

Metagenomic Functional Analysis

DO

2024-08-27

Introduction

The idea is to focus on the genes and functional metabolic pathways associated with the use or non-use of antibiotics at two different time points:

Before sampling Within a 60-40 window We are interested in two categorical variables for the comparative analysis of the modules:

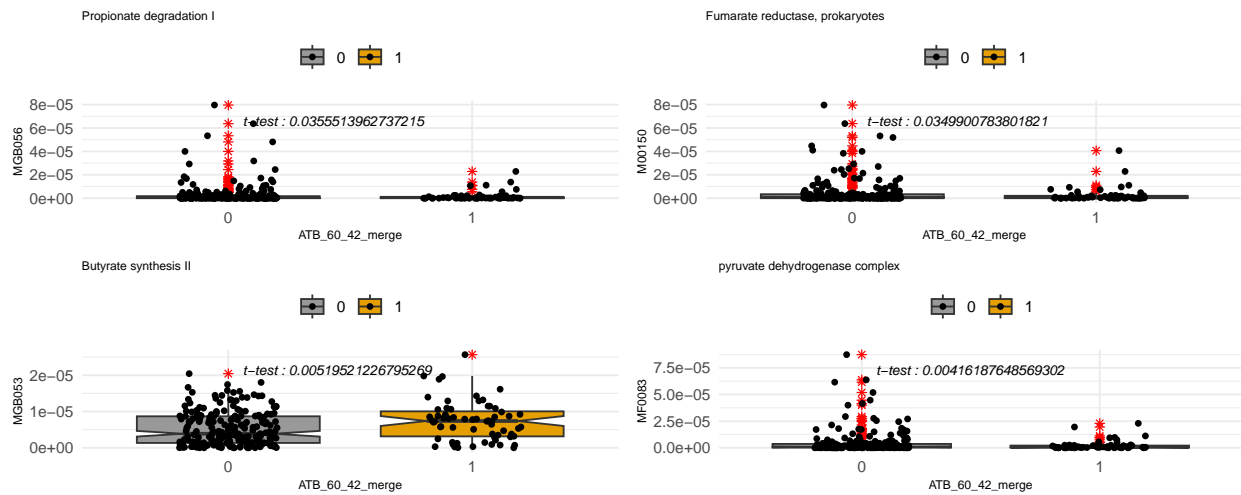
ATB_before_sample ATB_60_42 The functional data comes from the Shrcan pipeline.

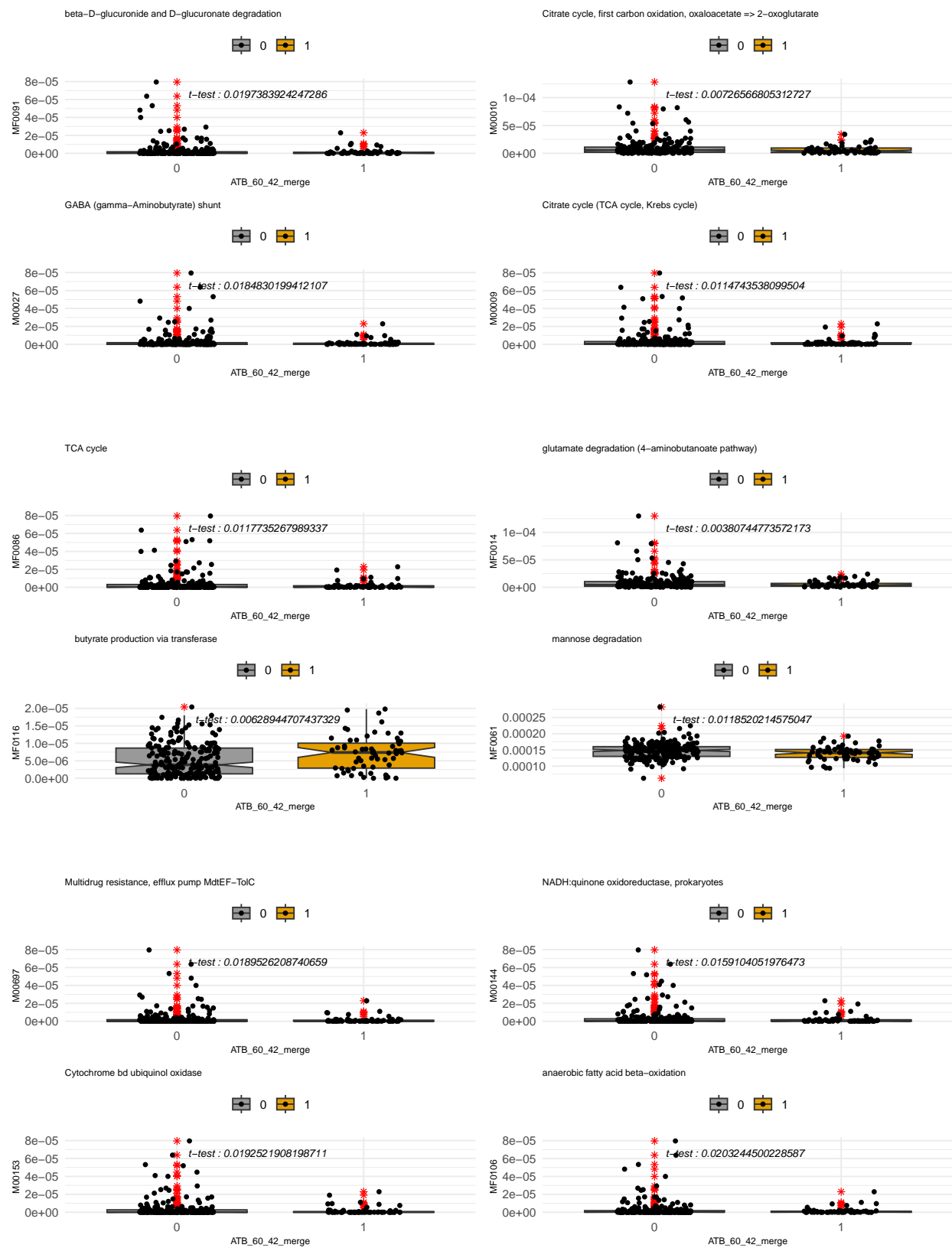
Check for each species/functional module/sample if the functional module has more than 90% of the necessary genes for module activity.

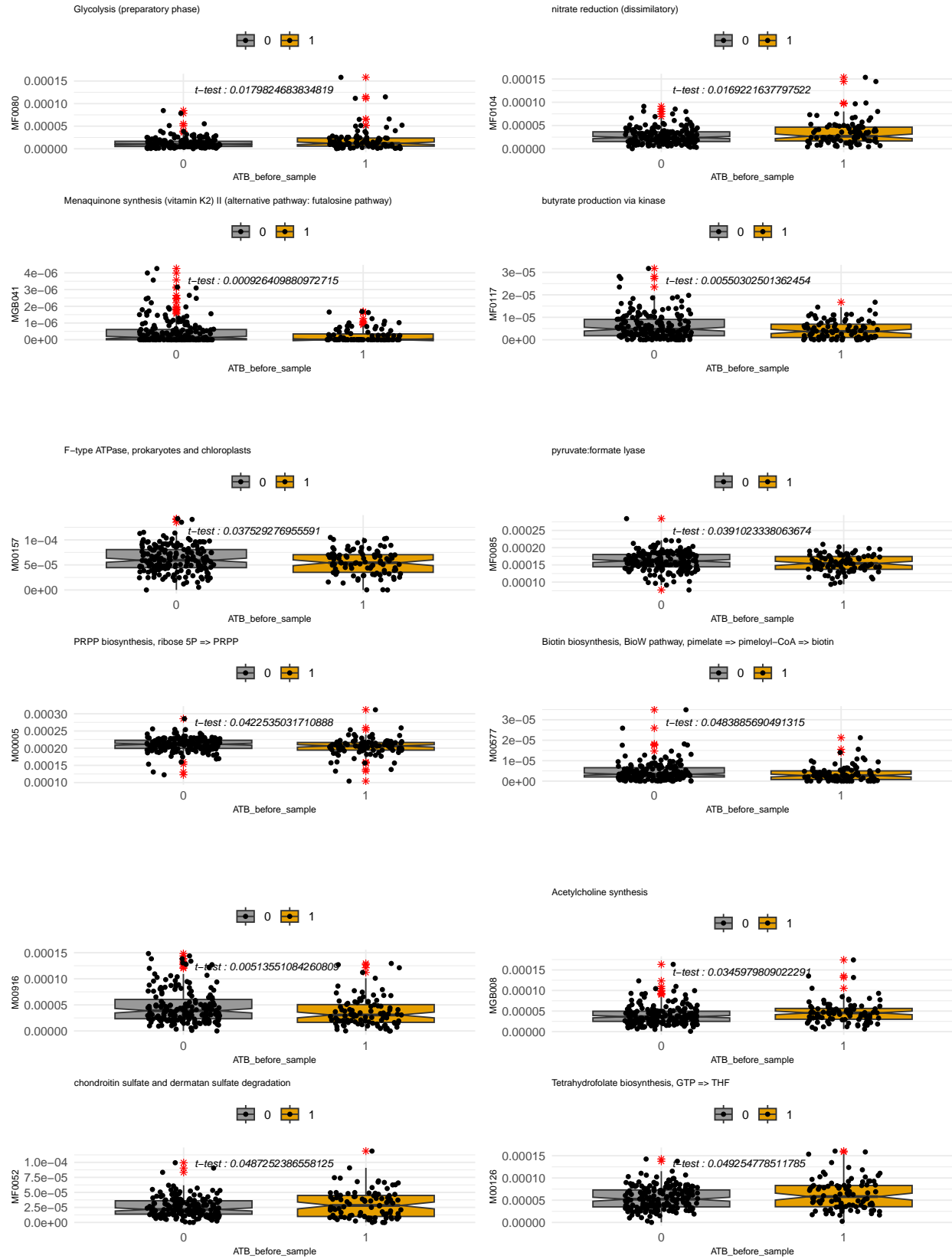
If so, consider that the abundance of this functional potential is equivalent to the abundance of the species carrying it.

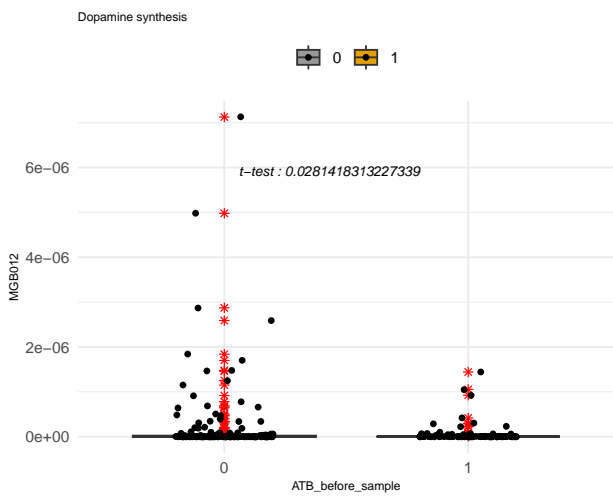
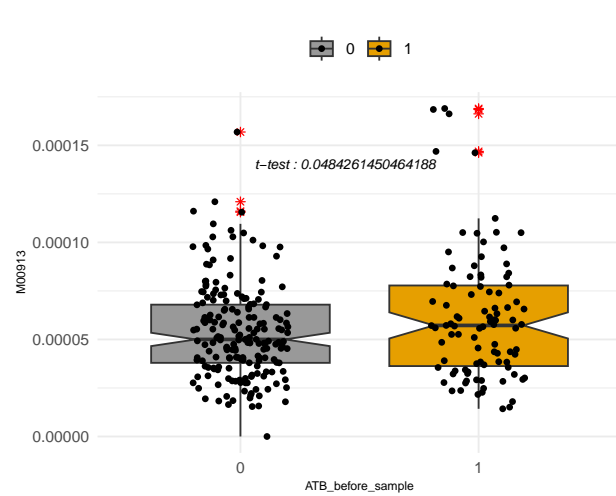
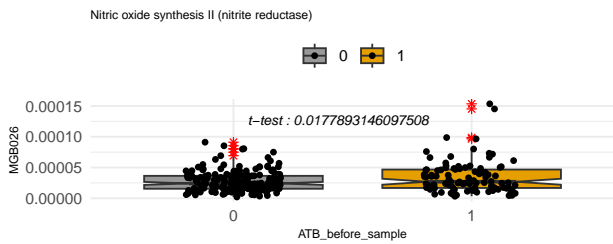
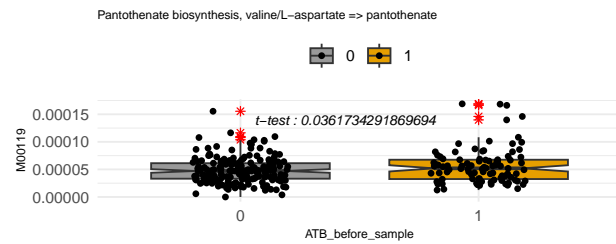
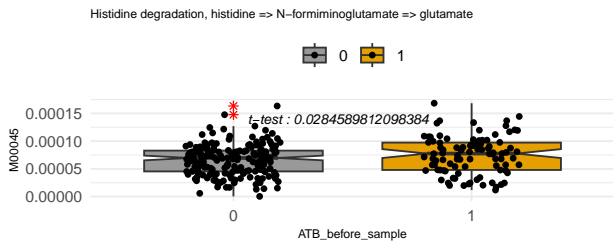
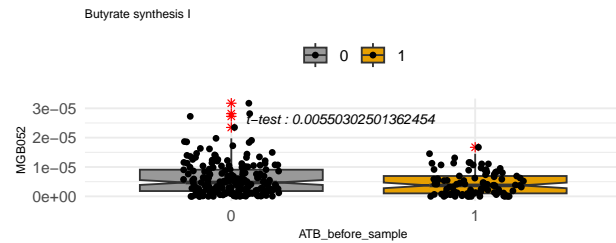
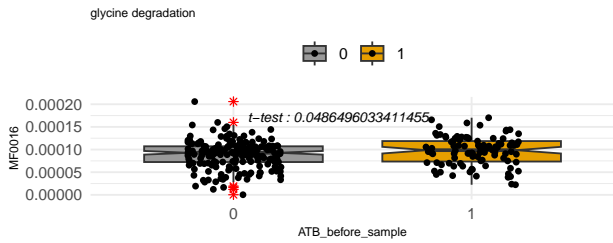
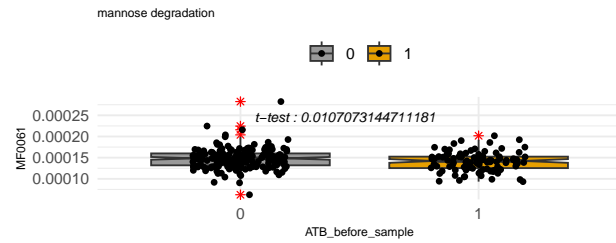
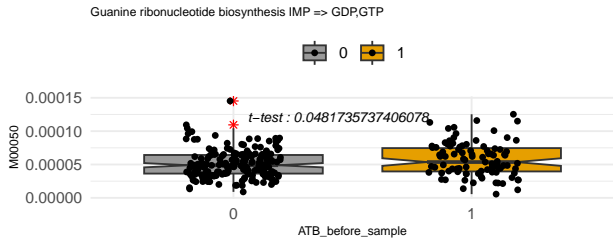
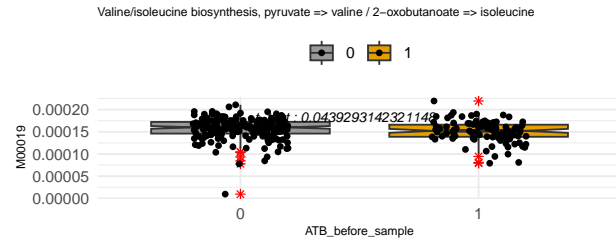
ATB_60_42_merge : les modules significativement differents entre les deux groupes

[1] 21









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