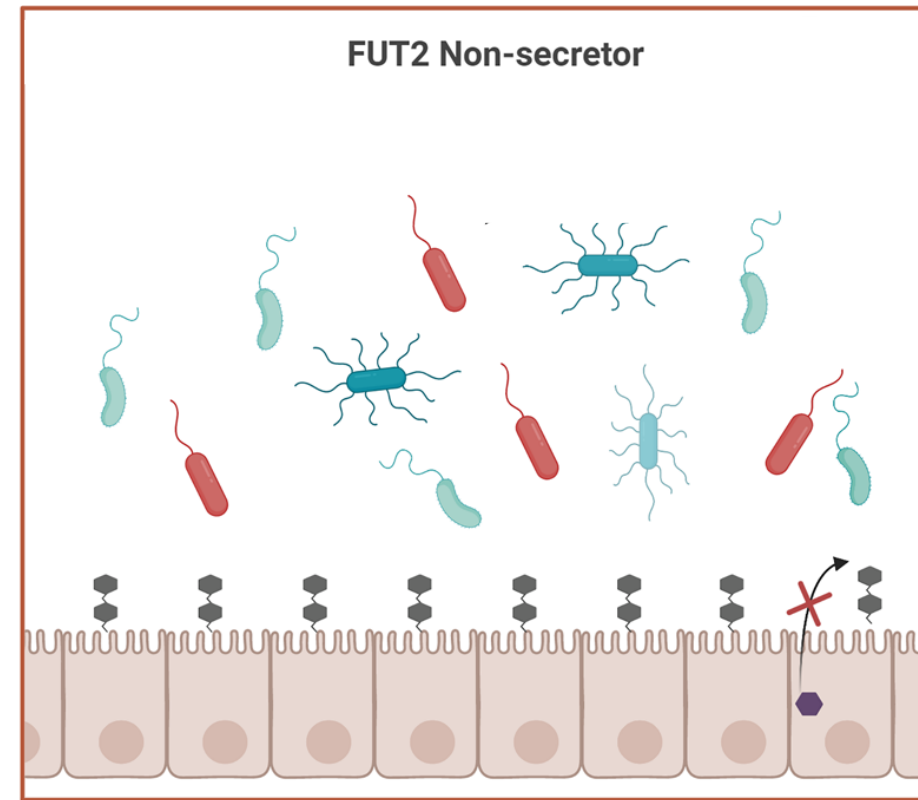
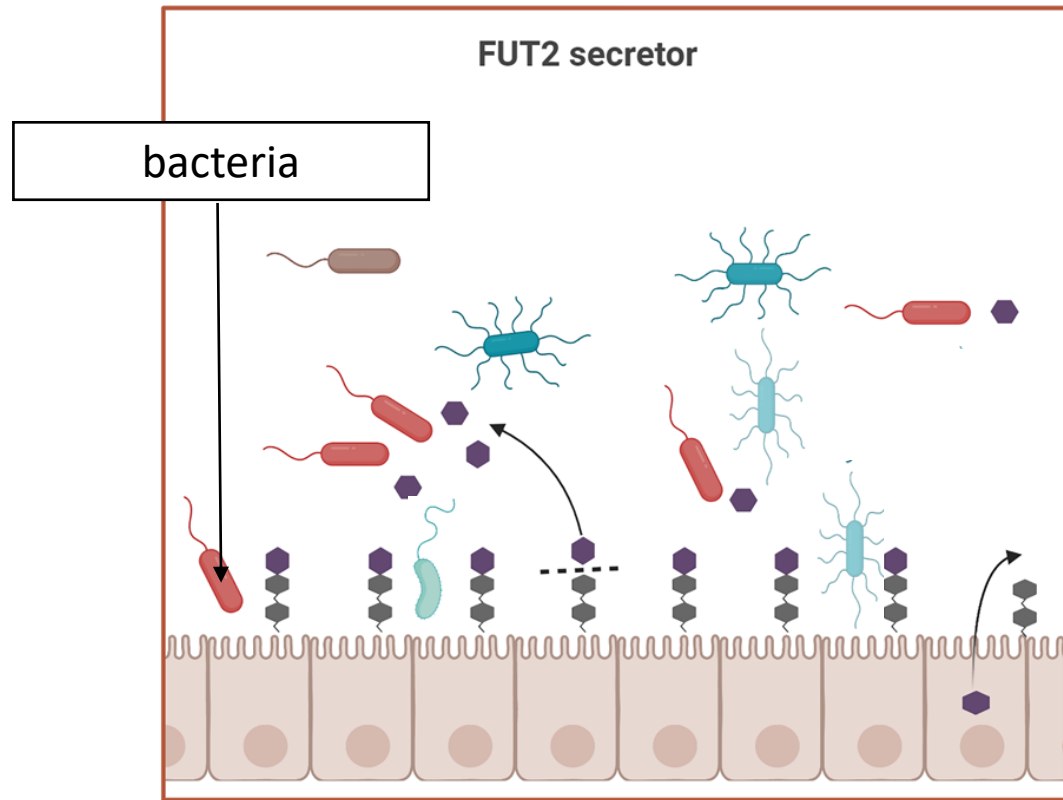
# ABO and *FUT2*

- Variation in DNA of *FUT2* determines secretor status

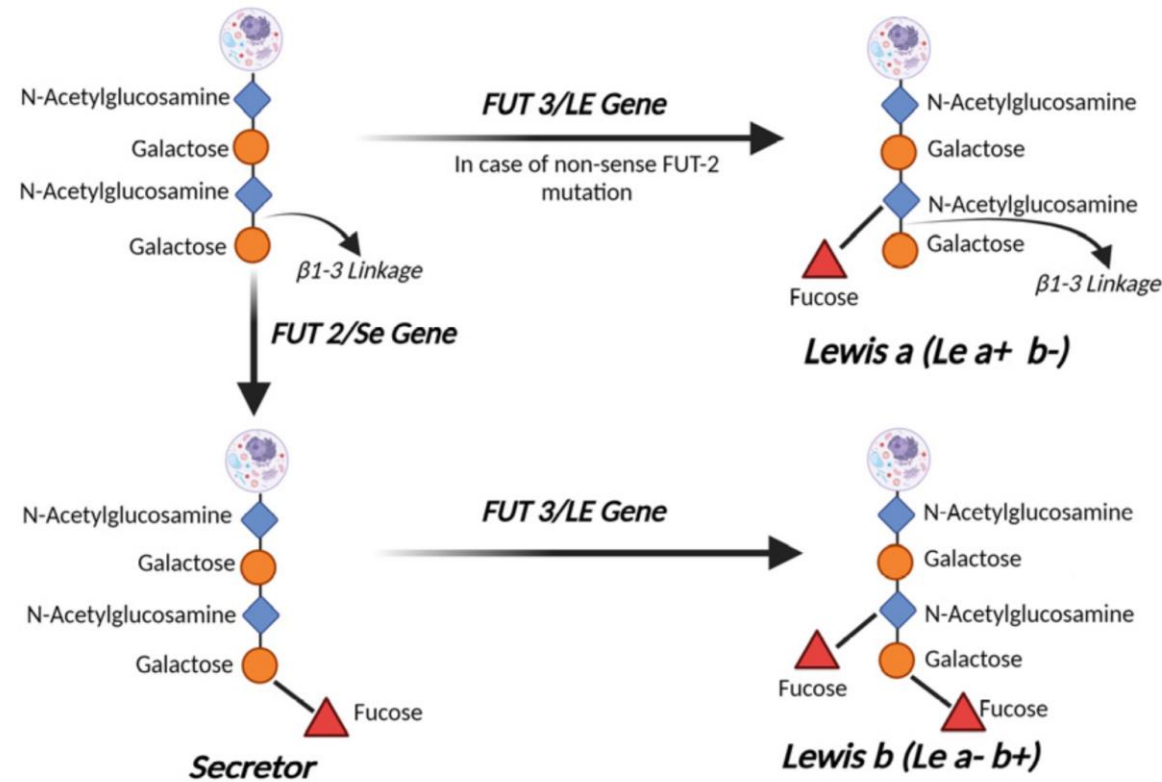




# ABO and *FUT2*

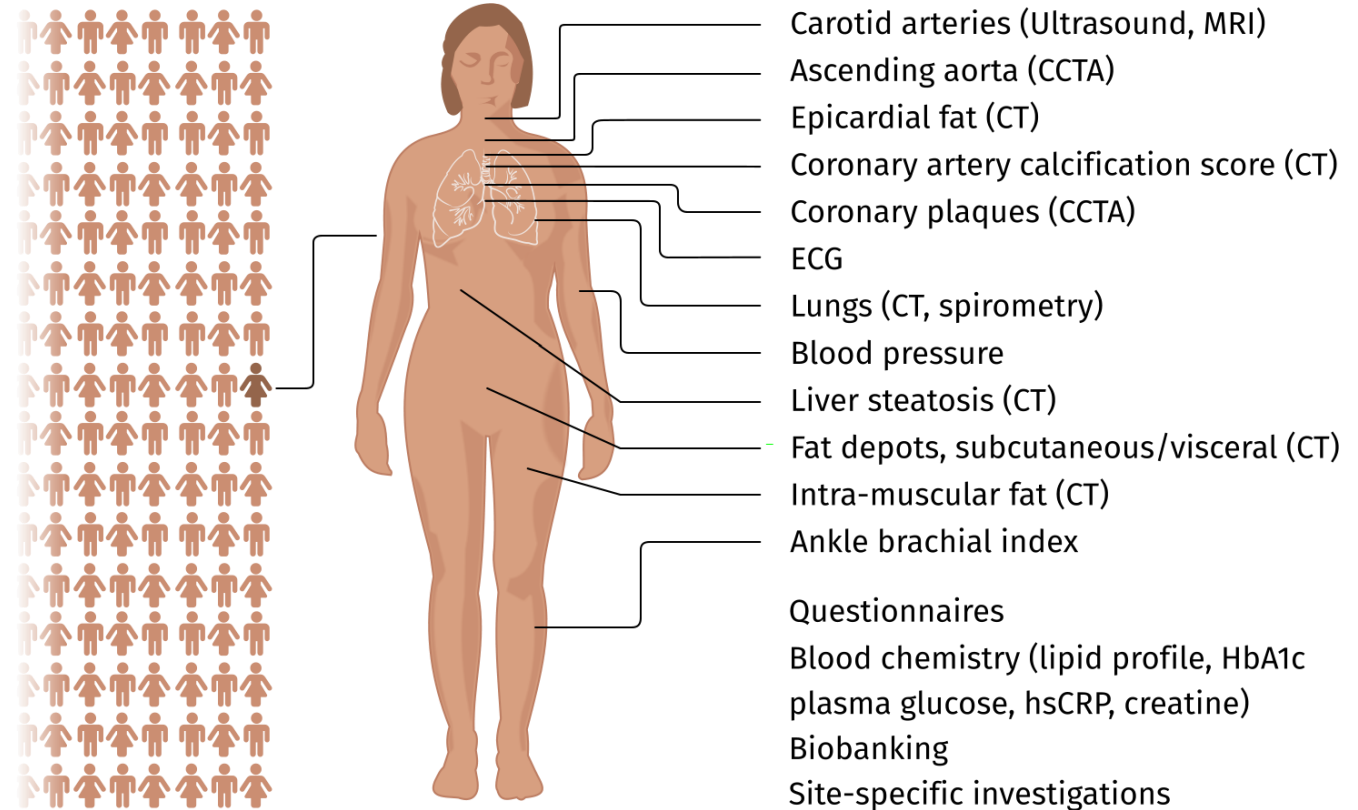


# *FUT2*, *FUT3* and *Clostridium* sp900540255



# Conclusion

- Amazing, but sensitive, data
- Requires a secure environment
- Including storage and compute



# Acknowledgements



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Huvudfinansier av SCAPIS

# SCAPIS

SWEDISH CARDIOPULMONARY BIOIMAGE STUDY



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