

# Investigating insulin resistance in human obesity with transcriptomics

Citation for published version (APA):

Kalafati, M. (2021). *Investigating insulin resistance in human obesity with transcriptomics: towards precision-based strategies*. [Doctoral Thesis, Maastricht University]. Maastricht University.  
<https://doi.org/10.26481/dis.20211112mk>

**Document status and date:**

Published: 01/01/2021

**DOI:**

[10.26481/dis.20211112mk](https://doi.org/10.26481/dis.20211112mk)

**Document Version:**

Publisher's PDF, also known as Version of record

**Please check the document version of this publication:**

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# Investigating insulin resistance in human obesity with transcriptomics: Towards precision-based strategies

by Marianthi Kalafati

1. An increased systemic inflammatory profile is a mechanism linking the increased expression of inflammatory genes in abdominal subcutaneous adipose tissue to muscle insulin resistance. (*Chapter 2*)
2. Adipose tissue insulin resistance and muscle insulin resistance do not always vary concordantly. (*Chapter 3*)
3. The combination of publicly available subcutaneous adipose tissue gene expression datasets with a deconvolution algorithm to calculate subcutaneous adipose tissue cell-type composition demonstrates the hidden strength of reusing publicly available data to gain cell-type specific insights into adipose tissue function. (*Chapter 4*)
4. Adjustment for white blood cell profile in the whole blood, in differential gene expression analyses, adds a layer of information that would otherwise remain elusive and adds substantially to the biological interpretation of the data. (*Chapter 5*)
5. Precision-based strategies have the potential to change the conventional standards of care in human obesity. Nevertheless, parallel efforts from governments, policy makers and food industry are needed to make environments less obesity-promoting and more supportive of healthy eating and physical activity.
6. Network and pathway analysis with transcriptomics data can help elucidate the pathways and mechanisms that are altered in human overweight and obese insulin resistant phenotypes.
7. When we all have data online it will be great for humanity; it is a perquisite to solving many problems that humankind faces. (*Robert Cailliau*)
8. Bioinformatics turns something unfathomable into something we can visualize. (*The Babraham Institute*)
9. I have not failed; I have just found 10,000 ways that won't work. (*Thomas Edison*)
10. In a world where you can be anything, be kind. (*Caroline Flack*)