Genotyping analysis: Ruminomics and the cow genome

Francesco Strozzi – Head of the Bioinformatics Core Facility

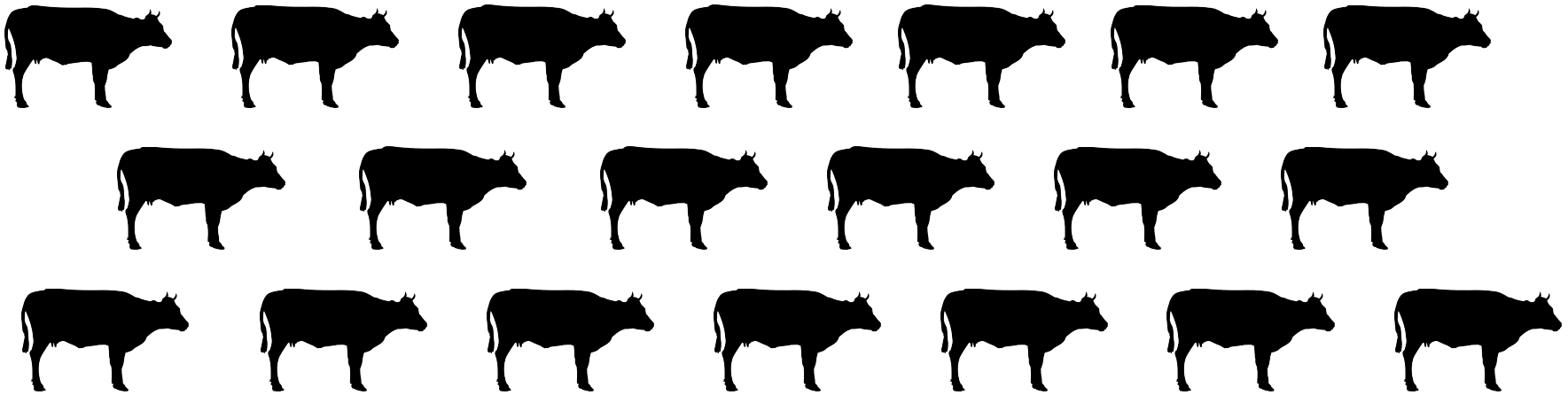
The population

800 Holstein from UK and Italy

The population

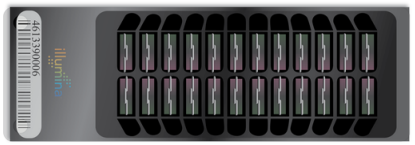
200 Nordic red from Sweden and Finland

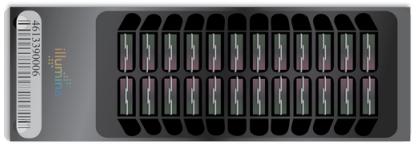
The Genotyping



GeneSeek GGP HD

GeneSeek GGP HD v2





TOOLS

SNPchimp + **SNPchimp** tools

DATASET 1 (raw)

GeneSeek GGP HD (76.883 SNPs)
208 samples

QC

Autosomes
Mapped SNPs
< 10% missing (ind)
< 20% missing (snp)
In common with GGPHDv2
"Double" SNPs (= chr/pos)

DATASET 2 (raw)

GeneSeek GGP HD v.2 (**138.892 SNPs**)
797 samples

QC

Autosomes
Mapped SNPs
< 10% missing (ind)
< 20% missing (snp)
"Double" SNPs (= chr/pos)

MERGED DATASET

Polymorphic SNPs

Imputation
Beagle v.4

FINAL (Imputed) DATASET

117.722 SNPs
982 samples

Zanardi (PLINK + BEAGLE)

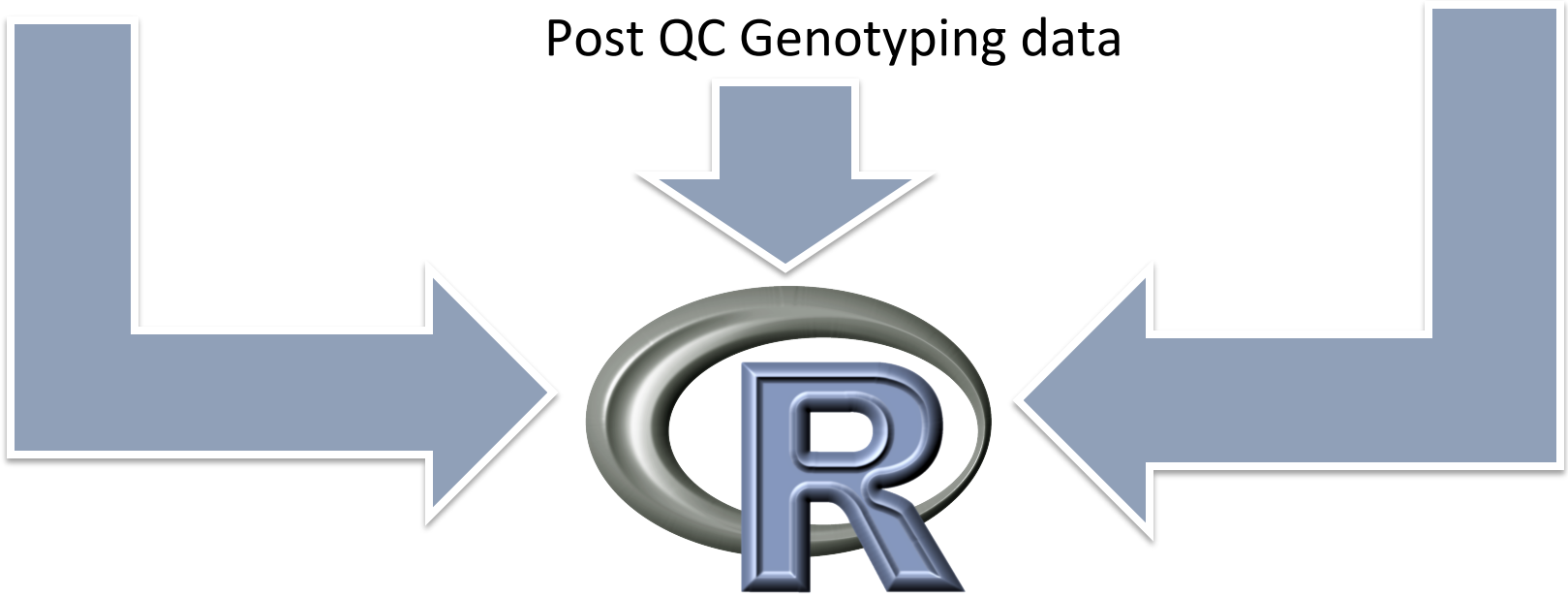
http://bioinformatics.tecnoparco.org/SNPchimp/
https://github.com/nicolazzie/SNPChimpRepo.git
https://github.com/bioinformatics-ptp/Zanardi

The Analysis

Phenotypes measurements
✓ CH4 emissions

Microbiome data
✓ Bacteria / Archaea

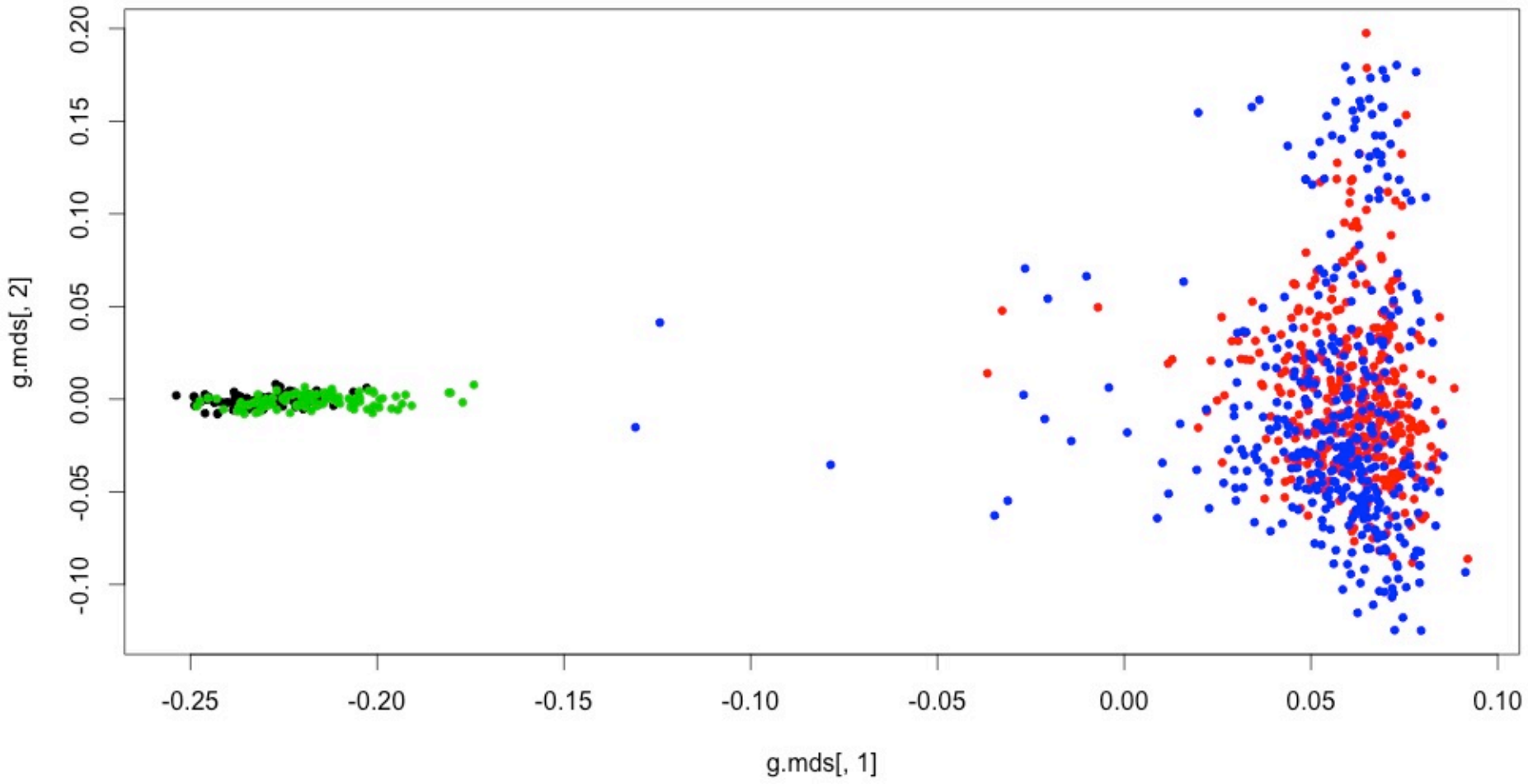
Post QC Genotyping data



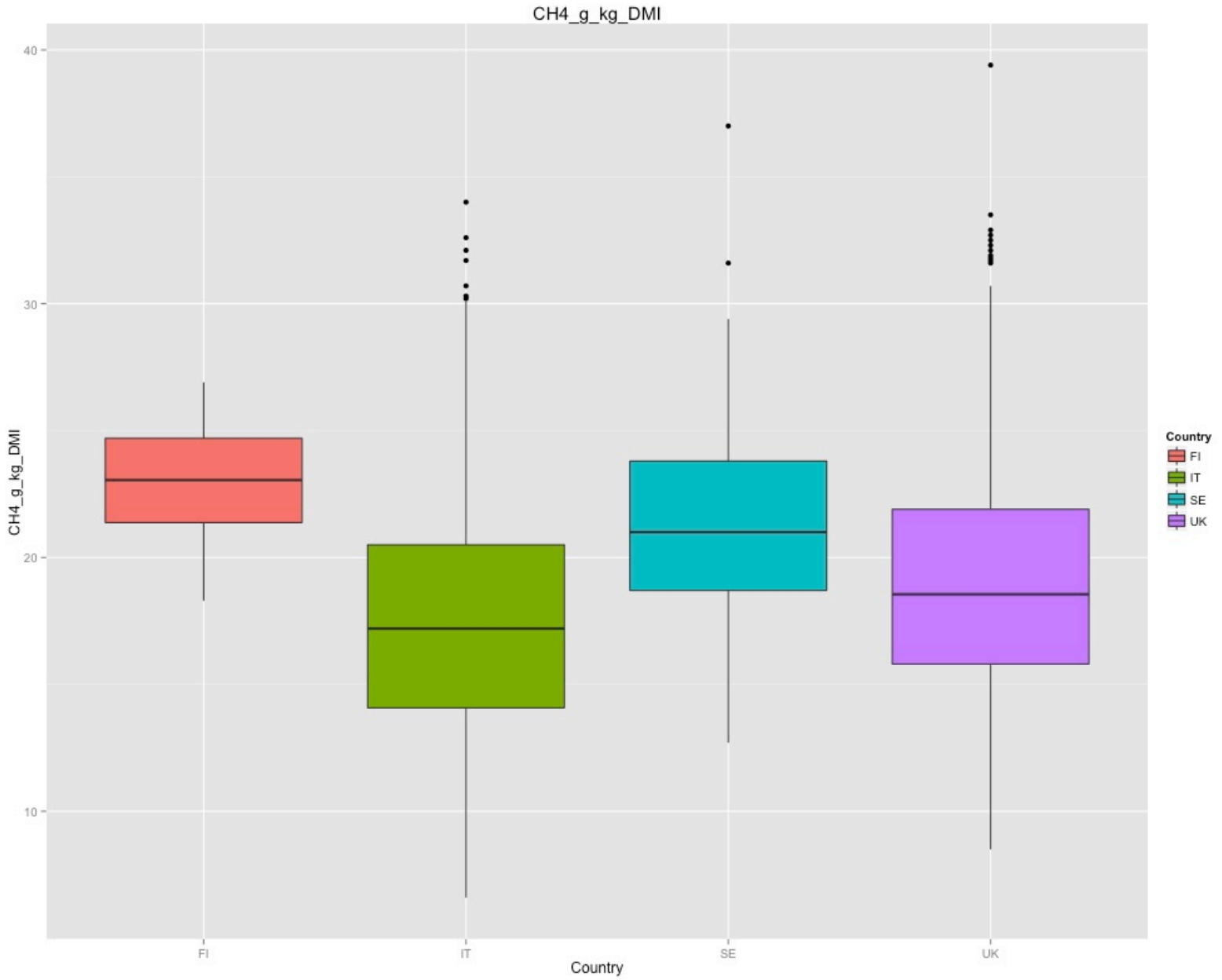
GenAbel

GENOME WIDE ASSOCIATION STUDY

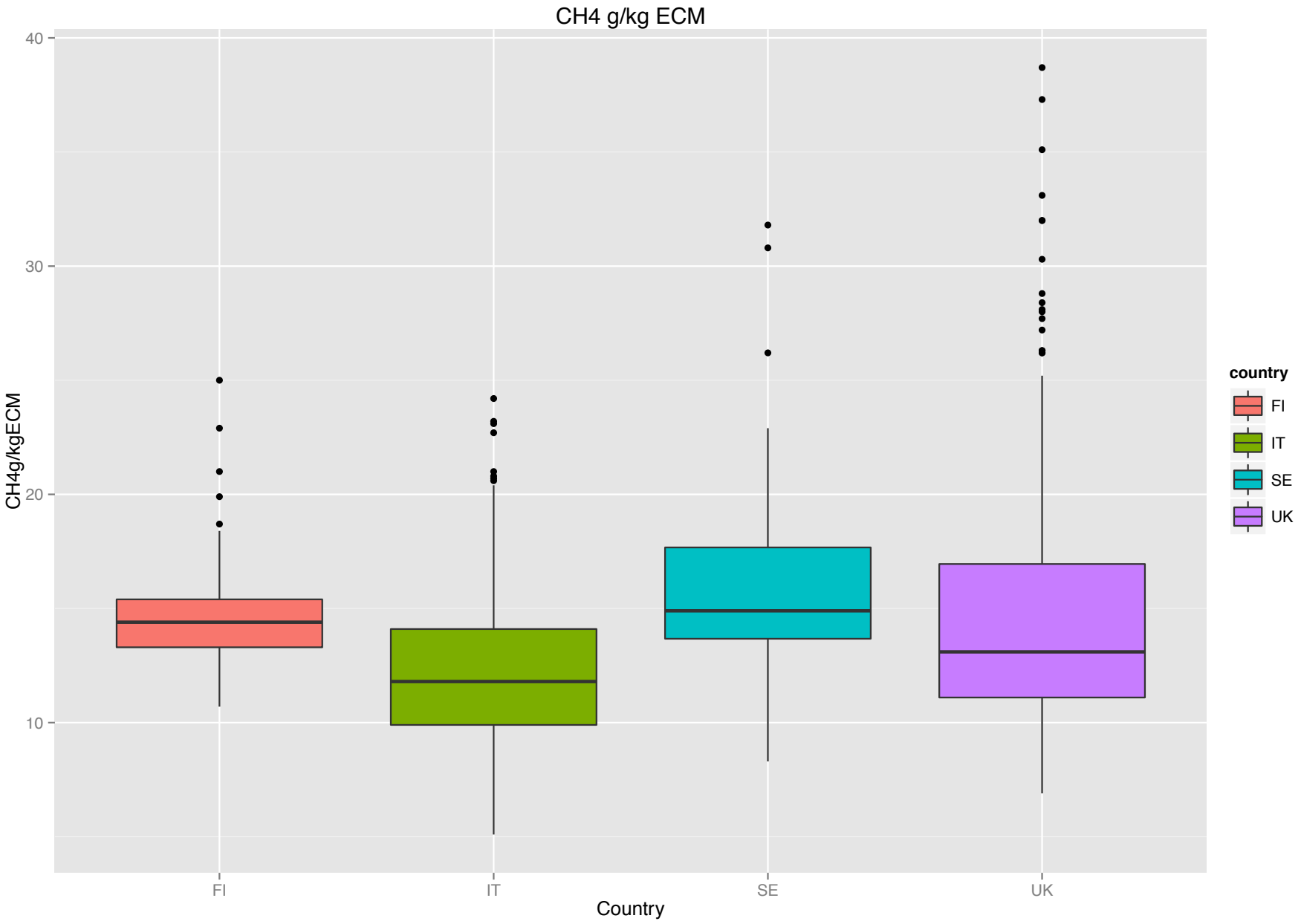
The Analysis – Population Structure



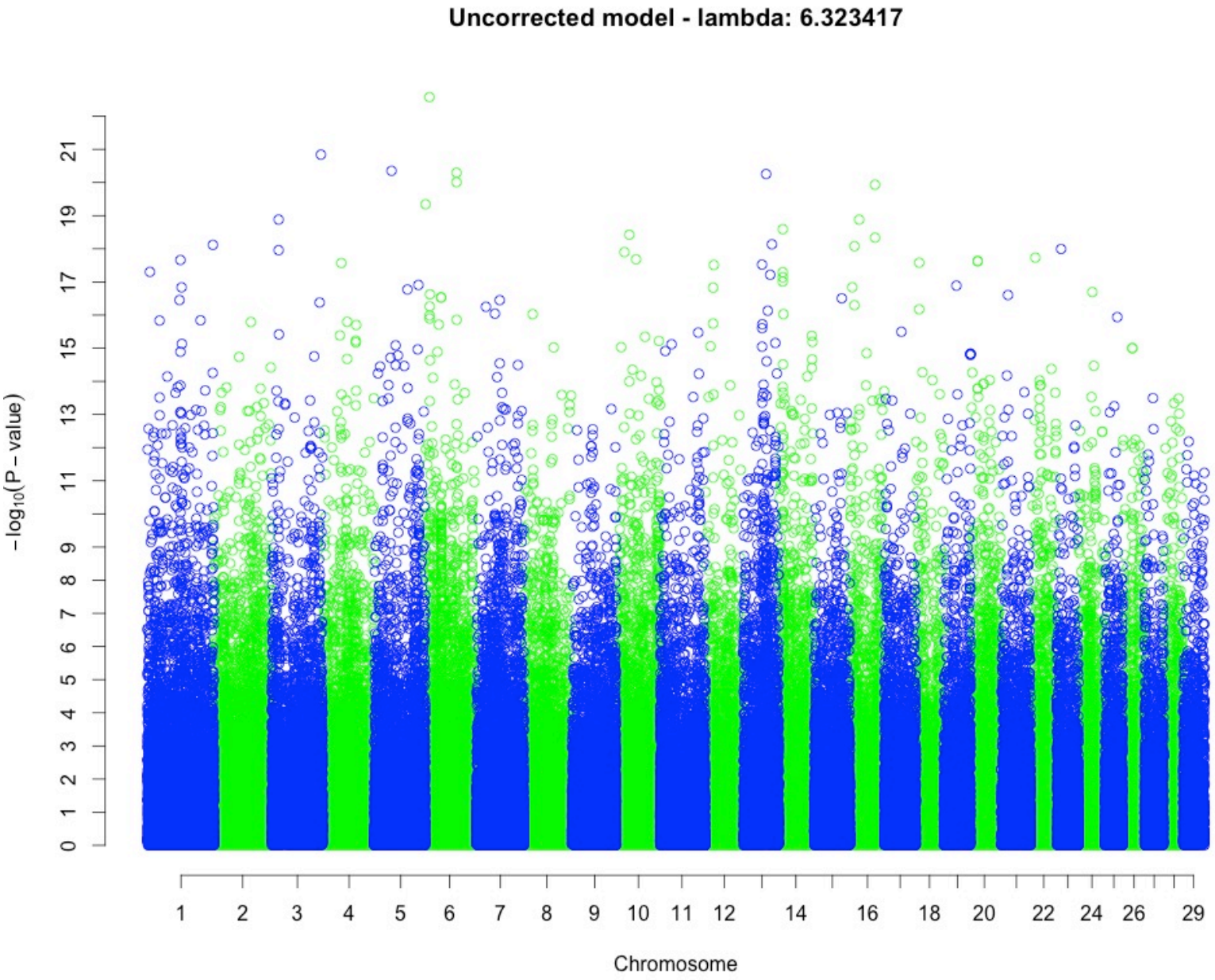
The Analysis – Methane Emissions



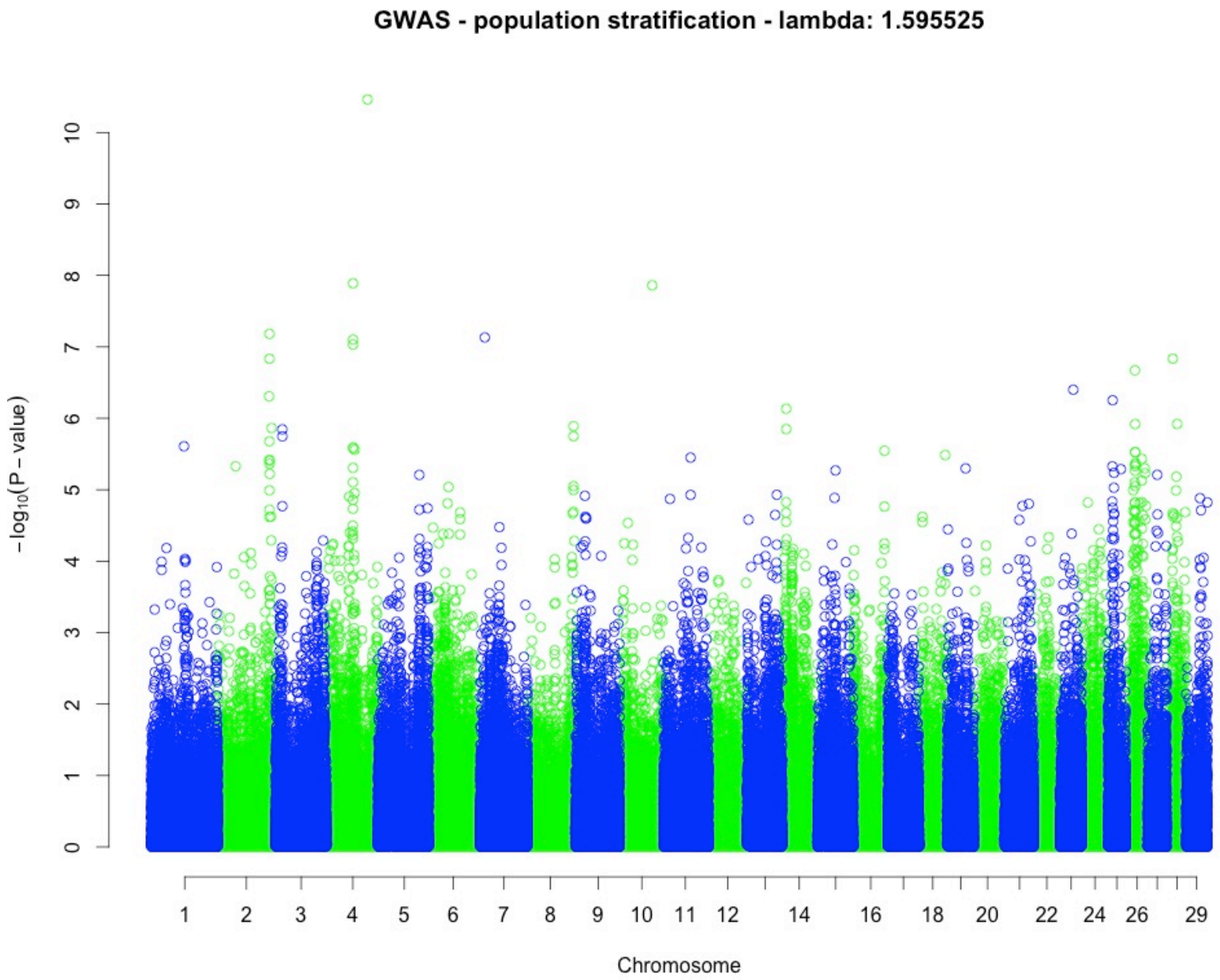
The Analysis – Methane Emissions



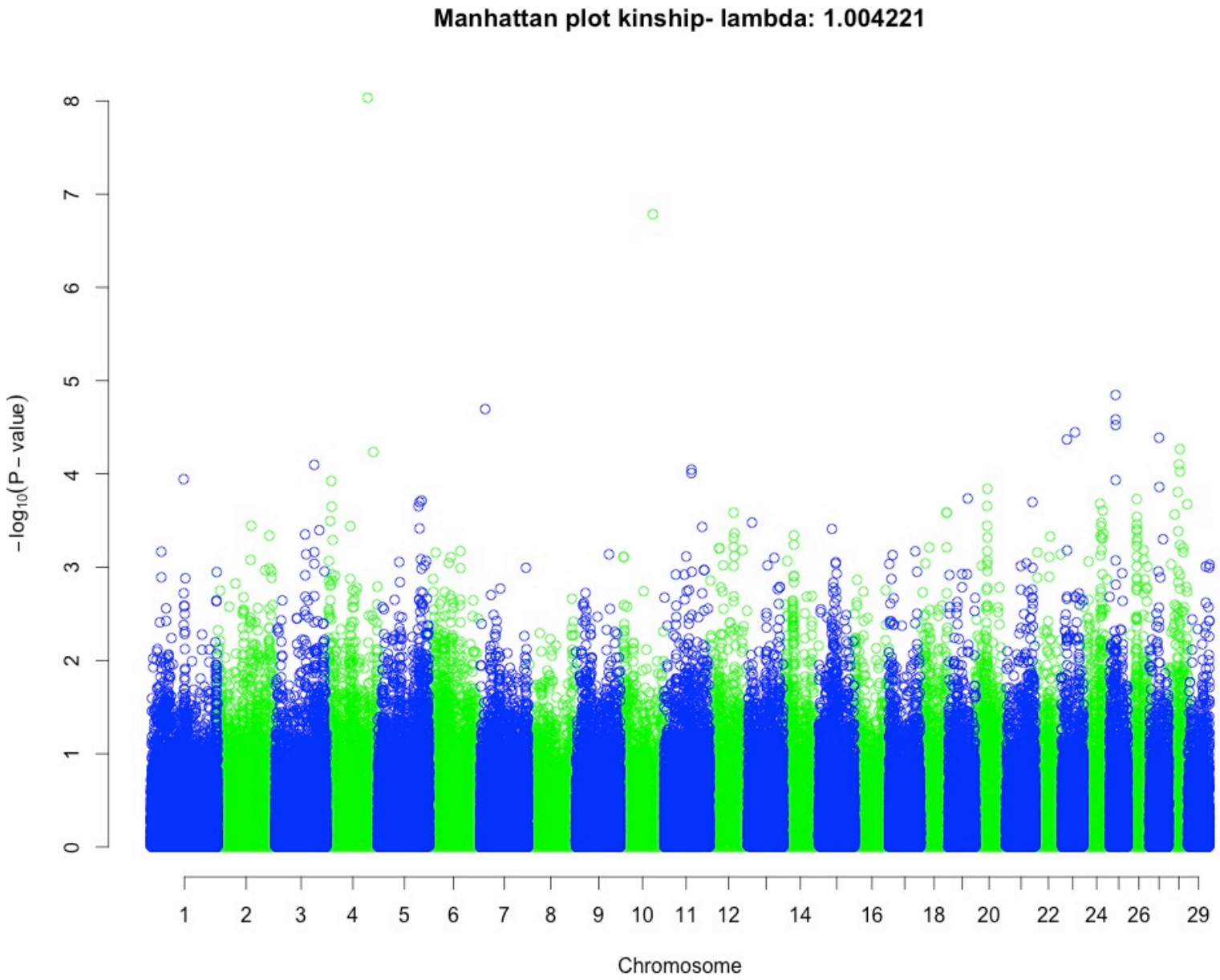
The Analysis – Model correction



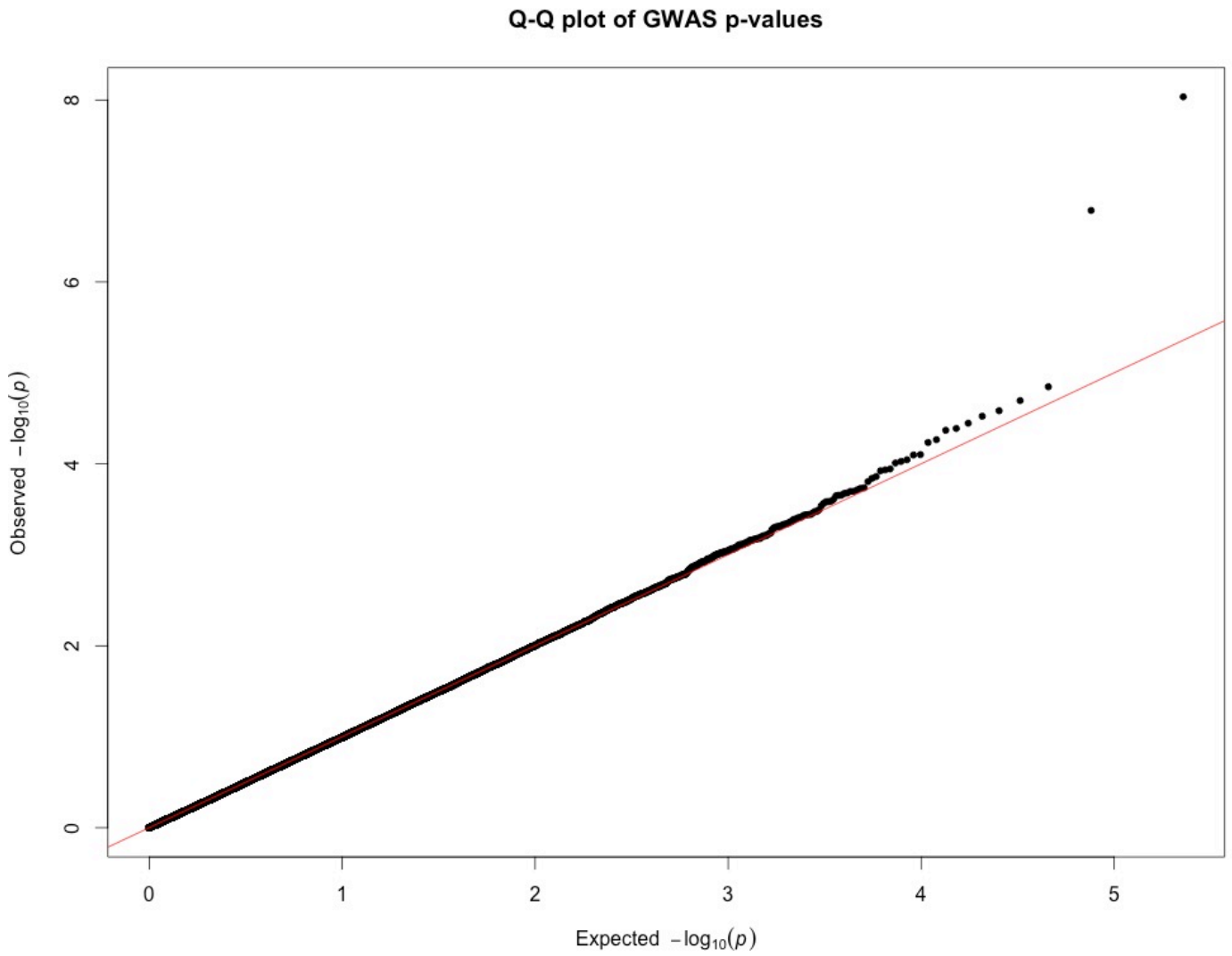
The Analysis – Model correction



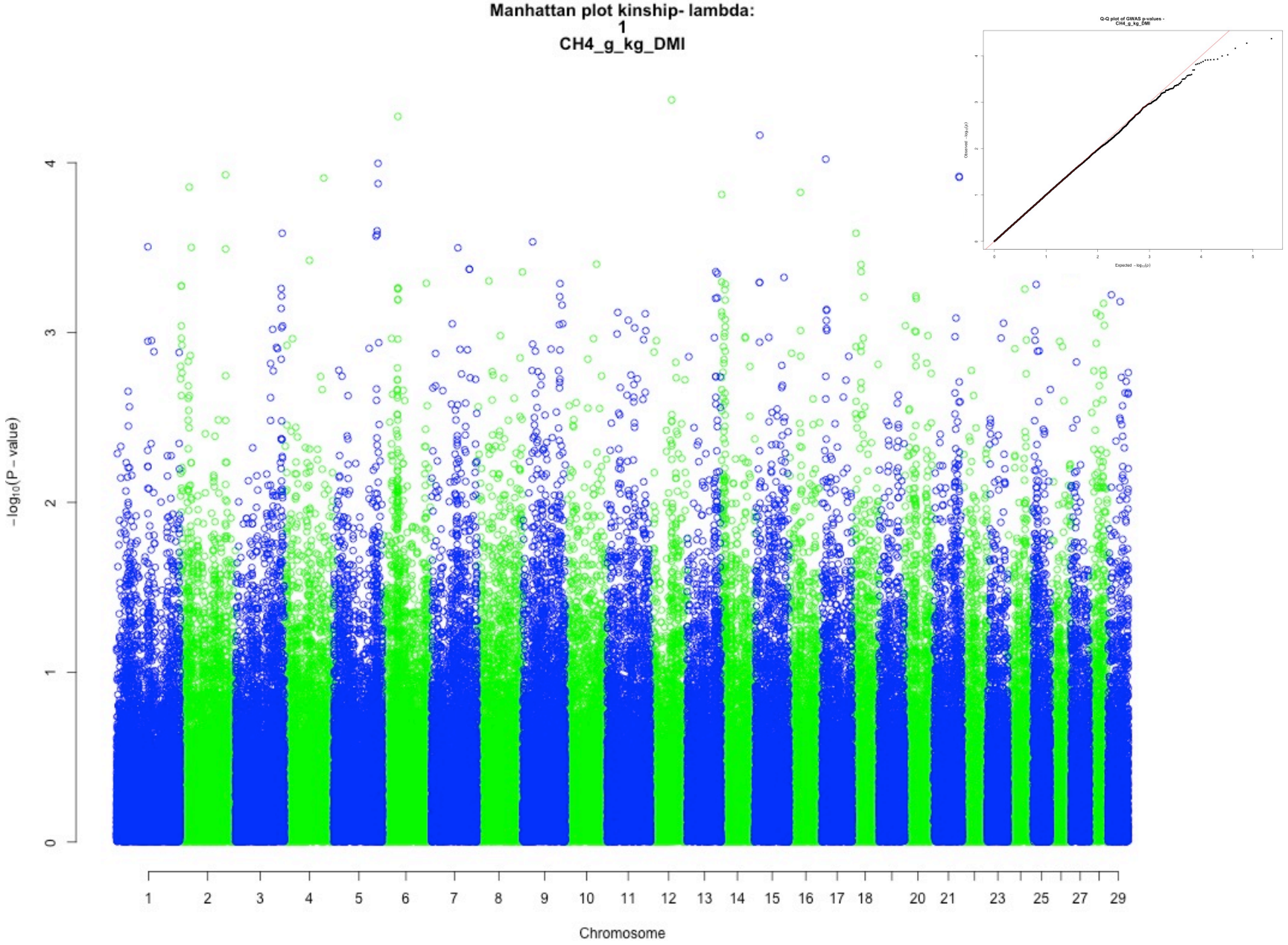
The Analysis – Model correction



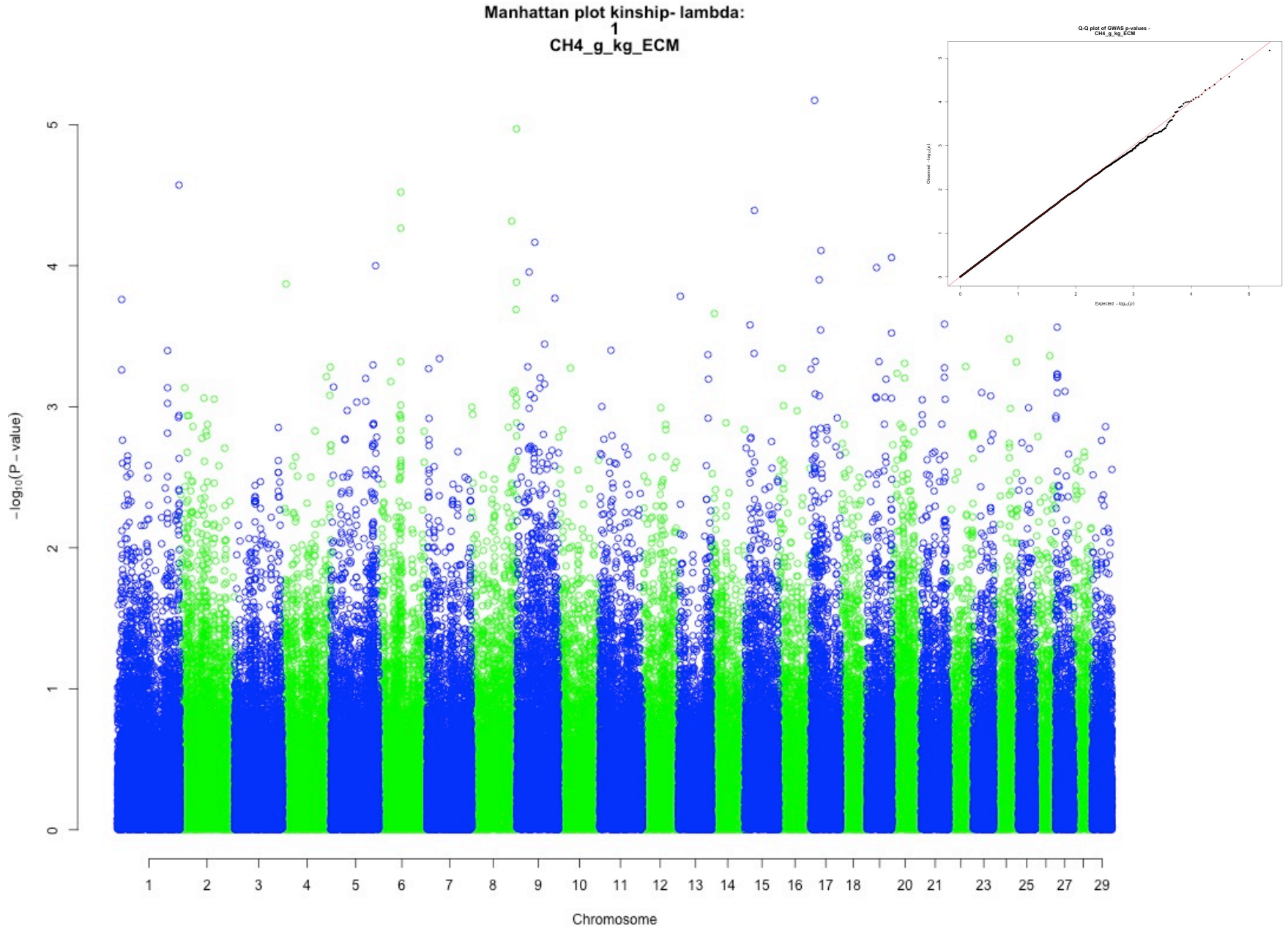
The Analysis – Model correction

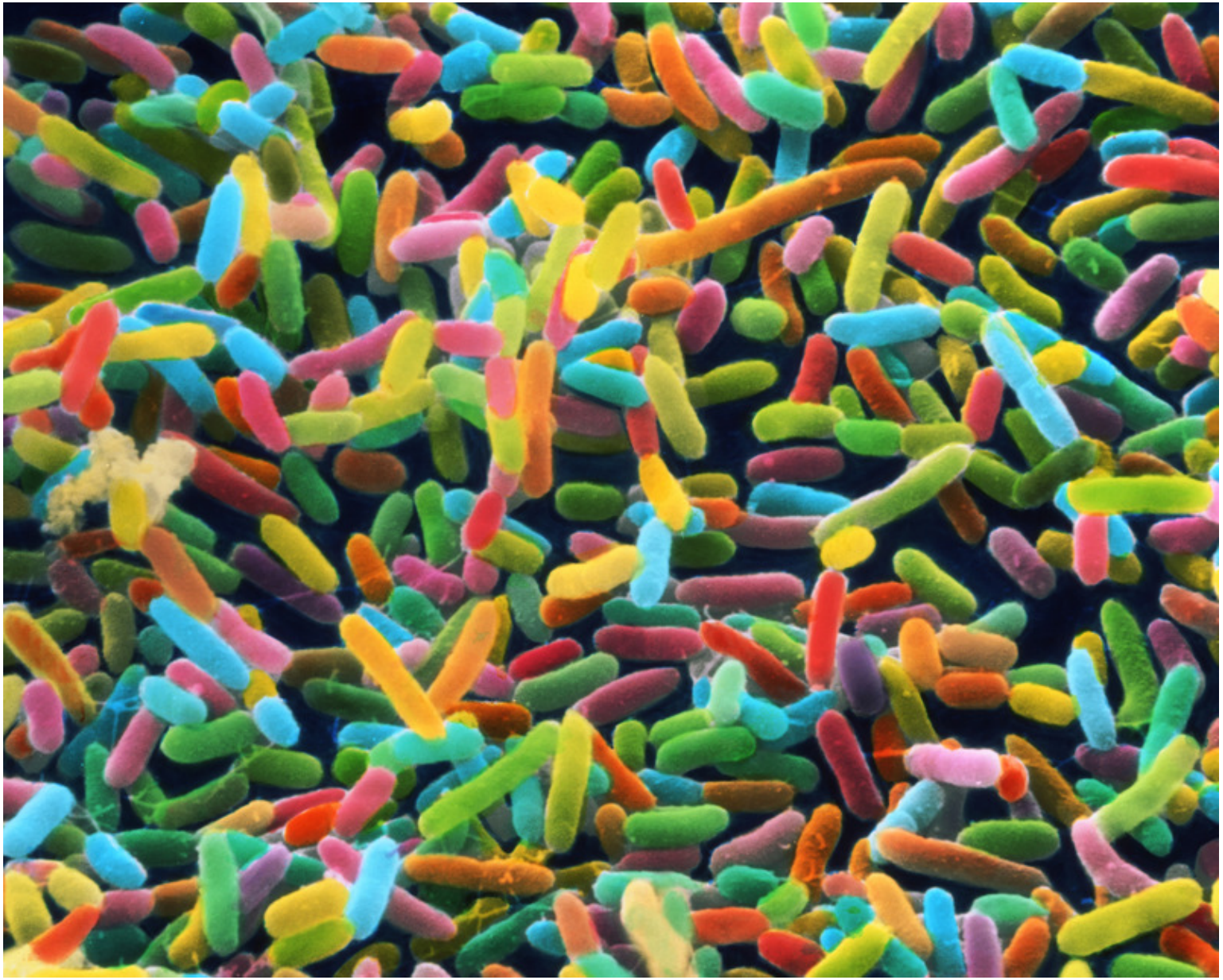


The Analysis – Methane Emissions DMI

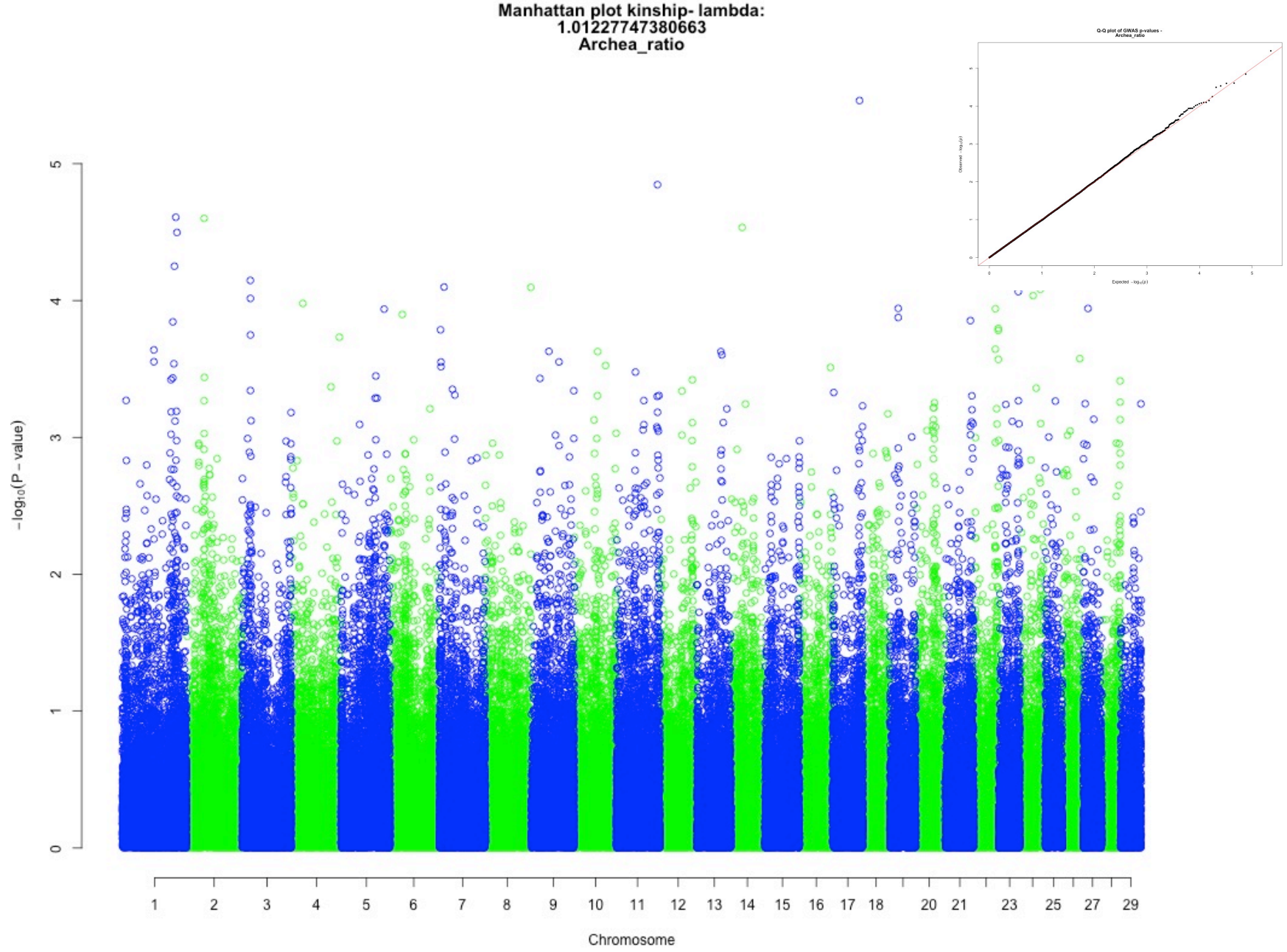


The Analysis – Methane Emissions ECM

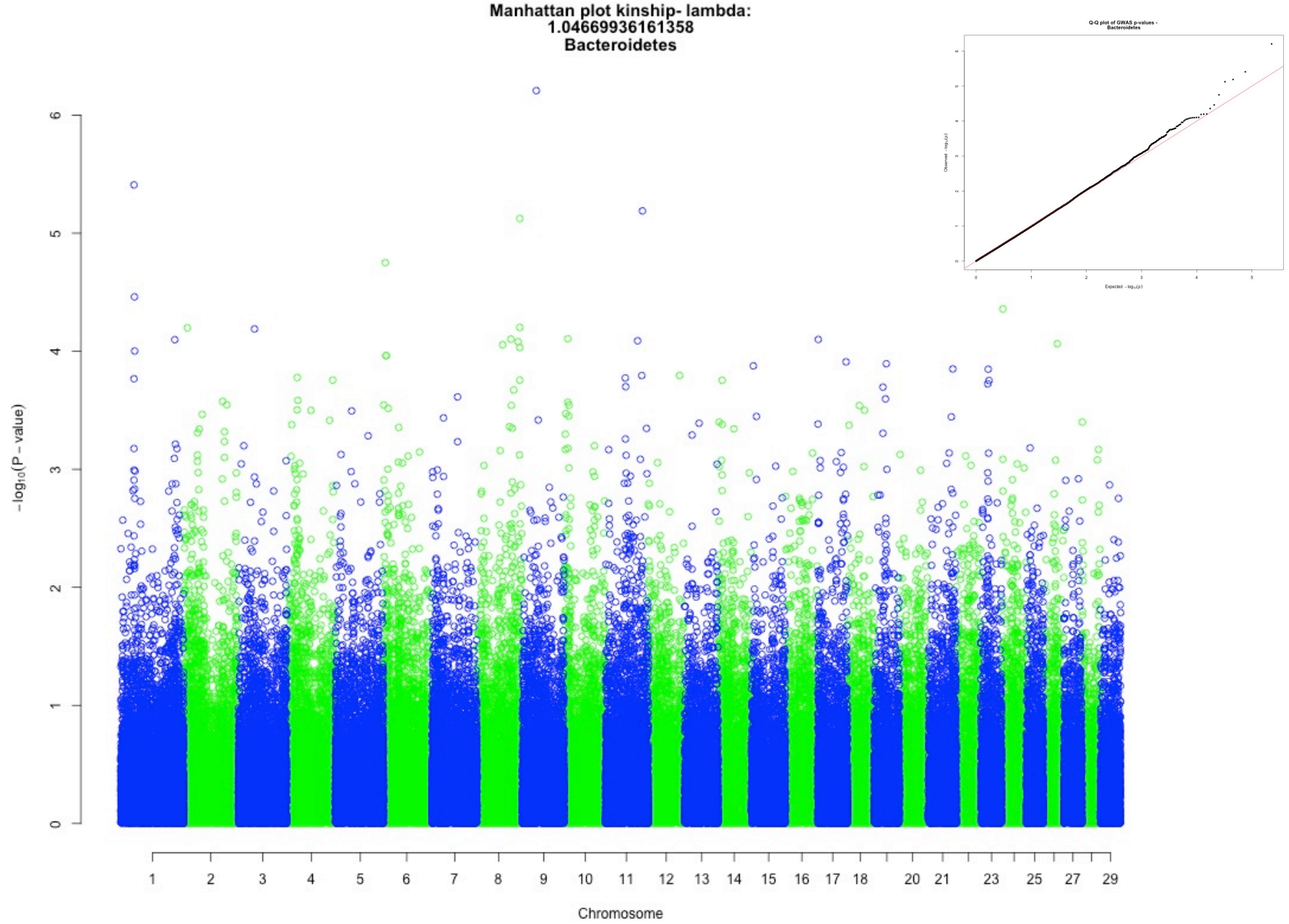




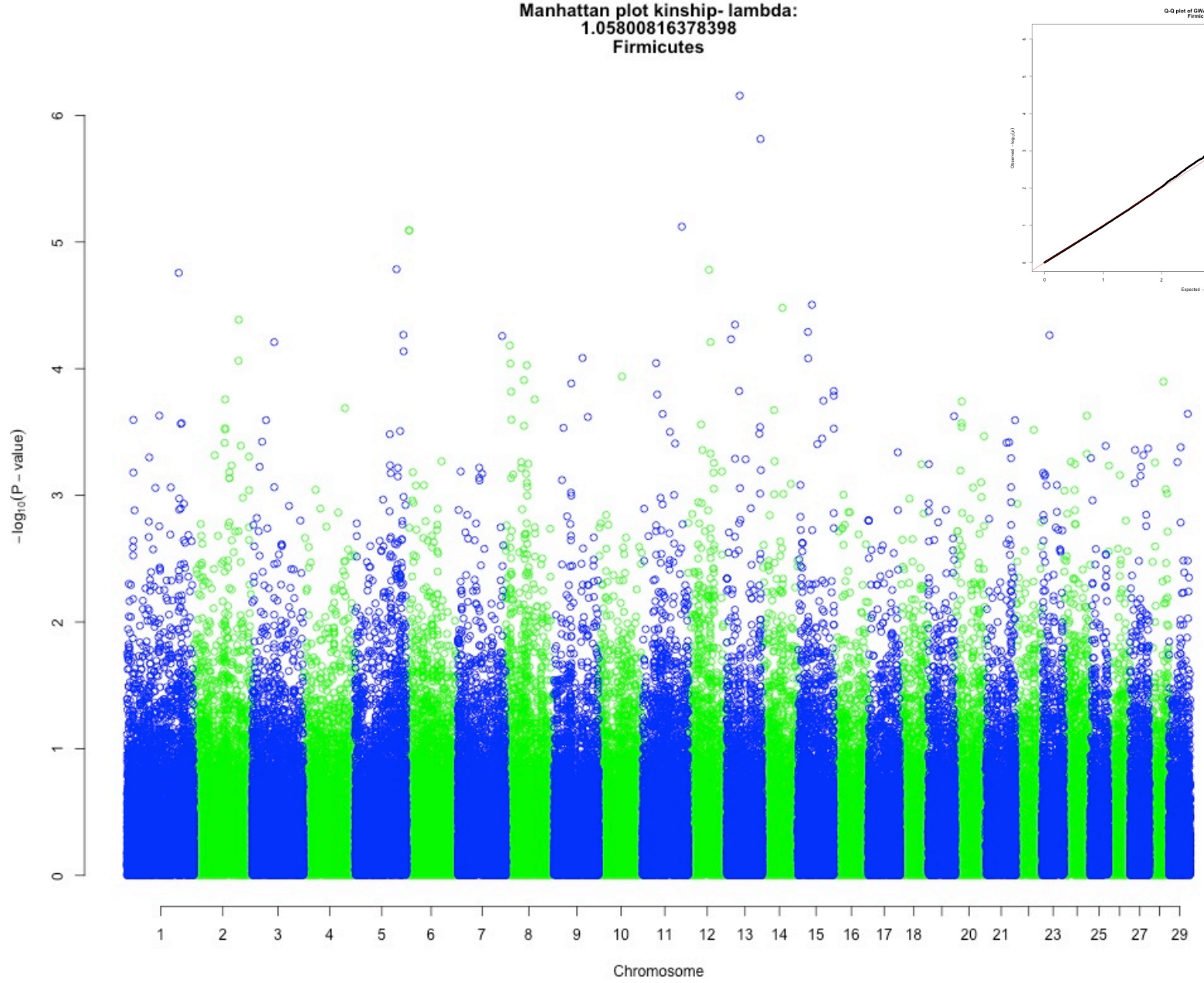
The Analysis – Archaea / Bacteria ratio



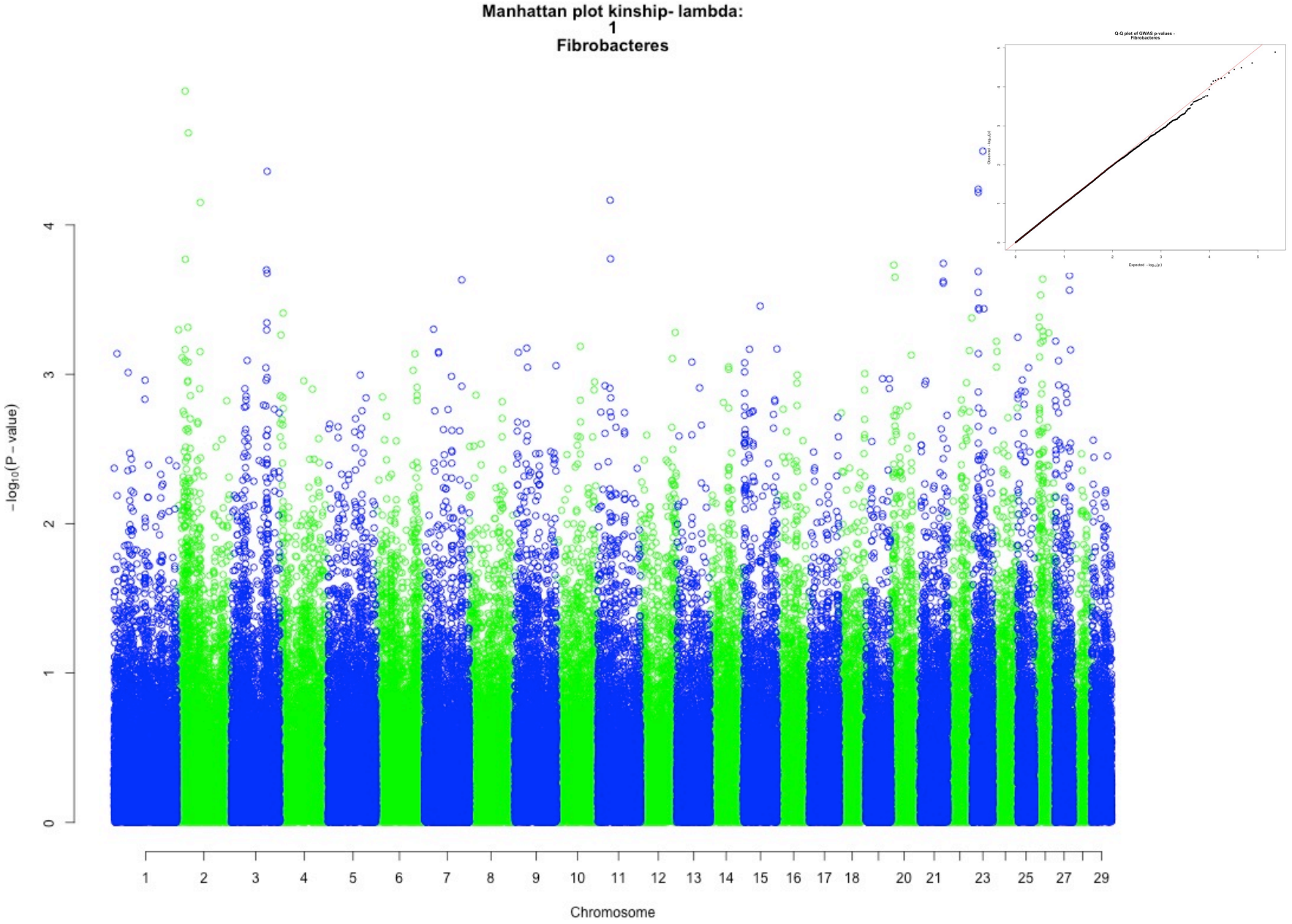
The Analysis – Bacteroidetes



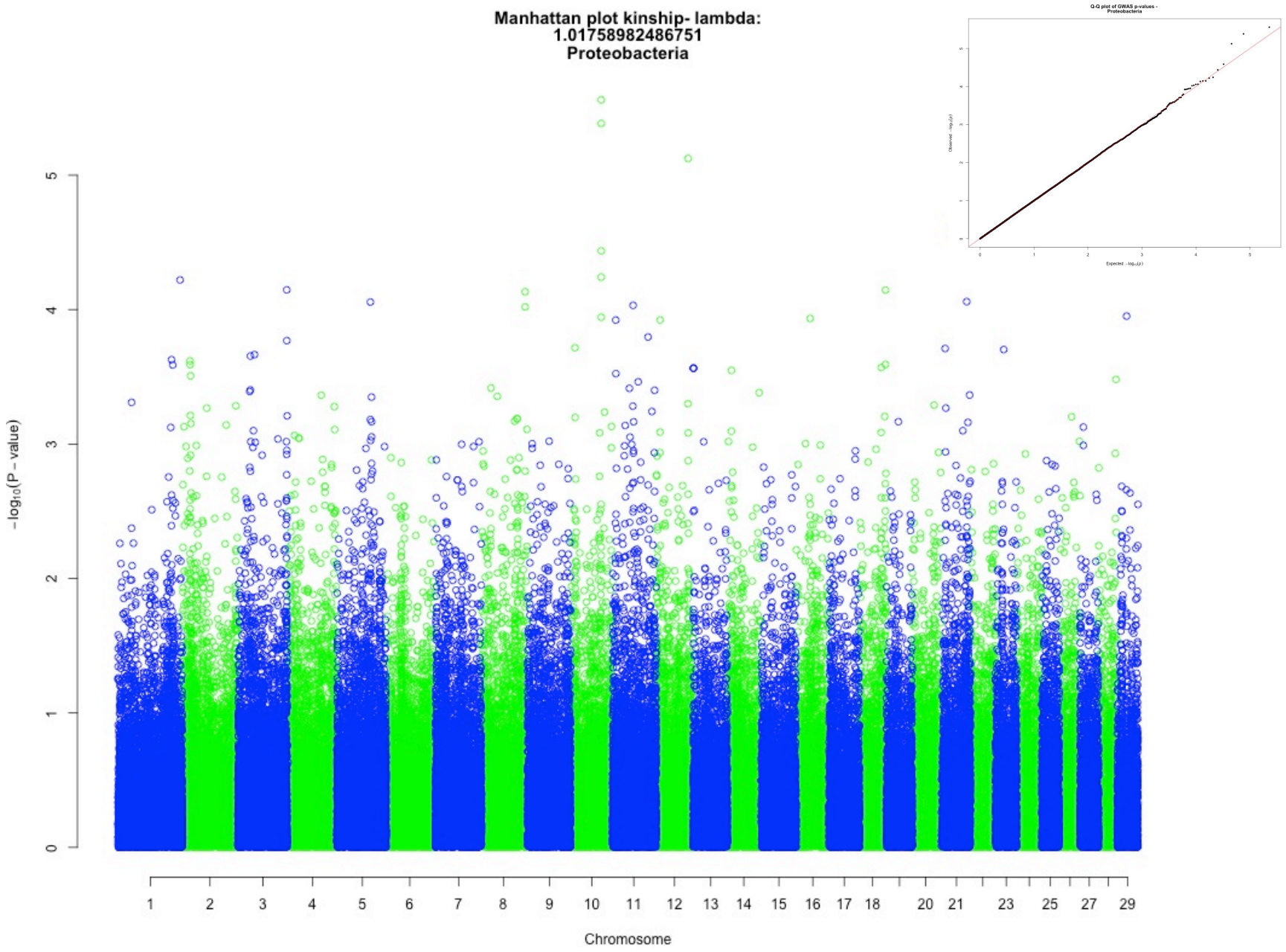
The Analysis – Firmicutes



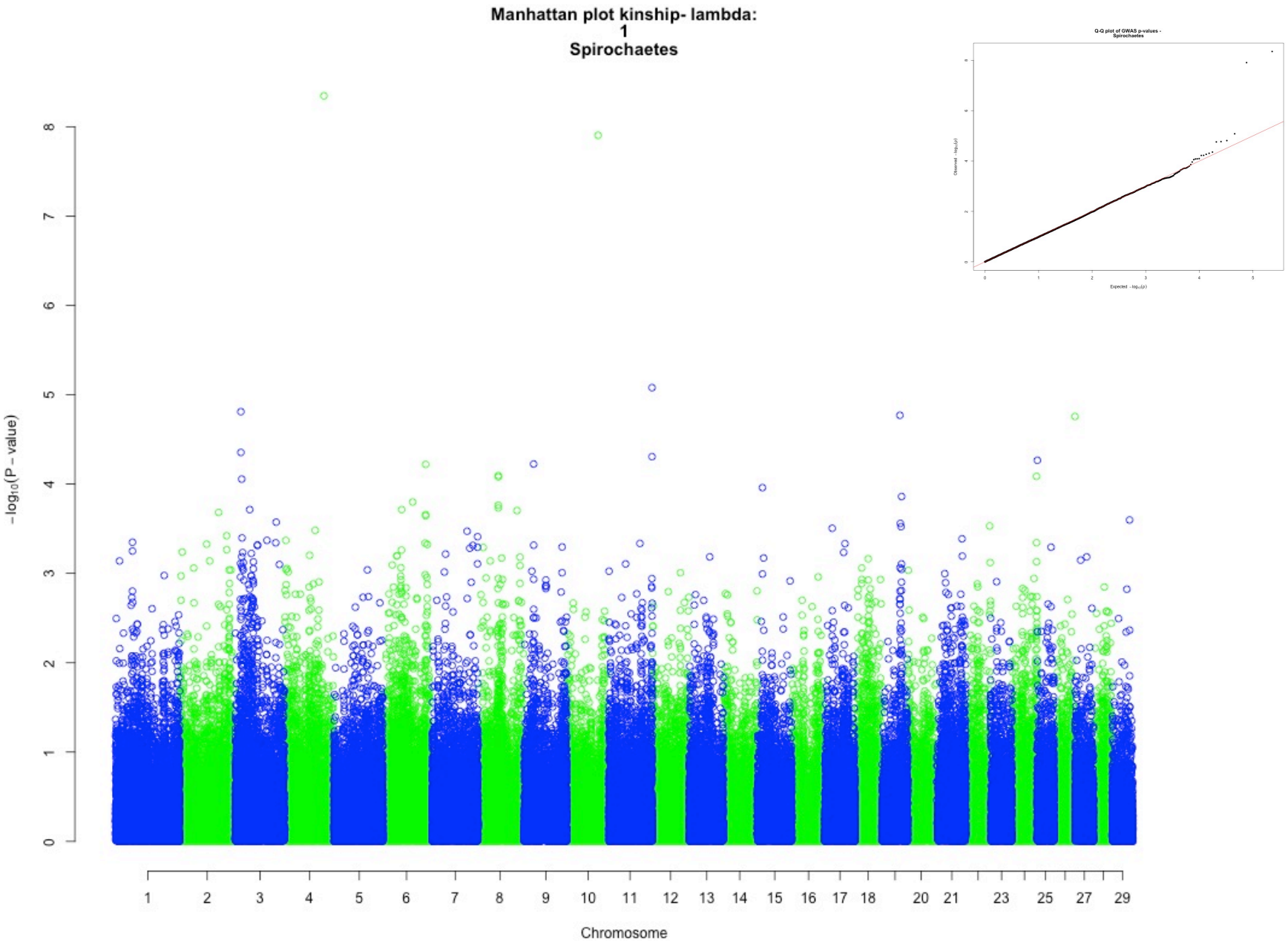
The Analysis – Fibrobacteres



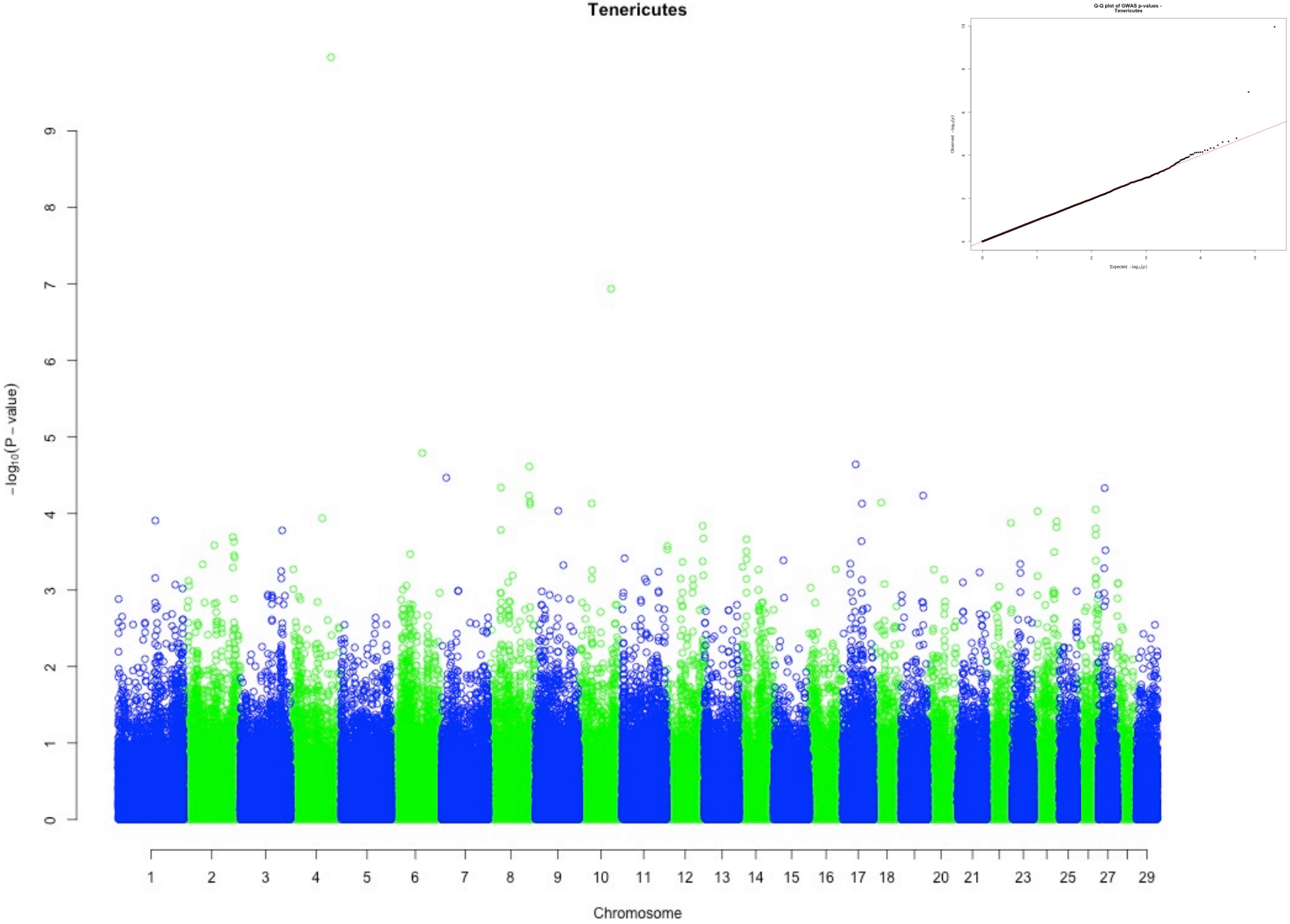
The Analysis – Proteobacteria



The Analysis – Spirochaetes



The Analysis – Tenericutes



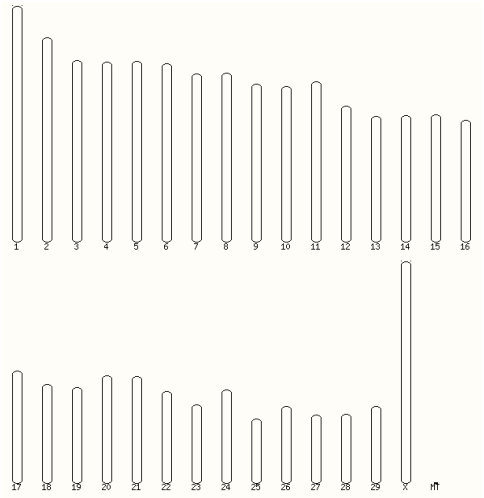
The Associations

Methane Emissions

Associations found on:

- ✓ Chromosome 12
- ✓ Chromosome 6
- ✓ Chromosome 15
- ✓ Chromosome 17
- ✓ Chromosome 8
- ✓ Chromosome 1

The Associations



Archaea/Bacteria ratio
- ✓ Chromosome 17
- ✓ Chromosome 11
- ✓ Chromosome 1
- ✓ Chromosome 2

Bacteroidetes:
- ✓ Chromosome 9
- ✓ Chromosome 1
- ✓ Chromosome 11
- ✓ Chromosome 8

Fibrobacteres:
- ✓ Chromosome 2
- ✓ Chromosome 23
- ✓ Chromosome 26
- ✓ Chromosome 3

Firmicutes:
- ✓ Chromosome 13
- ✓ Chromosome 11
- ✓ Chromosome 6
- ✓ Chromosome 24

Proteobacteria:
- ✓ Chromosome 10
- ✓ Chromosome 12
- ✓ Chromosome 21
- ✓ Chromosome 1

Spirochaetes:
- ✓ Chromosome 4
- ✓ Chromosome 10
- ✓ Chromosome 11
- ✓ Chromosome 3

Tenericutes:
- ✓ Chromosome 4
- ✓ Chromosome 10
- ✓ Chromosome 6
- ✓ Chromosome 17

The Conclusions

- First indications of cow genomic regions associated
  - with CH4 emissions
  - with archaea and bacteria proportions

- This information will be used as the basis to define genetic breeding values for these traits

What's Next

- Annotation of the genes found under the association peaks and exploration of the related pathways

- The phenotypic data gathered by the project is massive and there is much more to explore to find interesting associations (e.g. Digestibility, VFA, Rumen composition etc.)

Aknowledgements

Sampling and Phenotypic data

Prof. Phil Garnsworthy – UNOTT
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Dr. Gabriele Marras – PTP
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Project Coordinator

Prof. John Wallace - UNIABERDEEN

THANK YOU

"For cryin' out loud, roll down the window if you're going to emit greenhouse gases!"

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