Reasonable names and reasonable terms for *Bacteria* and *Archaea*

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"The beginning of wisdom is to call things by their proper name"

Chinese proverb

Carl von Linné

A universal name would provide a means of access to all that is known about an organism and and its relationship to all others in a natural hierarchy

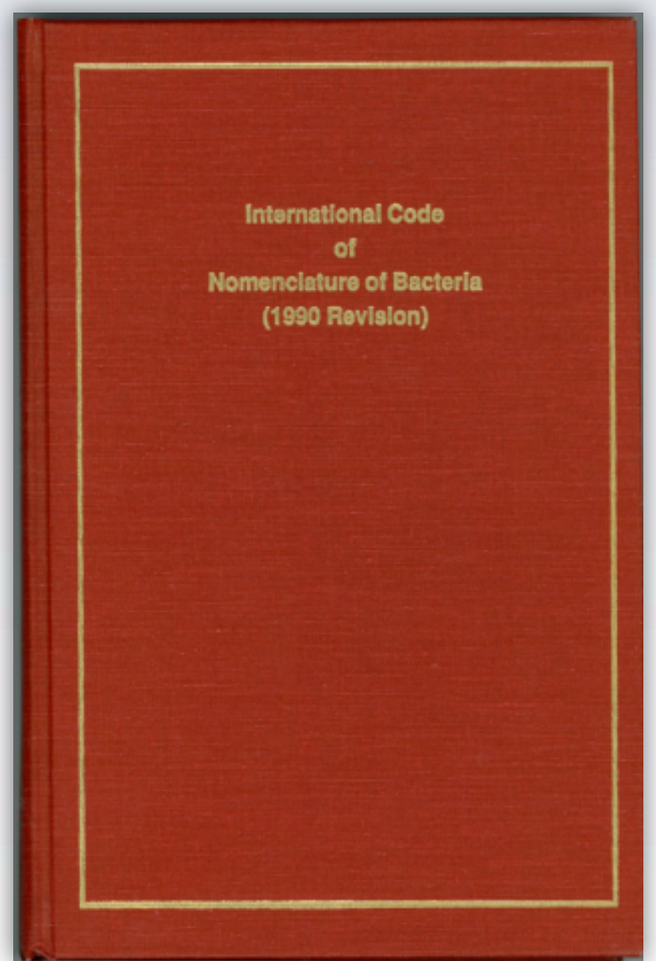
Description of *Ottowia beijingensis* sp. nov.

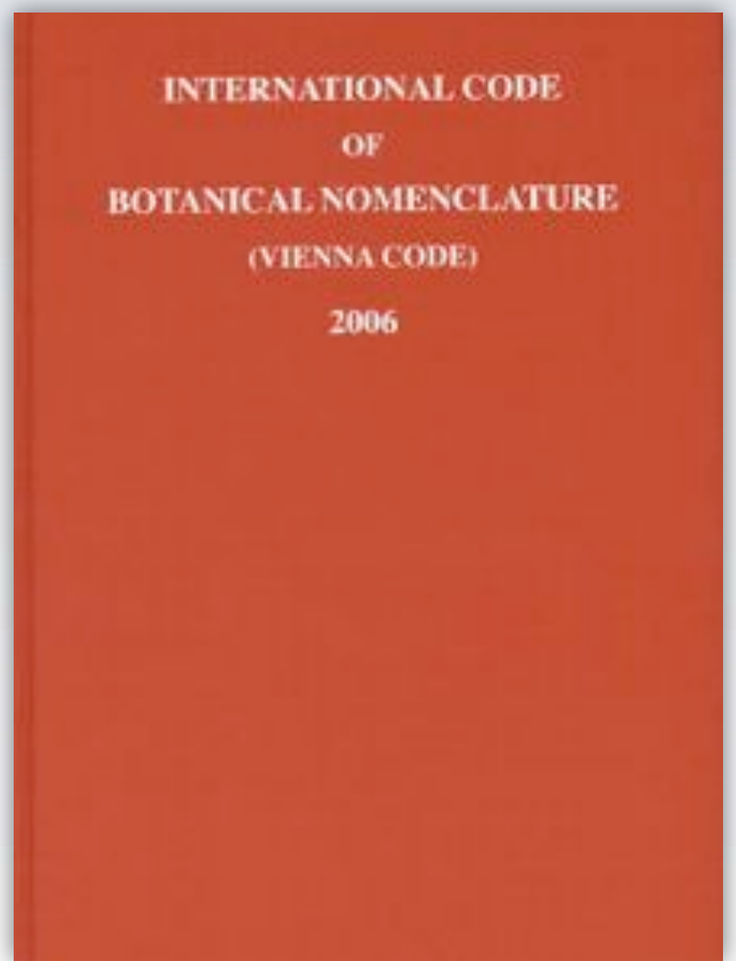
Ottowia beijingensis (bei.jing.en′sis. N.L. fem. adj. *beijingensis* of Beijing, the capital of PR China, where the type strain was isolated).

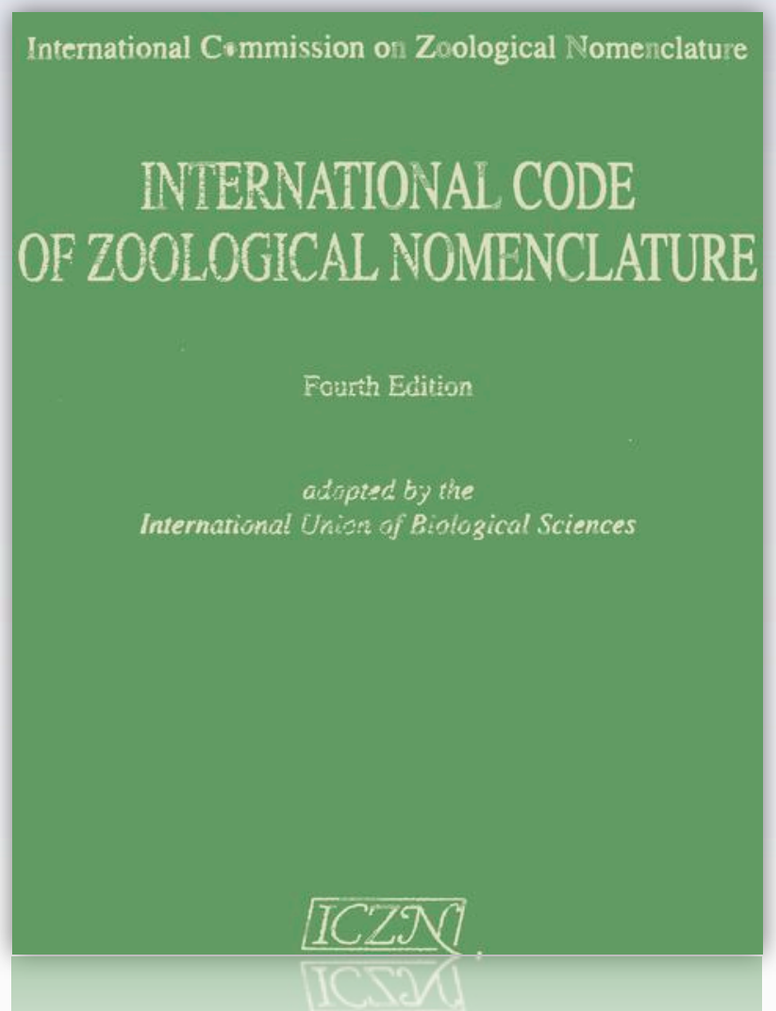
Cells are short rods, about 1.3 μm long and 0.7 μm wide, non-motile, with no flagellum, positive for catalase and oxidase, and Gram-stain-negative. On LB agar medium, produces smooth beige colonies with regular edges that are 1 mm in diameter and slightly raised in the centre after 2 days of incubation at 28 °C. Grows in 0–2.5 % NaCl (optimum 1 %) at 10–37 °C (optimum 30 °C), but not at 41 °C within 1 week. Negative for autotrophic growth with H_2. Polyhydroxyalkanoate granules are absent inside cells grown on LB. Thiosulfate can be utilized as co-substrate for aerobic growth and is oxidized to sulfate. Principal fatty acids are summed feature 3 ($C_{16:1}\omega7c/C_{16:1}\omega6c$), $C_{16:0}$, summed feature 8 ($C_{18:1}\omega7c/C_{18:1}\omega6c$) and cyclo $C_{17:0}$. In the API ZYM test, positive for acid phosphatase, alkaline phosphatase, cystine aminopeptidase (weak), esterase (C4), lipase (C14), leucine aminopeptidase, naphthol-AS-BI-phosphoamidase, valine aminopeptidase and esterase lipase (C8); negative for α-glucosidase, *N*-acetyl-β-glucosaminidase, trypsin, α-chymotrypsin, α-galactosidase, α-mannosidase, β-galactosidase, β-glucosidase, β-glucuronidase and α-fucosidase. In the API 20NE test, can utilize adipic acid, phenylacetic acid and malic acid, but not capric acid, d-glucose, d-mannose, *N*-acetylglucosamine, l-arabinose, d-mannitol or trisodium citrate. Of the 95 substrates in the Biolog GN2 system, positive for d-glucuronic acid; weakly positive for *N*-acetyl-d-glucosamine, glucuronamide, l-alanyl glycine and l-asparagine; negative for all others. The major respiratory quinone is Q-8. The polar lipids comprise phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine and an unknown phospholipid.

The type strain, GCS-AN-3^T (=LMG 27179^T=CGMCC 1.12324^T=MCCC 1A01410^T) was isolated from coking wastewater activated sludge from Beijing Shougang Company Limited, Beijing, China. The G+C content of the DNA of the type strain is 67.6 mol%.

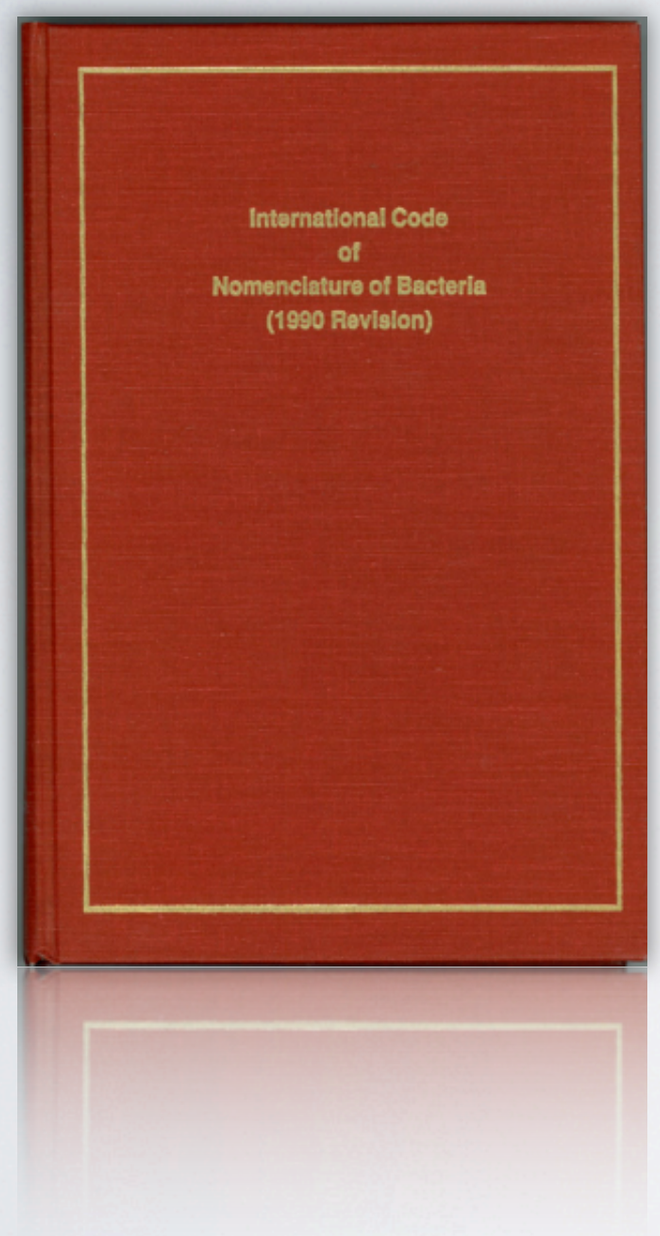
Cao J, et al, Int J Syst Evol Microbiol 2014; 64:963-967





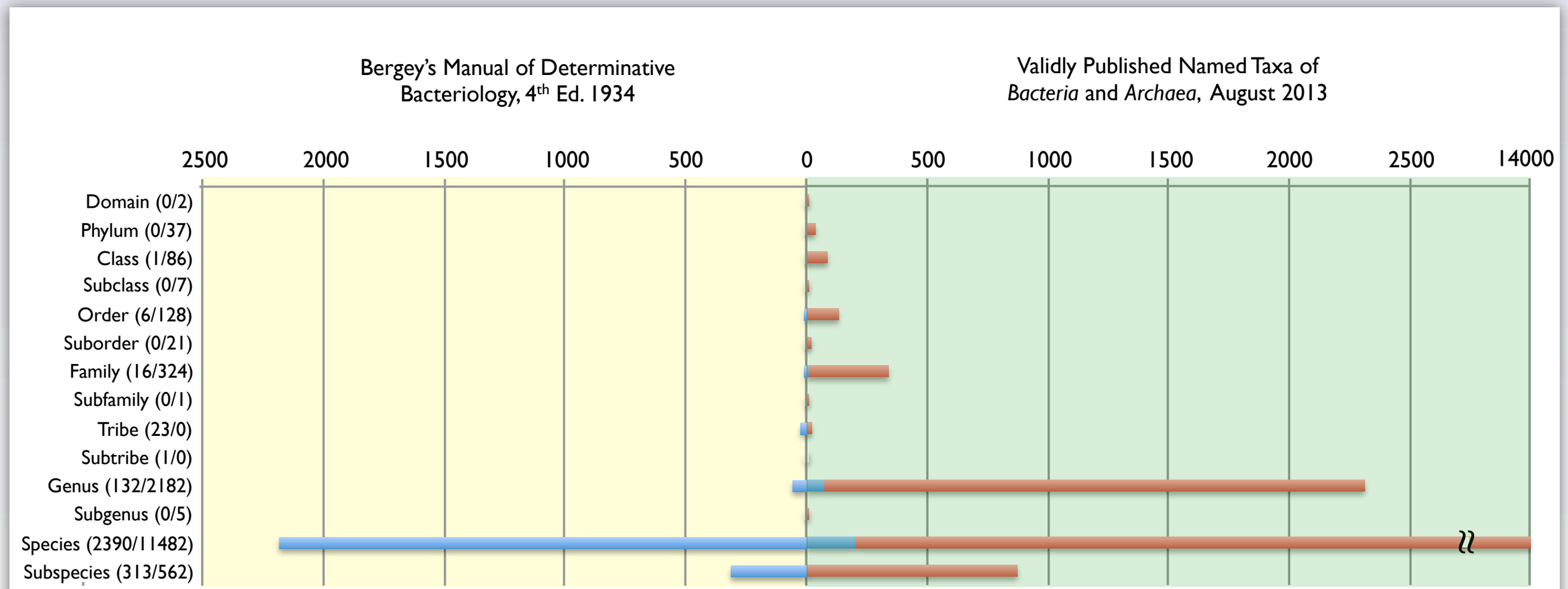


The Major Codes of Nomenclature



- Freedom of taxonomic thought
  - Only the names are regulated
- Correct names
  - Priority
  - Synonymy and homonymy
- Registration and valid publication
  - New priority date (January 1, 1980)
  - Effectively and validly published names
  - Legitimate names
  - Authorship (authorities)
- Typification and live types
- Emendations

Important concepts of the ICPN to be considered



Oren, A. and Garrity, GM. Antonie van Leeuwenhoek. 2014, DOI:10.1007/s10482-013-0084-1

Names = identifiers?
Names ≠ identifiers
- Names are not unique
- Names are not persistent
- Names are not “dumb”

Classification = identification?
Classification ≠ identification
- Classification is open-ended
- Identification is not

Misunderstanding and misuse of names

Question 1

How well does the nomenclature agree with current taxonomy of *Bacteria* and *Archaea*?

- Identify and correct problems
- Maintain compliance with the Code

Question 2

Is it possible to automatically disambiguate biological names?

- "Future-proof" names
  - Maintain links to metadata and data
  - Prior to assignment of name or taxon

Question 3

Is it possible to develop an ontology and apply machine reasoning to determine the correct name and to support inference and consistency checking?

The Self-Organizing Self-Correcting Classifier

What it is:

Method to visualize taxonomic misplacements and to optimize placement in compliance with the Code

Input

- **Classification matrix**
- **Nomenclature matrix**

Output

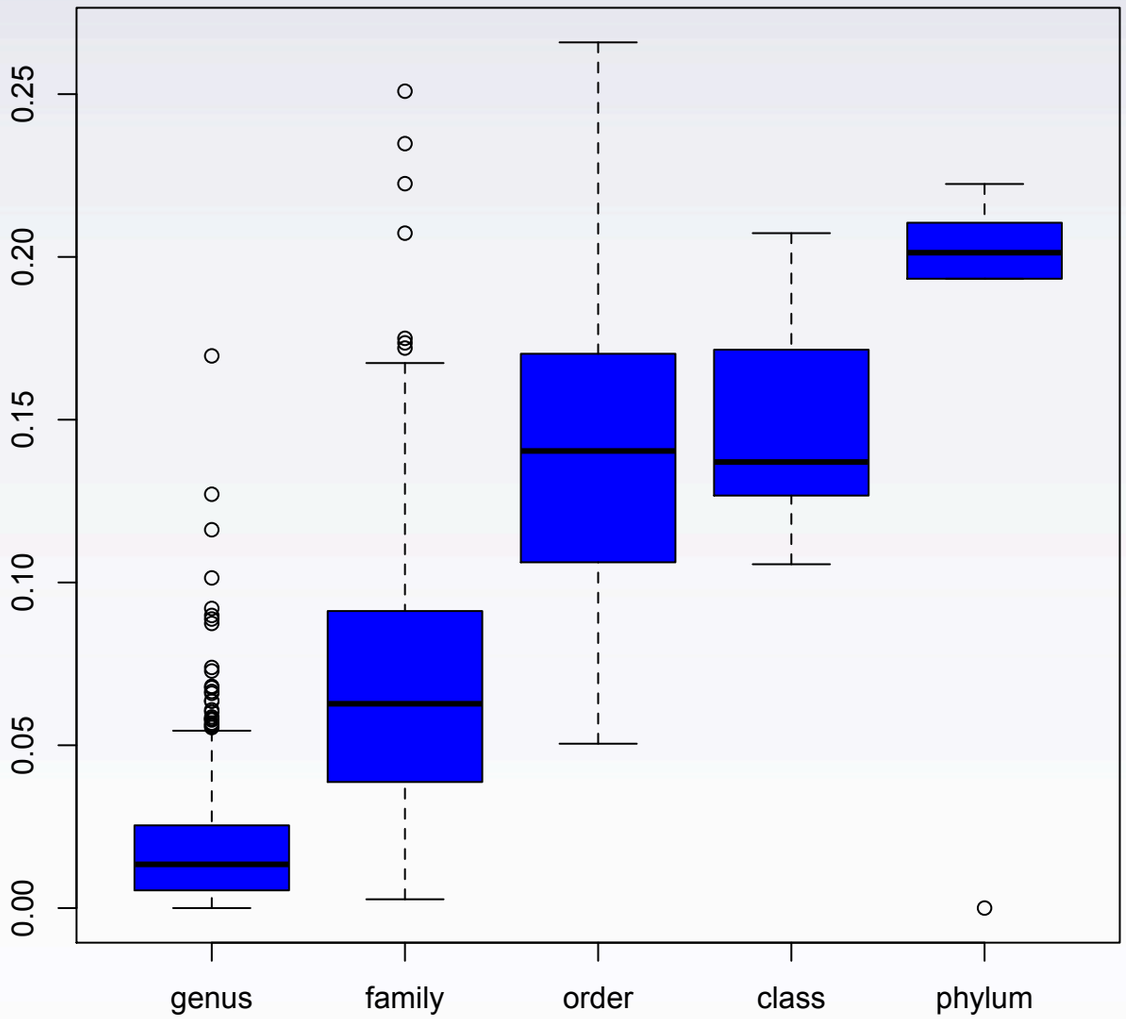
- **Smoothed distance/similarity matrices**
- **Summary statistics at each level of hierarchy**
- **Sets of reordered heatmaps**

- Input
  - Classification matrix
    - 11,402 aligned 16S rRNA
      - Source - NamesforLife Feb 2014 release
      - Greengenes alignment
      - Evolutionary distance computed
  - Nomenclature hierarchy
    - Coverage
      - 17,549 validly published names
        - 11 ranks
      - 2,911 synonyms
    - Transformed to a binary distance matrix
    - Source - NamesforLife Feb 2014 release

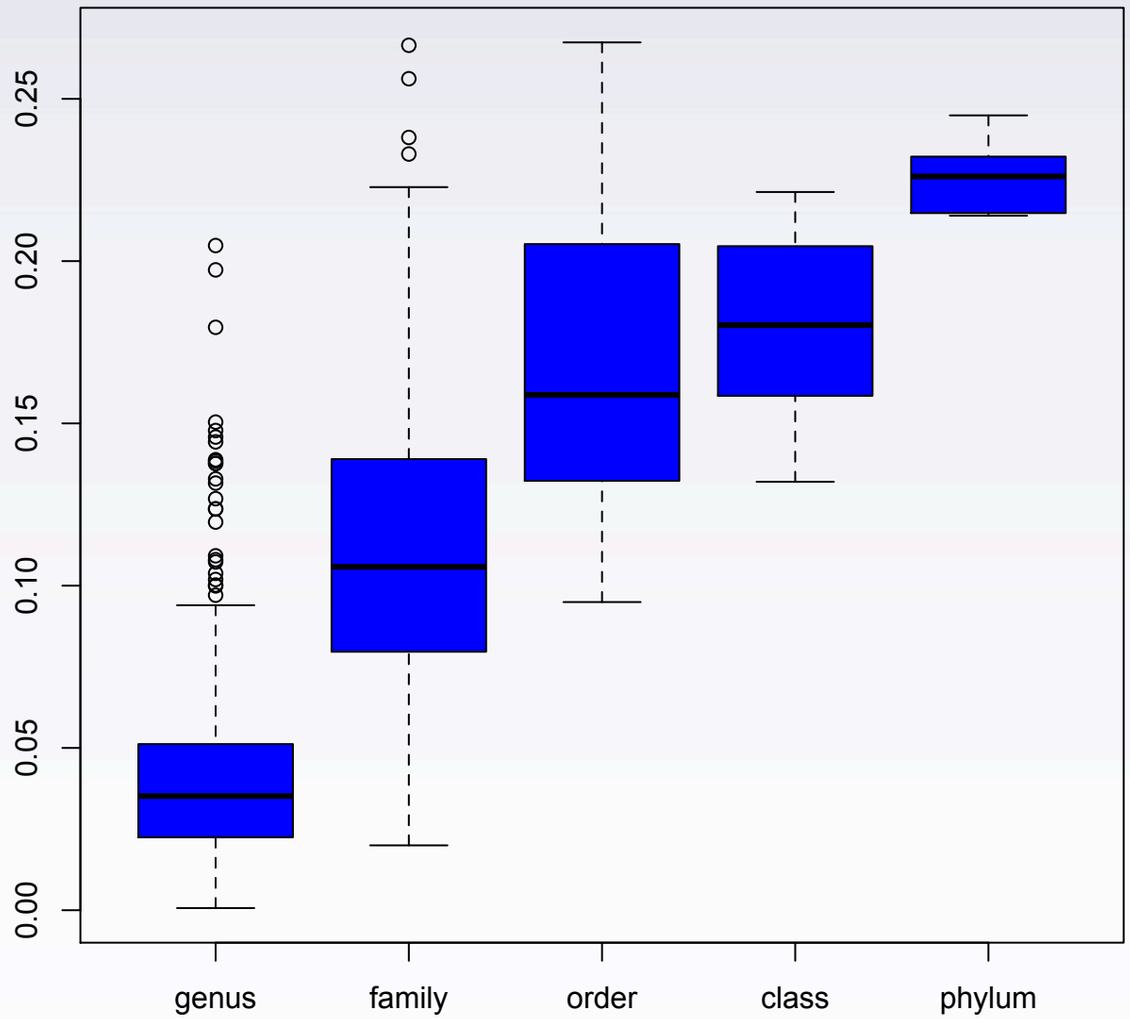
Rank	Validly published	Analyzed	Synonyms	Single member	Two members	3-5 members	6-10 members	> 10 members
Domain*	2	2	0	0	0	0	0	2
Phylum*	39	33	6	4	2	4	2	21
Class	106	75	31	18	7	6	9	35
Subclass	6	6	0	1	1	1	1	2
Order	197	170	27	46	18	15	19	74
Suborder	23	23	0	2	1	2	4	14
Family	465	410	55	109	41	48	49	163
Genus	2,511	2,245	266	1,088	397	369	195	196
Subgenus	5	5	0	1	4	0	0	0
Species	13,757	11410	2347	11,410	0	0	0	0
Subspecies	438	438	179	179	2	204	19	2

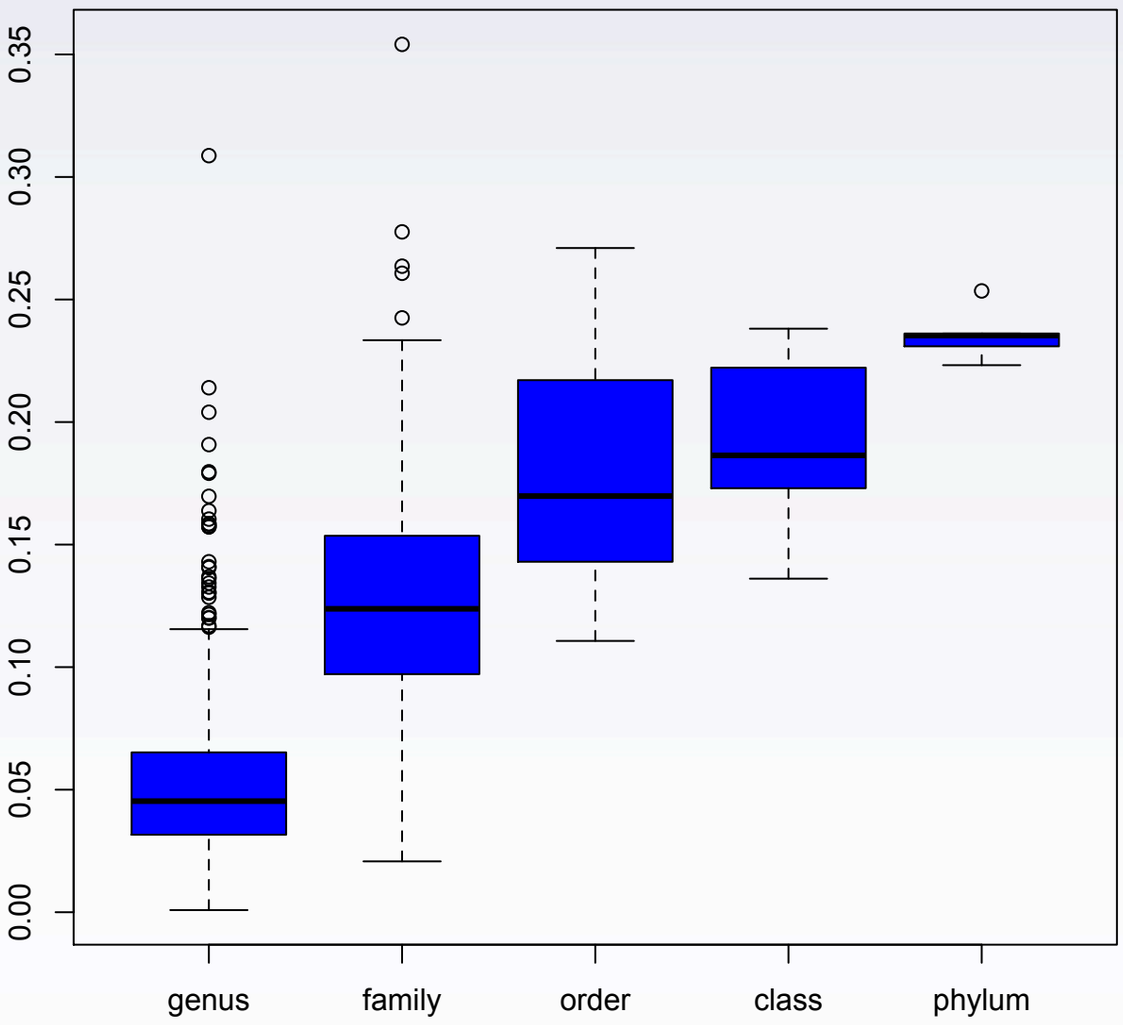
NamesforLIfe nomenclatural hierarchy for validly published *Bacteria* and *Archaea,* February 2014

Minimum taxon boundaries



First quartile taxon boundaries

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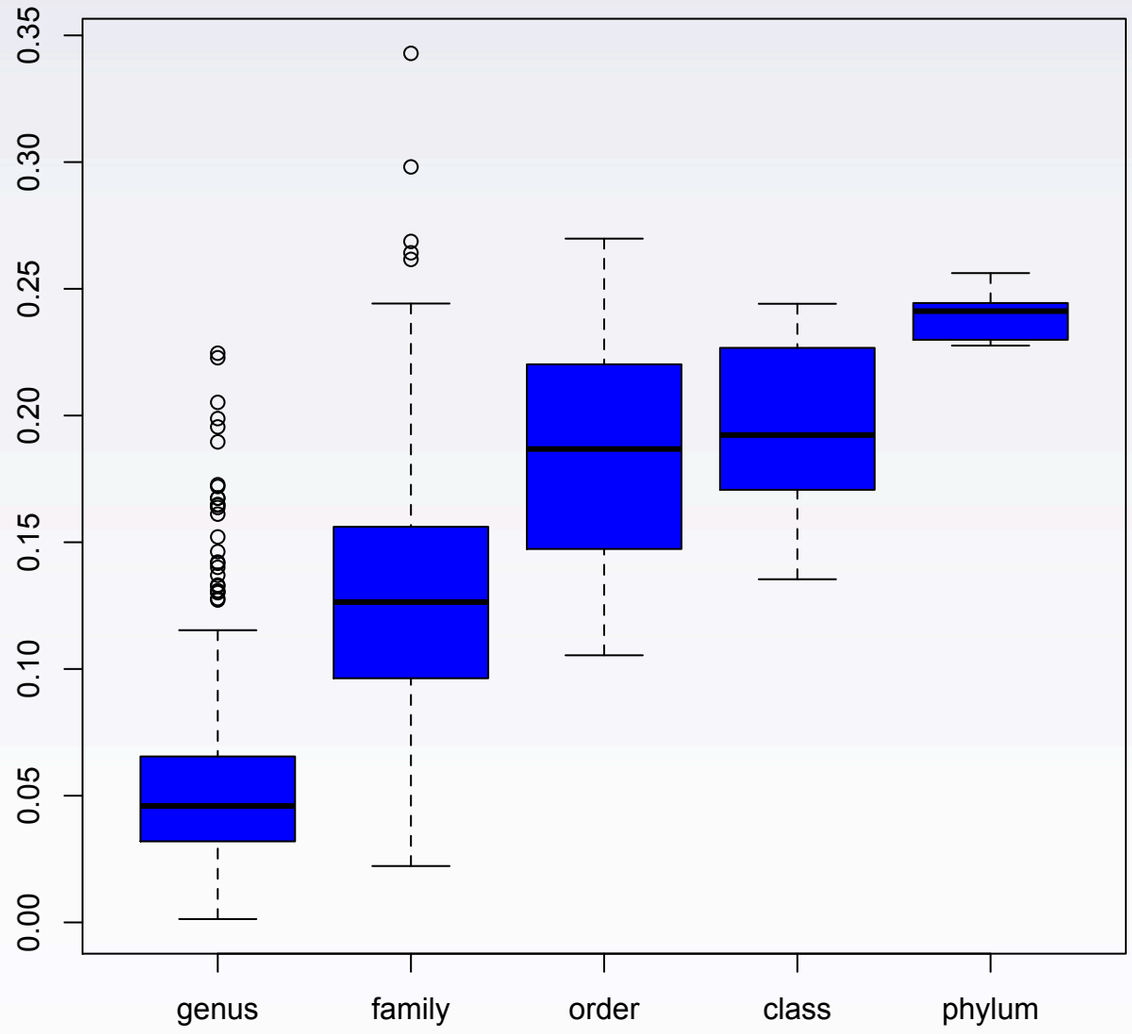
0.35
genus
family
order
class
phylum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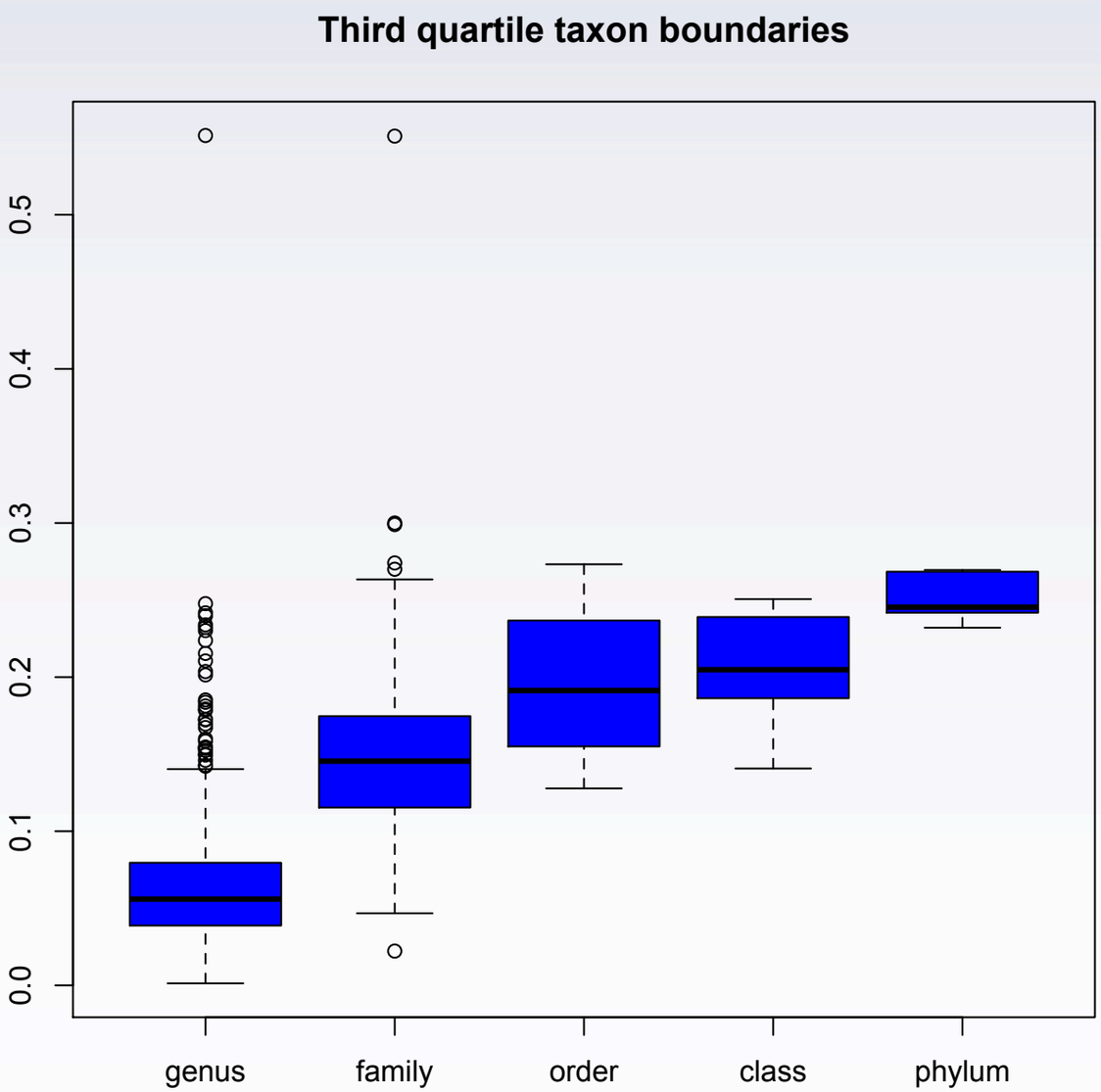
family
order
class
phylum


Third quartile taxon boundaries
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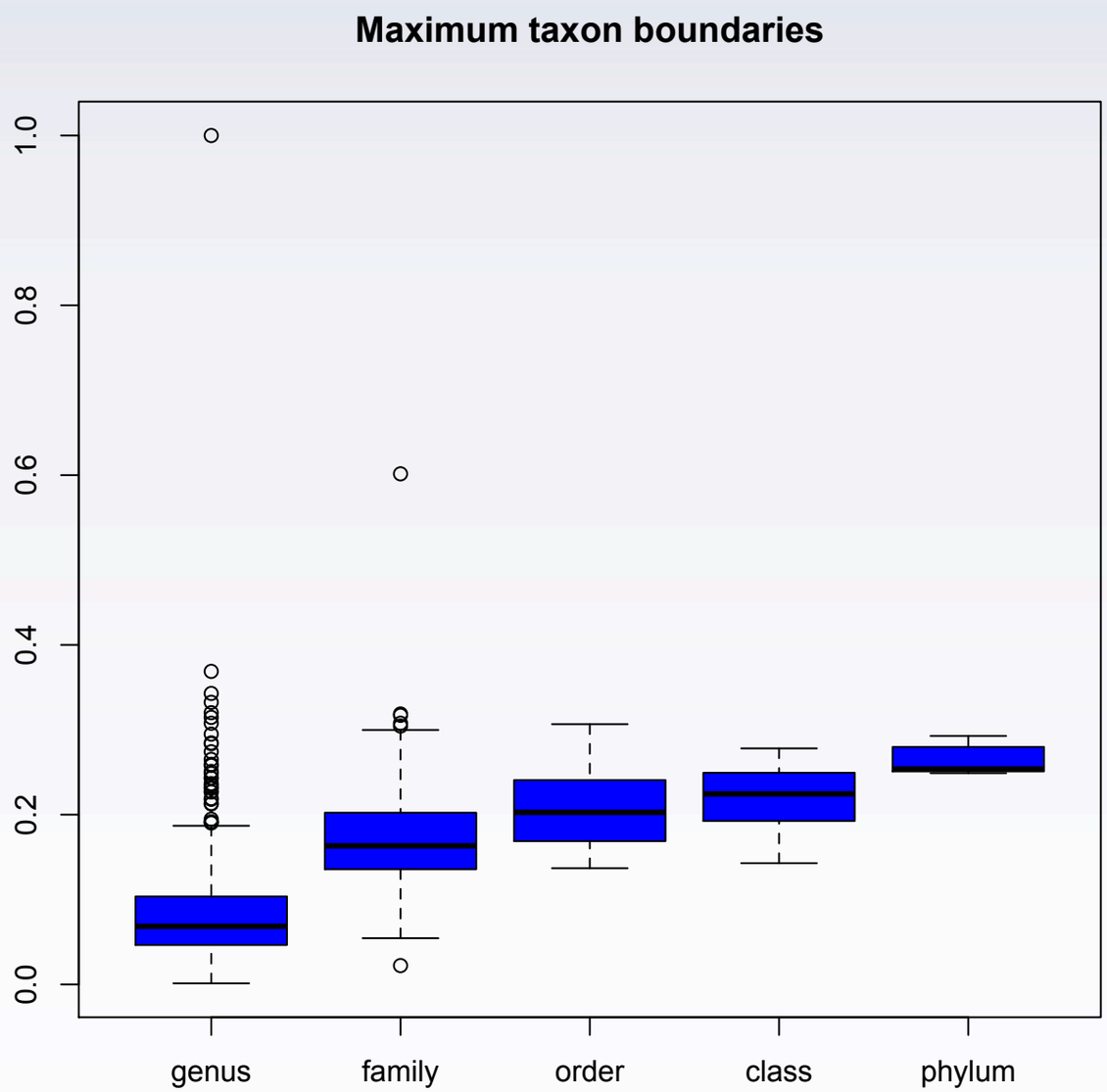
order
class
phylum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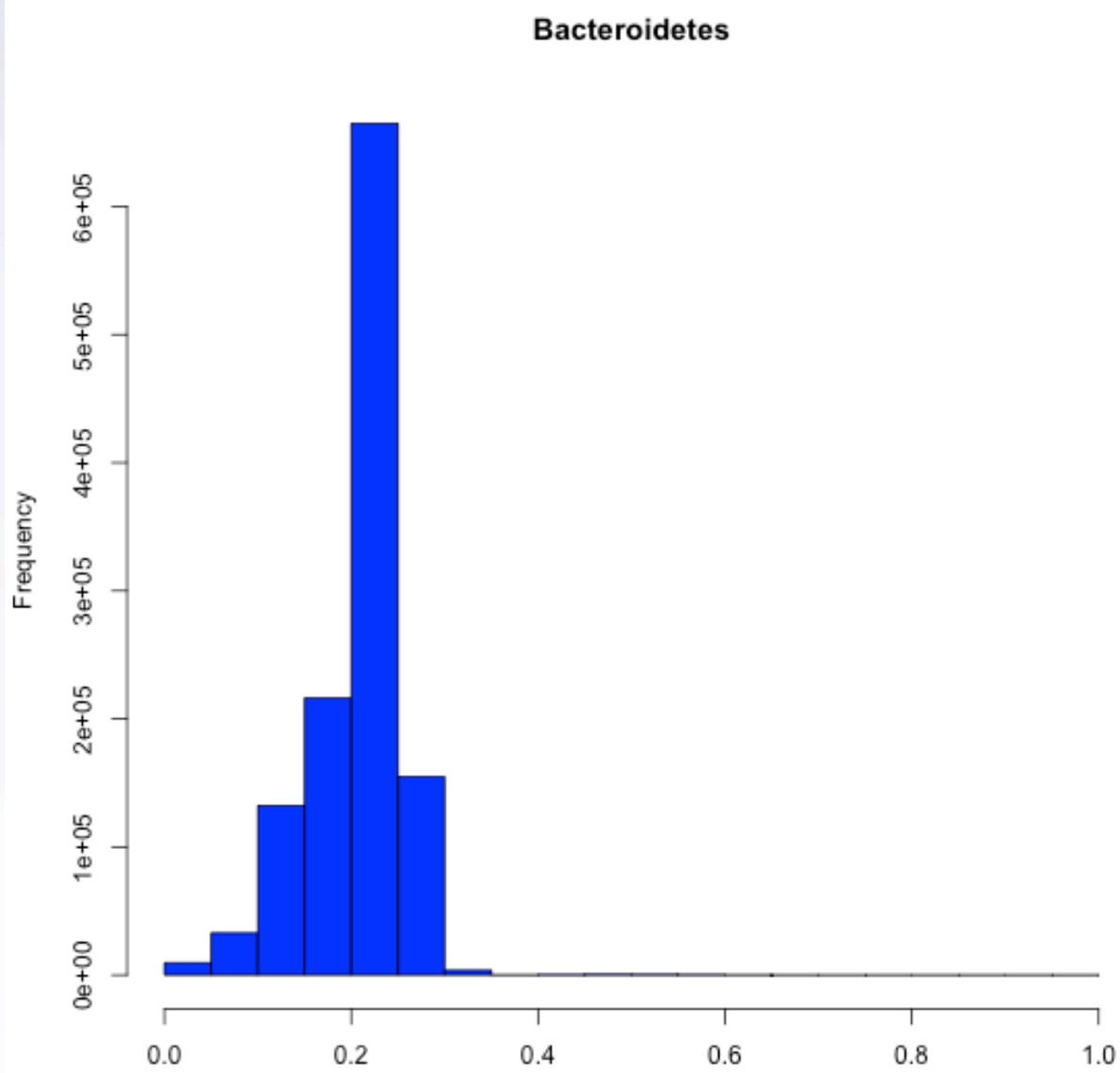
order
class
phylum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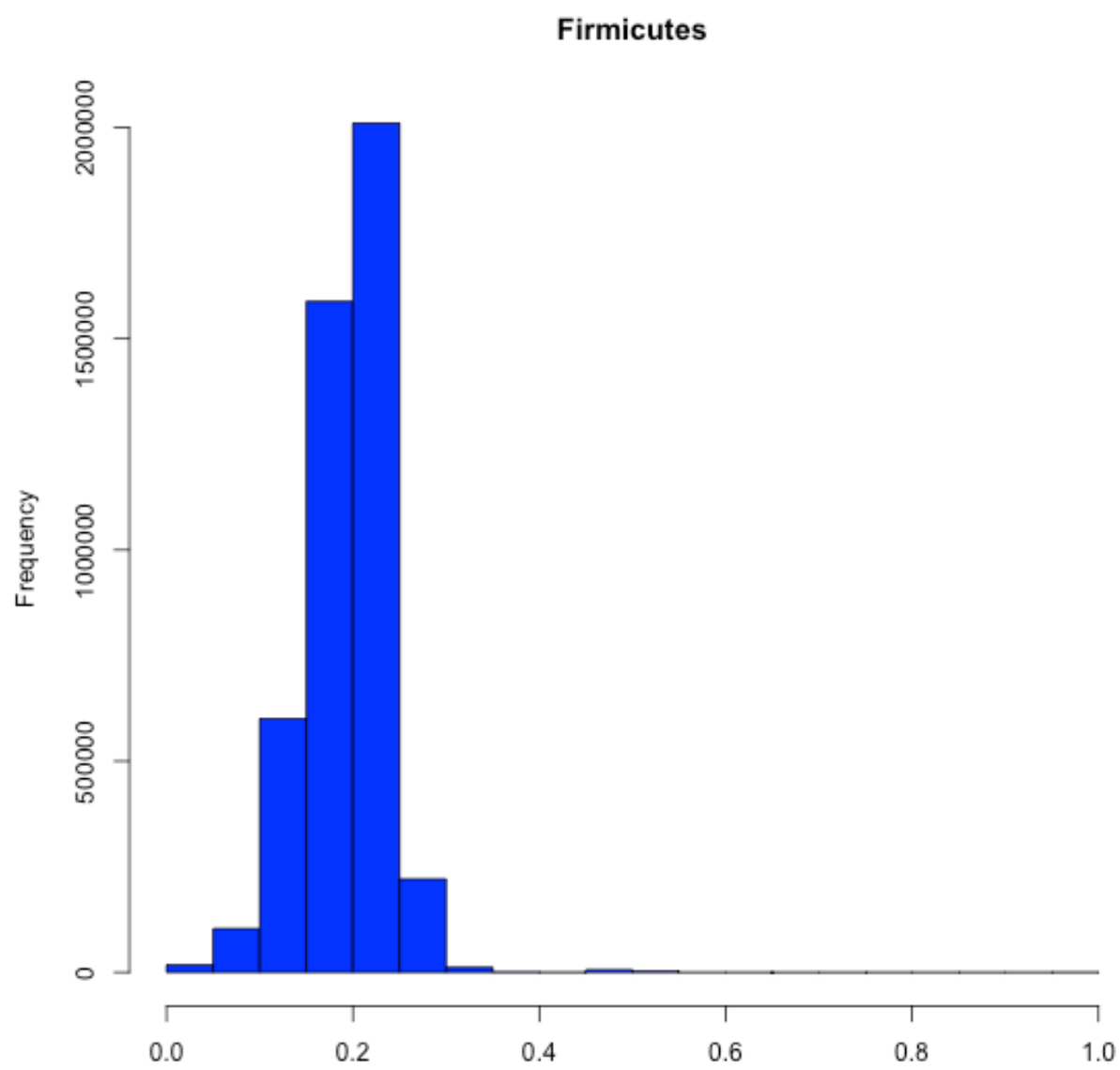
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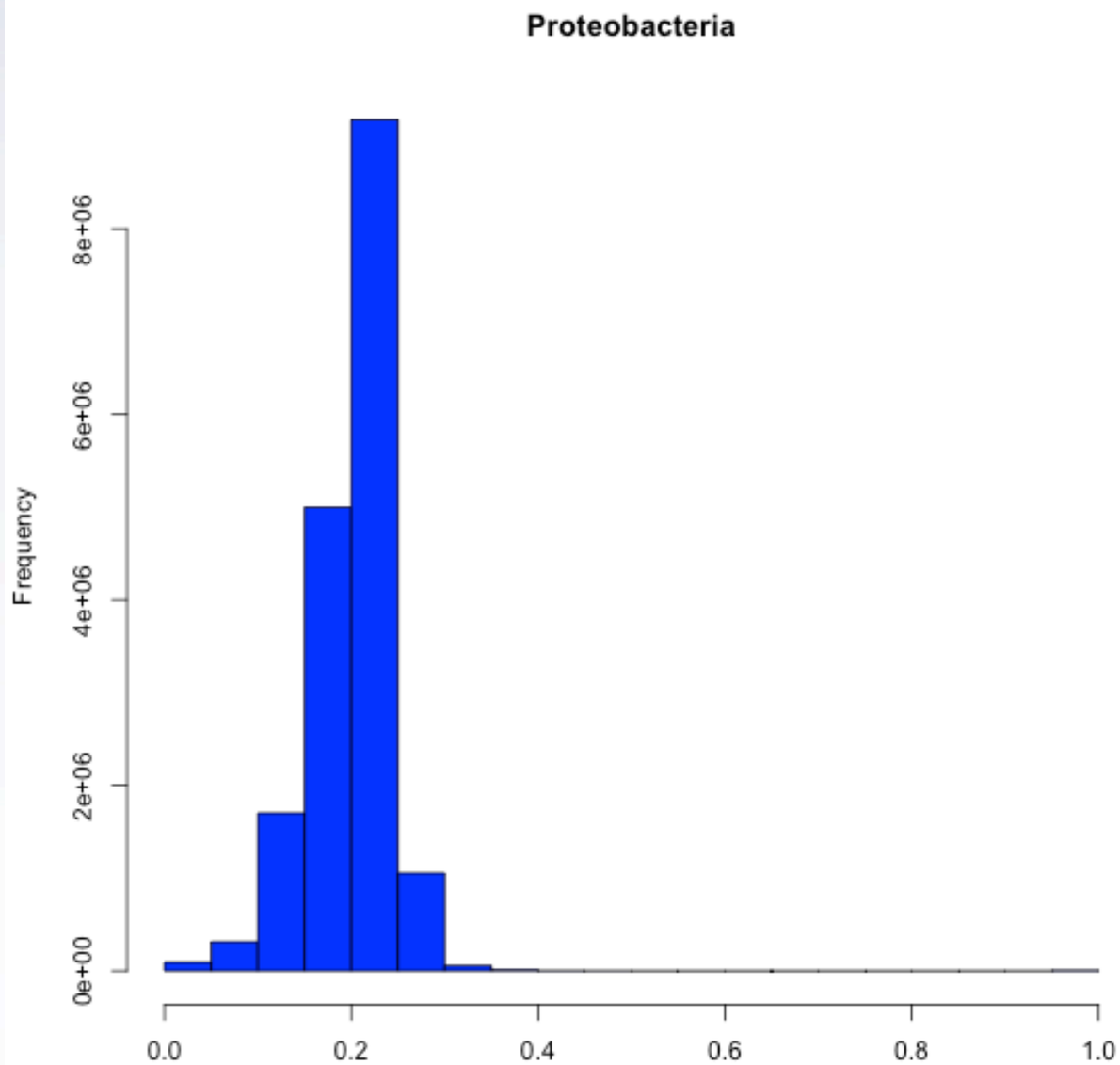
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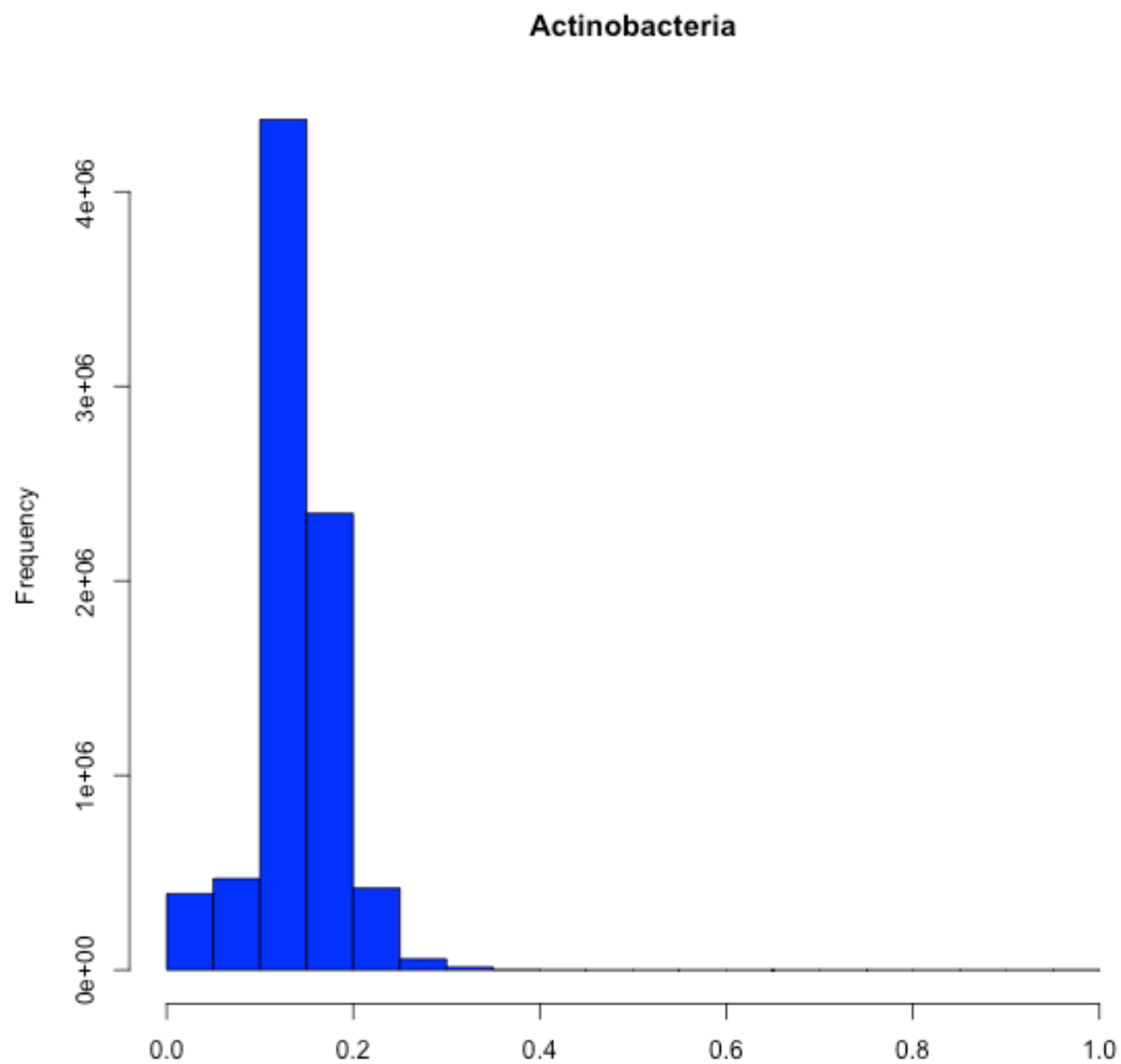
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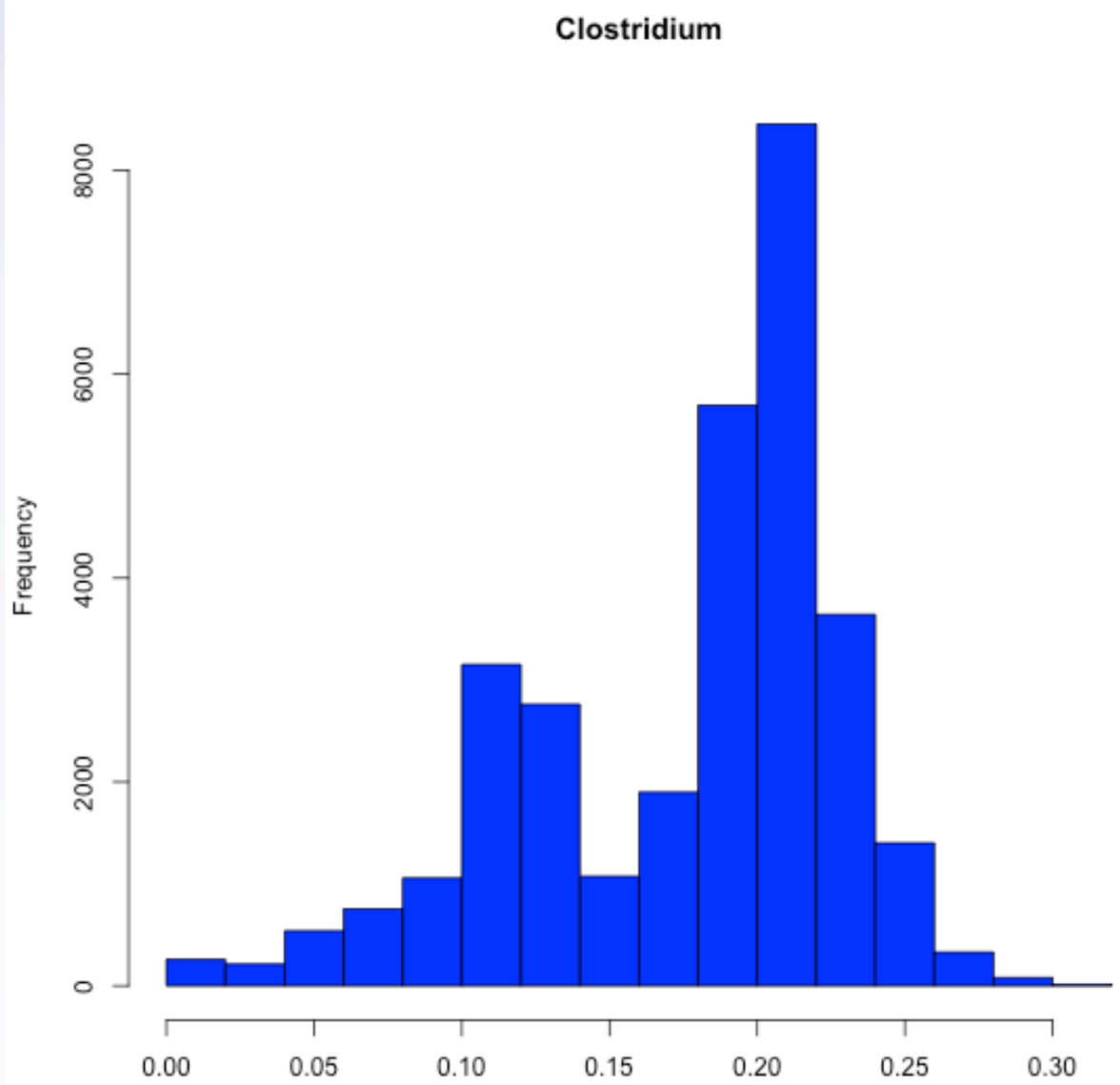
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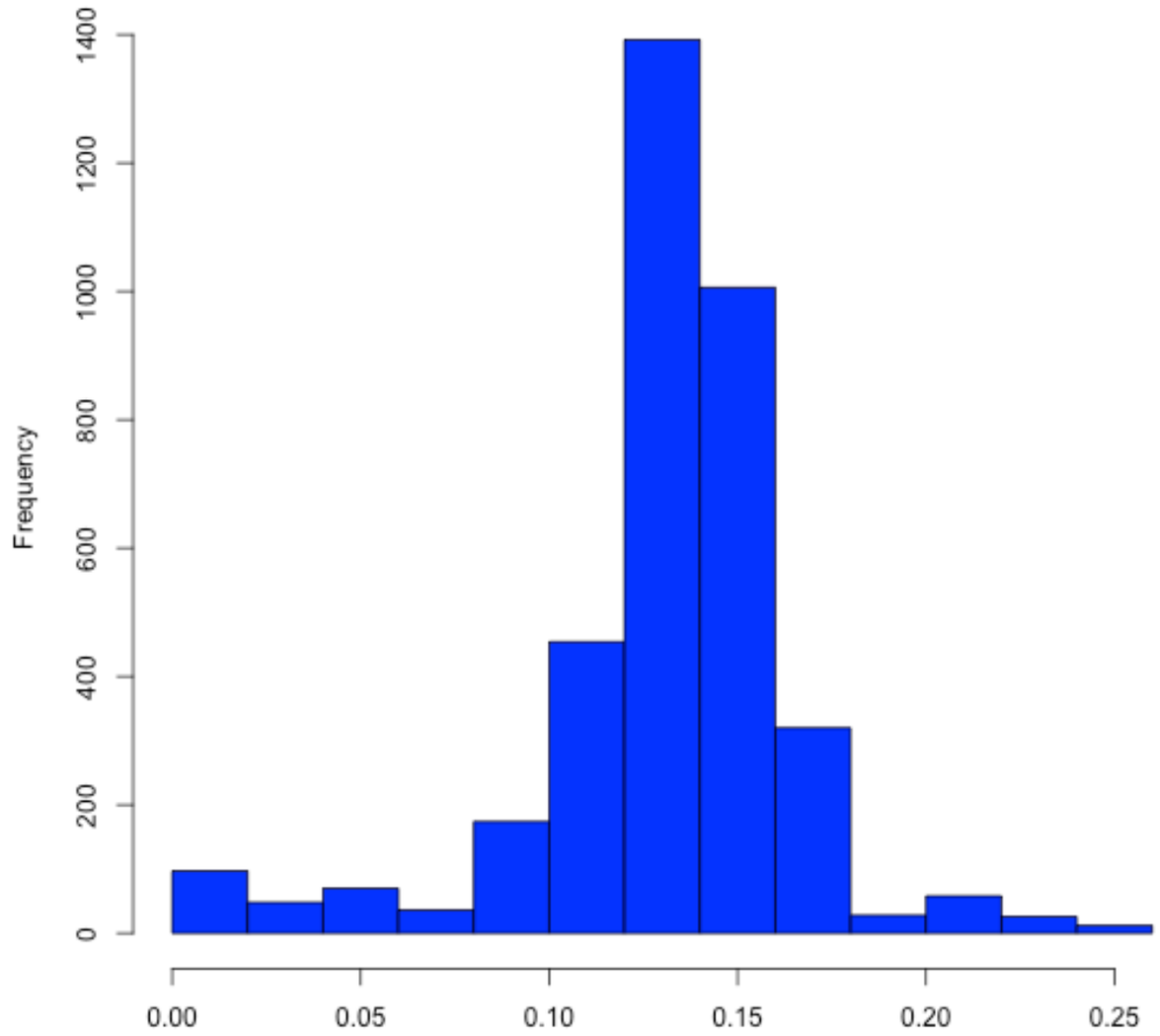
Desulfovibrio
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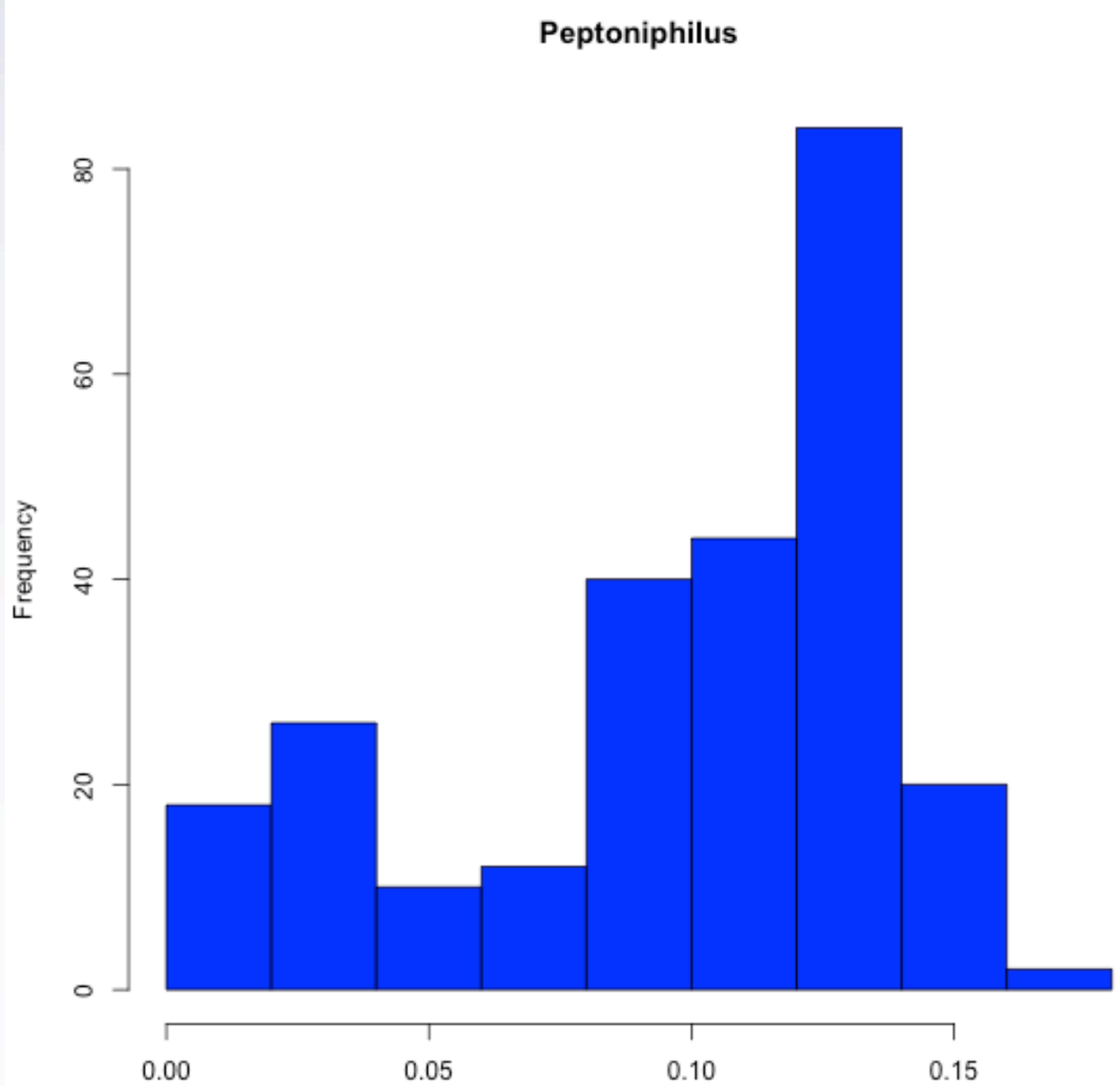
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0.10
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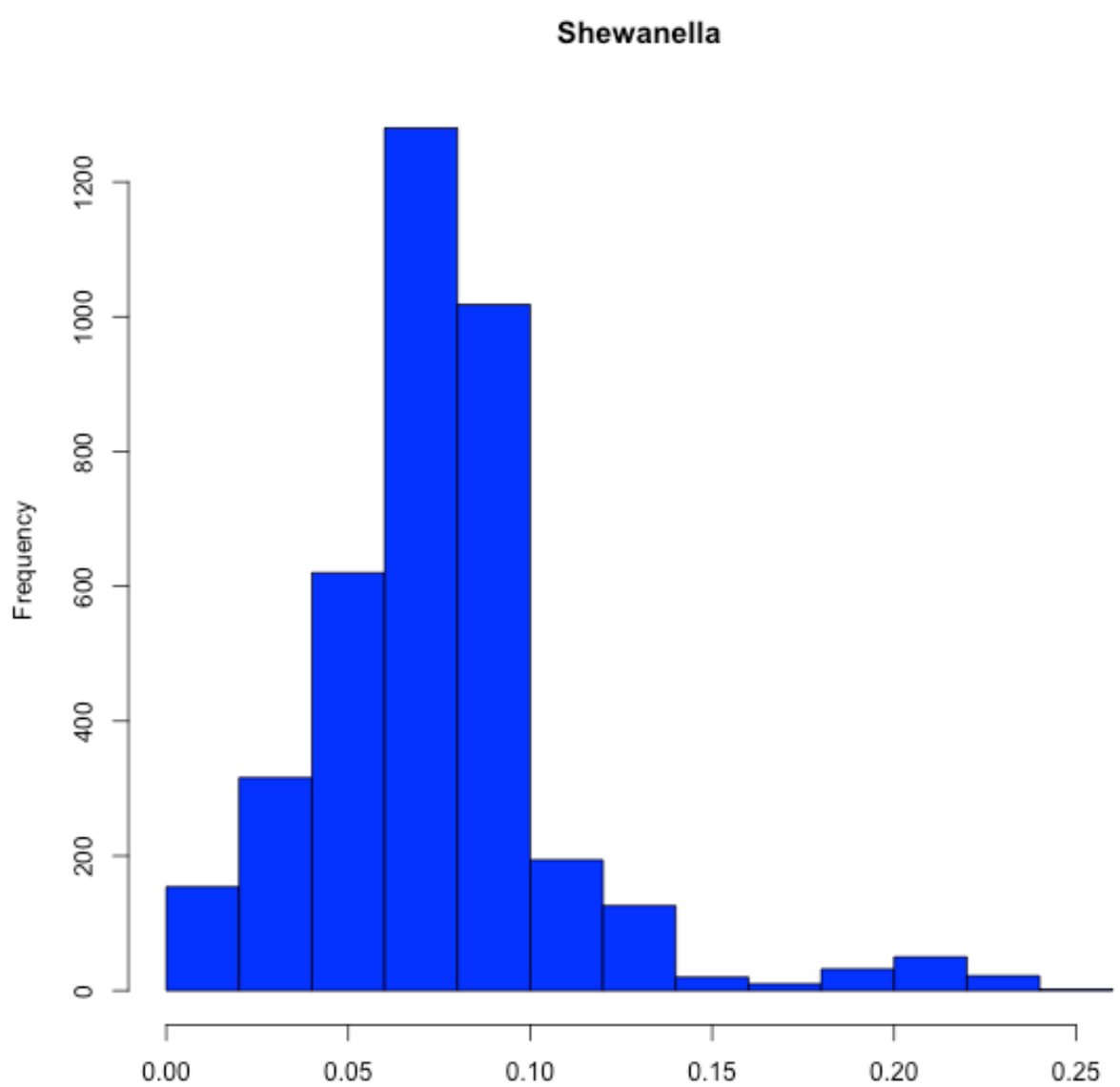
Shewanella
Frequency
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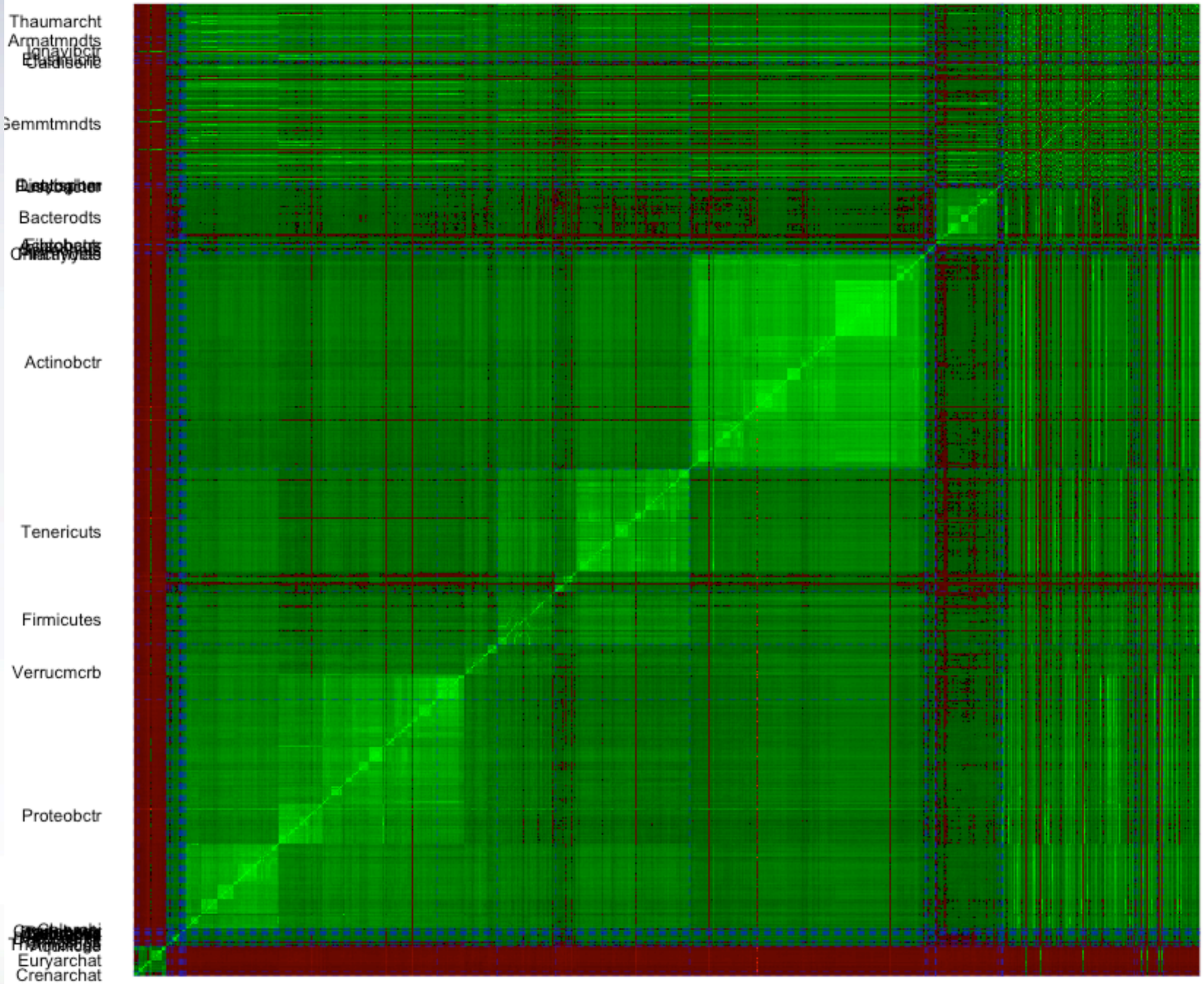
400
600
800
1000
1200
0.00
0.05
0.10
0.15
0.20
0.25

Rank	Min	Max		Min	Q1	Median	Mean	Q3	Max
Genus	2	597	**average**	0.026	0.040	0.048	0.048	0.056	0.075
			min	0.000	0.000	0.000	0.000	0.000	0.000
			max	1.000	1.000	1.000	1.000	1.000	1.000
Family	2	668	**average**	0.021	0.070	0.095	0.092	0.115	0.187
			min	0.000	0.004	0.006	0.006	0.006	0.006
			max	0.225	0.239	0.260	0.347	0.781	1.000
Order	2	2725	**average**	0.022	0.090	0.120	0.115	0.139	0.257
			min	0.000	0.009	0.009	0.009	0.009	0.009
			max	0.207	0.208	0.235	0.220	0.296	1.000
Class	2	2796	**average**	0.021	0.116	0.146	0.138	0.164	0.364
			min	0.000	0.009	0.009	0.009	0.009	0.009
			max	0.207	0.208	0.244	0.222	0.265	1.000
Phylum	2	4173	**average**	0.023	0.136	0.172	0.164	0.197	0.467
			min	0.000	0.047	0.047	0.047	0.047	0.047
			max	0.206	0.222	0.257	0.241	0.275	1.000
Domain	428	11004	**average**	0.000	0.216	0.250	0.241	0.275	1.000
			min	0.000	0.206	0.250	0.238	0.275	1.000
			max	0.000	0.226	0.251	0.244	0.275	1.000

Input ordering based on TOBA 7.7



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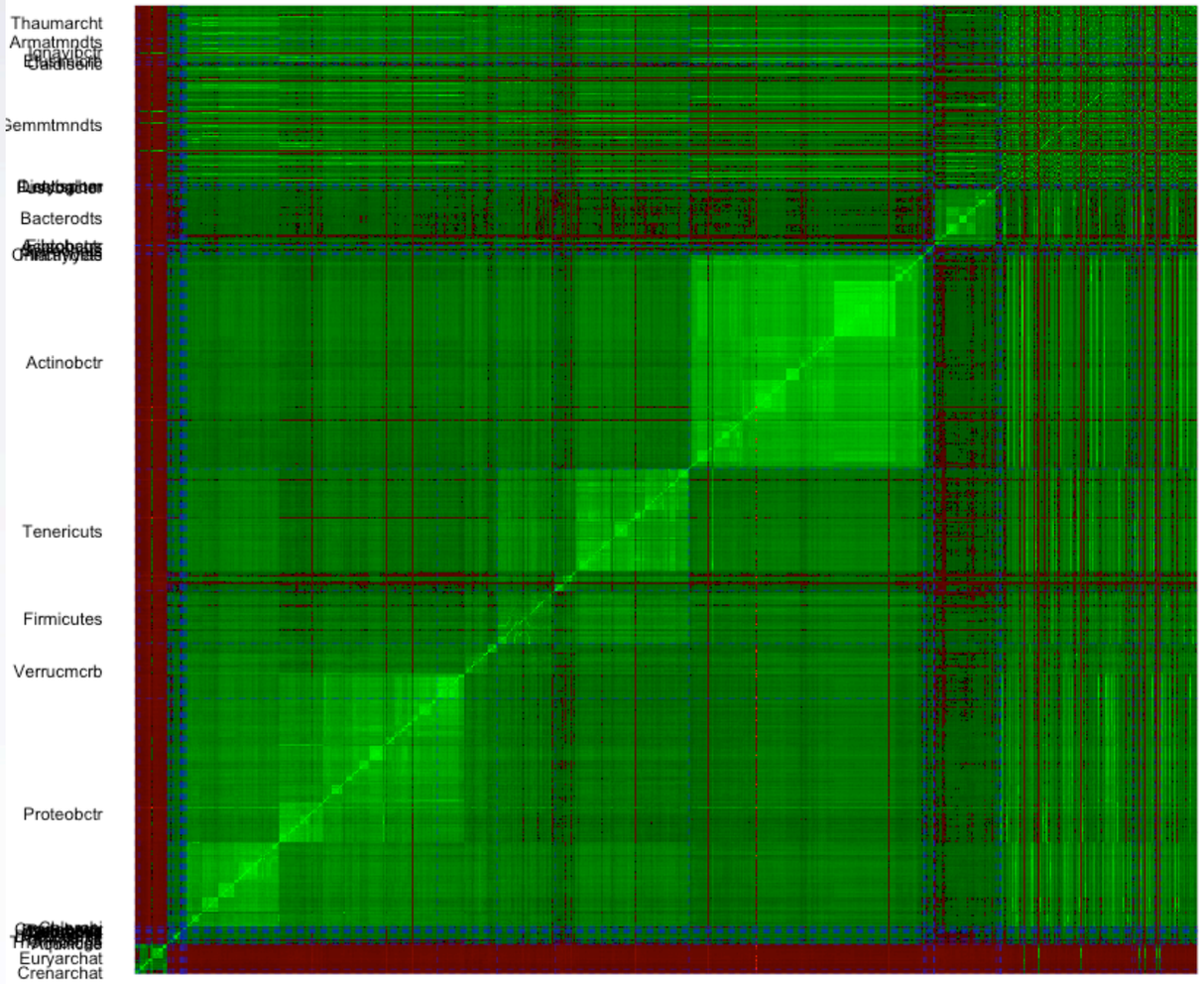

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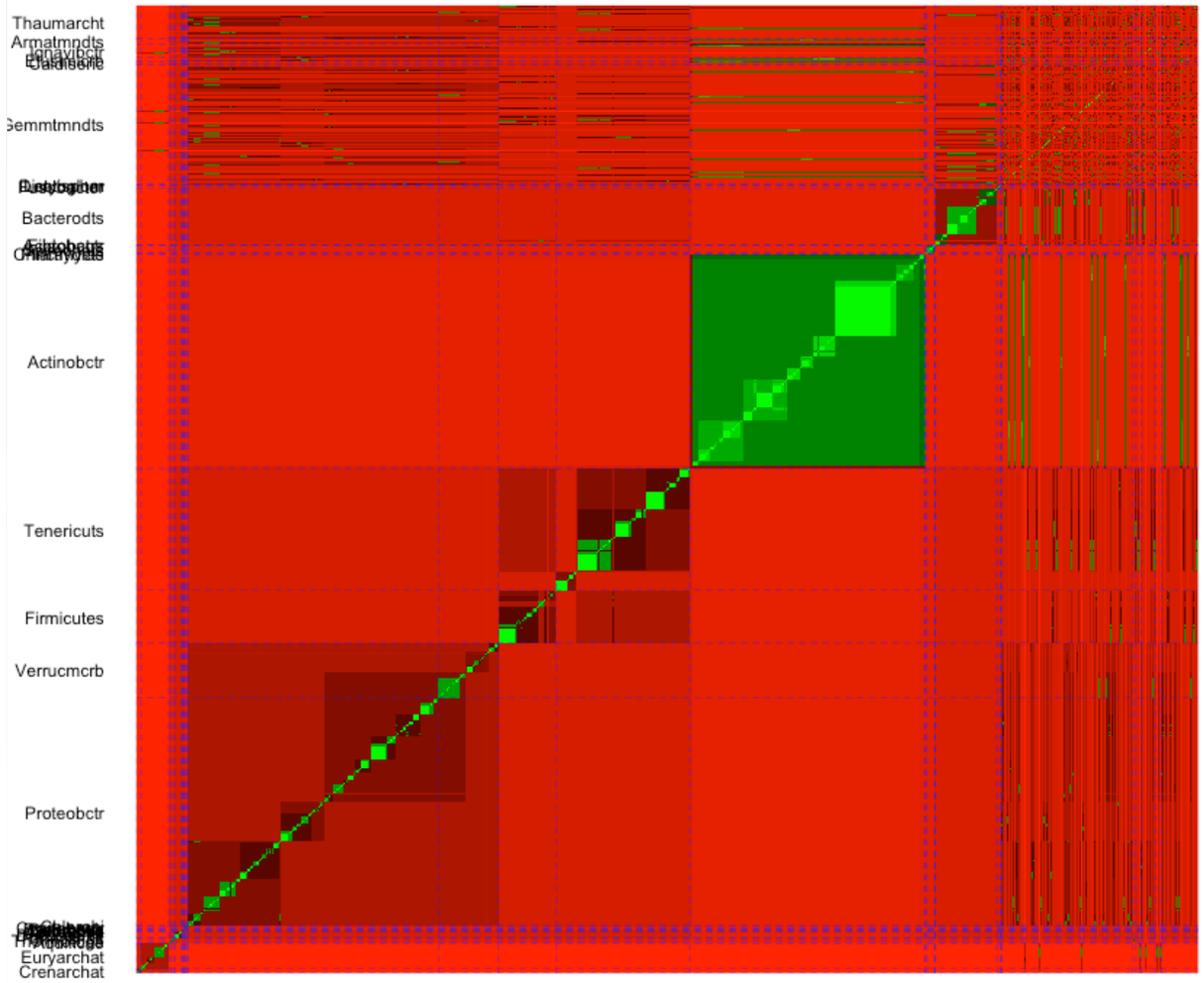

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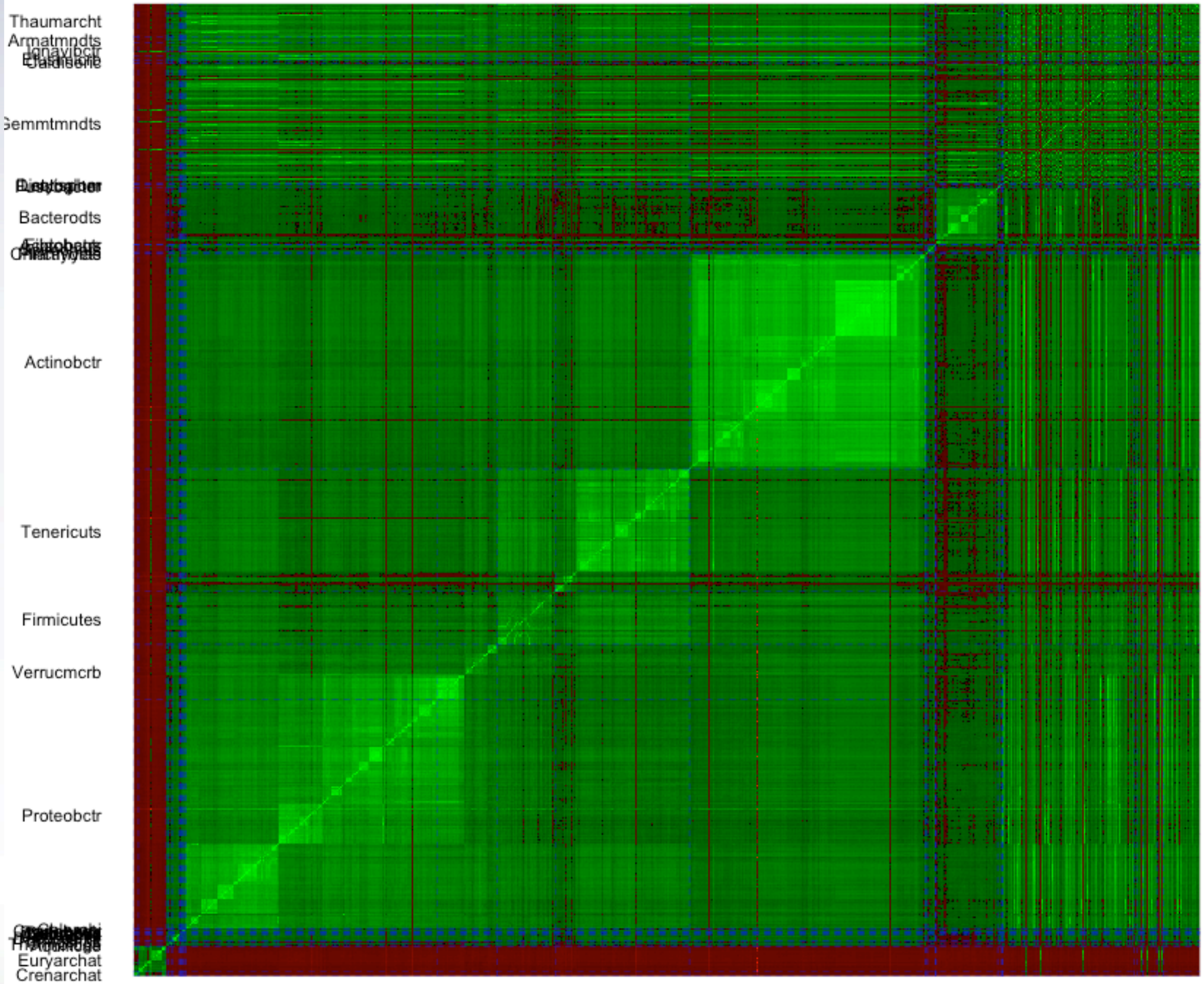
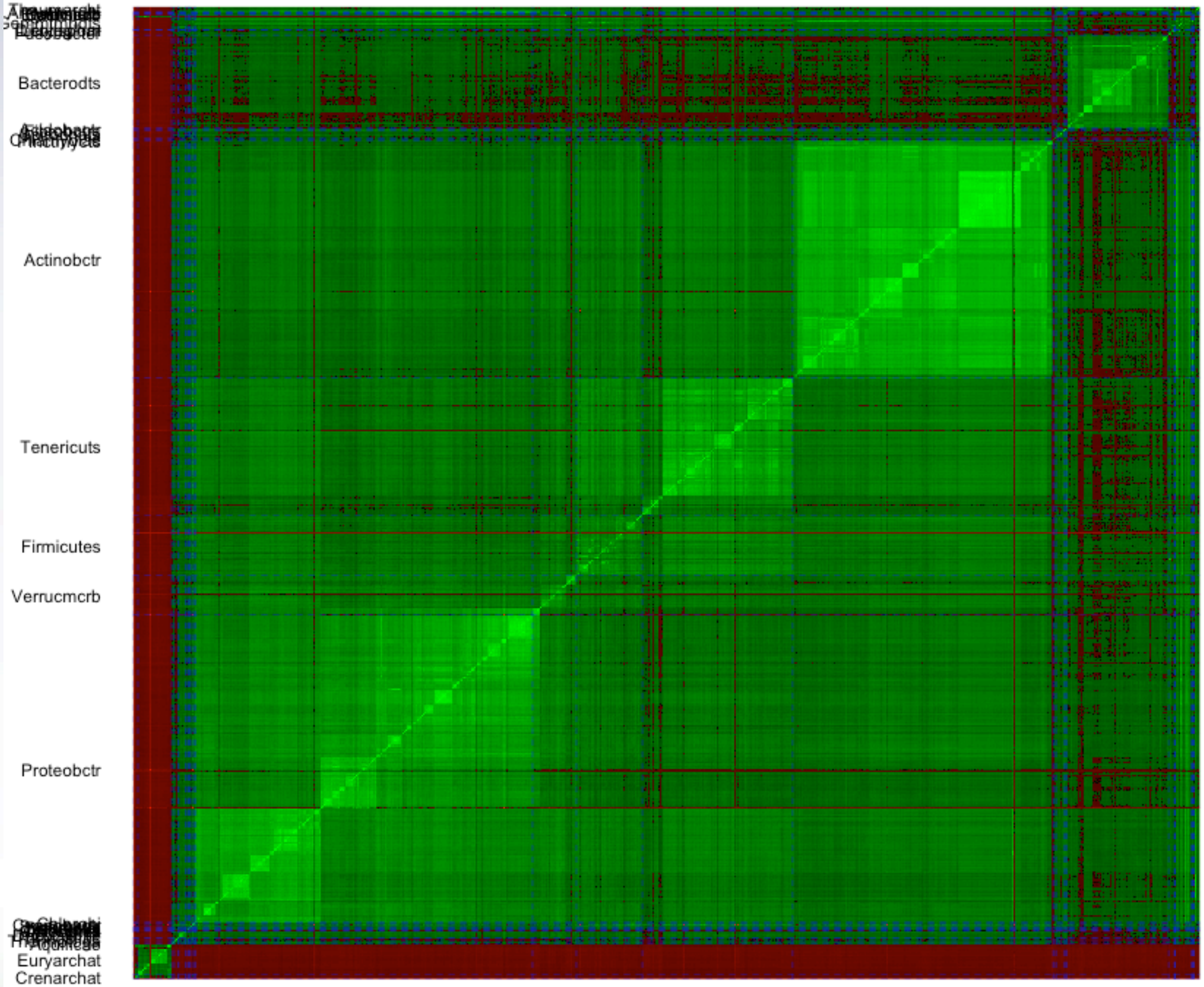
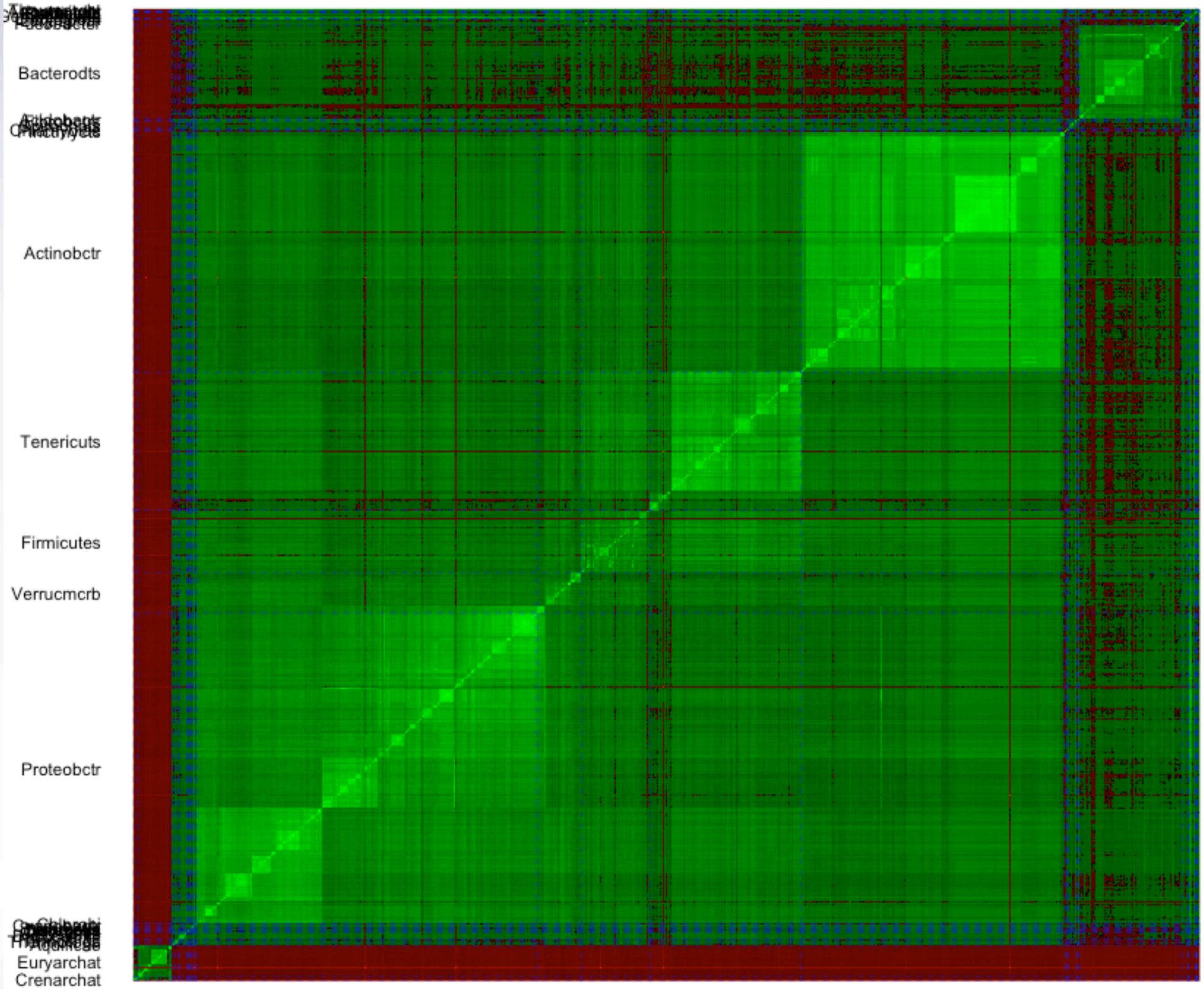


Rearranged at genus level



Rearranged at family level



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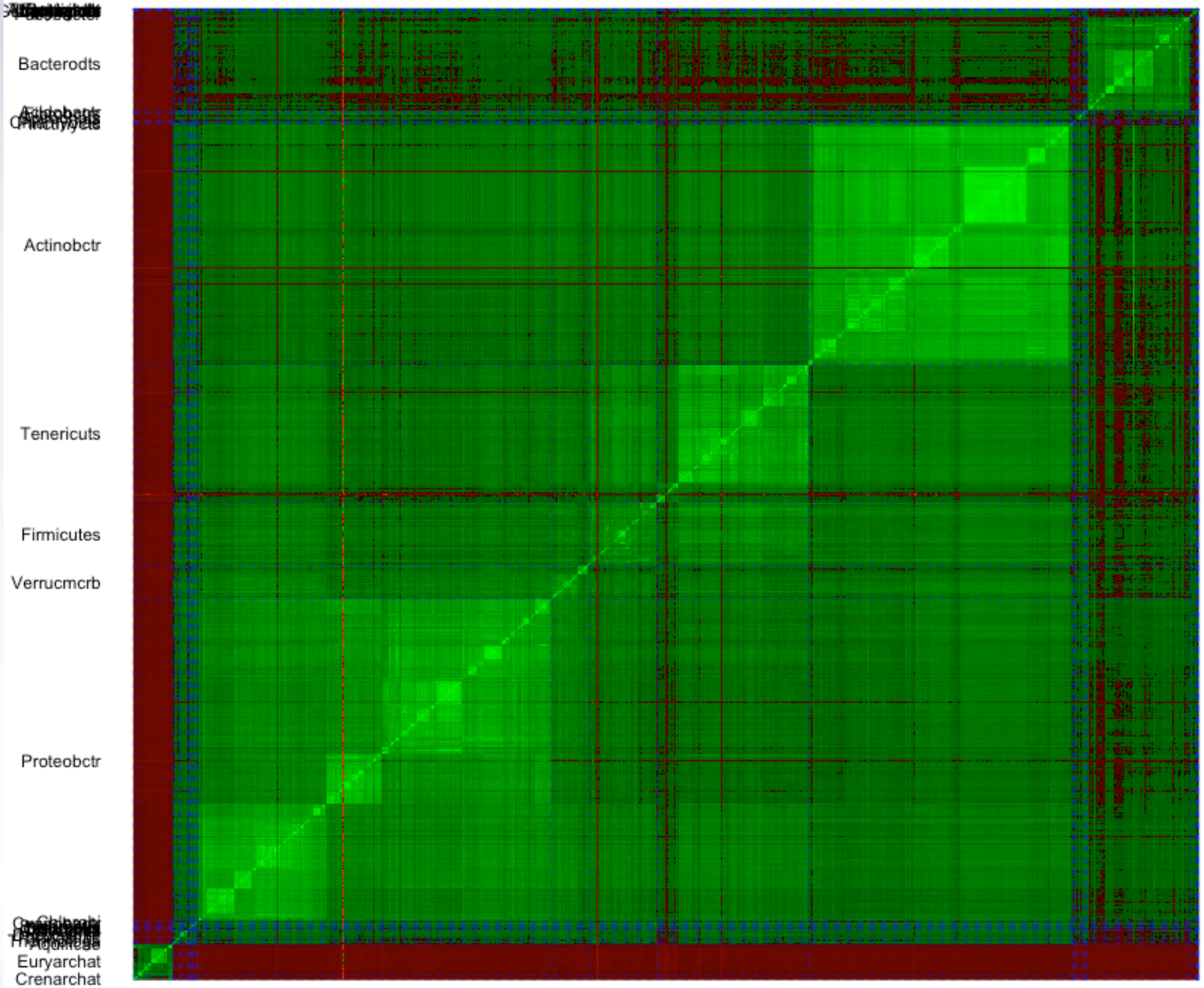

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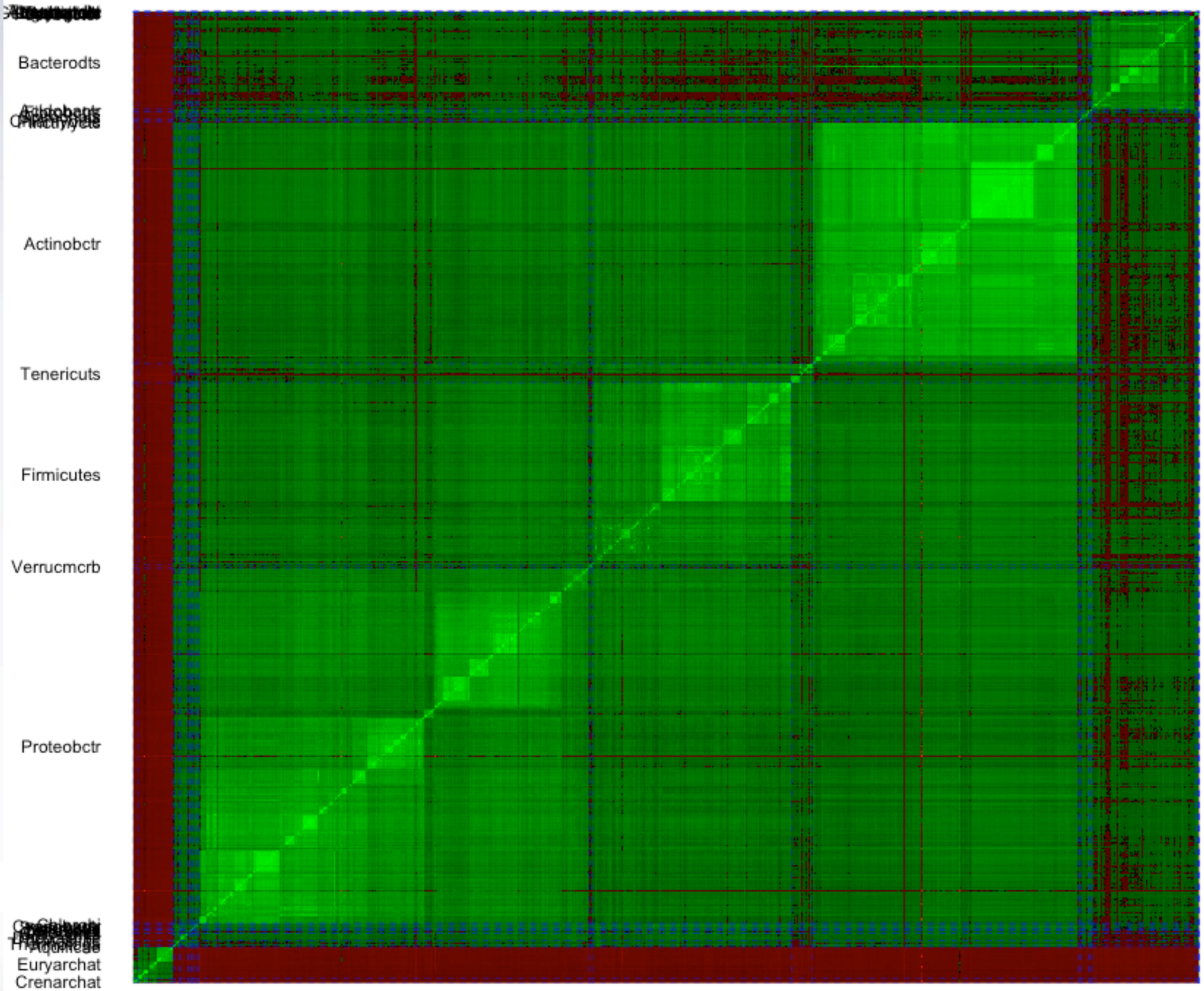

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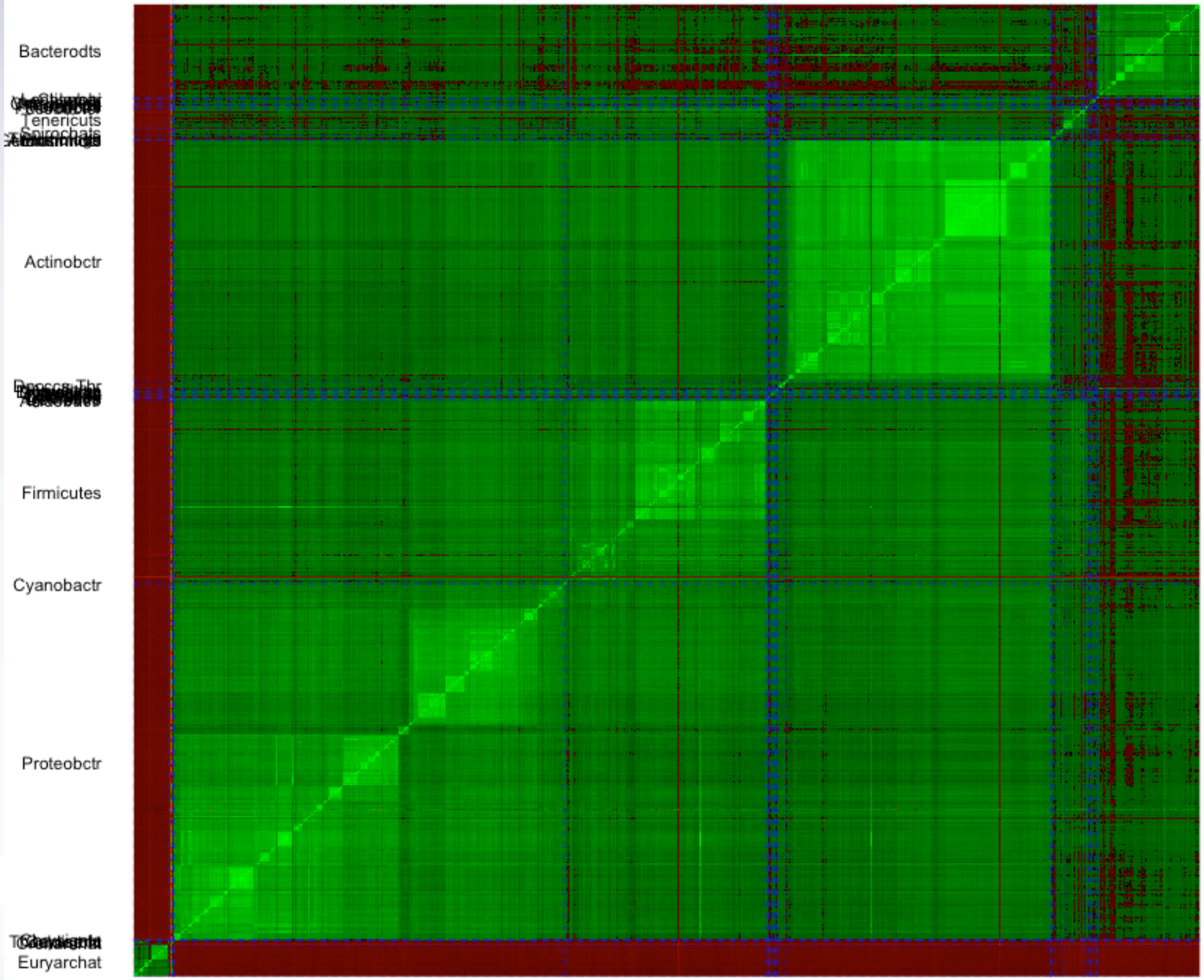

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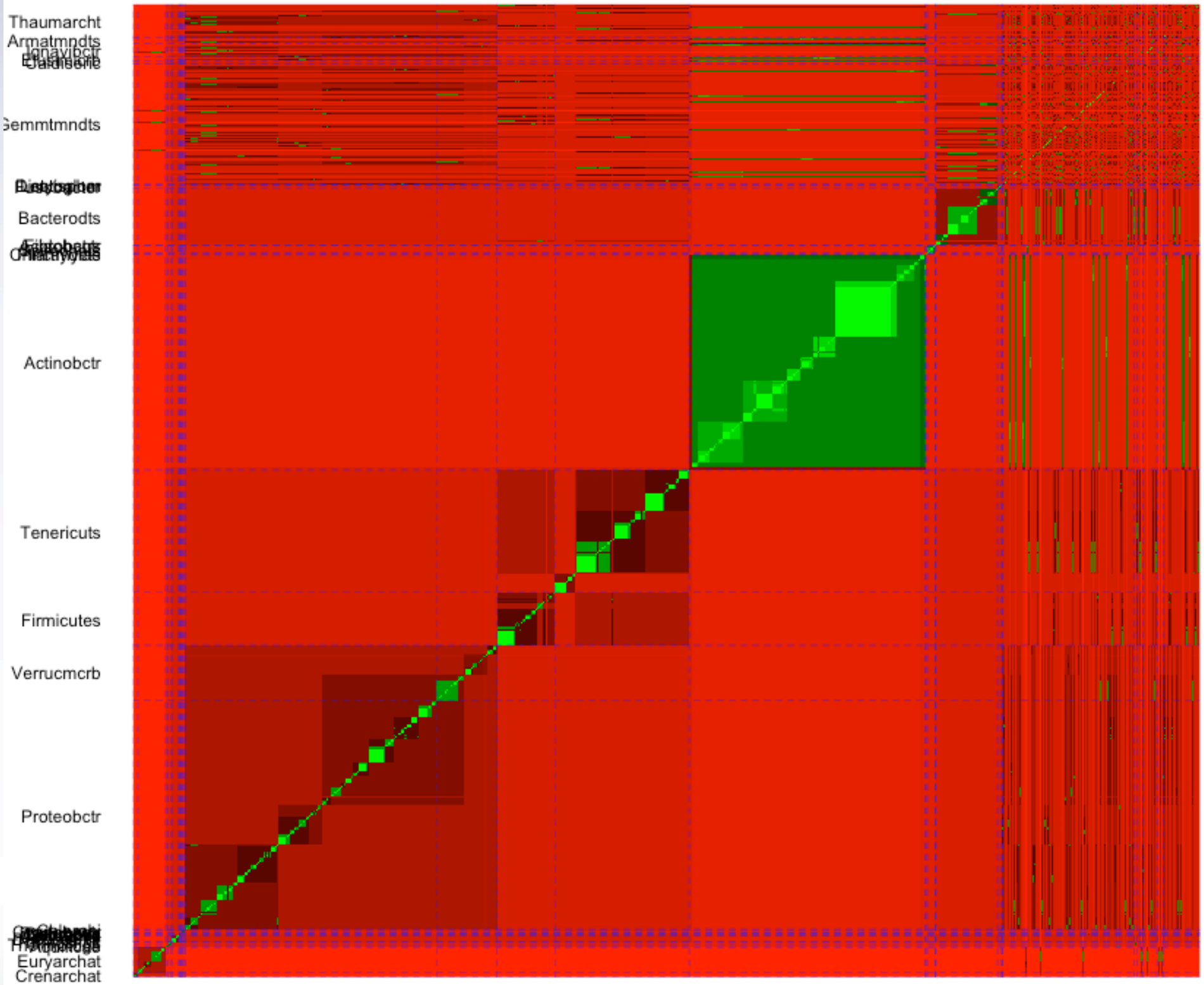

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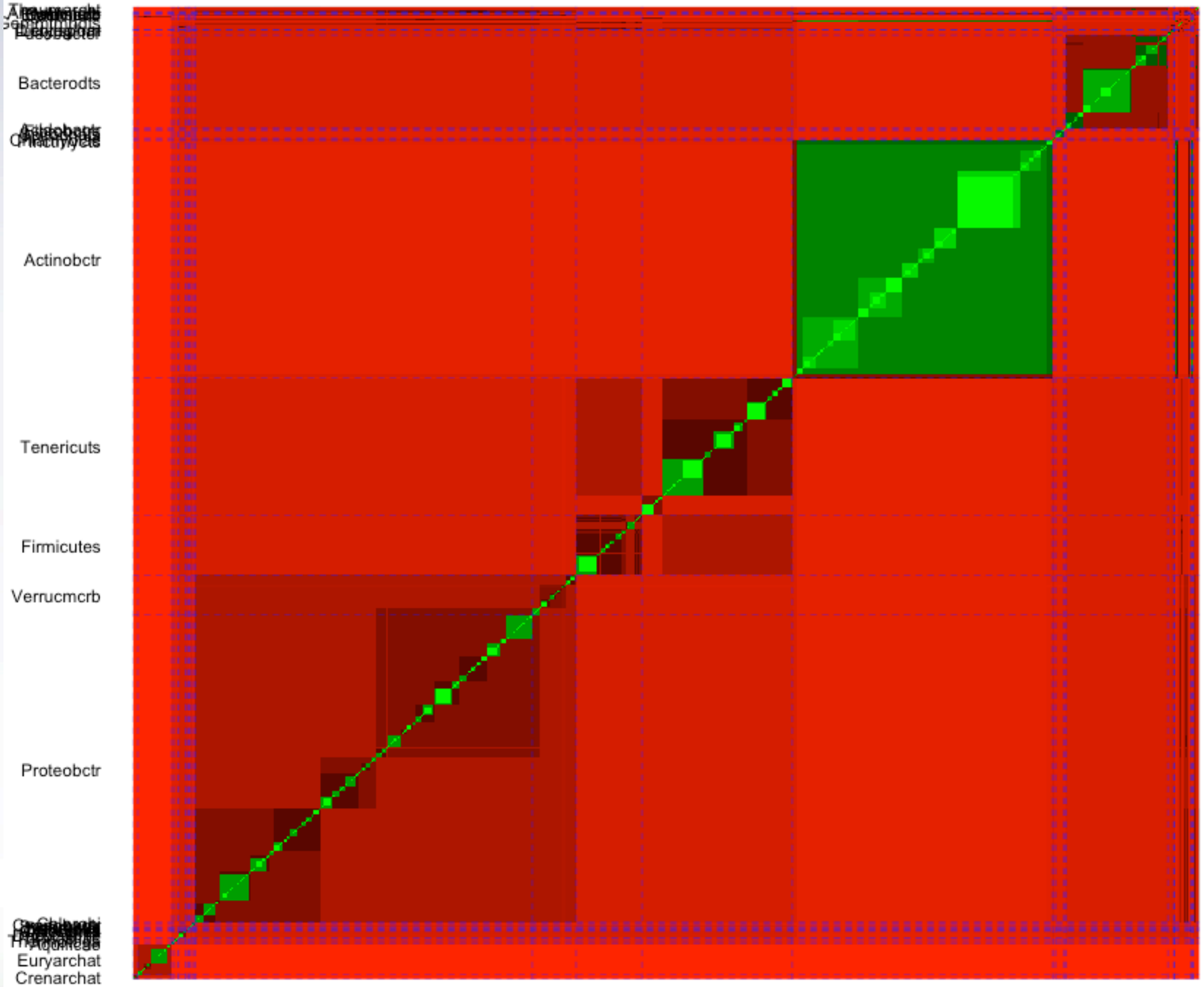

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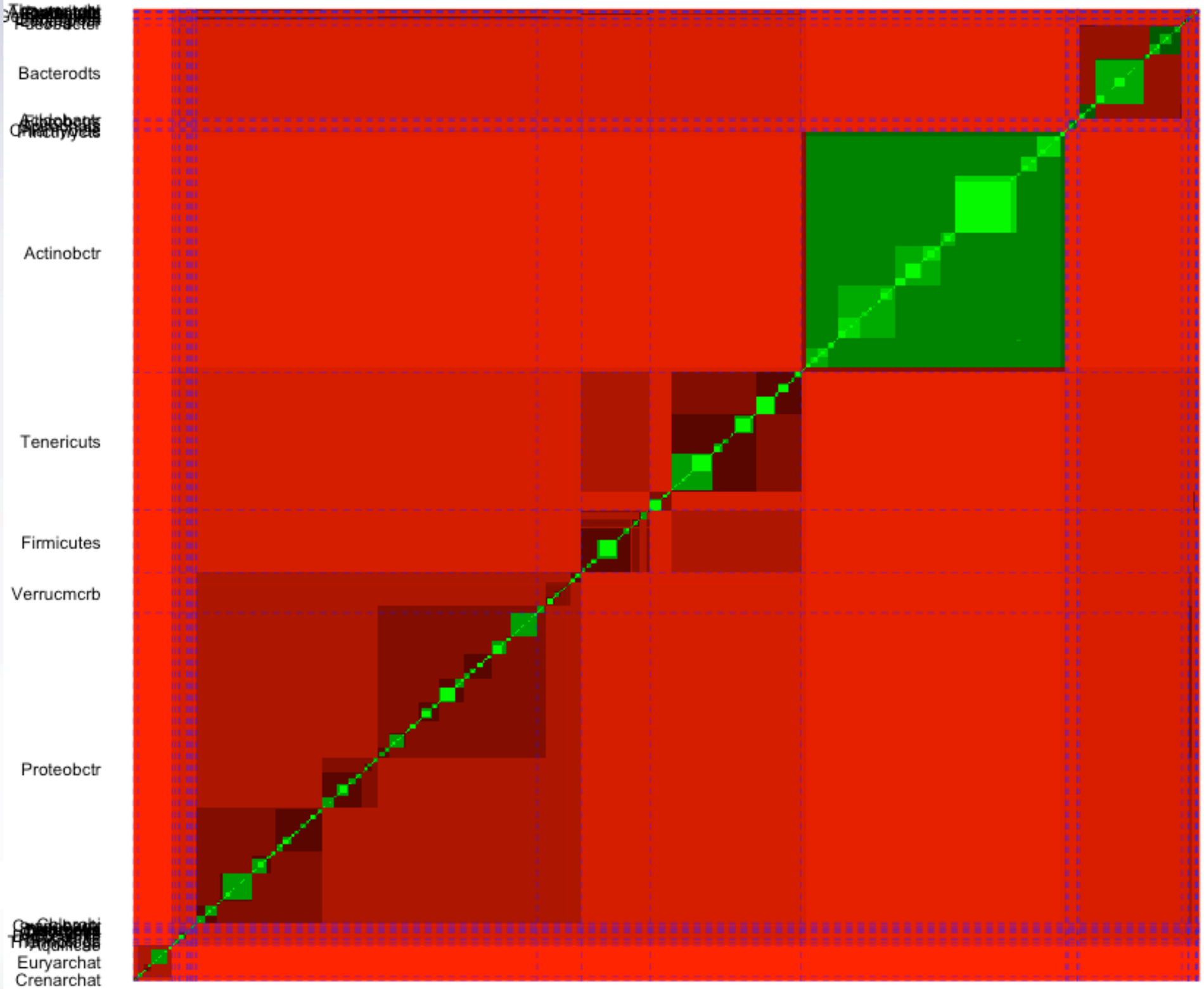

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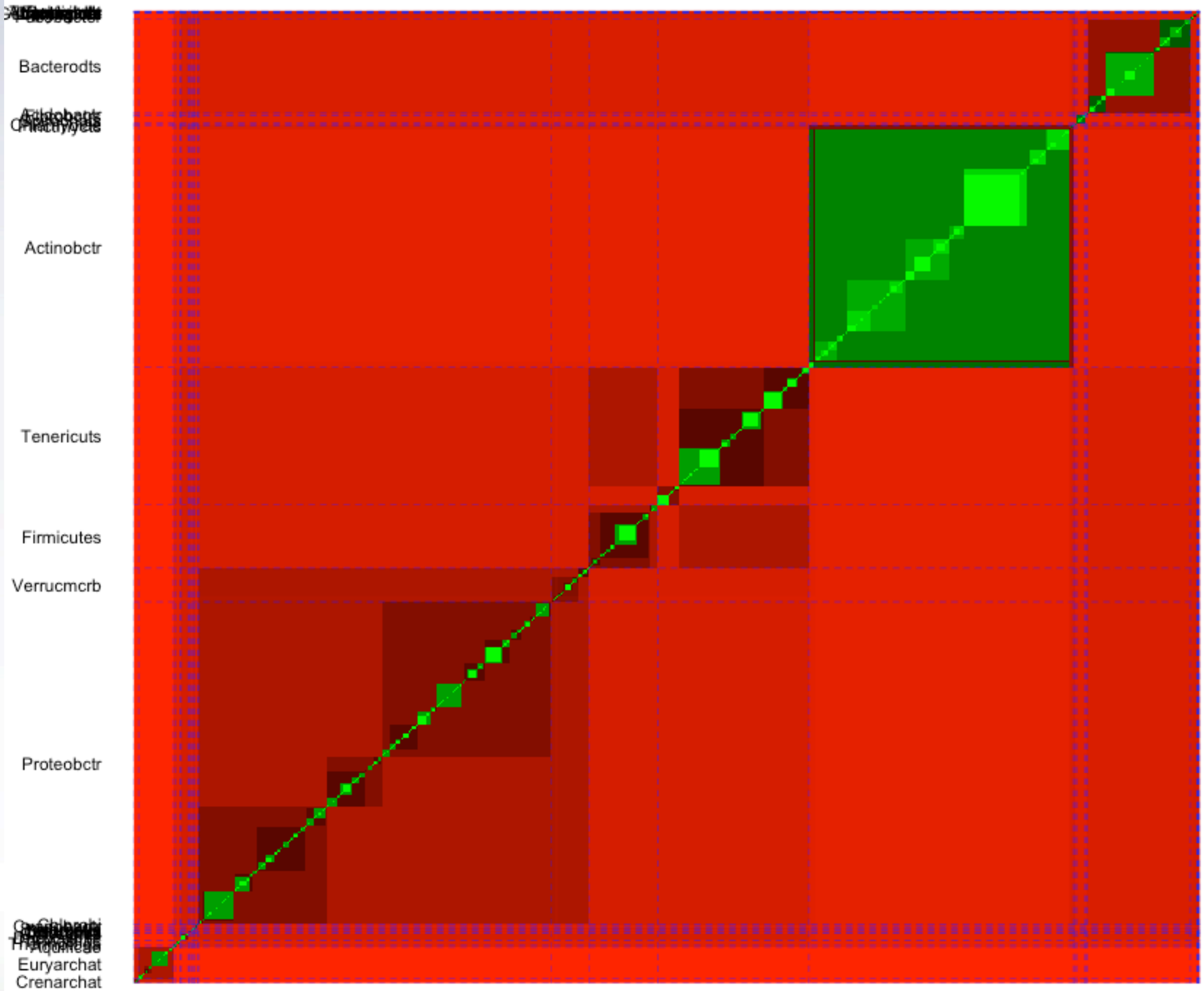

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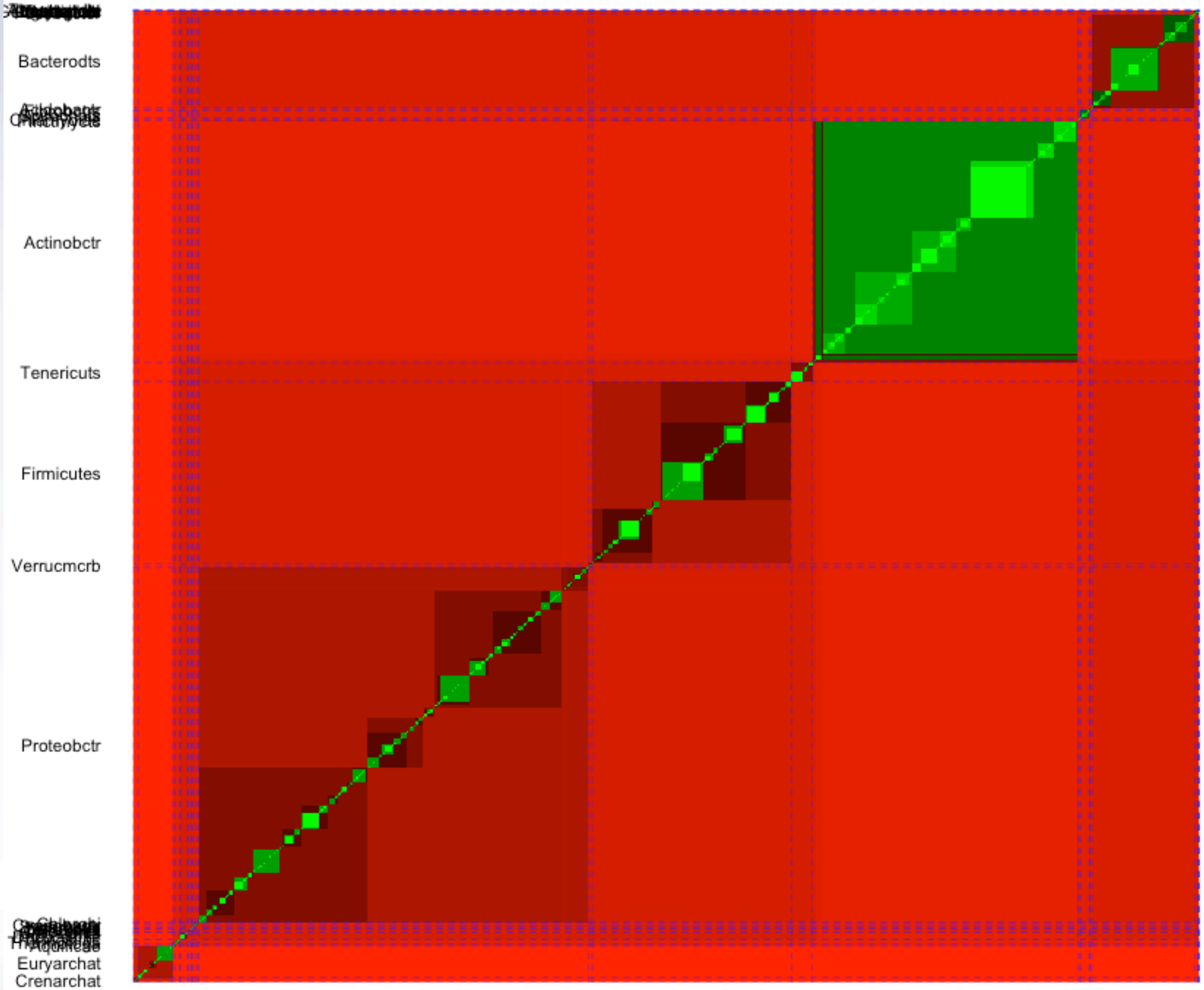

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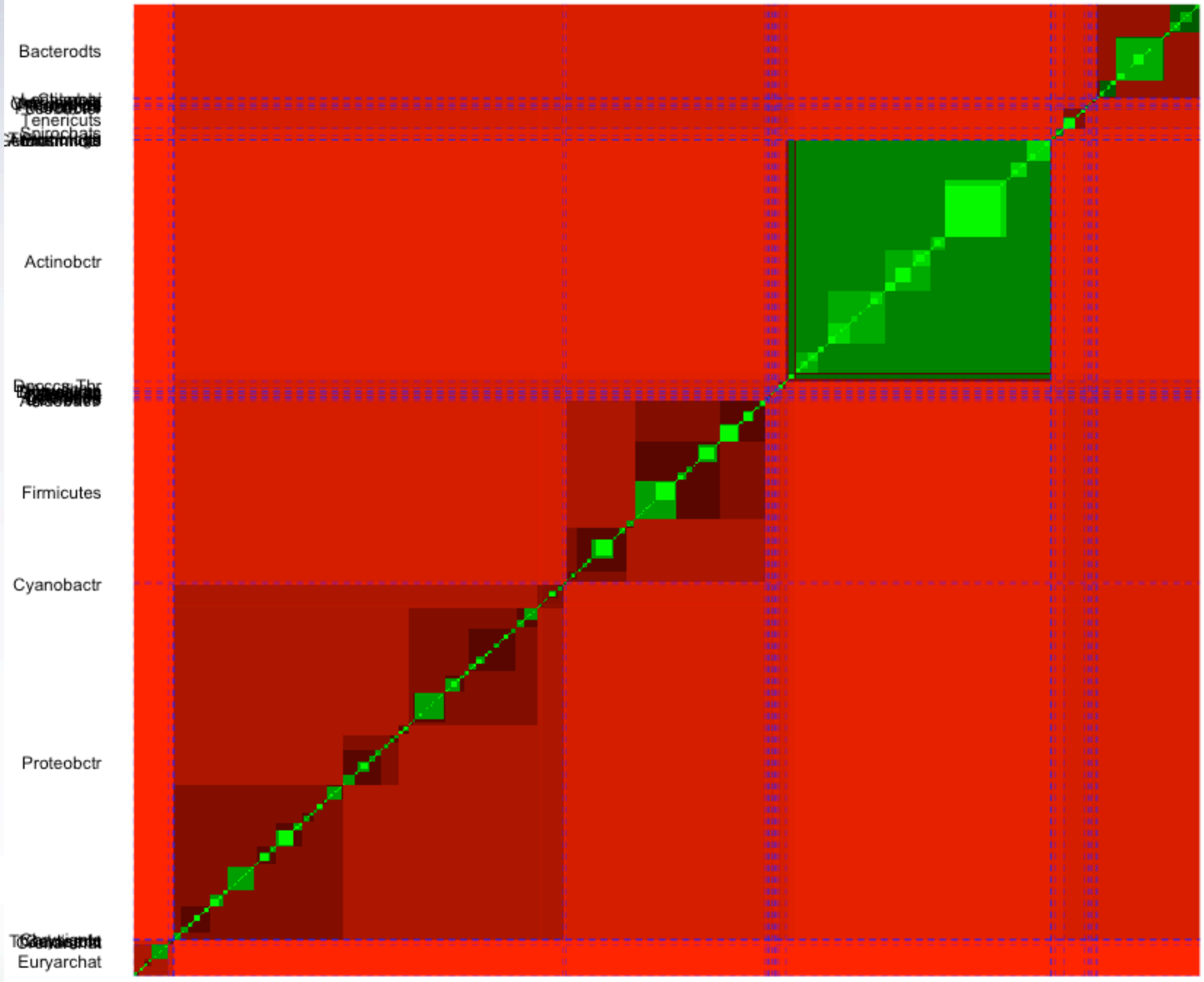
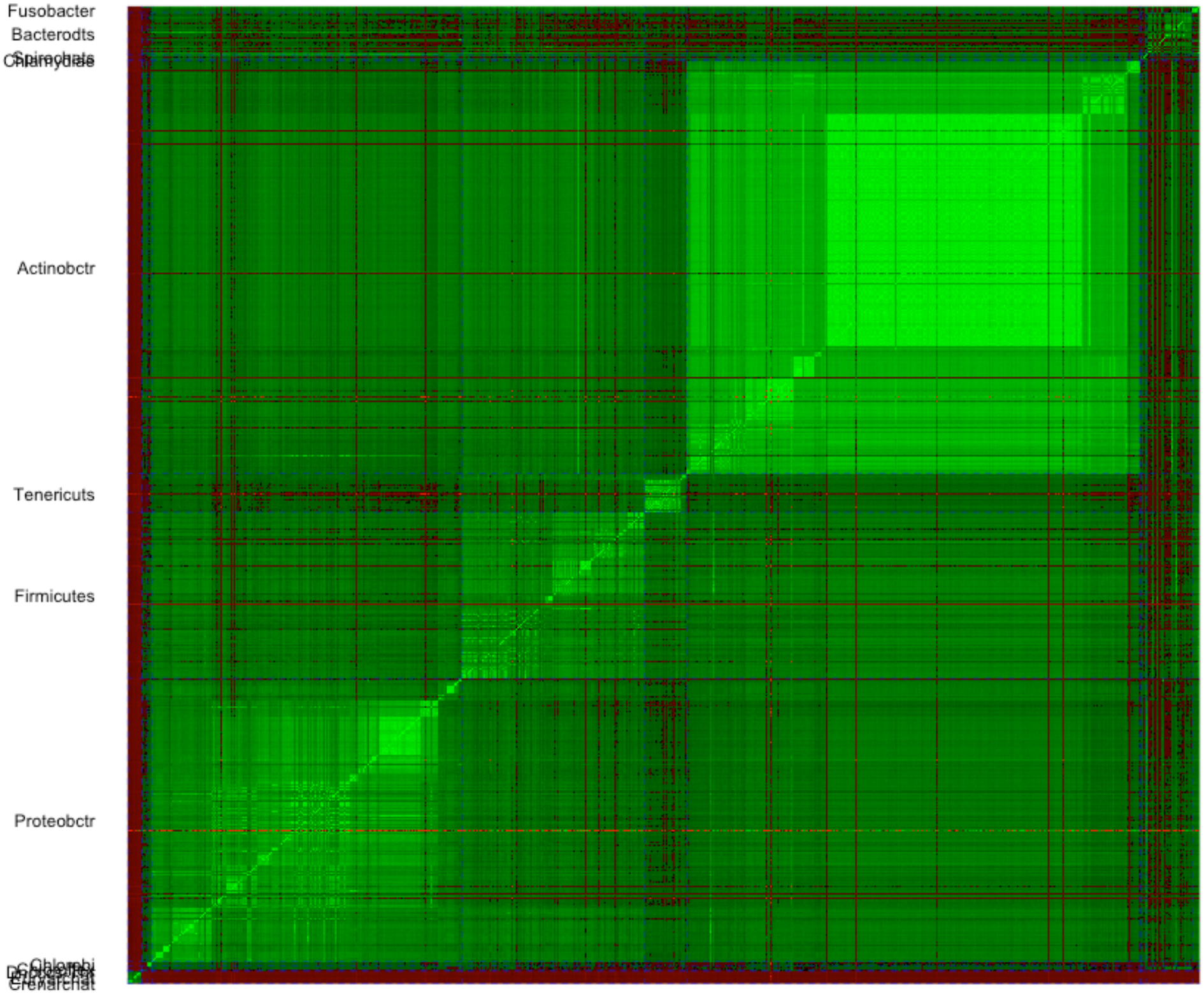
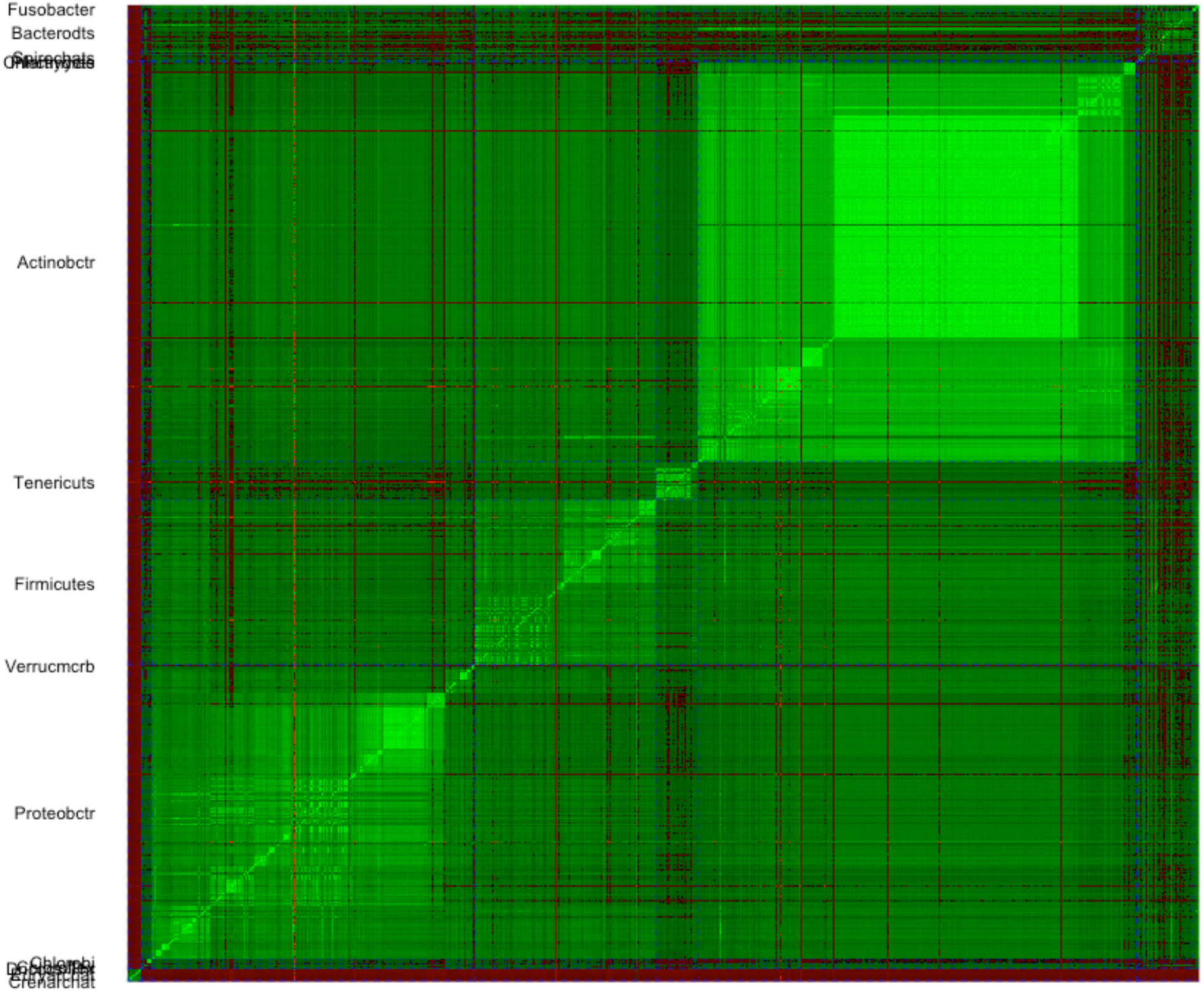


The effect of time

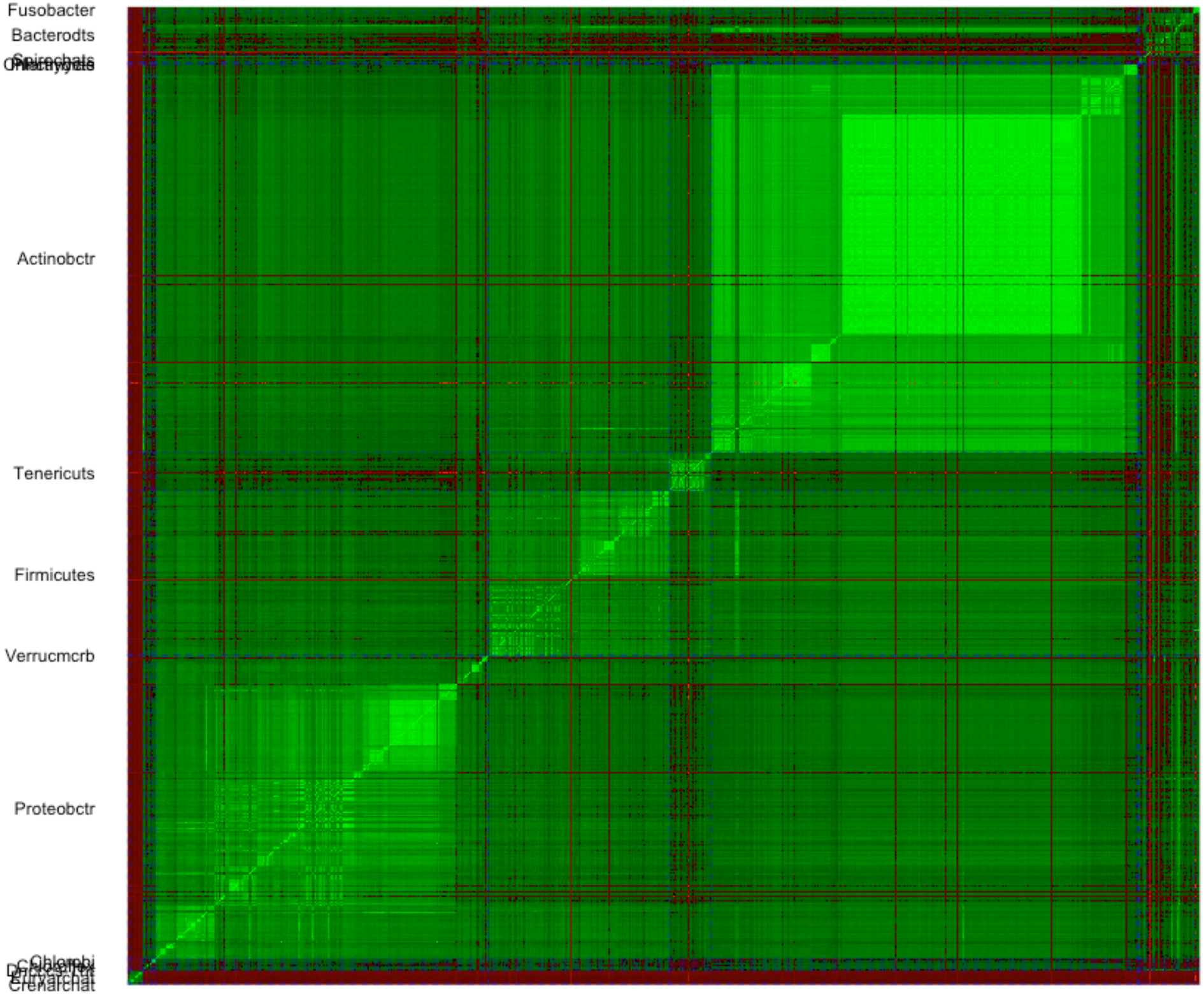
16S rRNA similarity of type strains of Bacteria and Archaea 1980



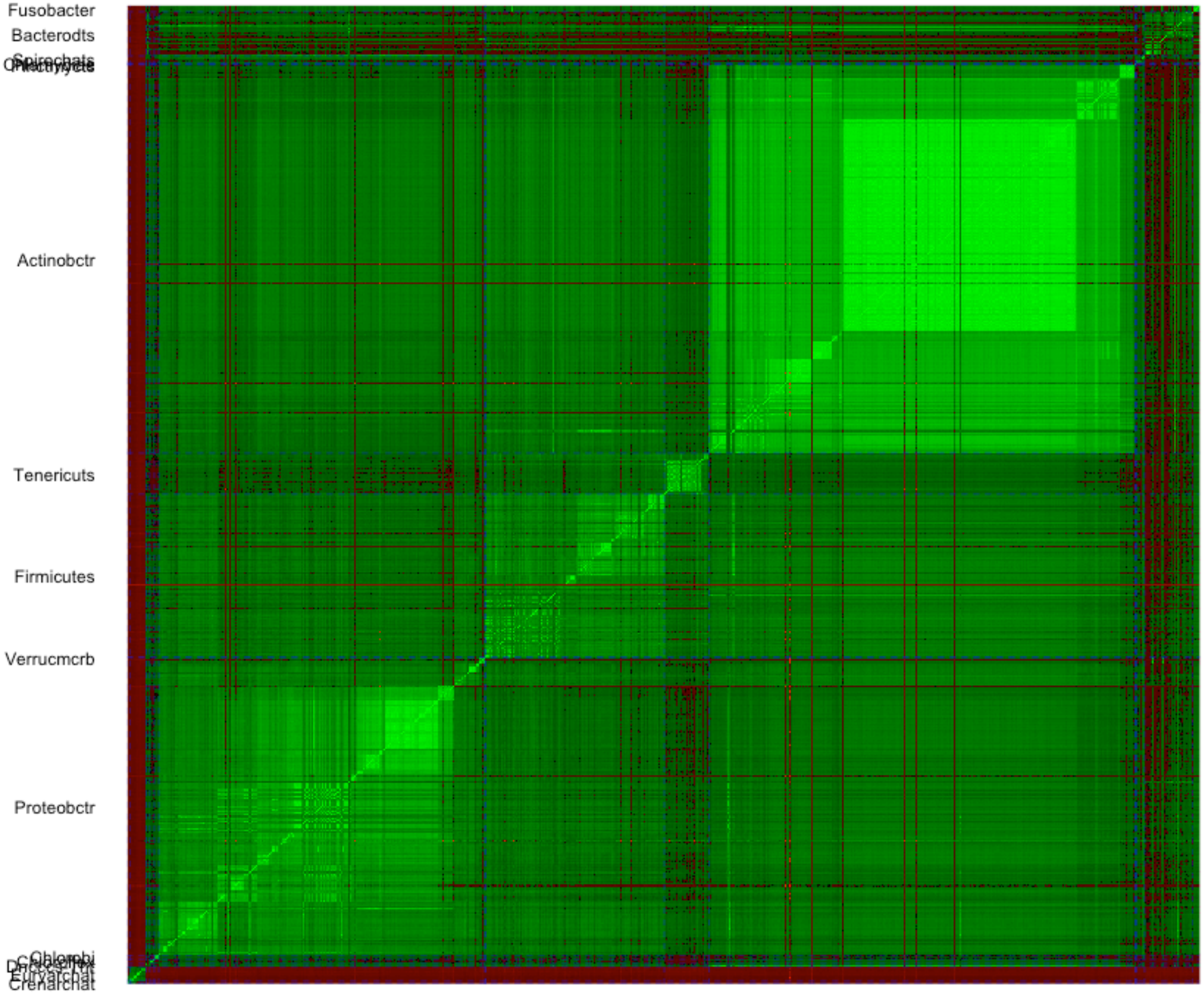
16S rRNA similarity of type strains of Bacteria and Archaea 1981



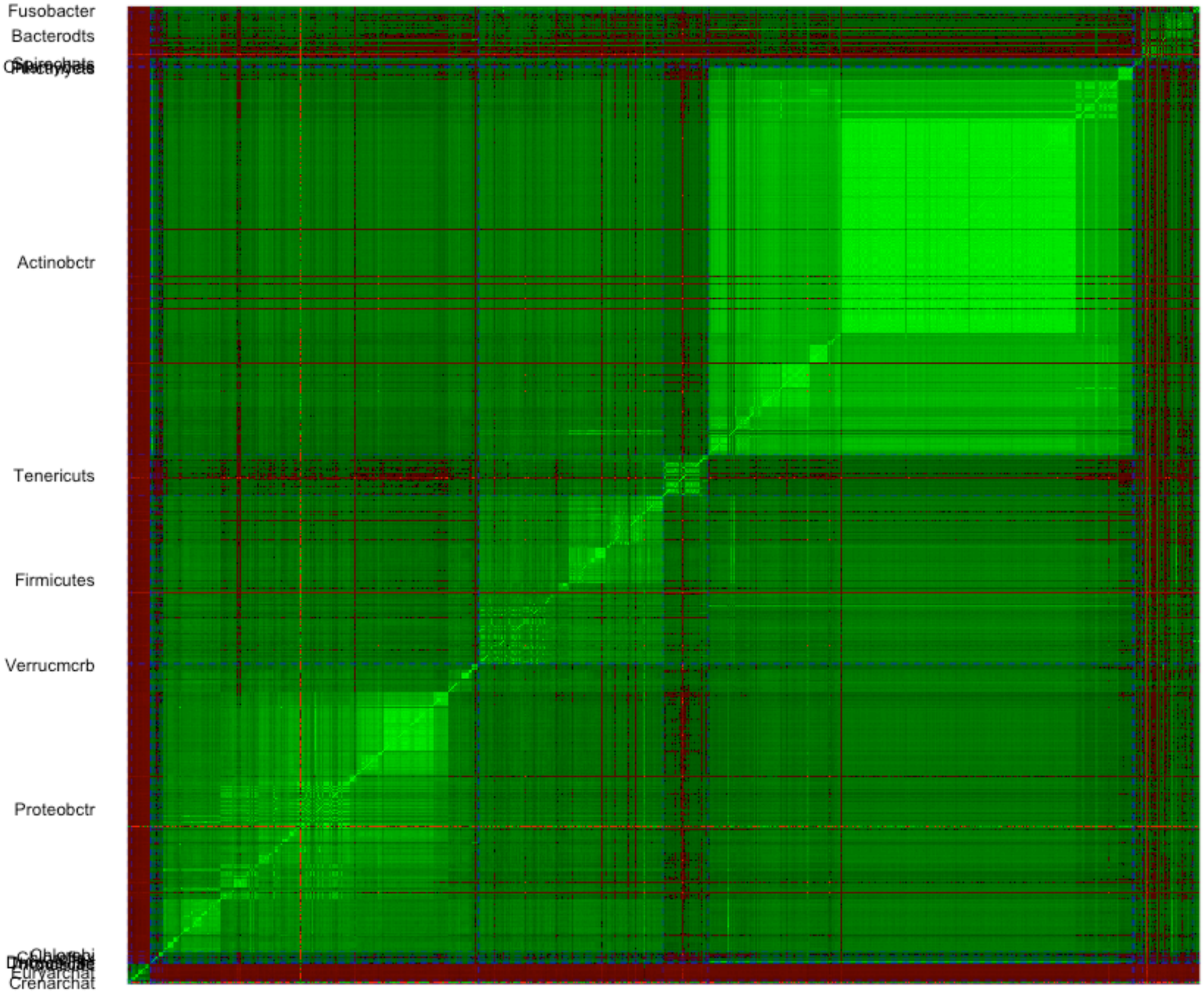
16S rRNA similarity of type strains of Bacteria and Archaea 1982



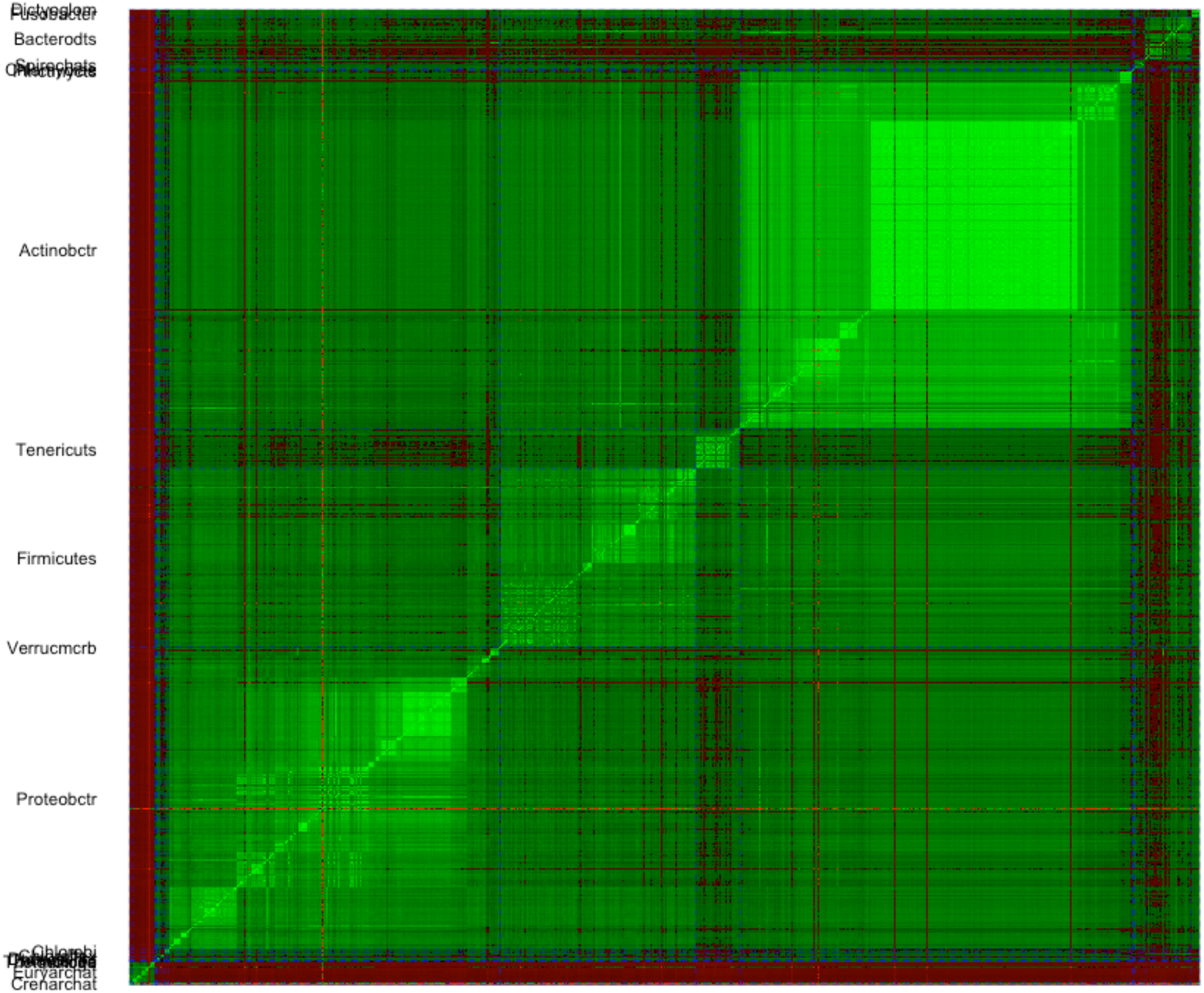
16S rRNA similarity of type strains of Bacteria and Archaea 1983



16S rRNA similarity of type strains of Bacteria and Archaea 1984



16S rRNA similarity of type strains of Bacteria and Archaea 1986



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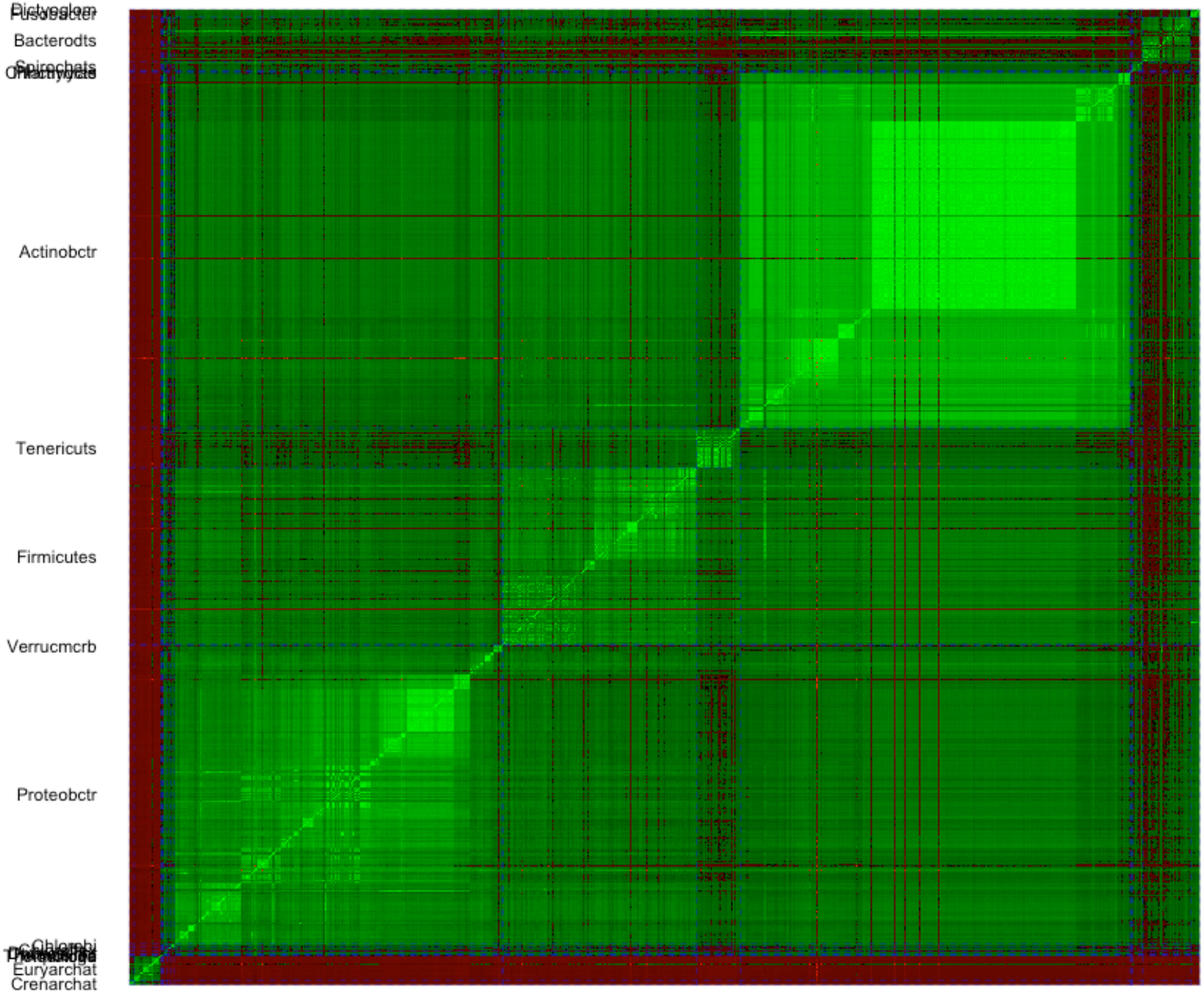

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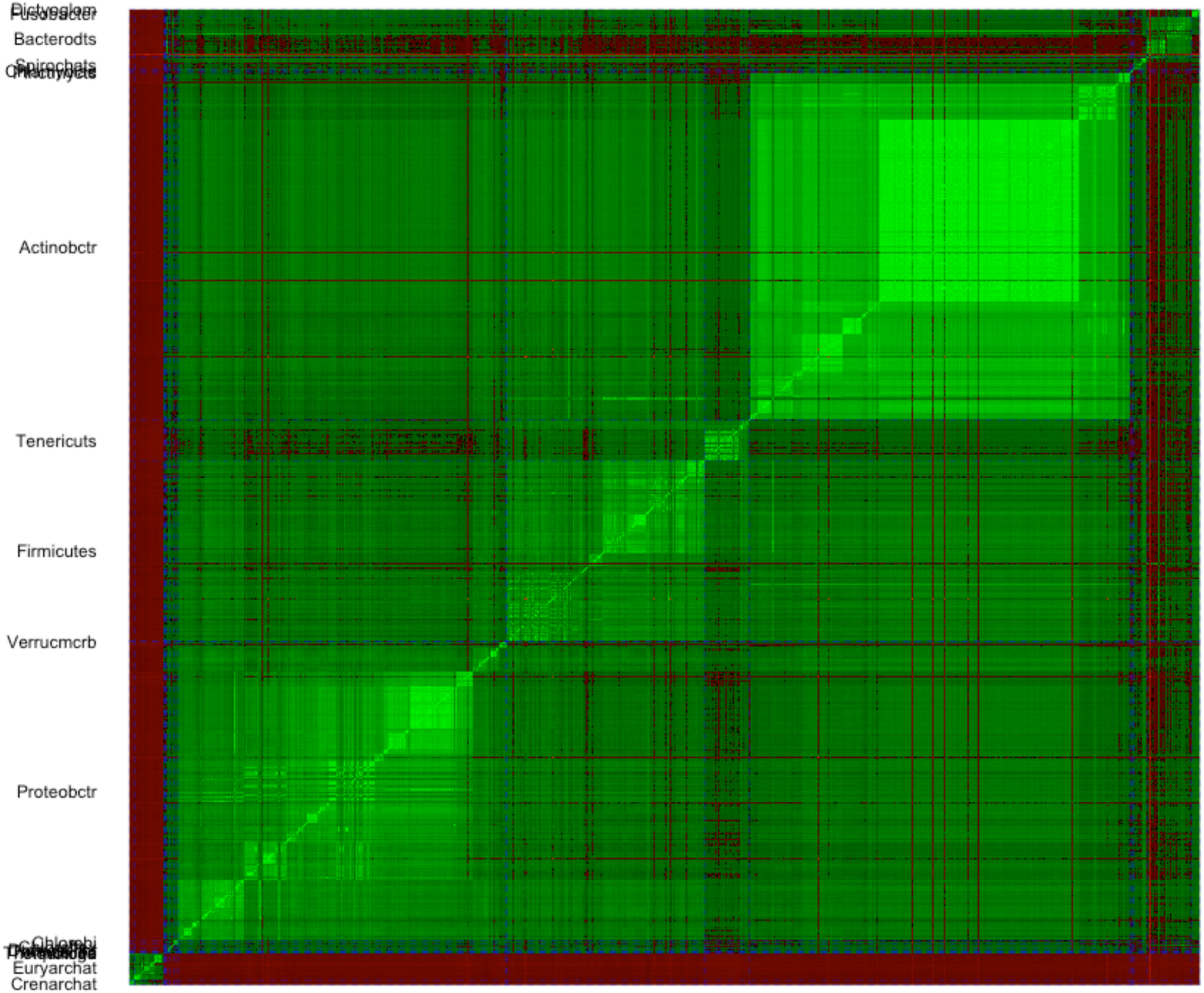

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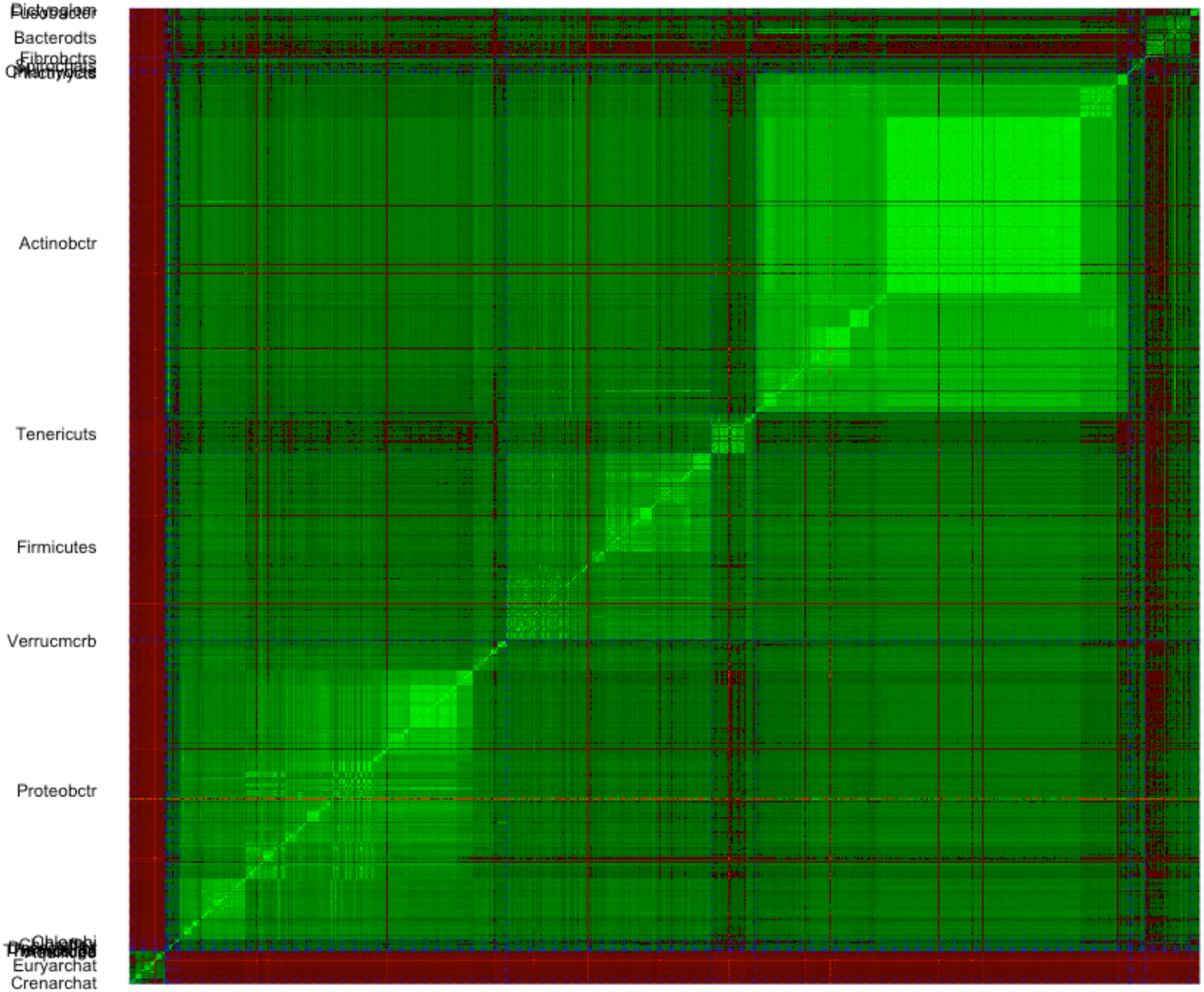

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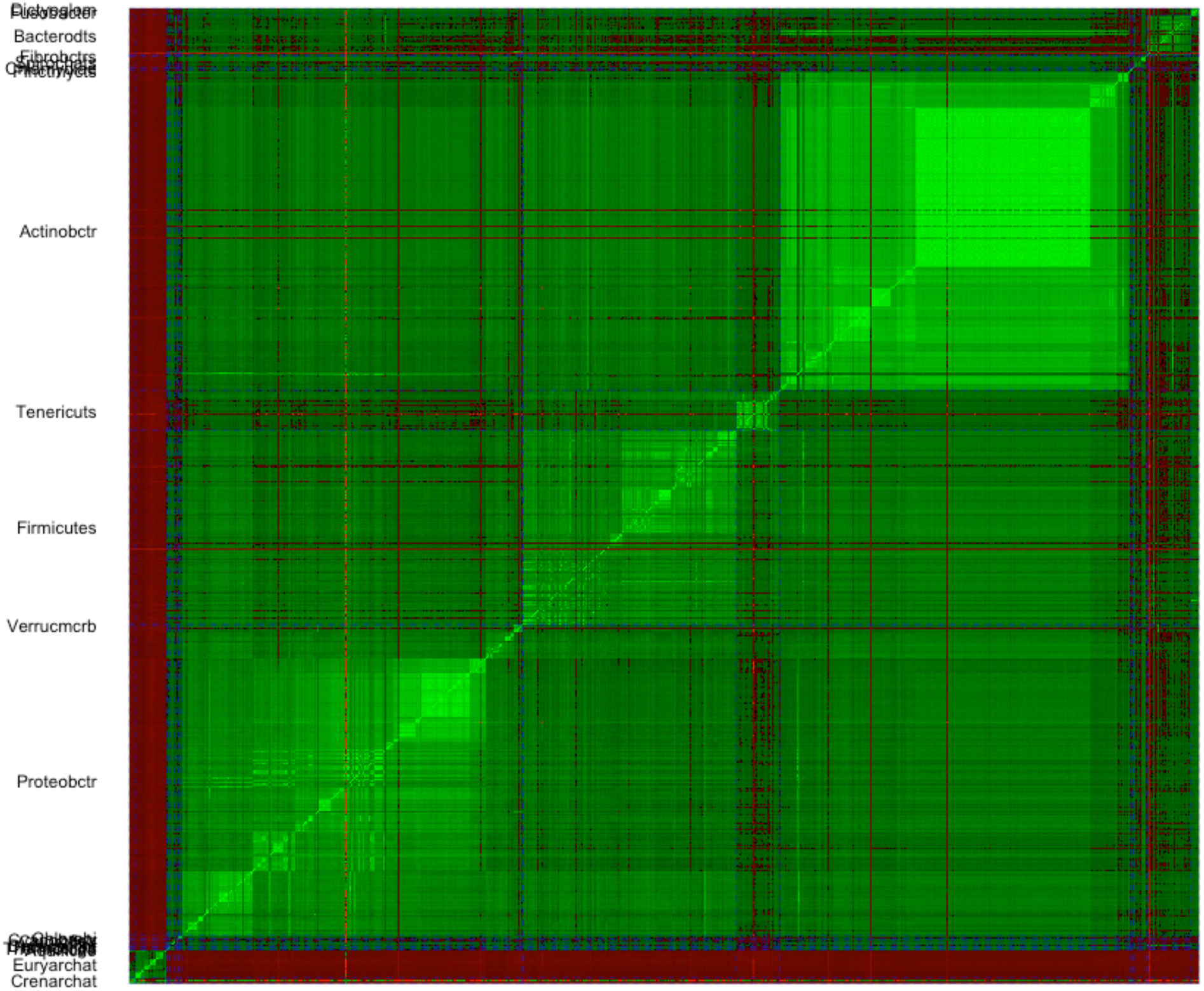

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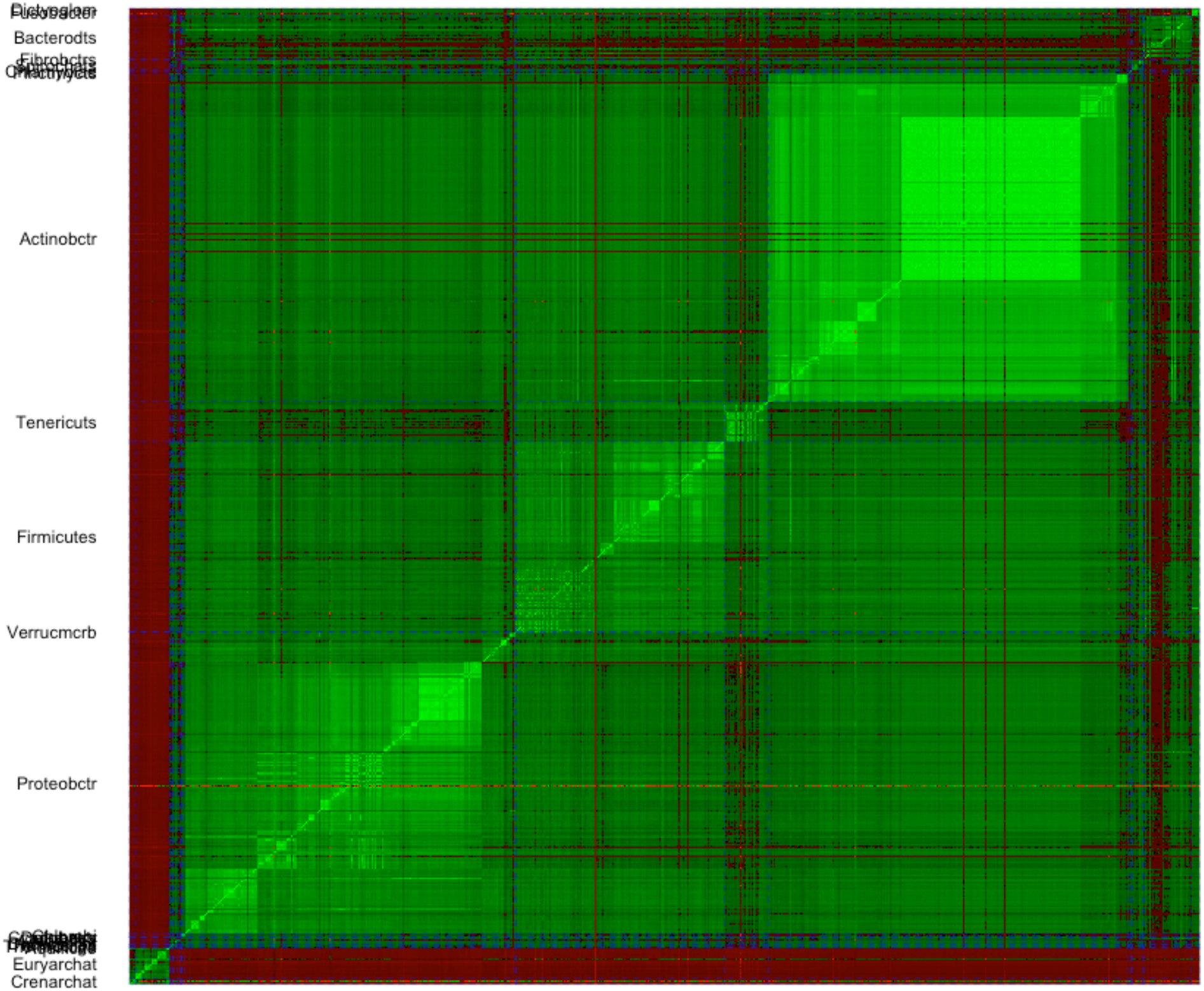

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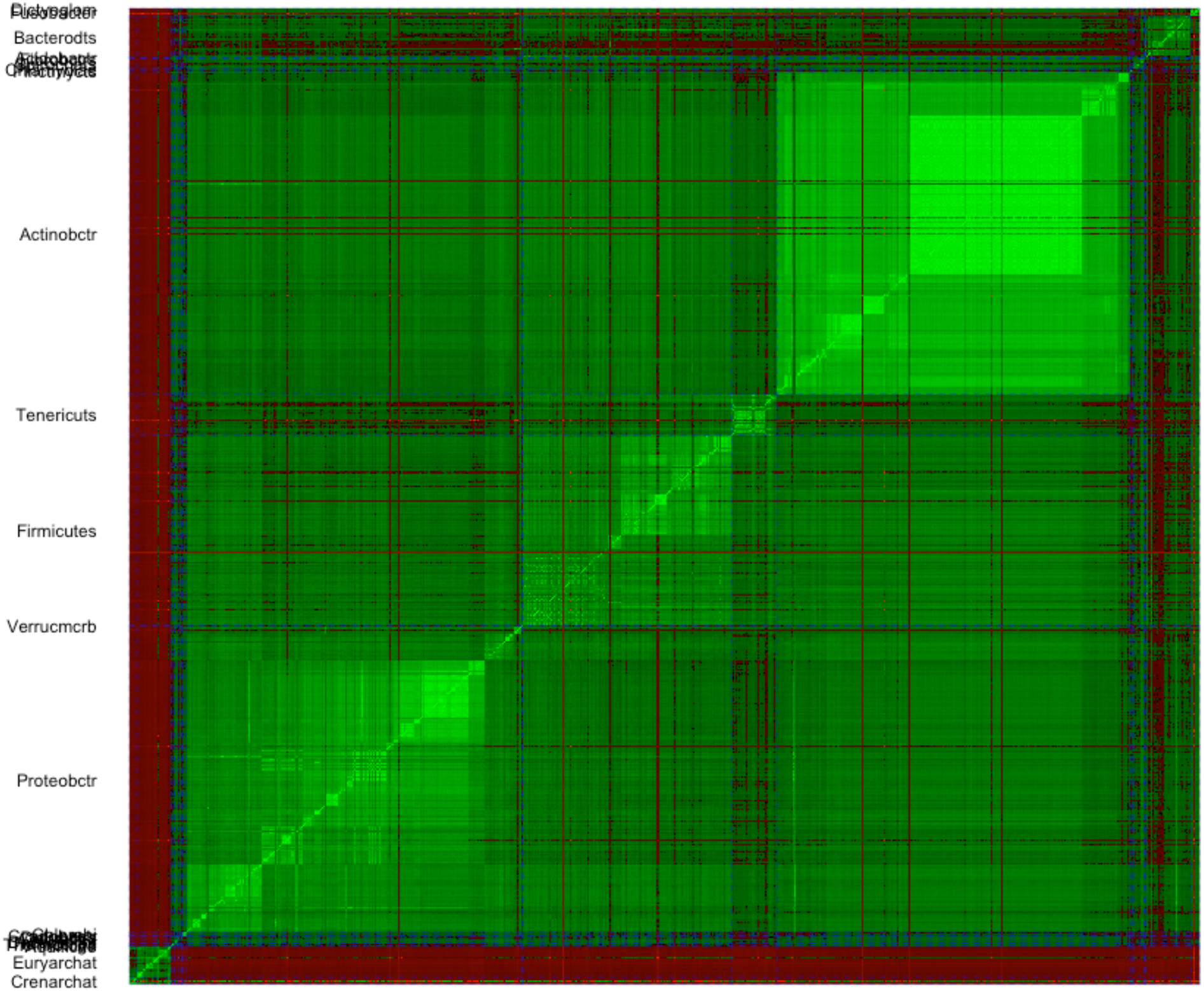

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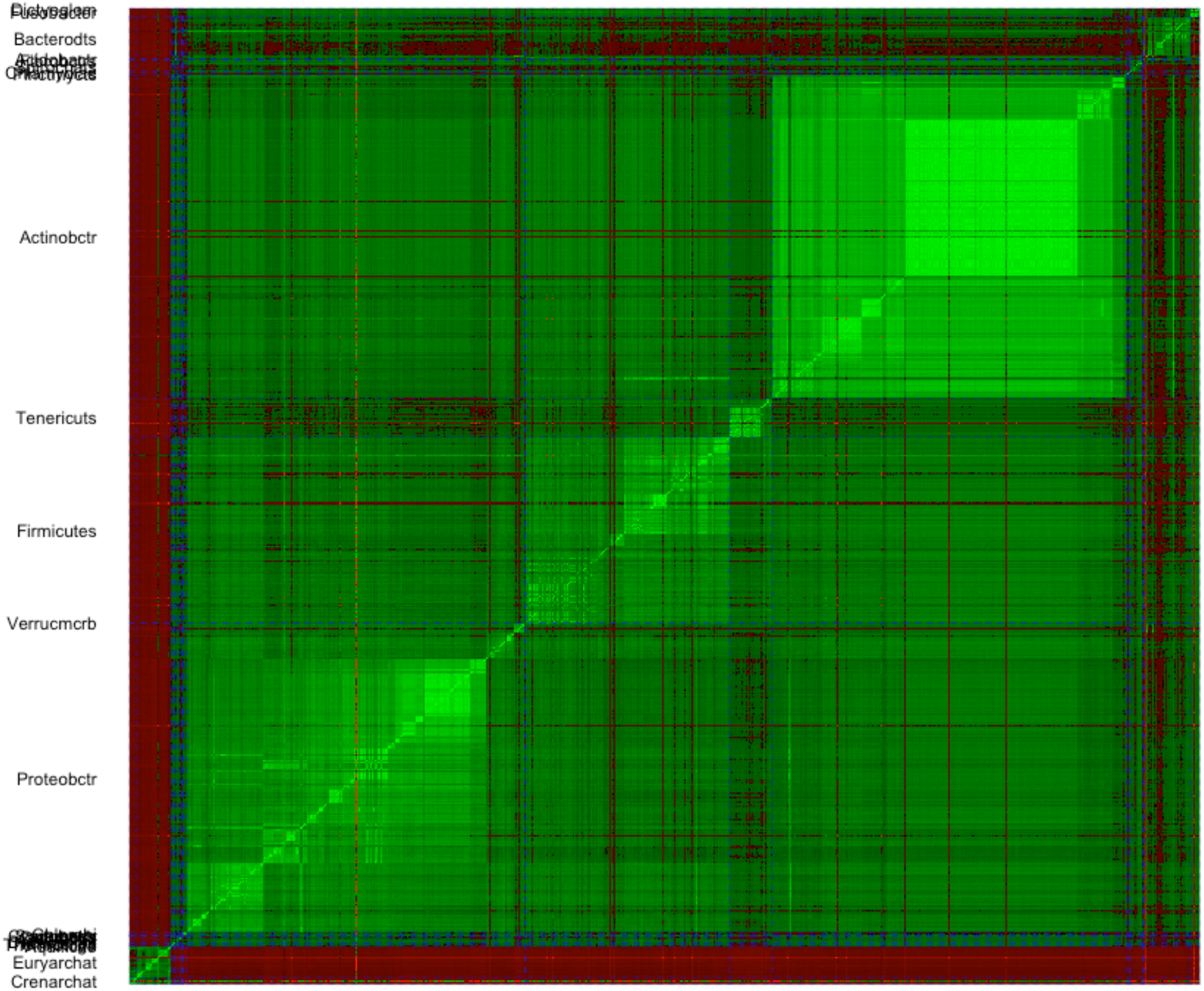

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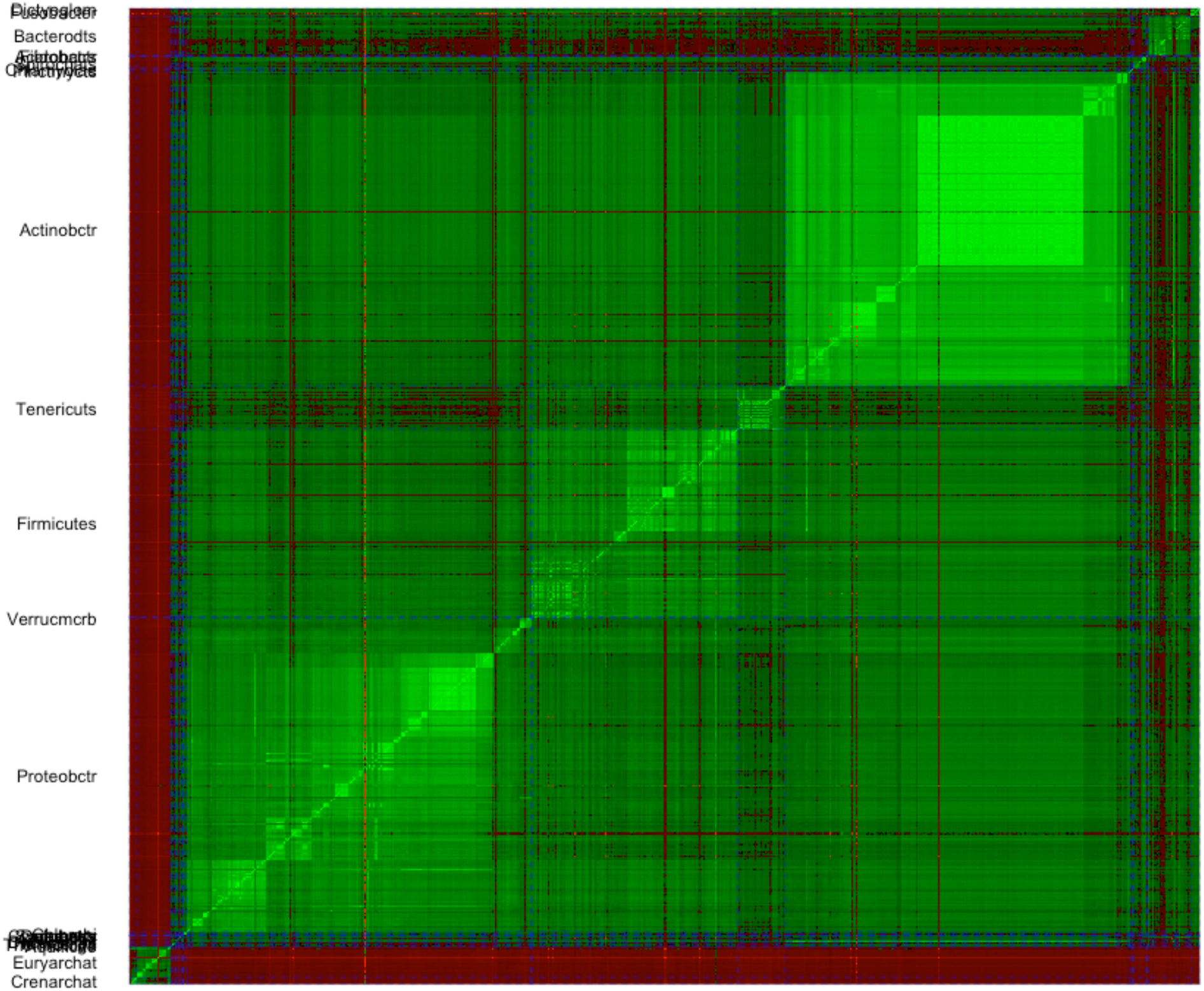

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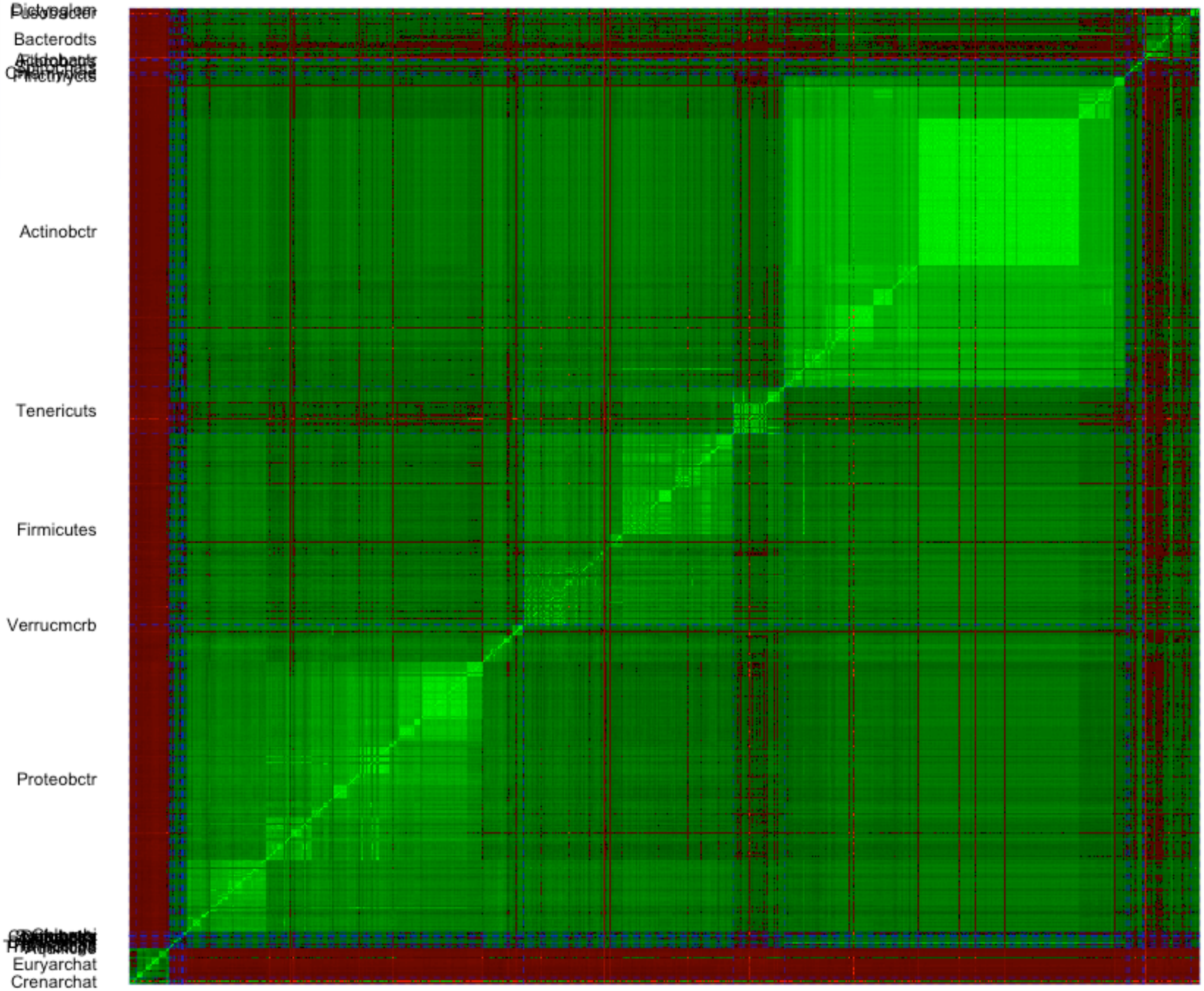

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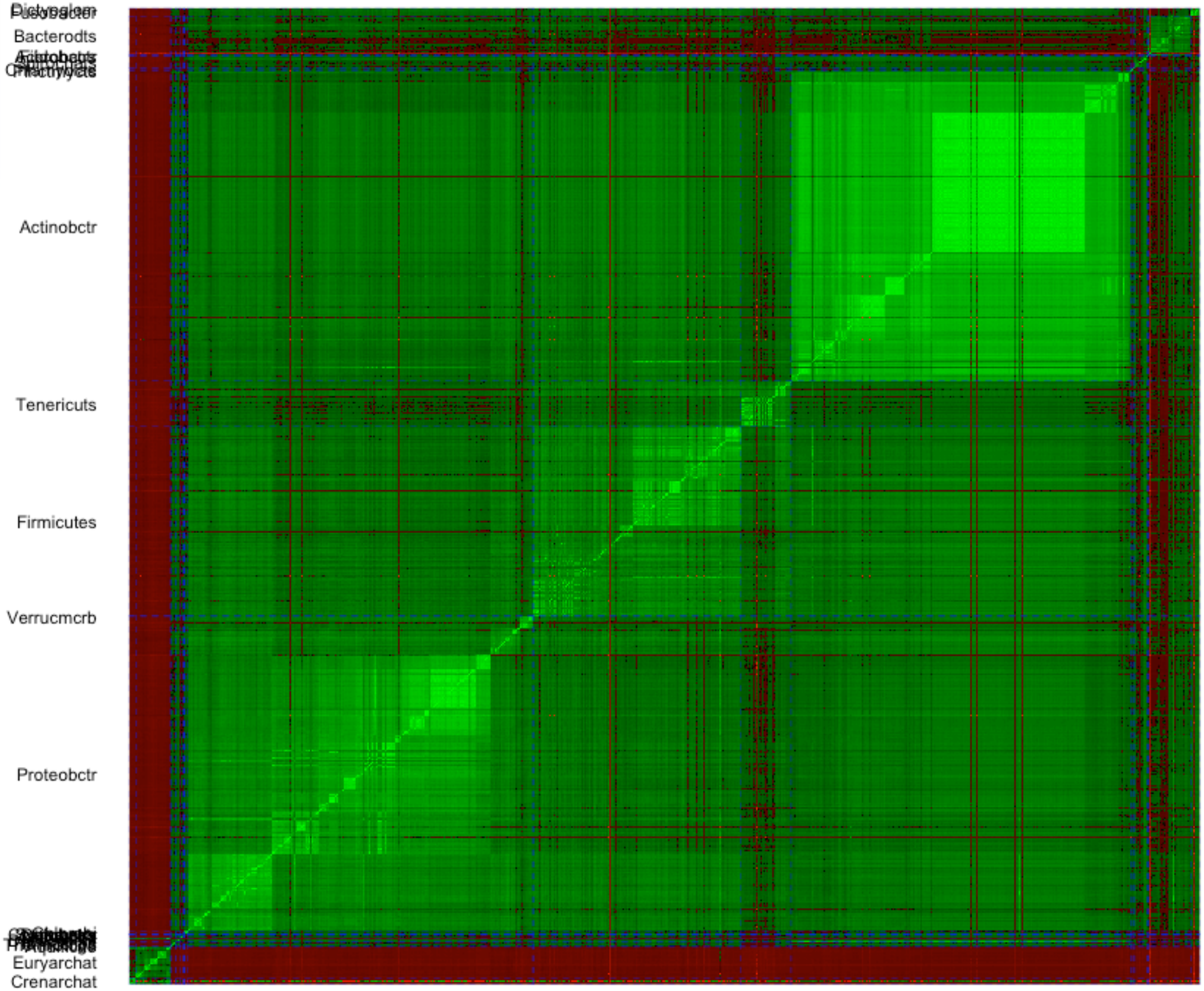

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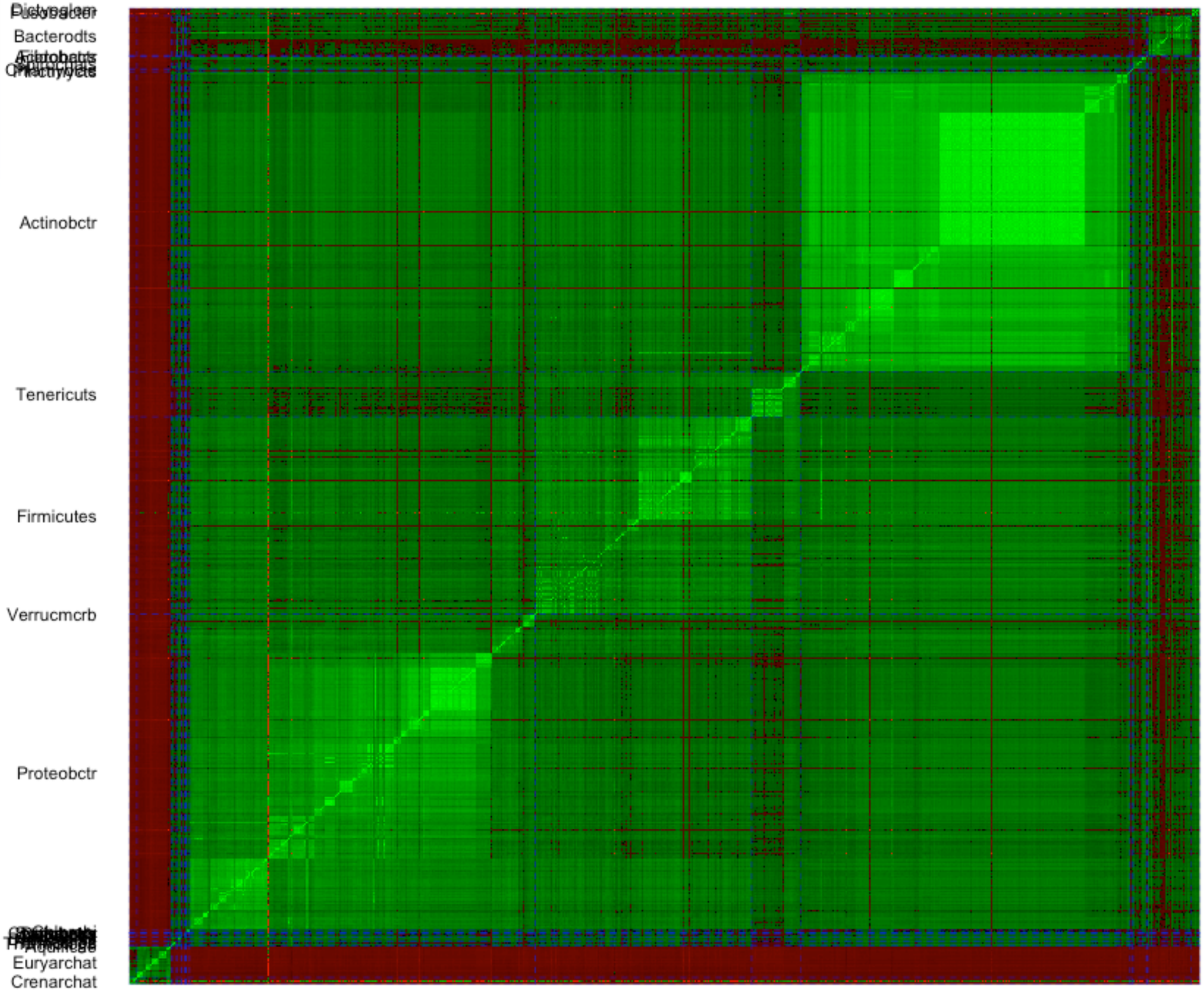

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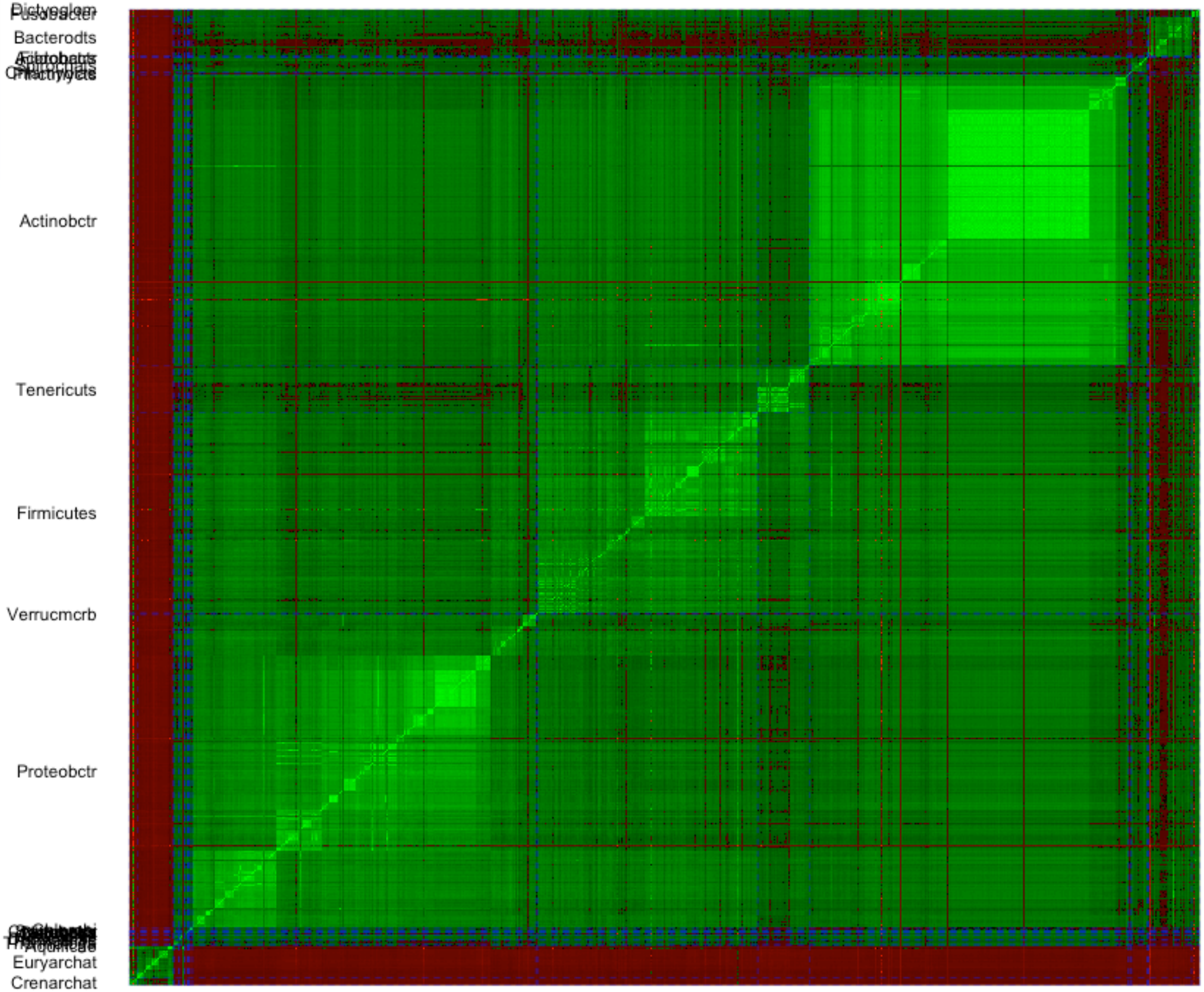
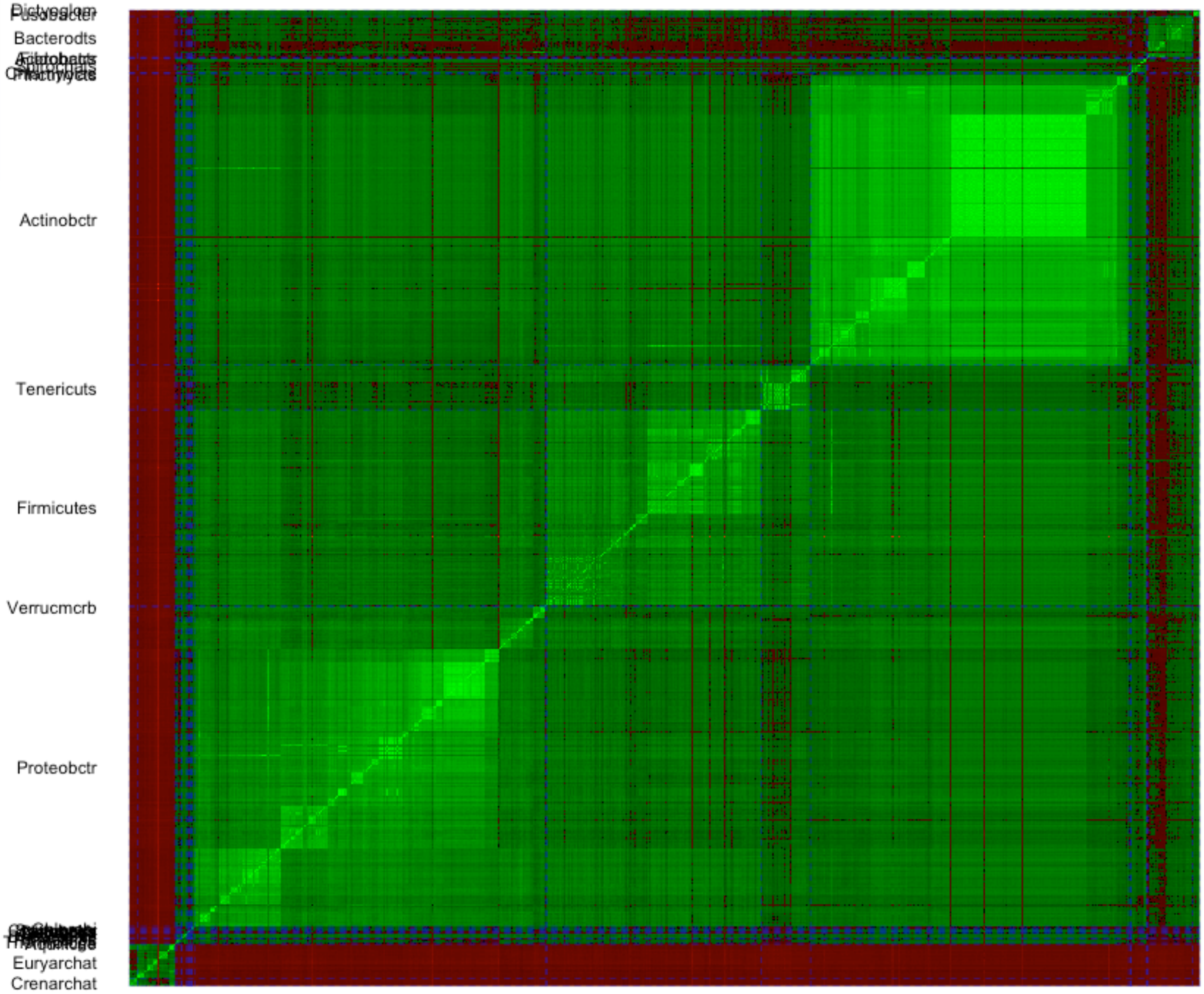


16S rRNA similarity of type strains of Bacteria and Archaea 1999



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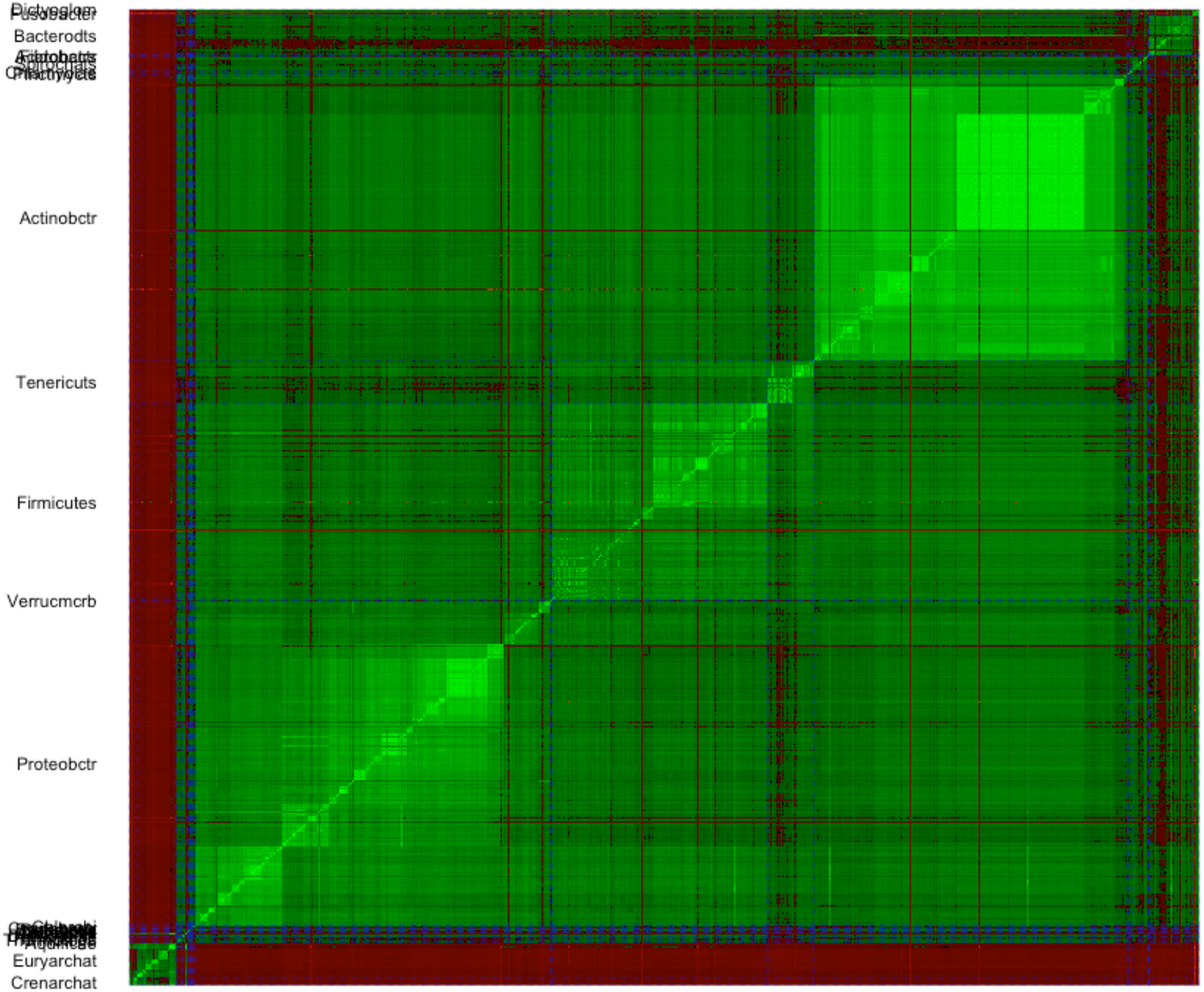
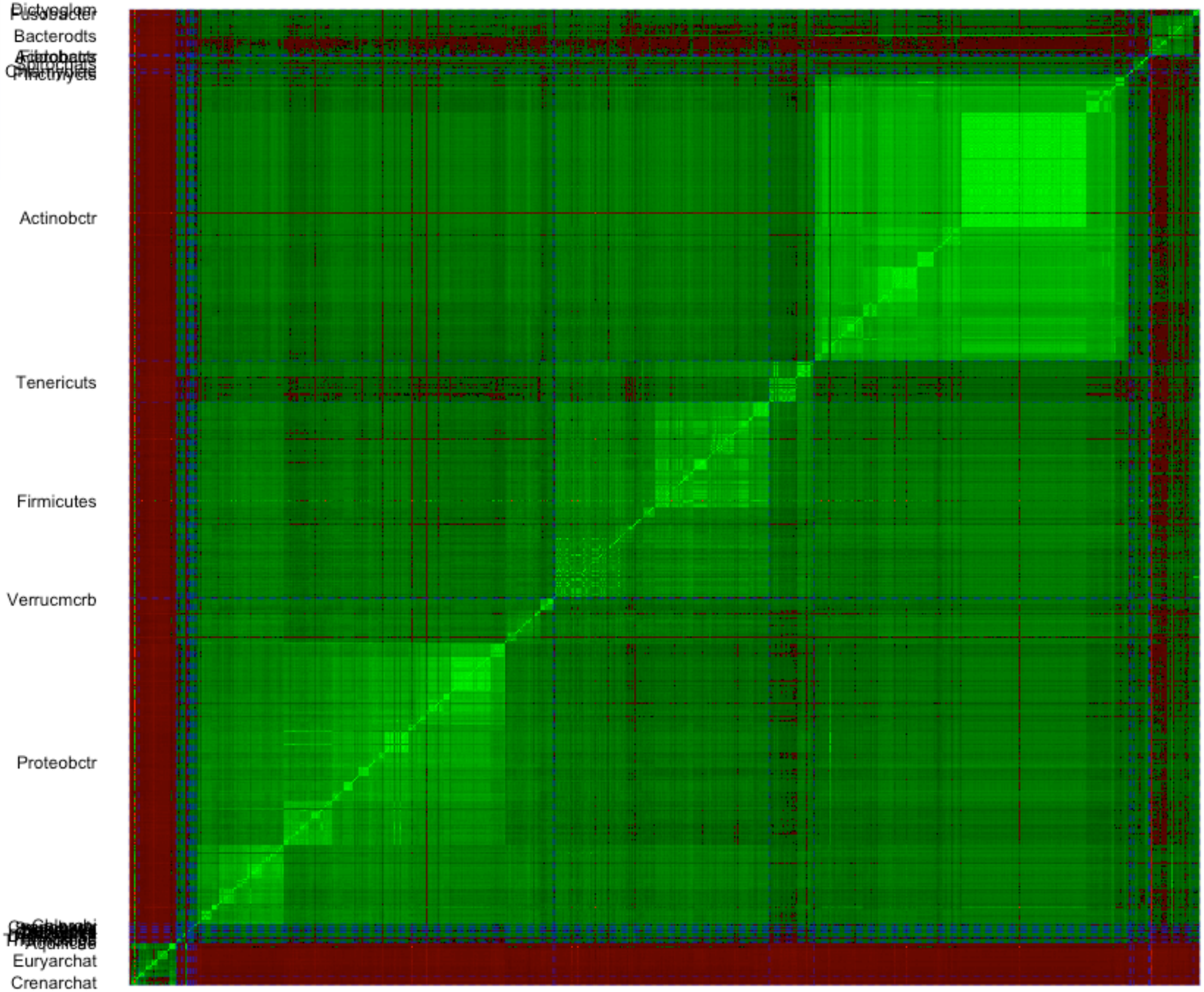


16S rRNA similarity of type strains of Bacteria and Archaea 2001



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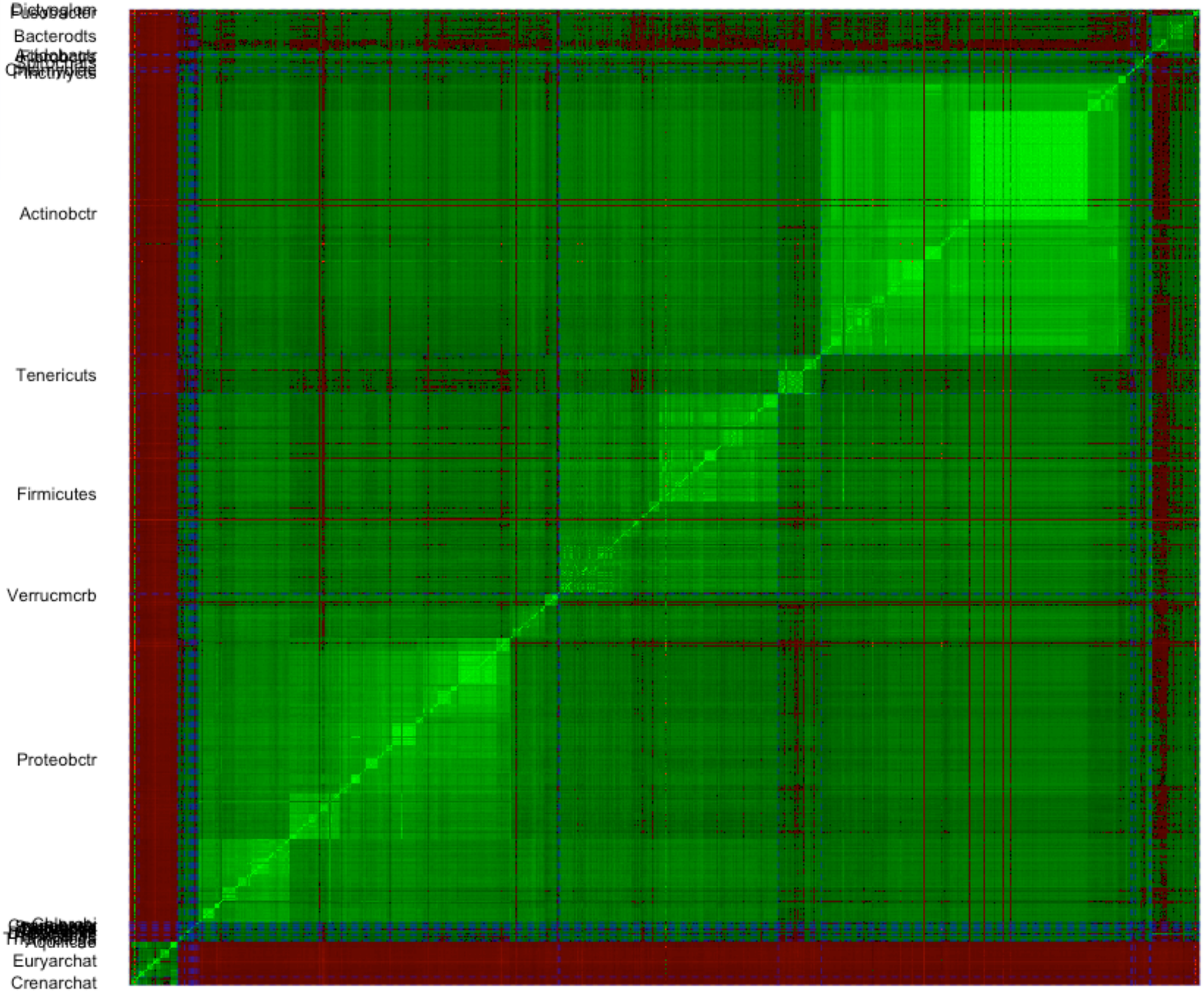

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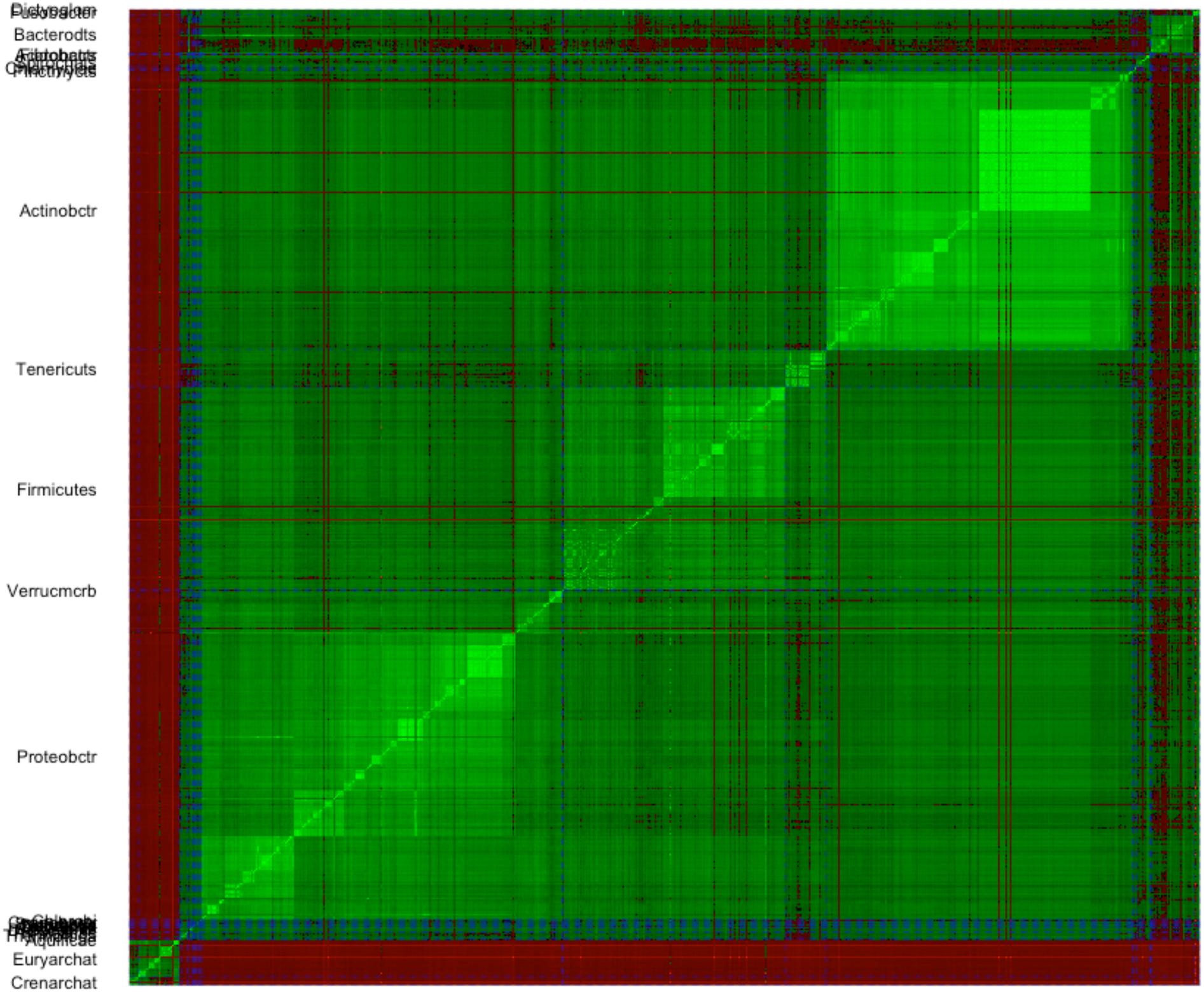

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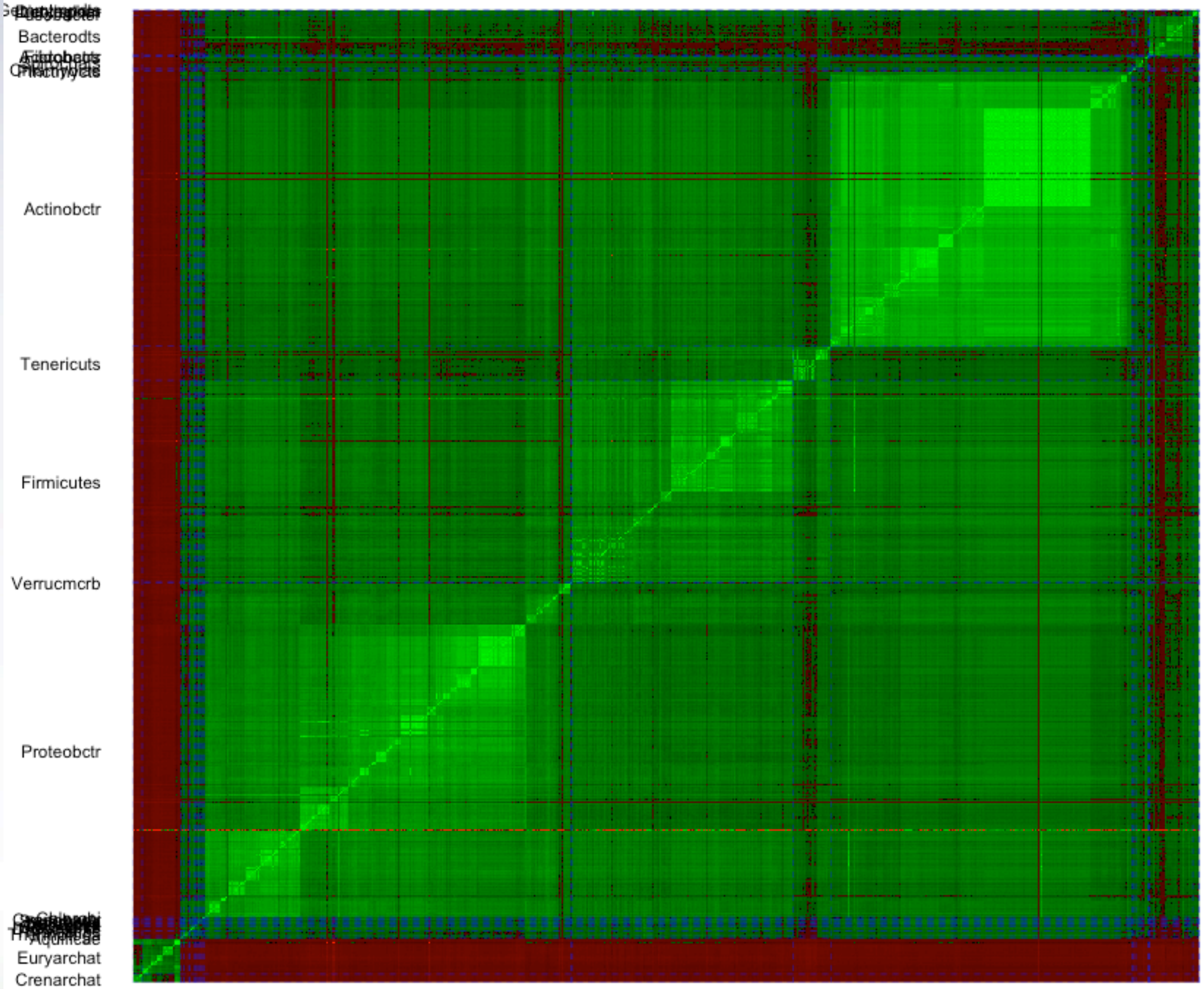

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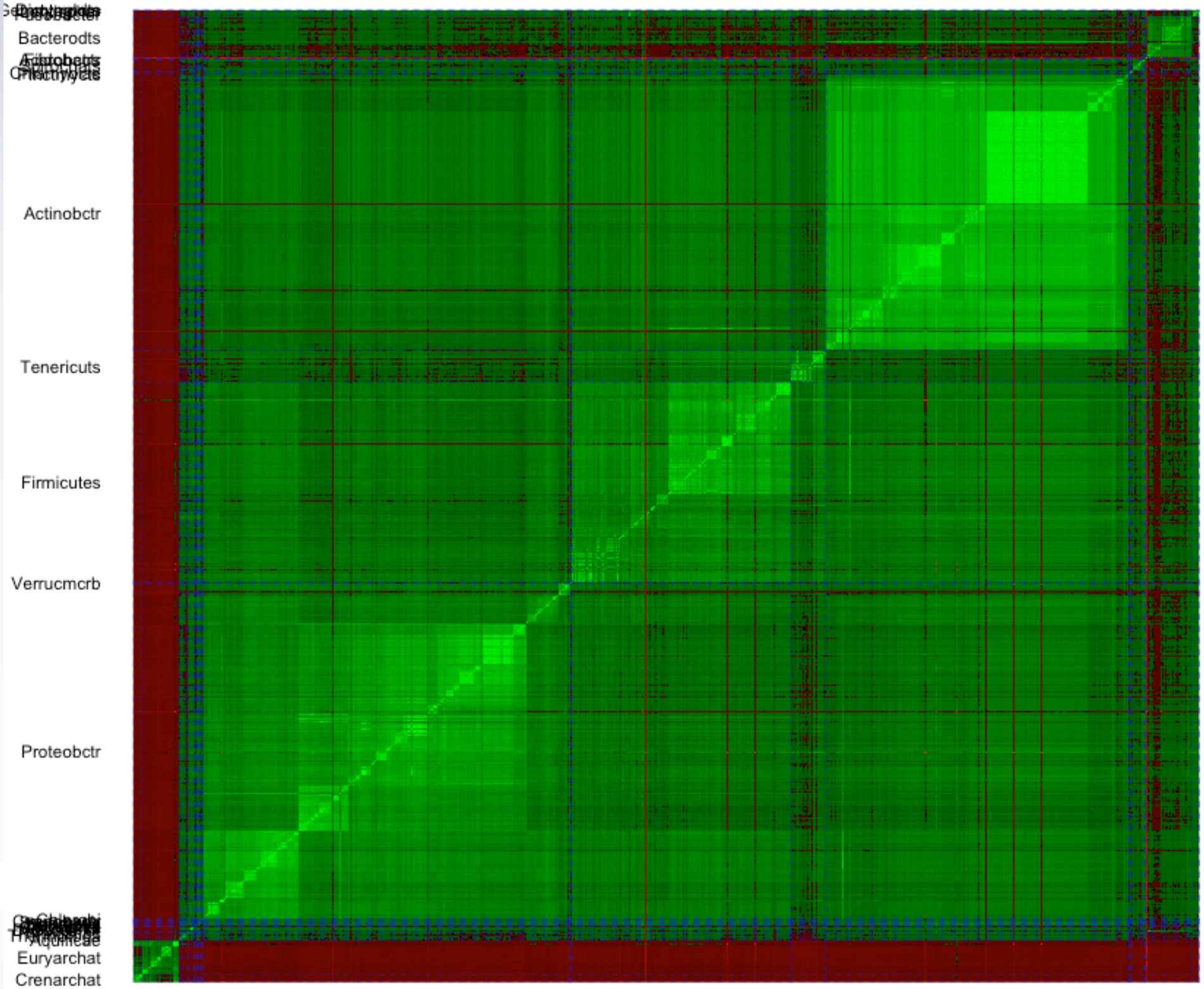

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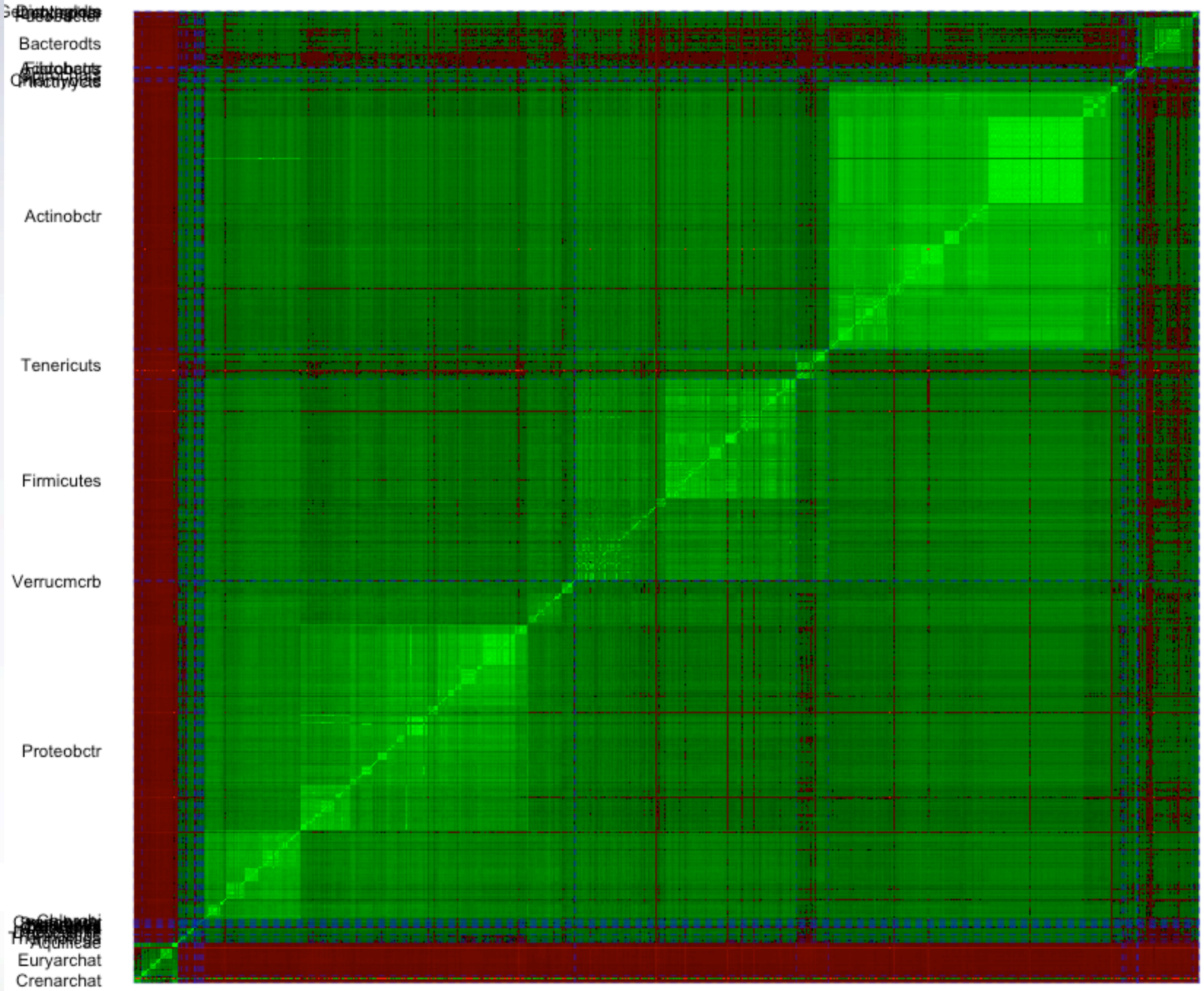

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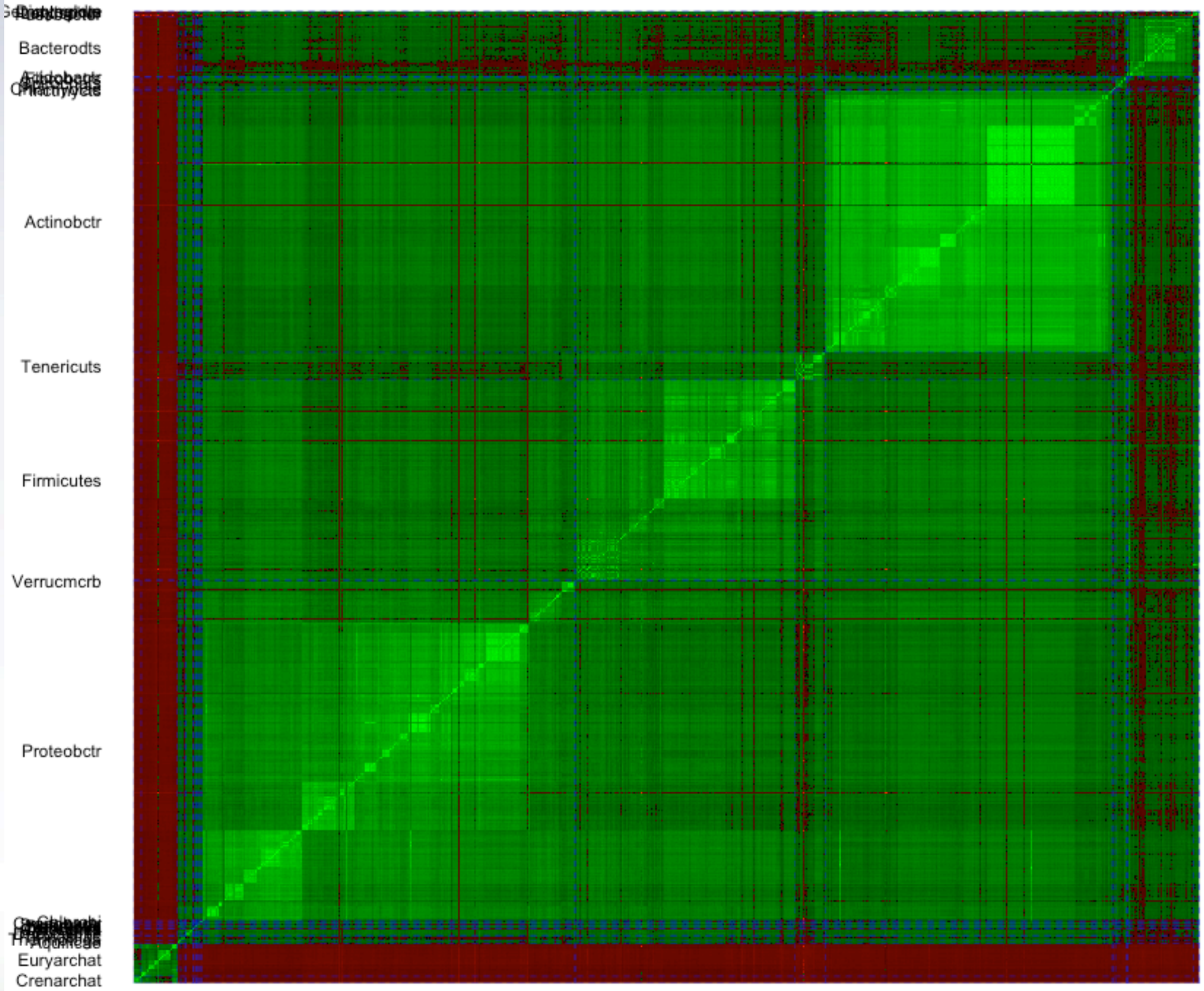
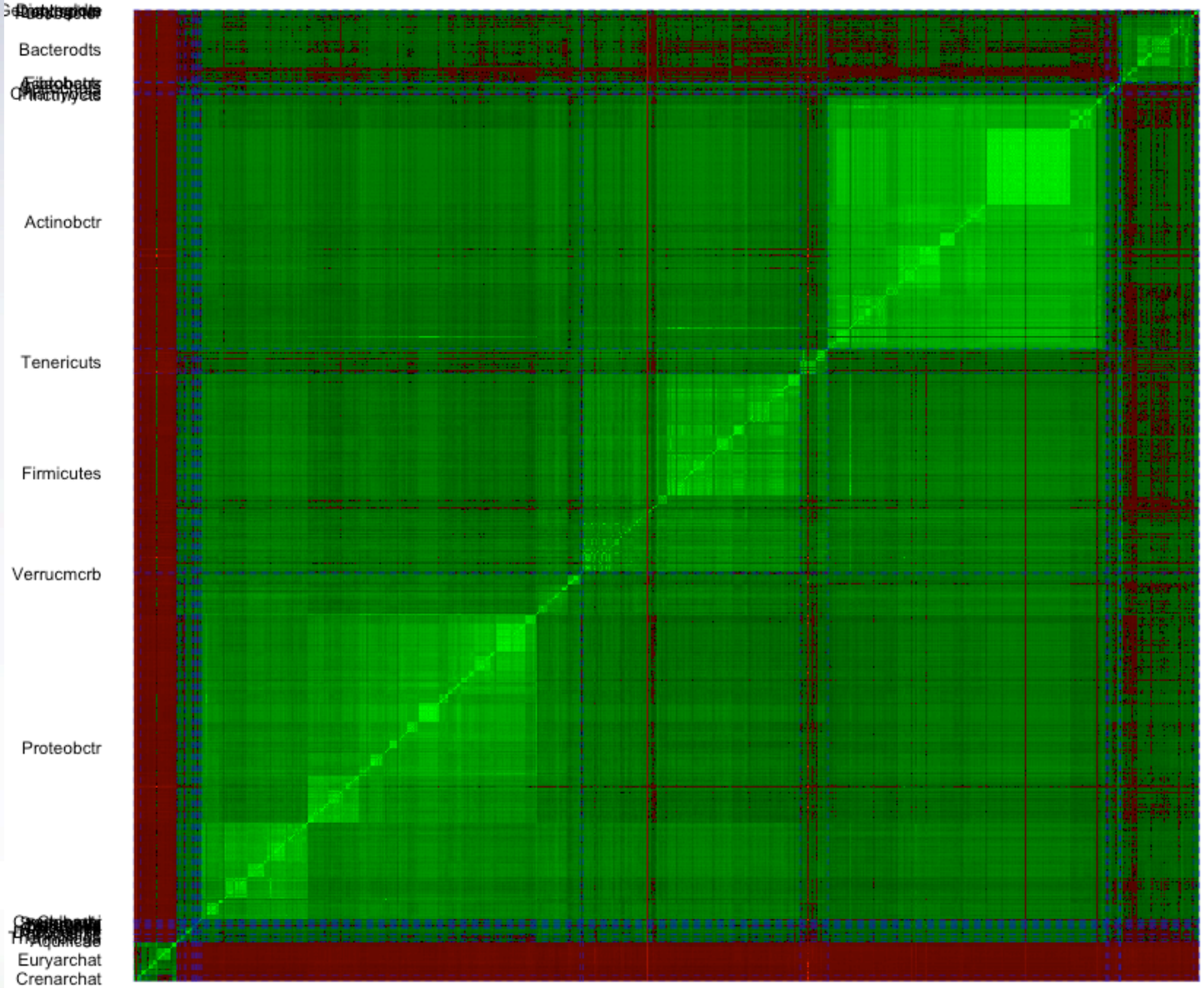
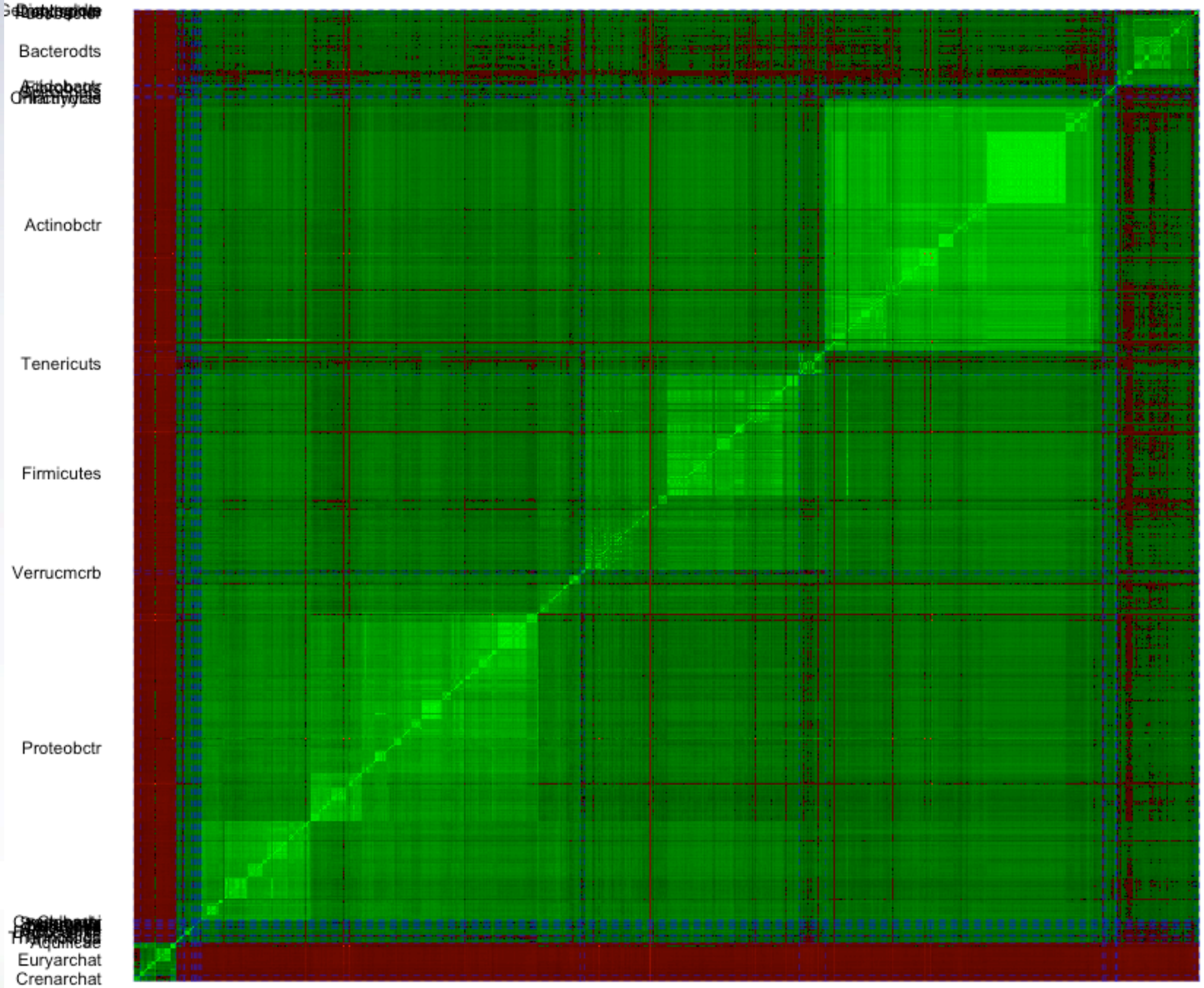


16S rRNA similarity of type strains of Bacteria and Archaea 2008



16S rRNA similarity of type strains of Bacteria and Archaea 2009



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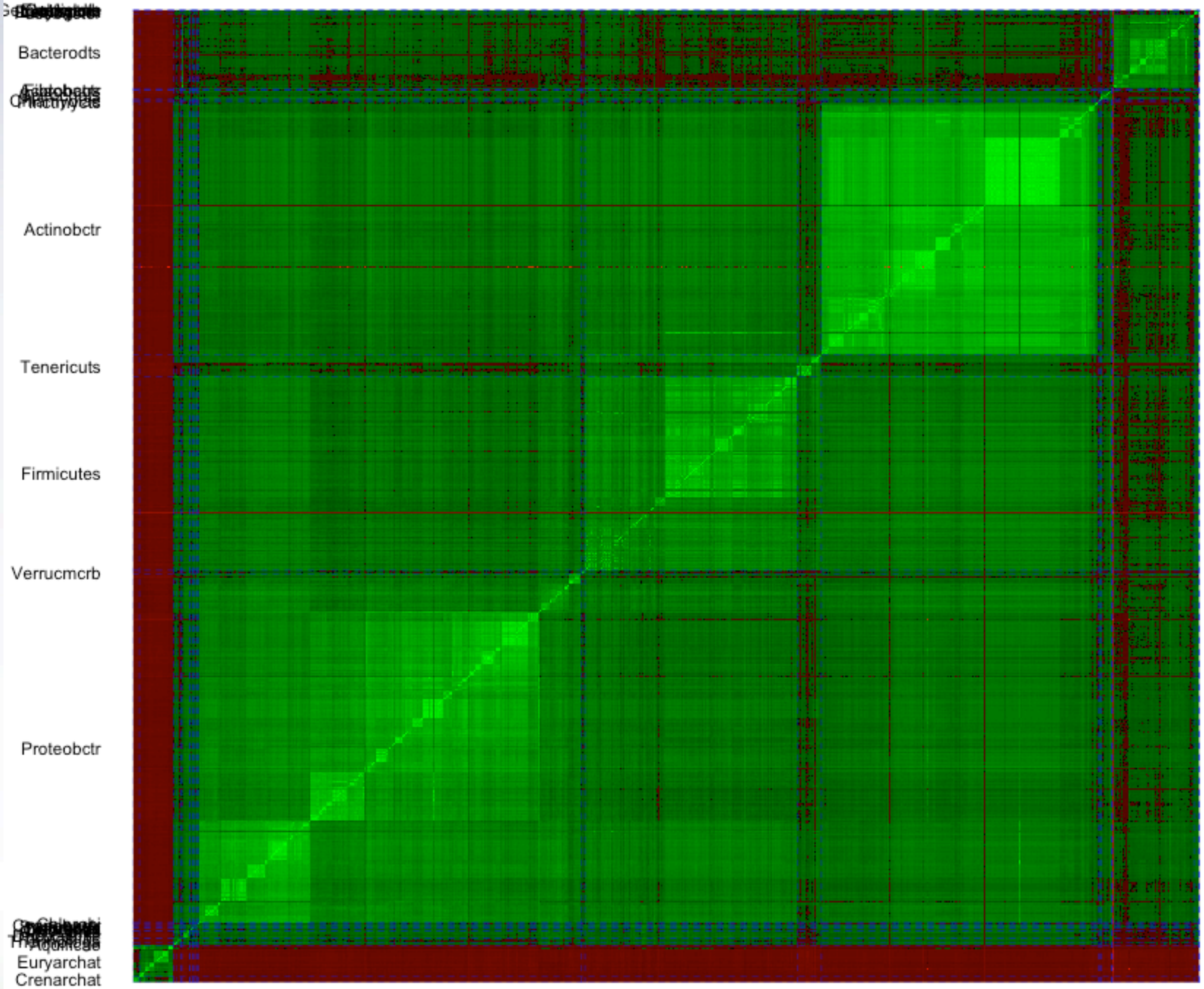
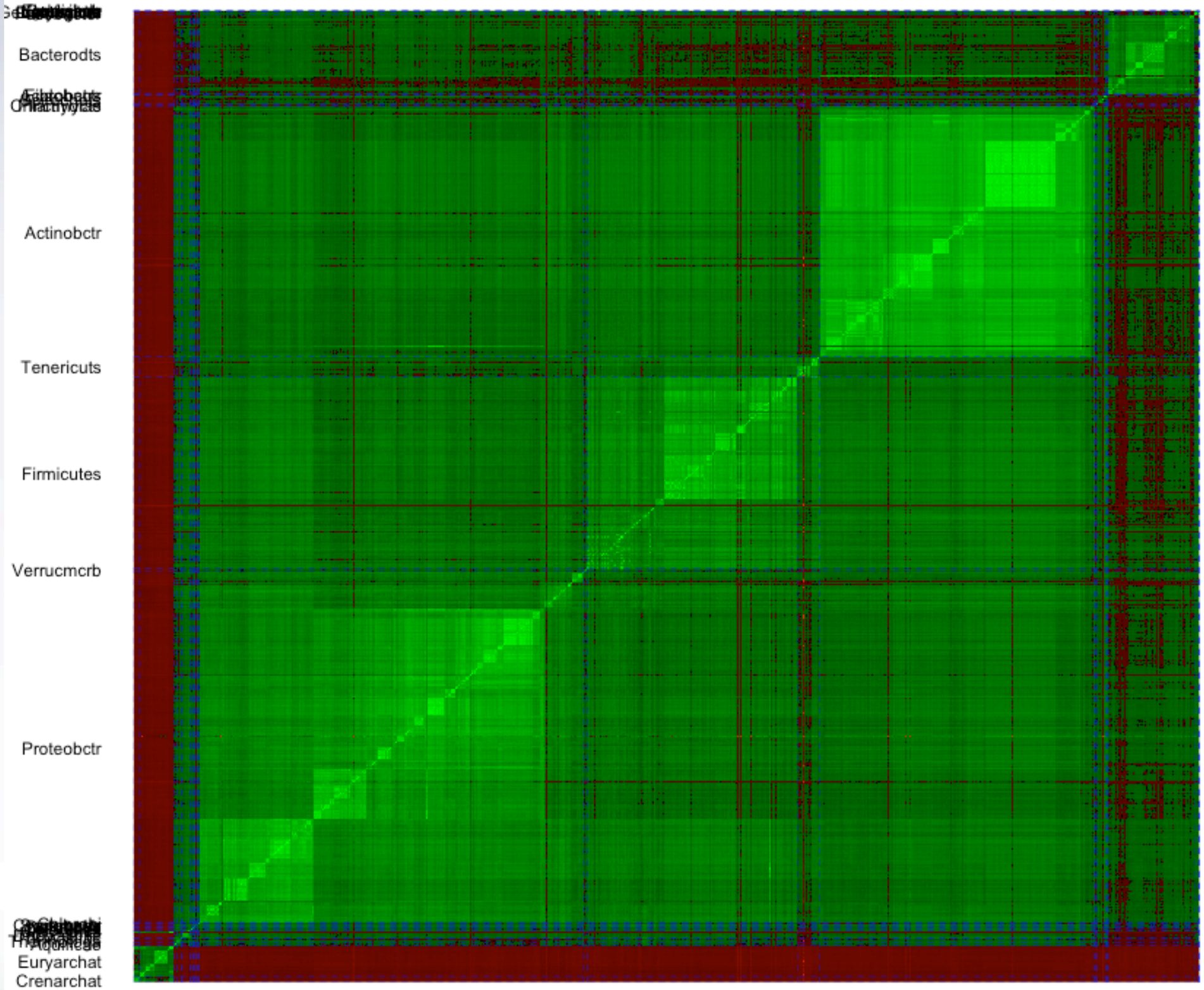


16S rRNA similarity of type strains of Bacteria and Archaea 2011



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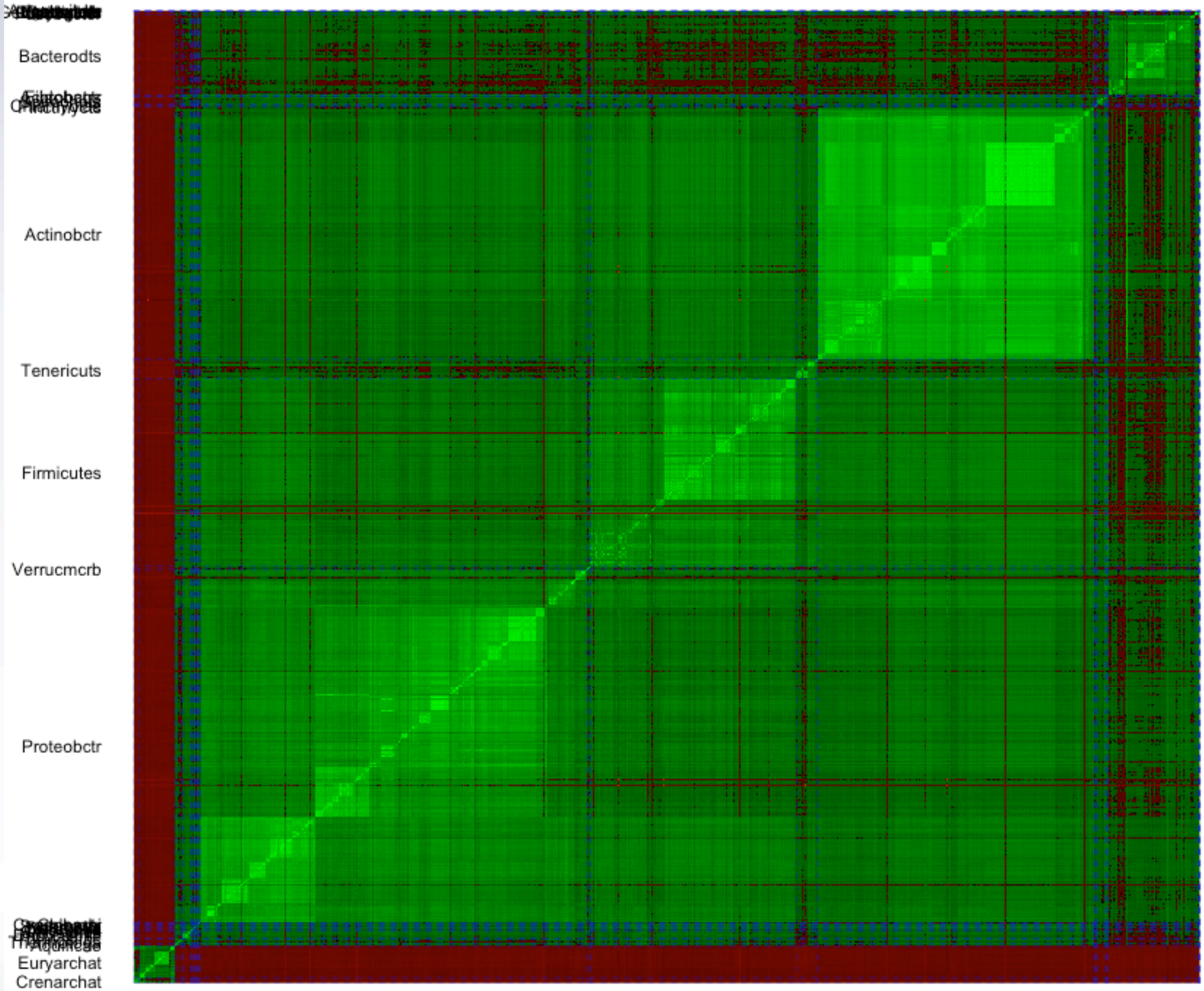

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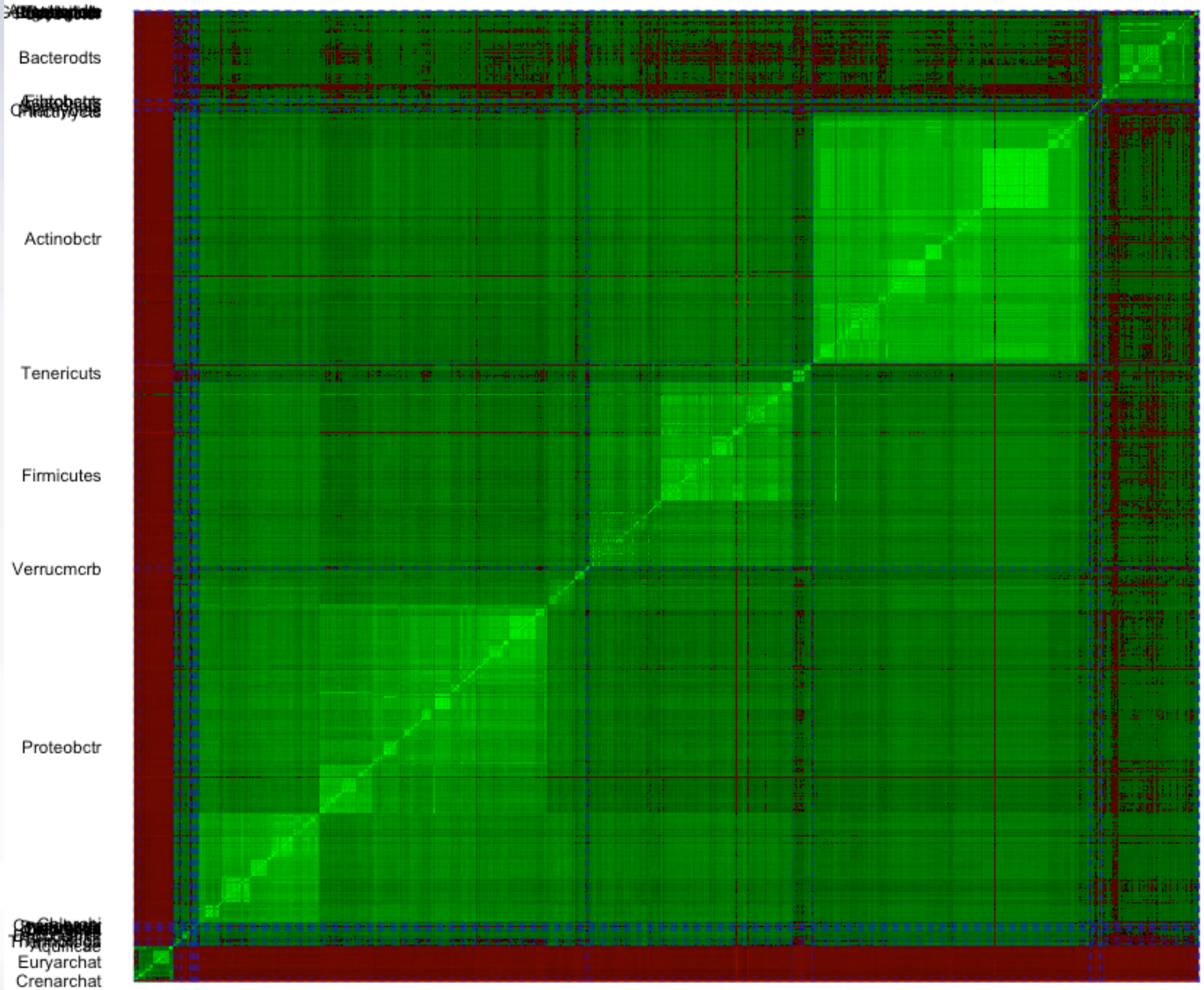
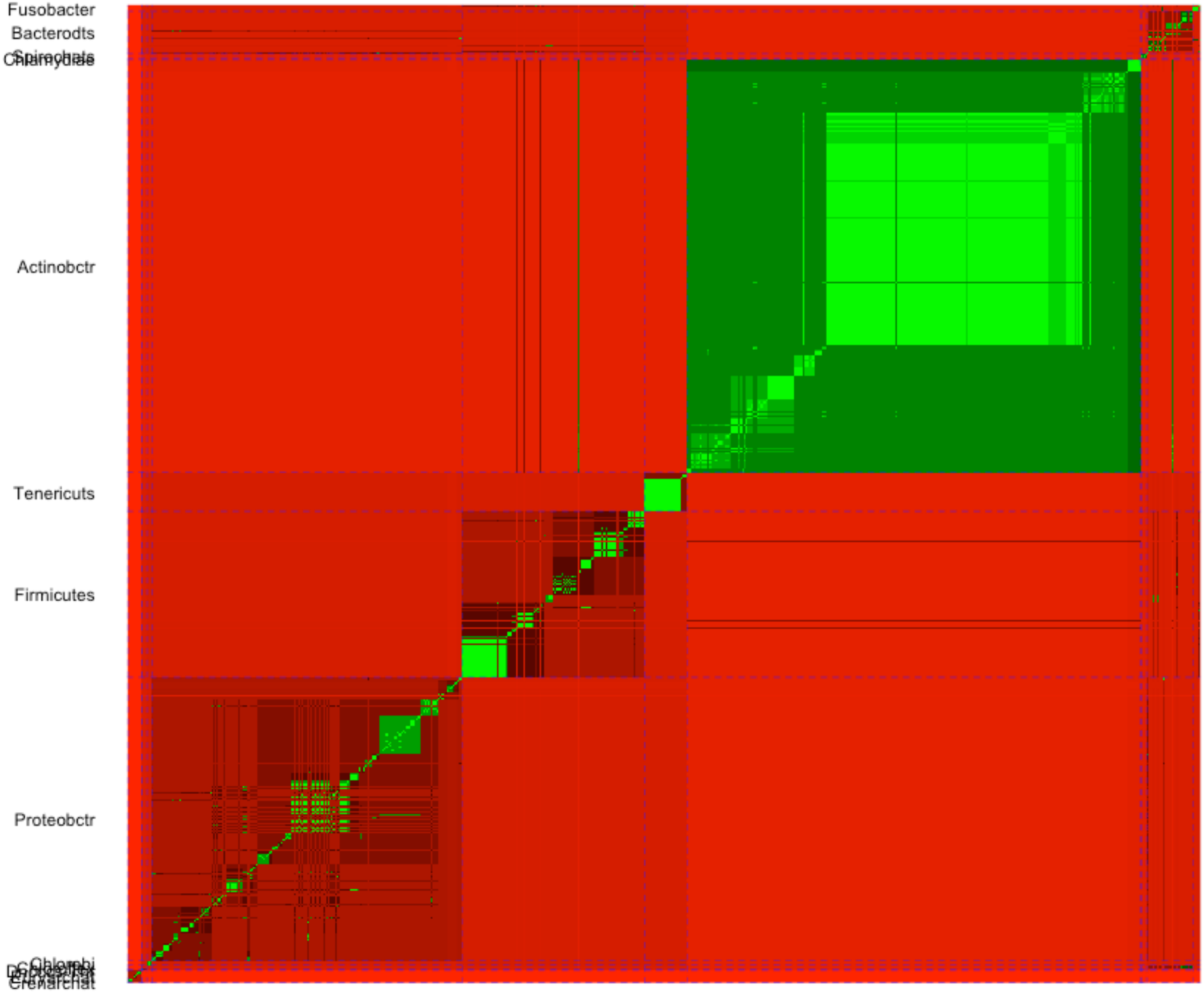
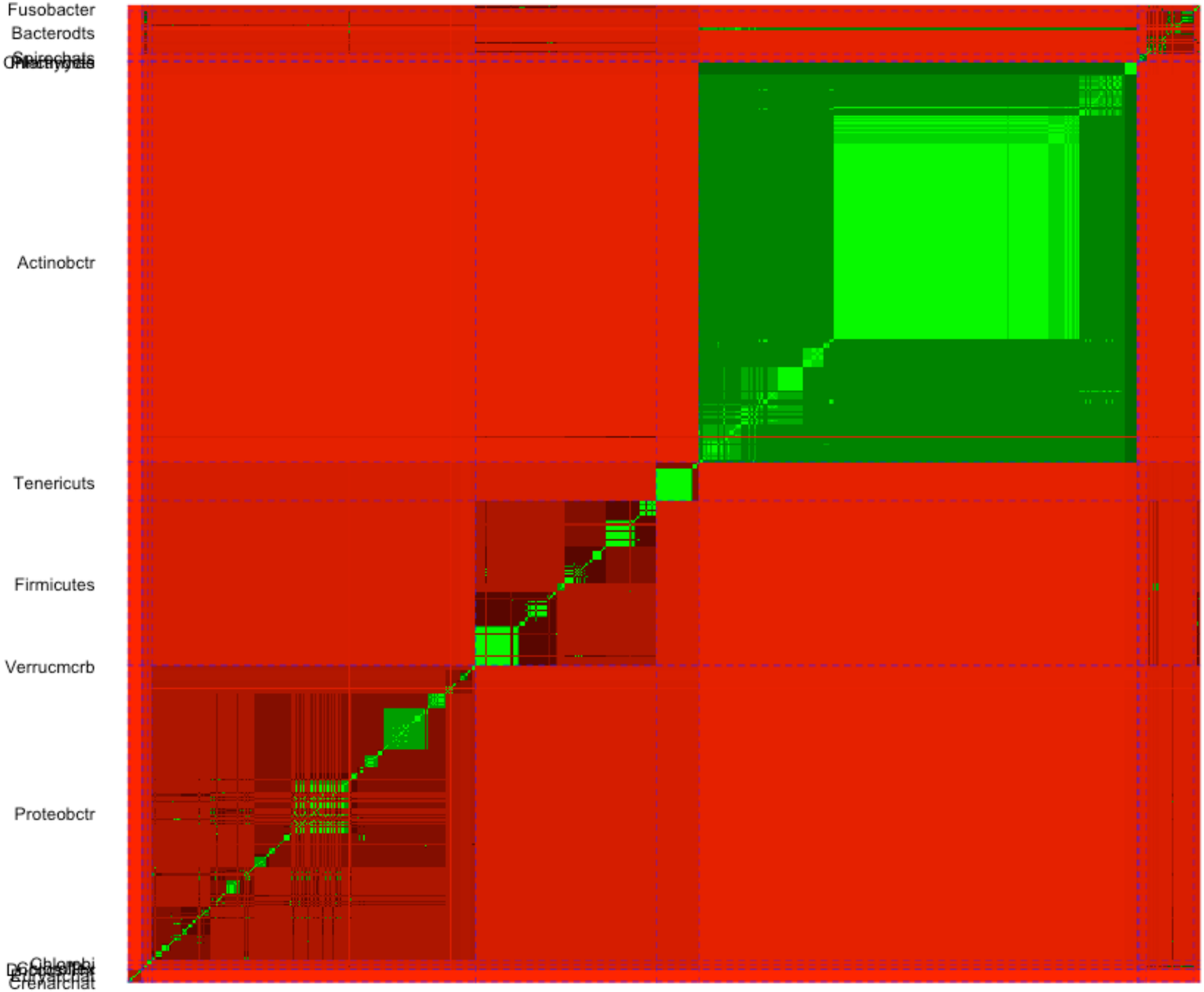


Taxonomy of type strains of Bacteria and Archaea 1980



Taxonomy of type strains of Bacteria and Archaea 1981



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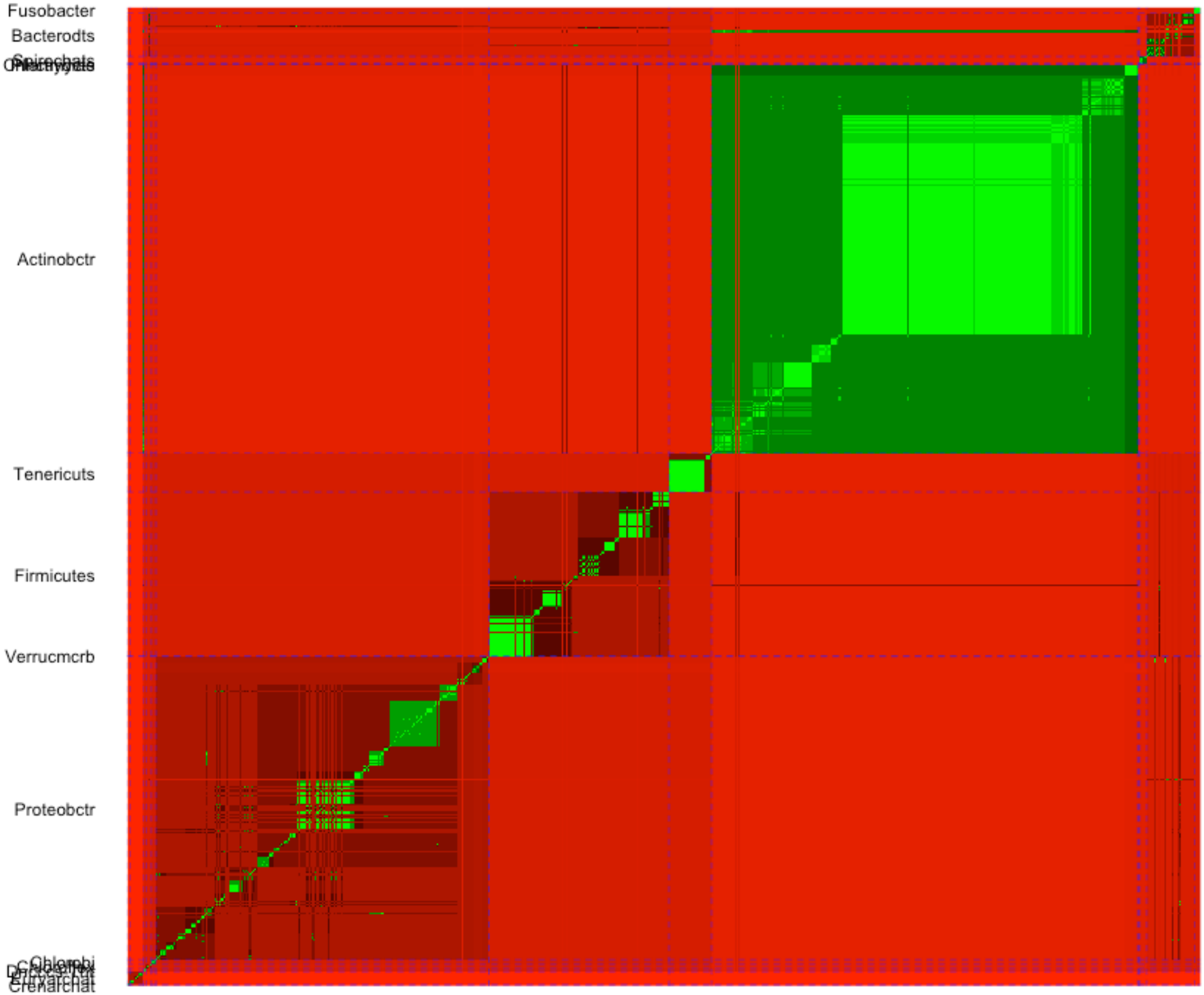

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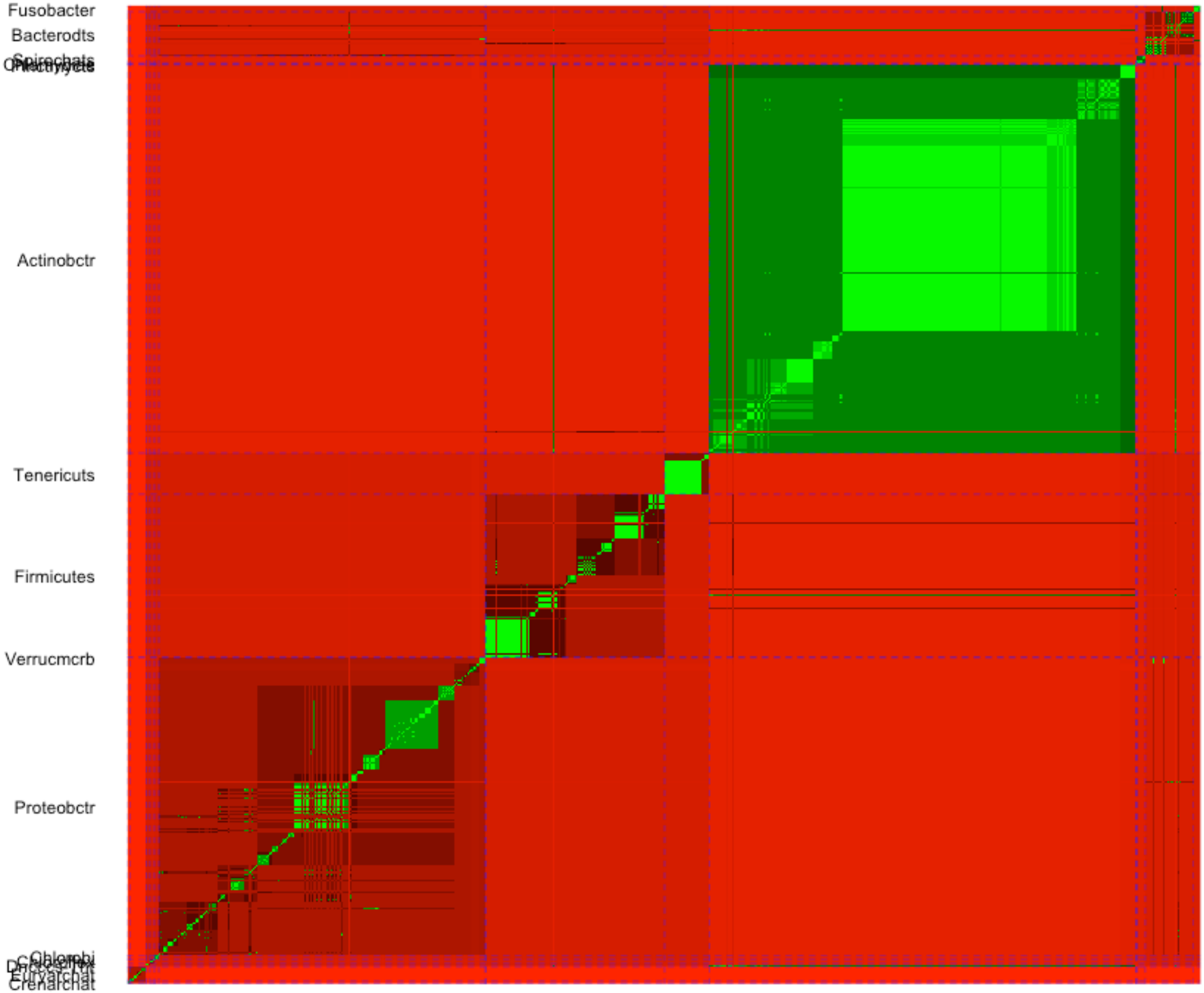

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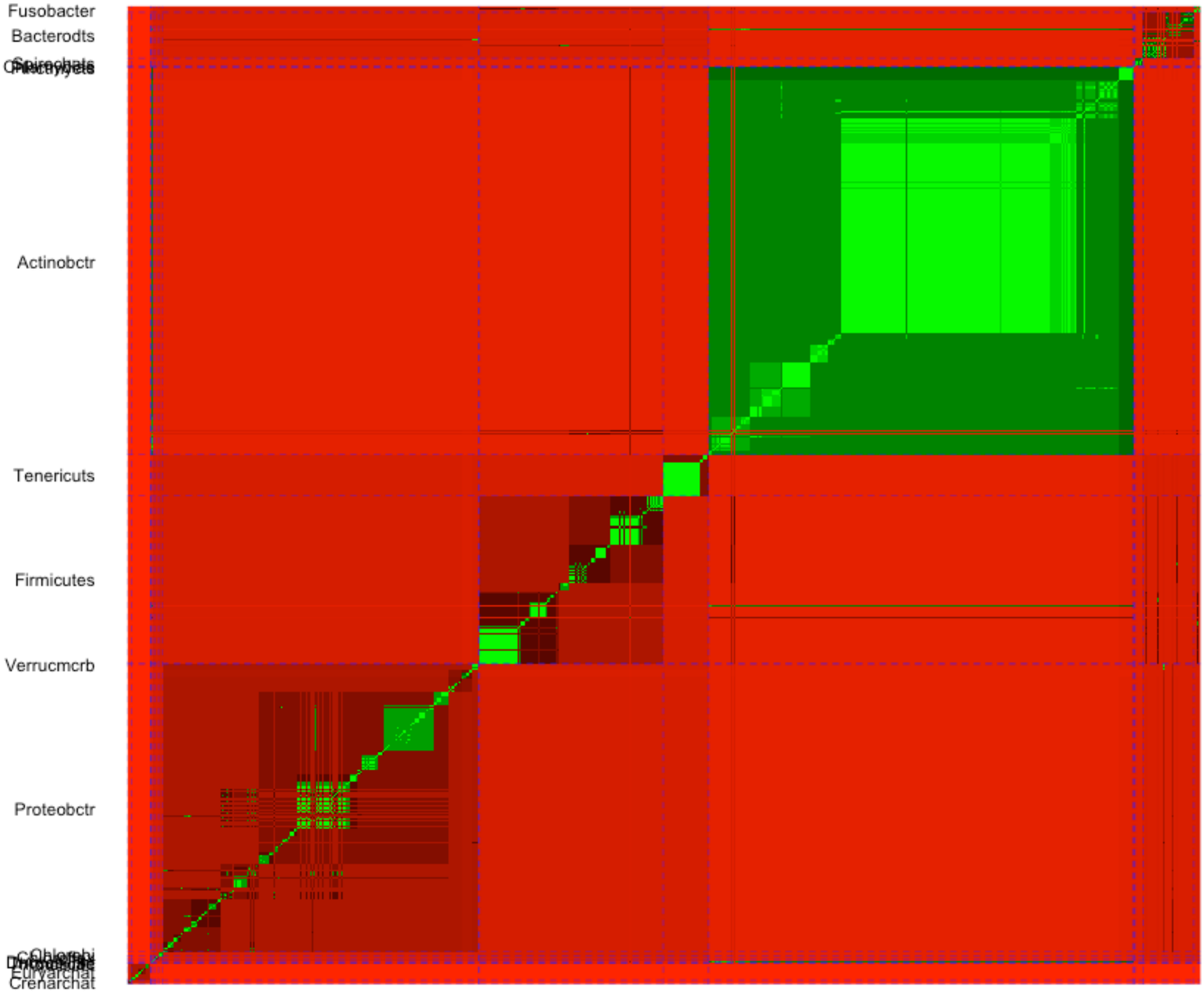

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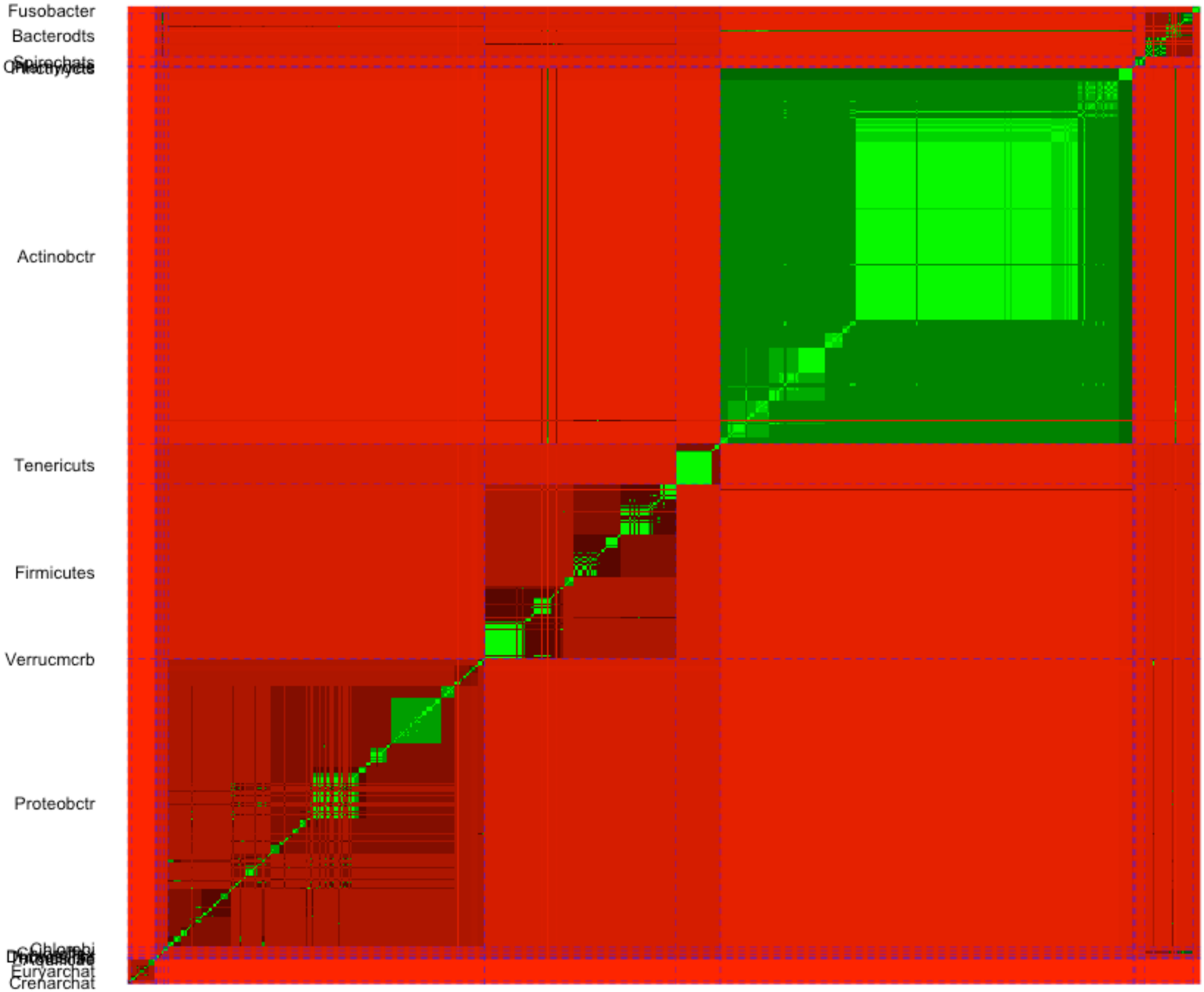

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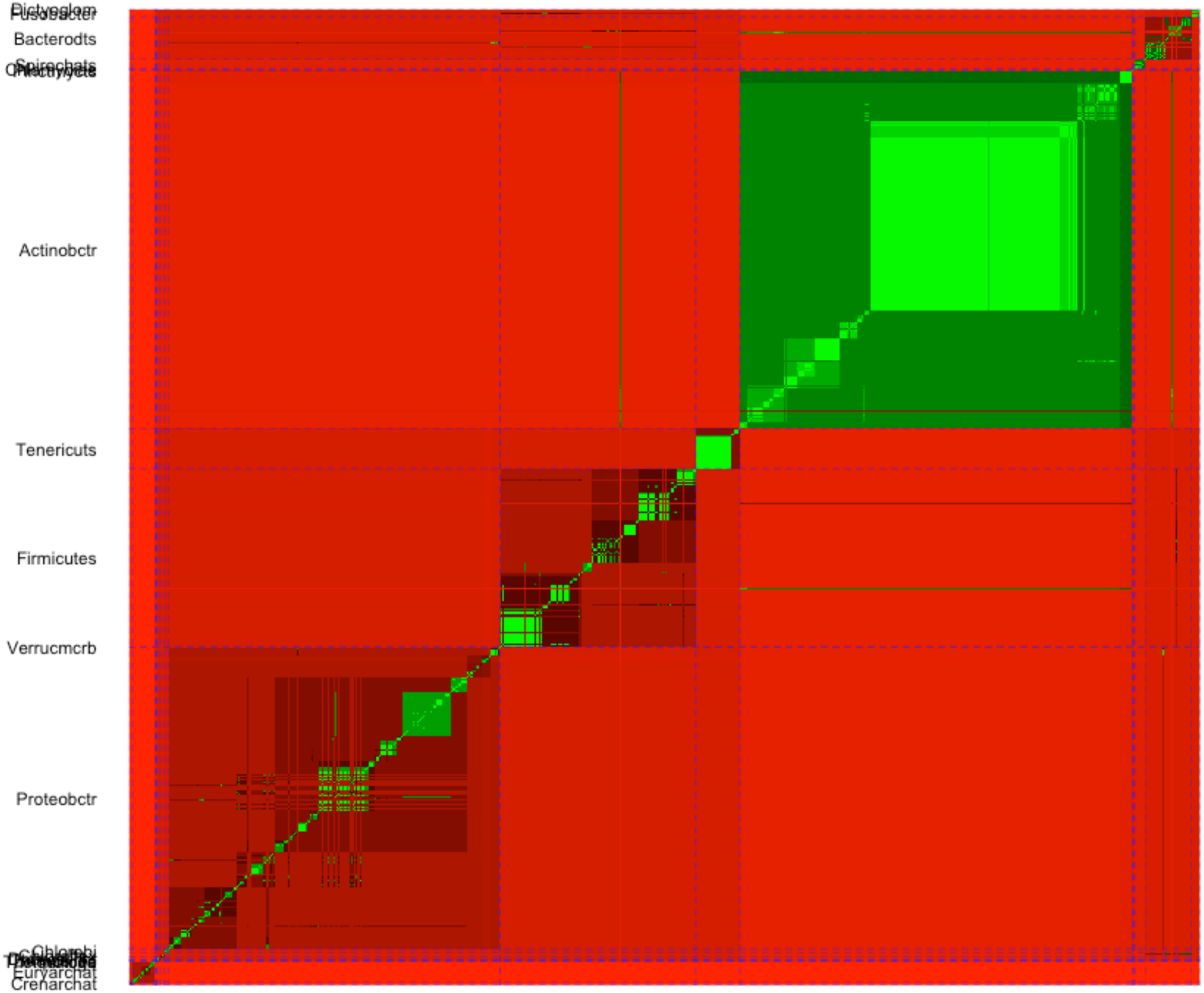

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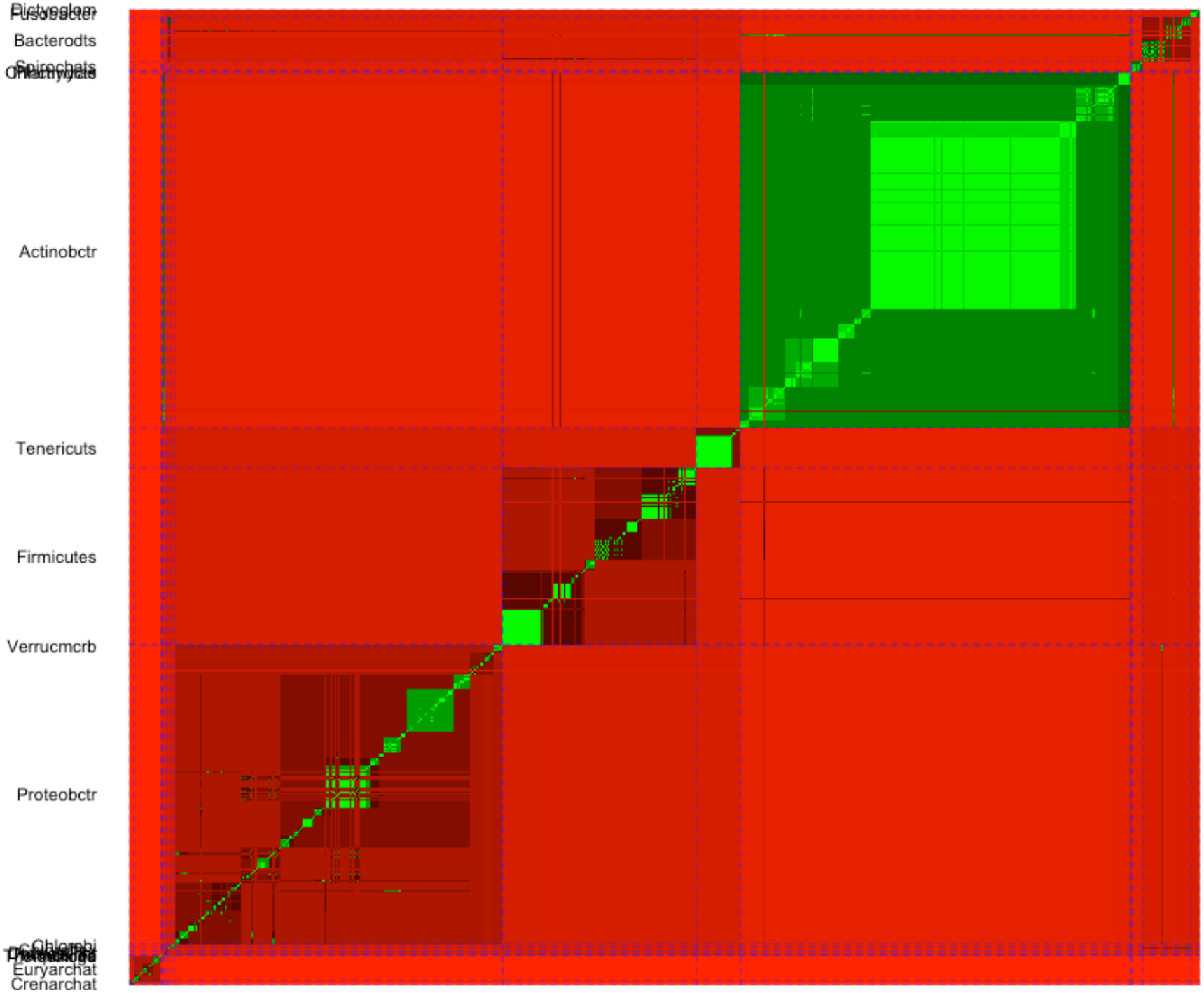

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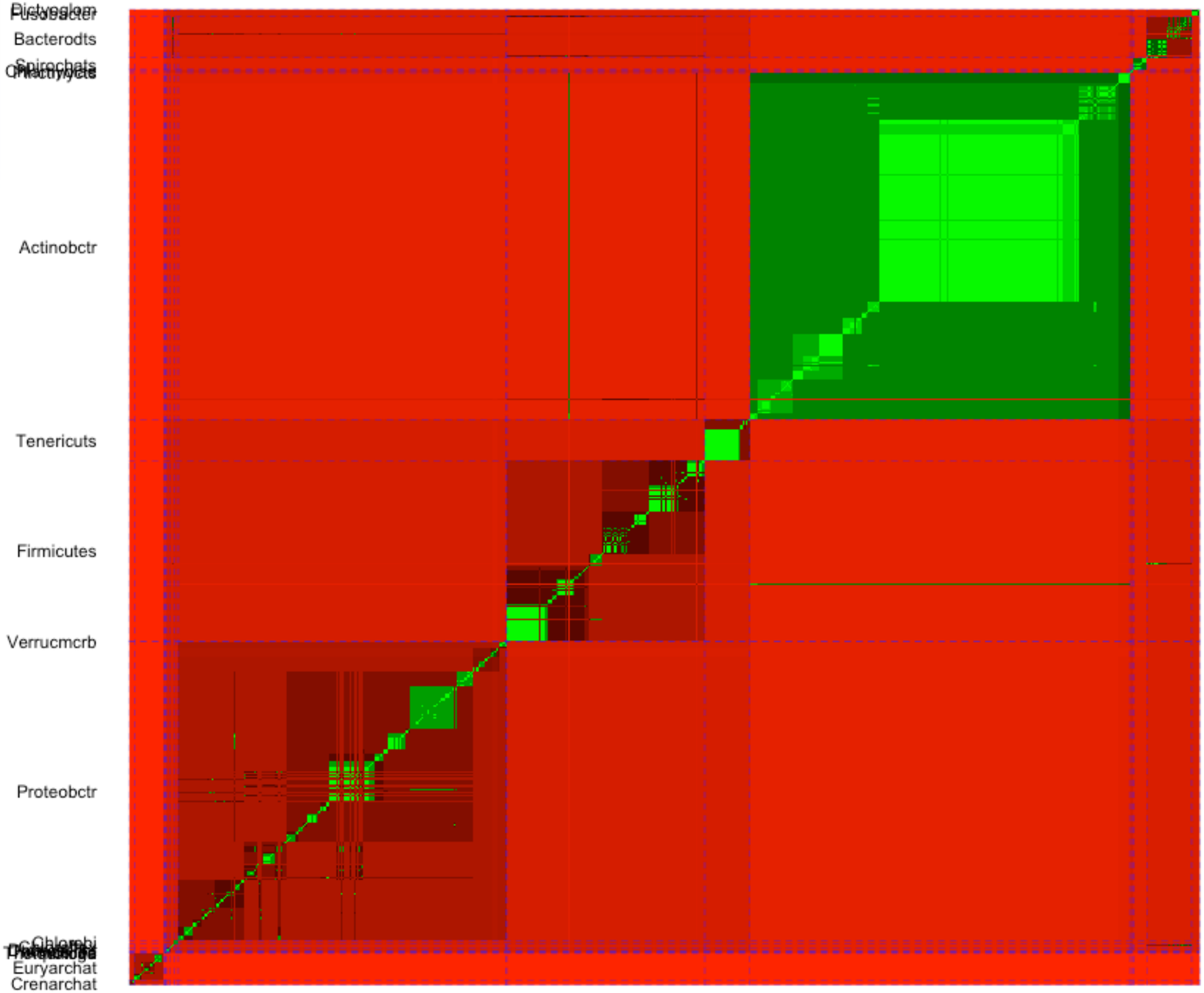

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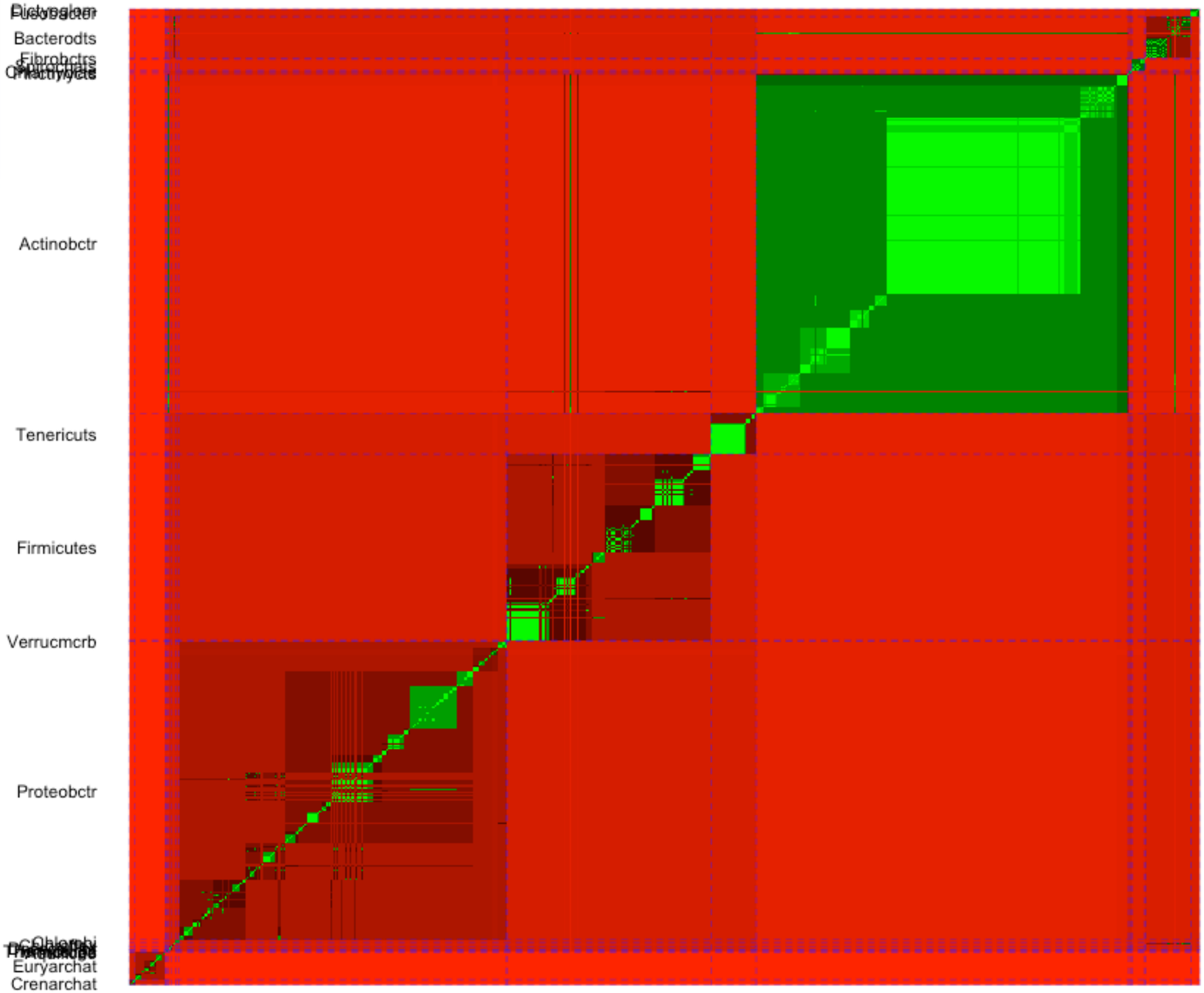

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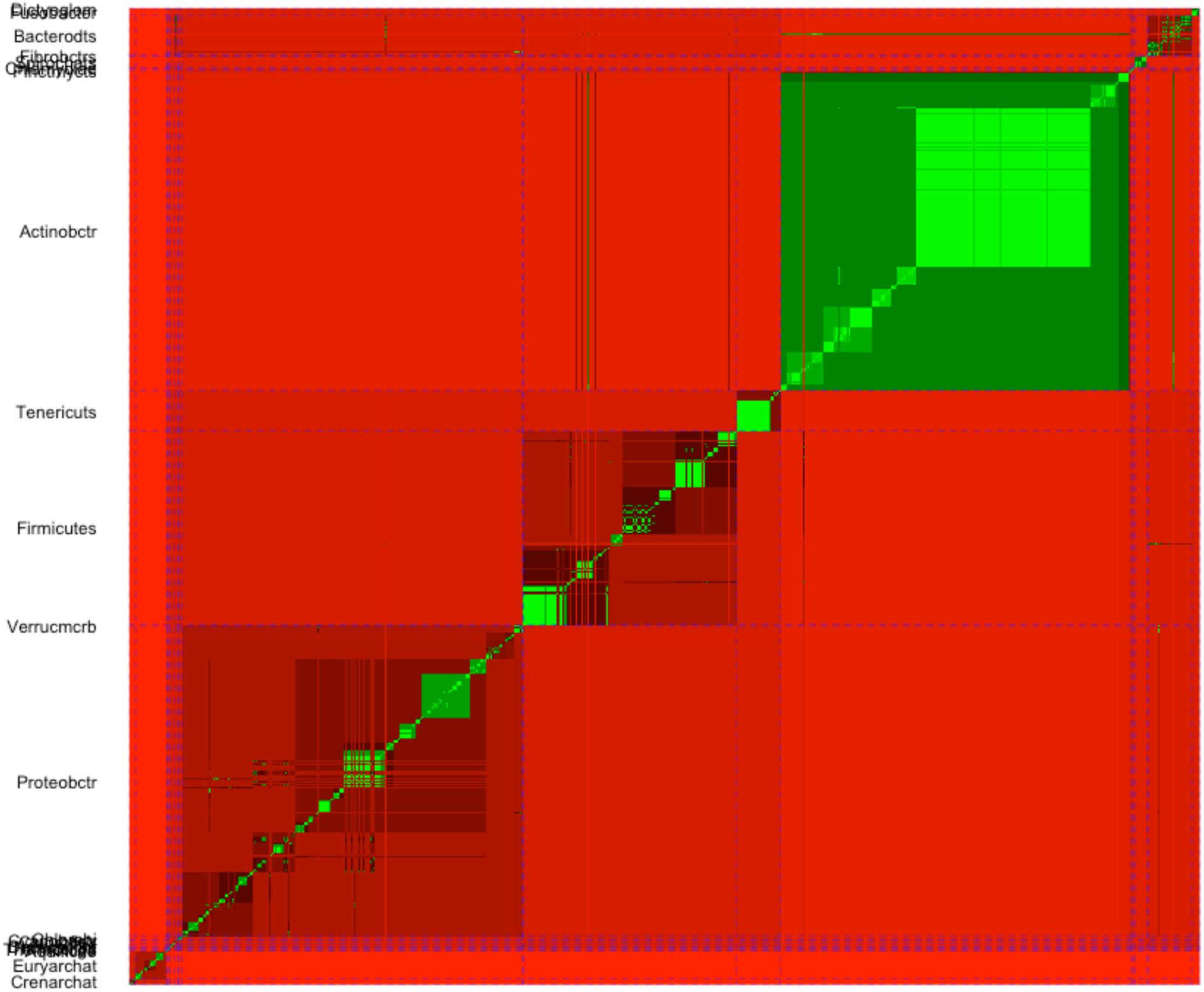

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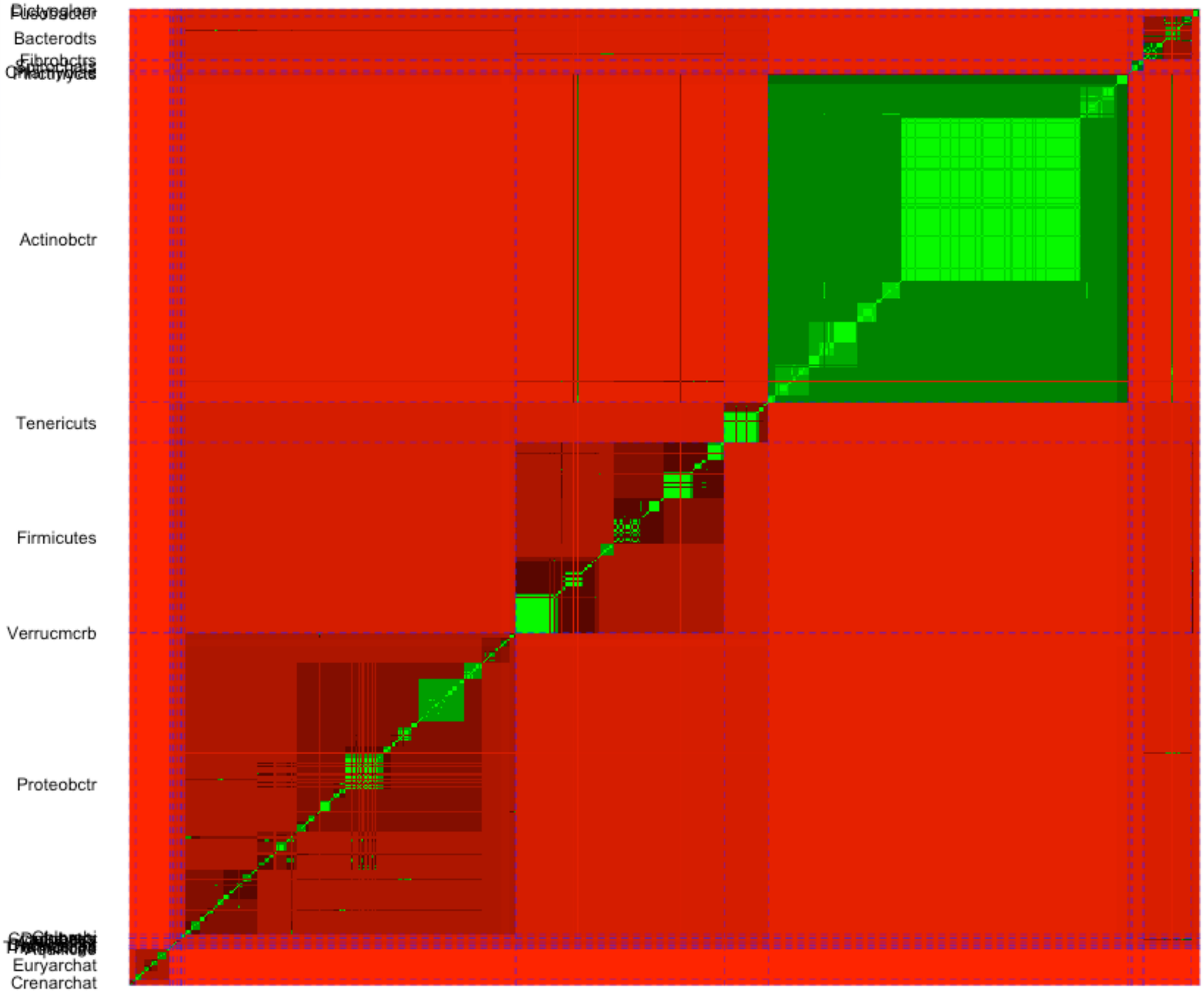

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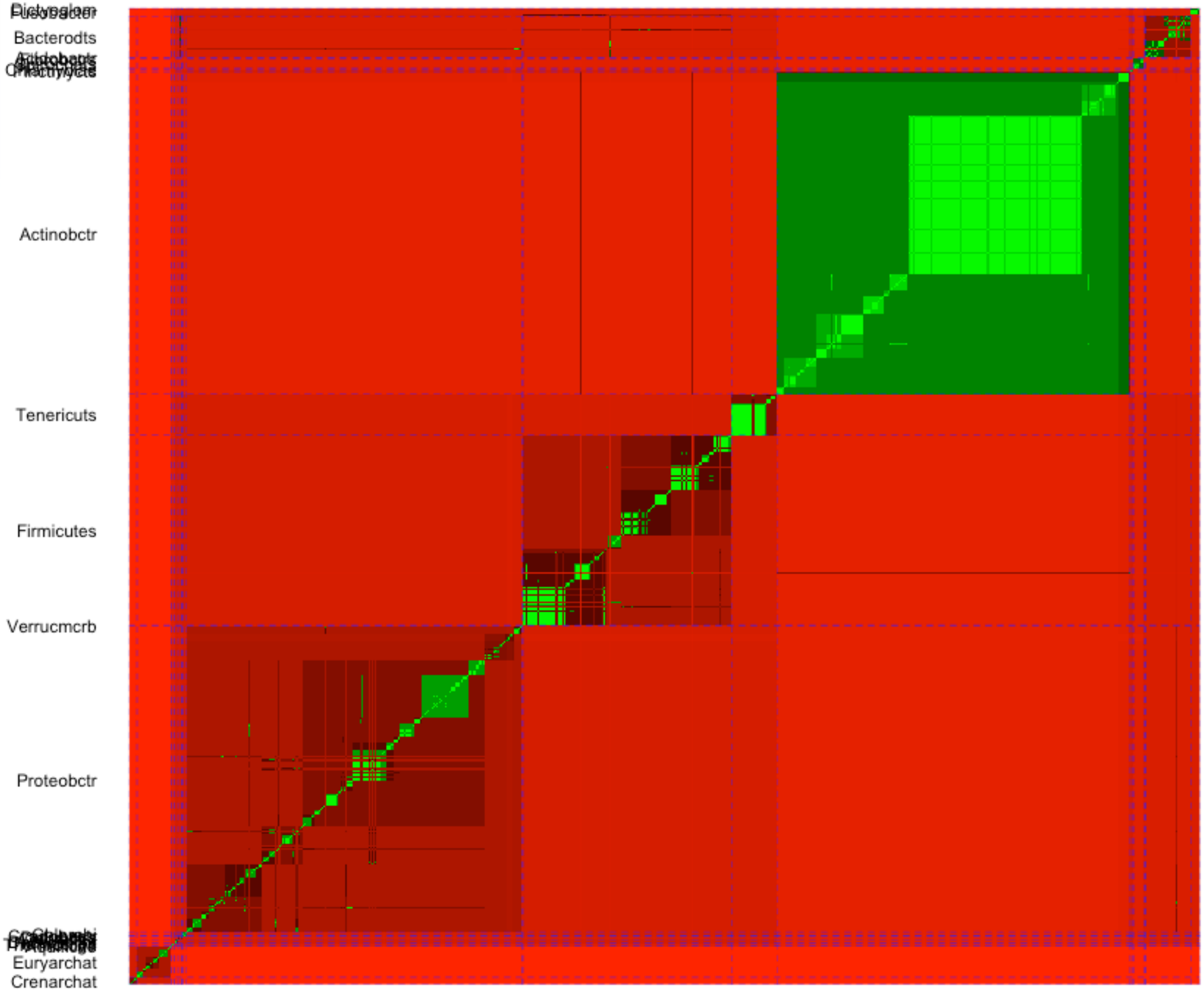

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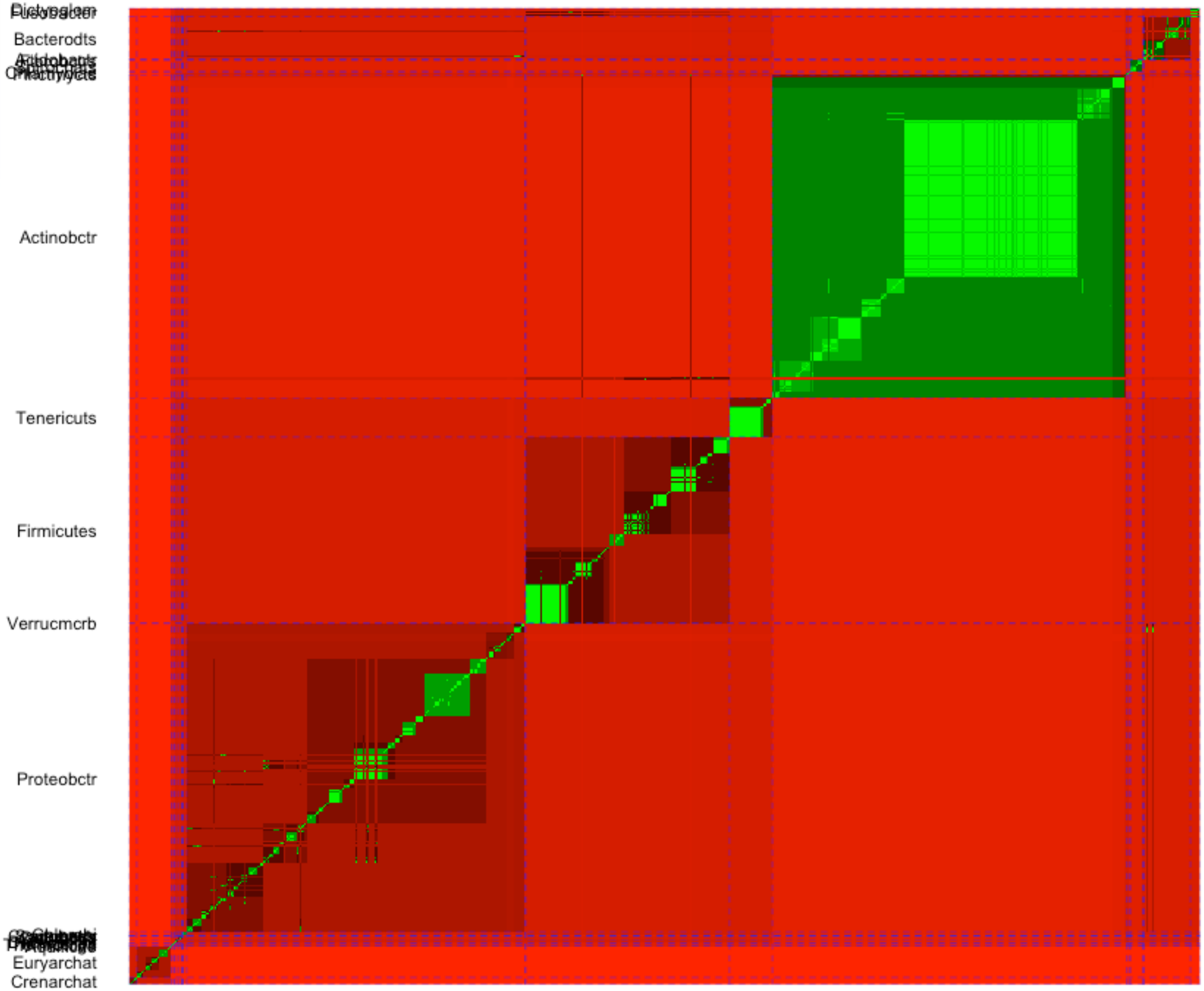

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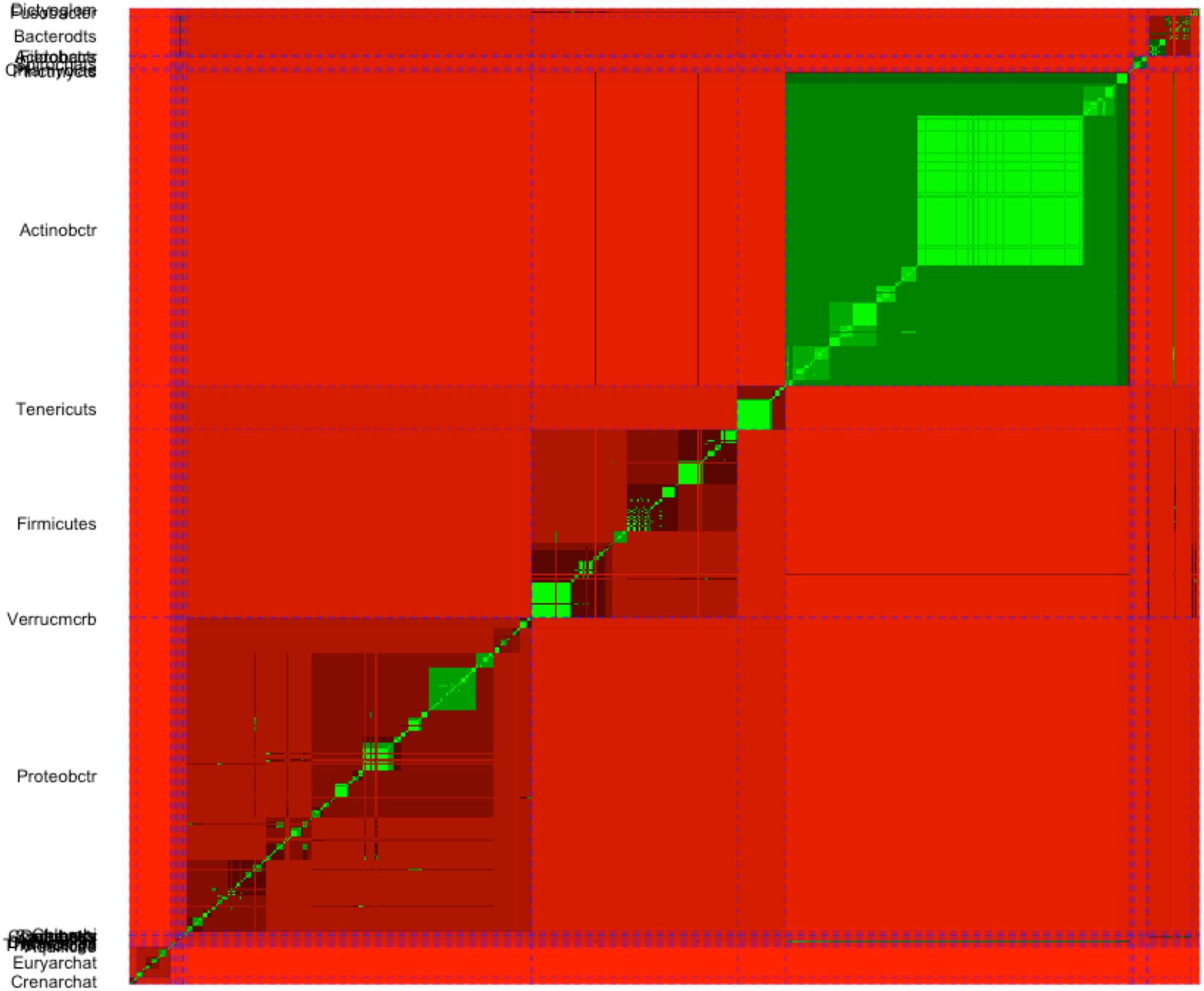

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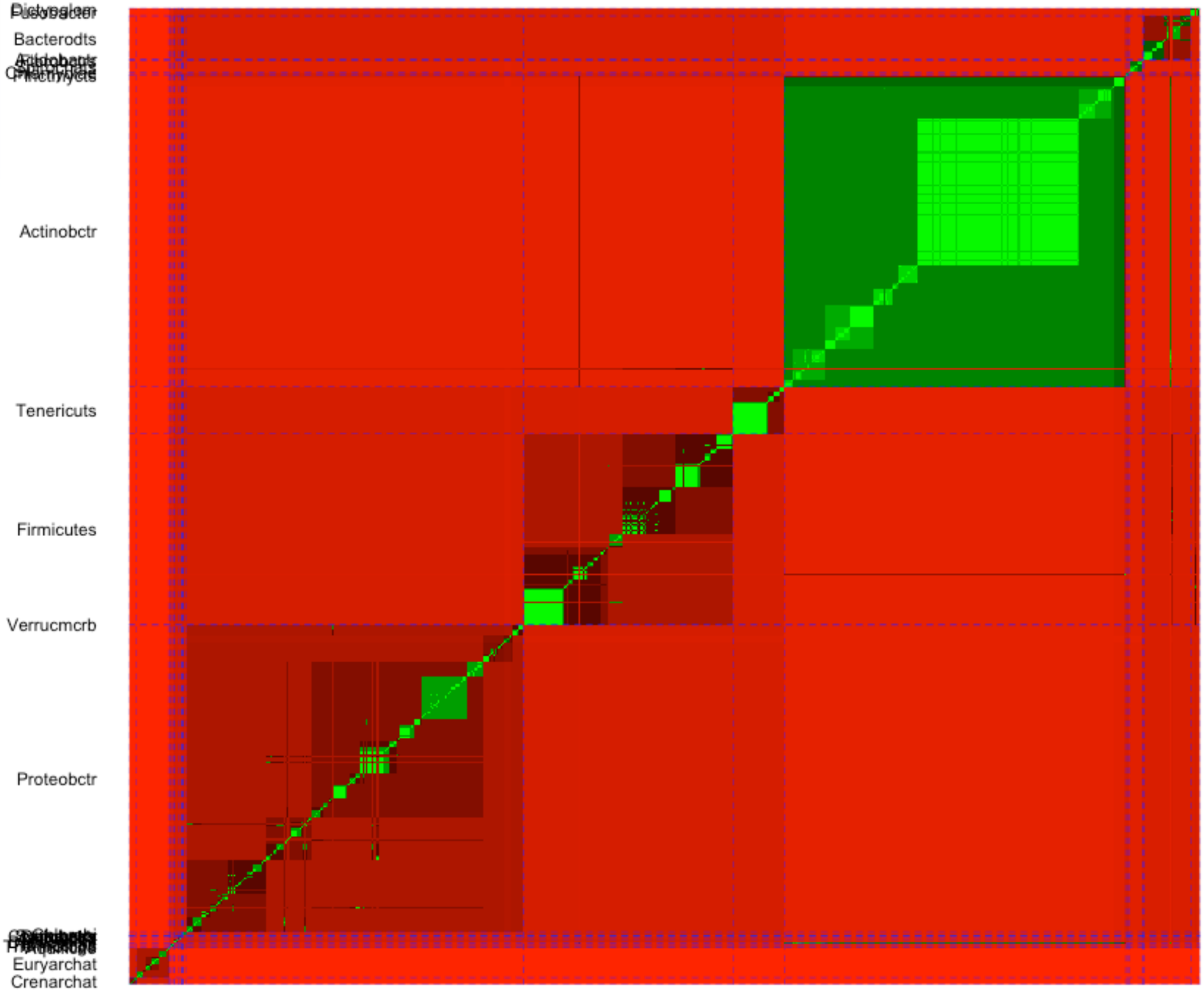

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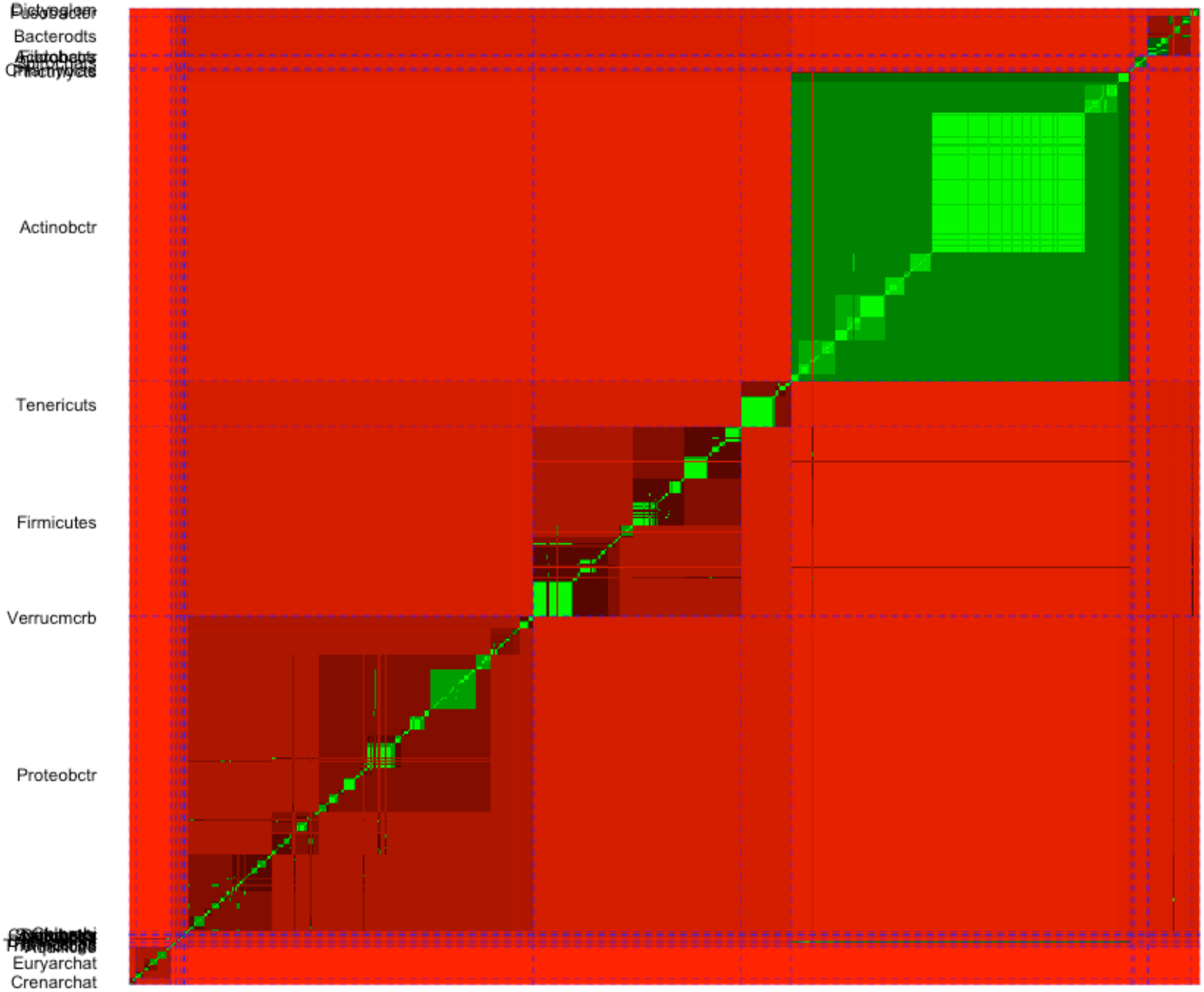

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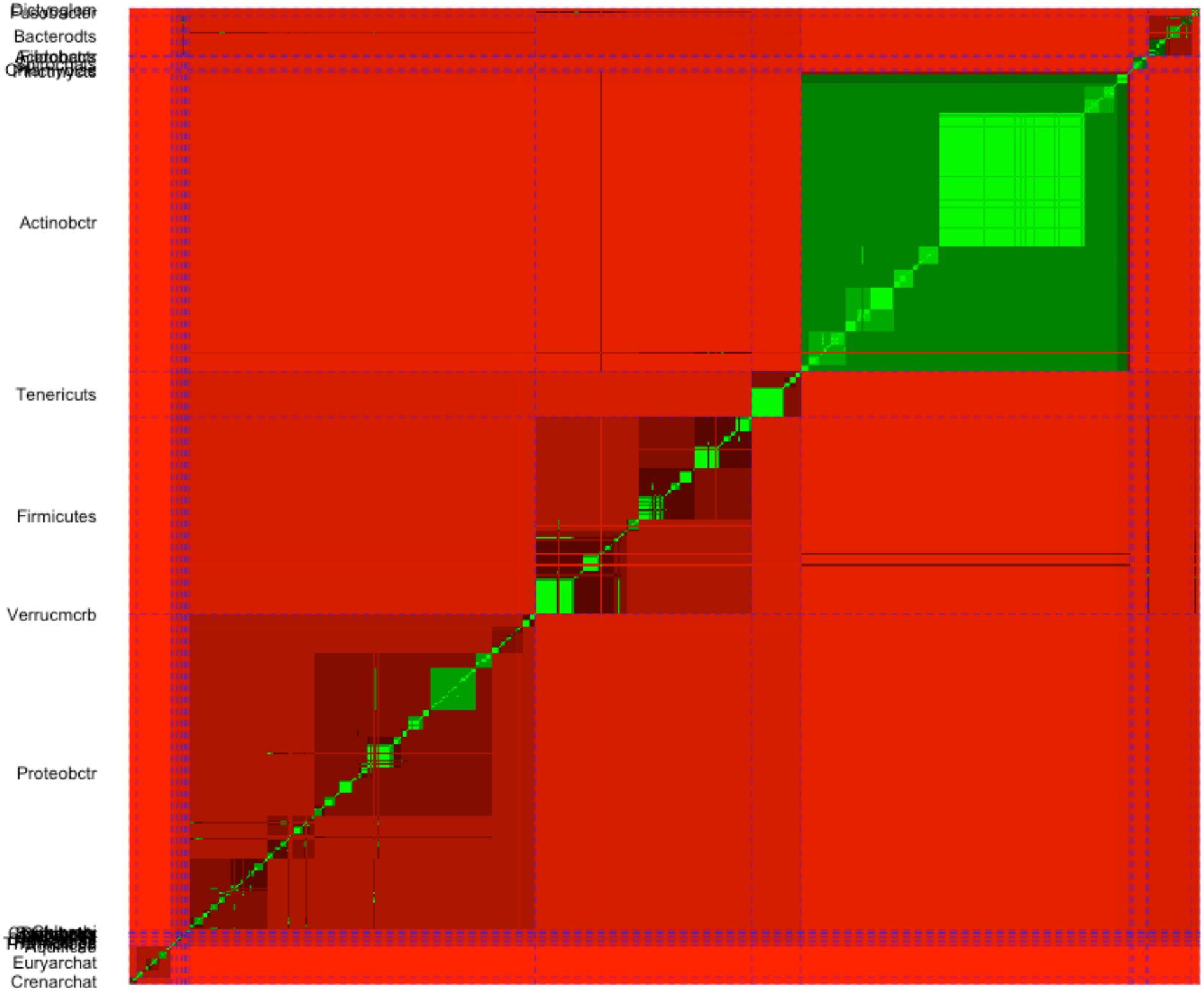

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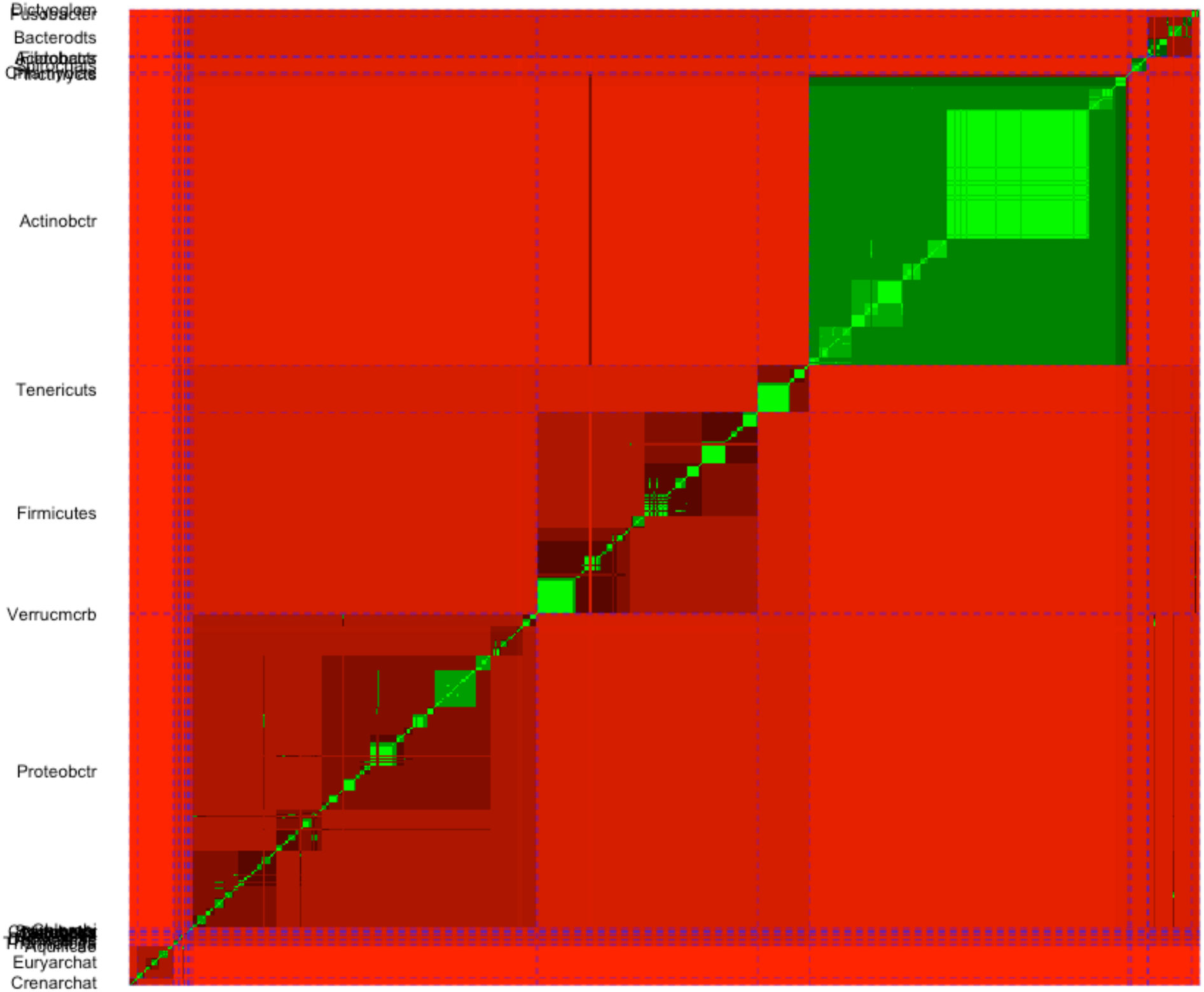

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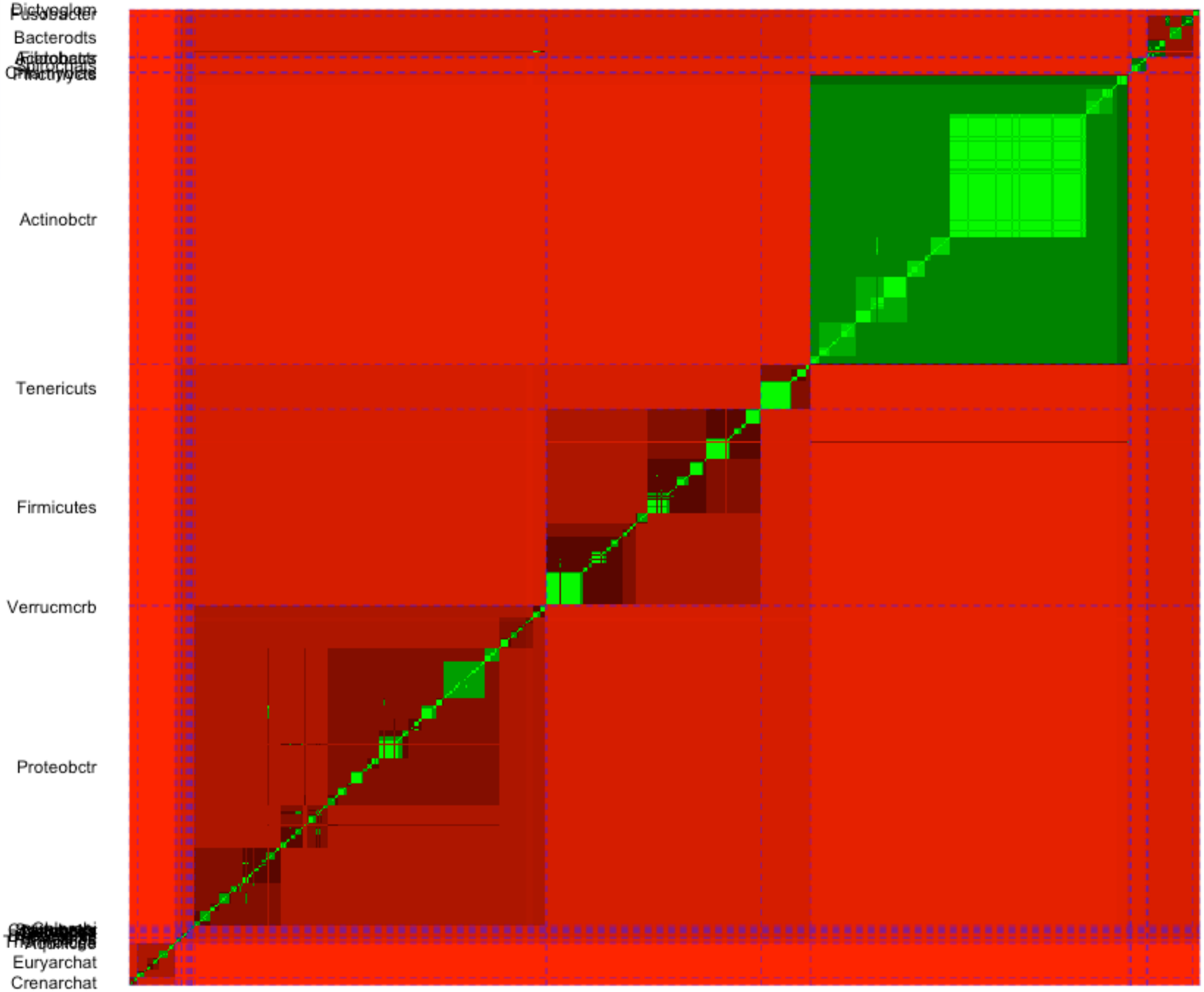

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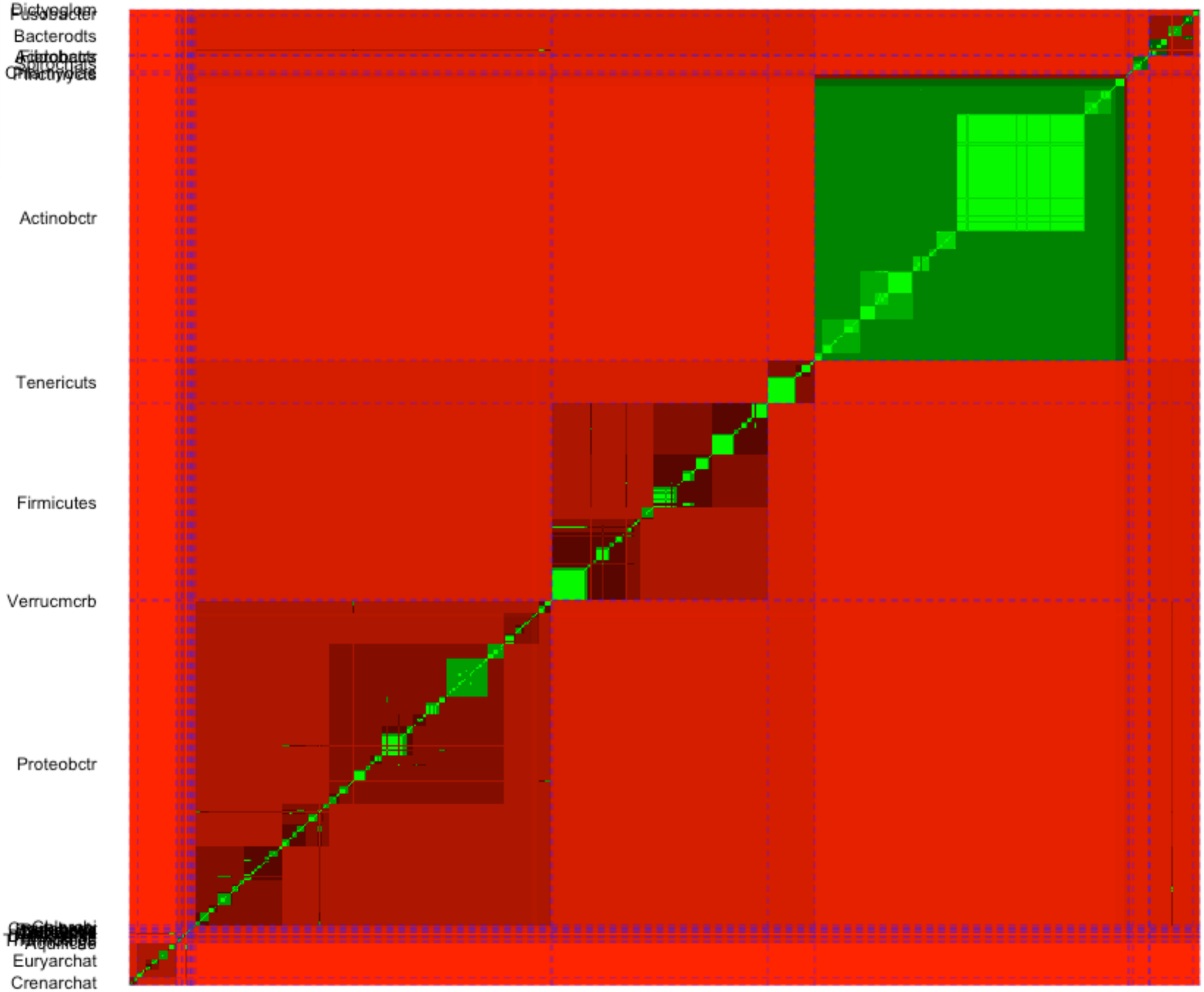

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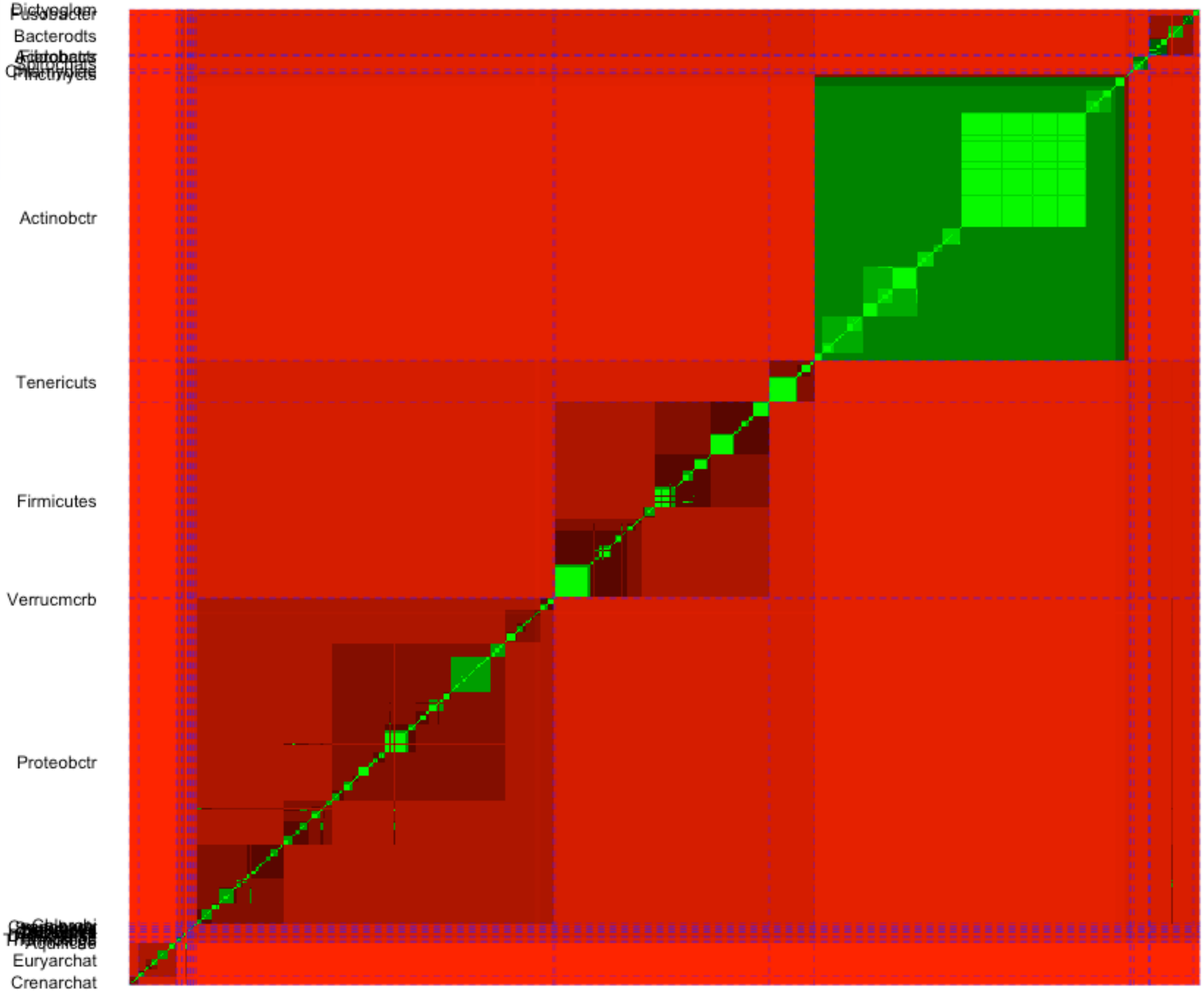

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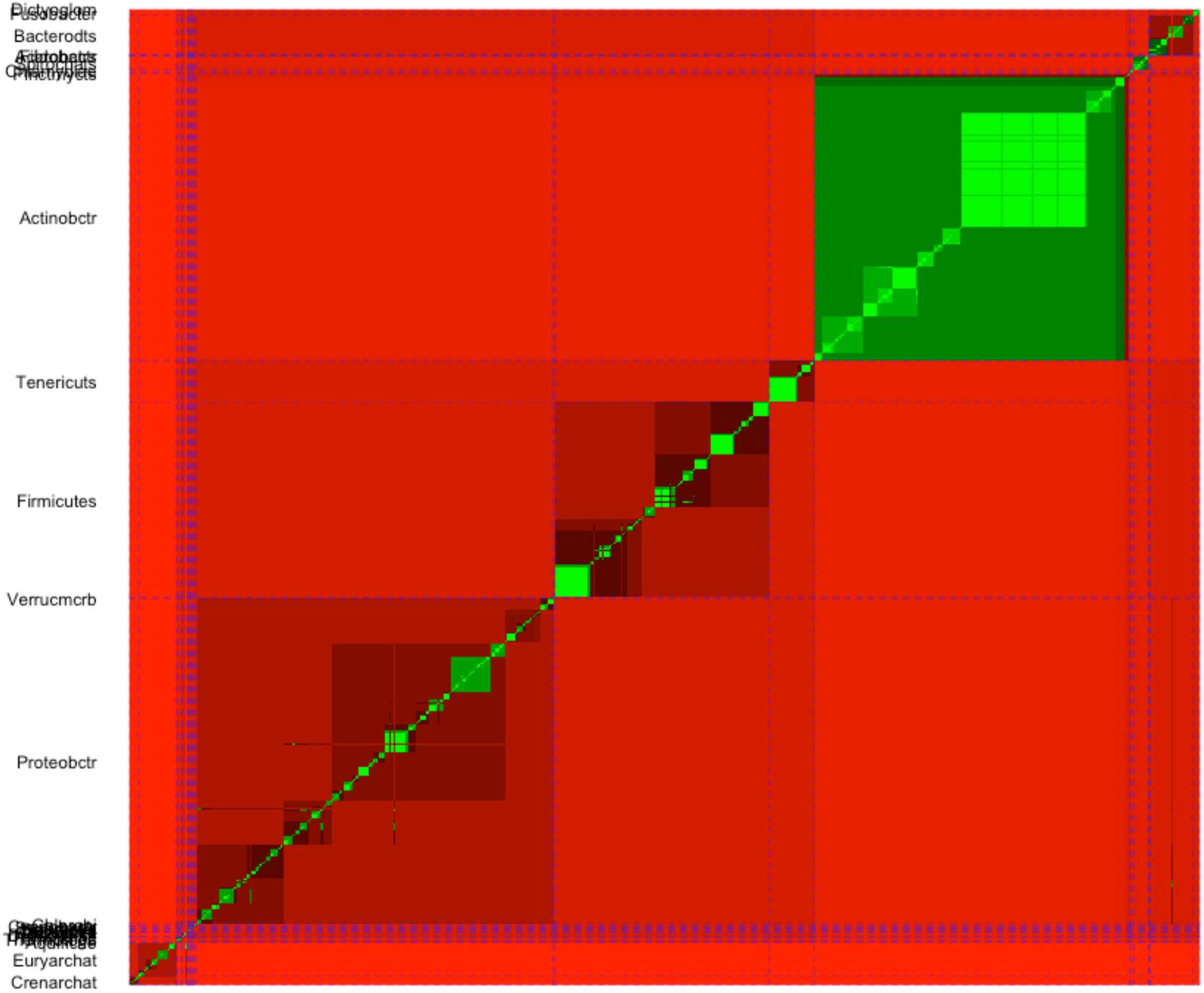

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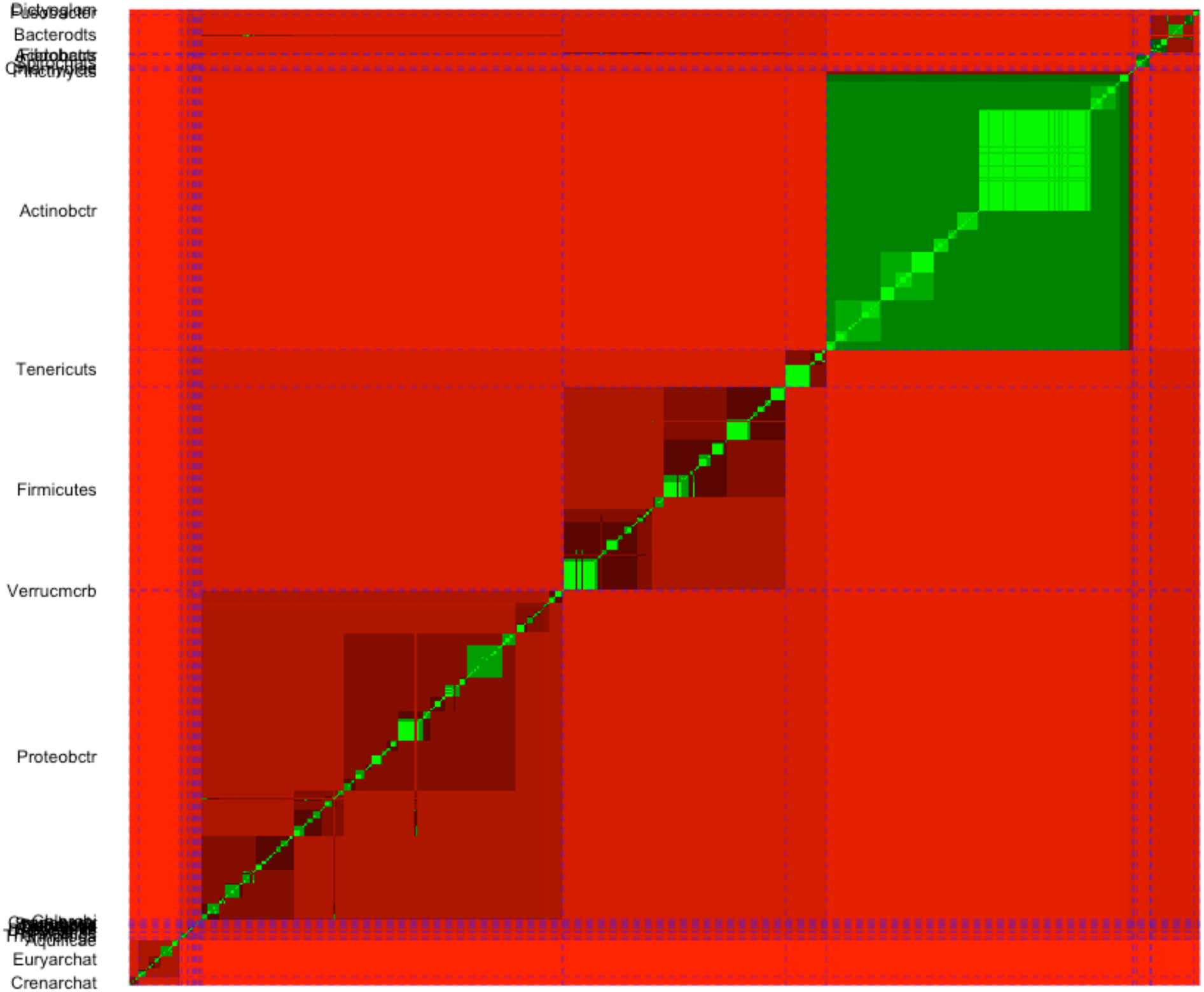

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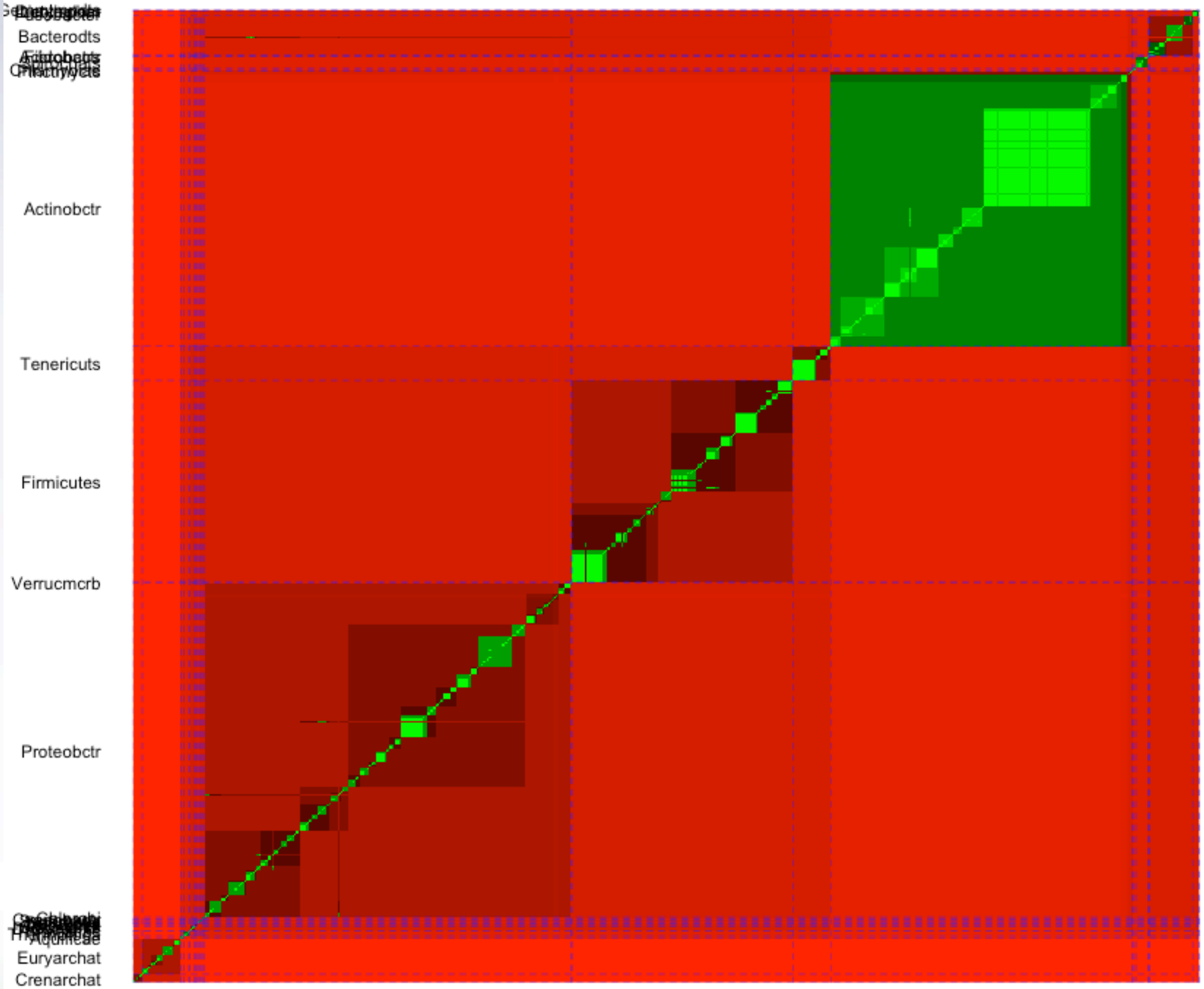

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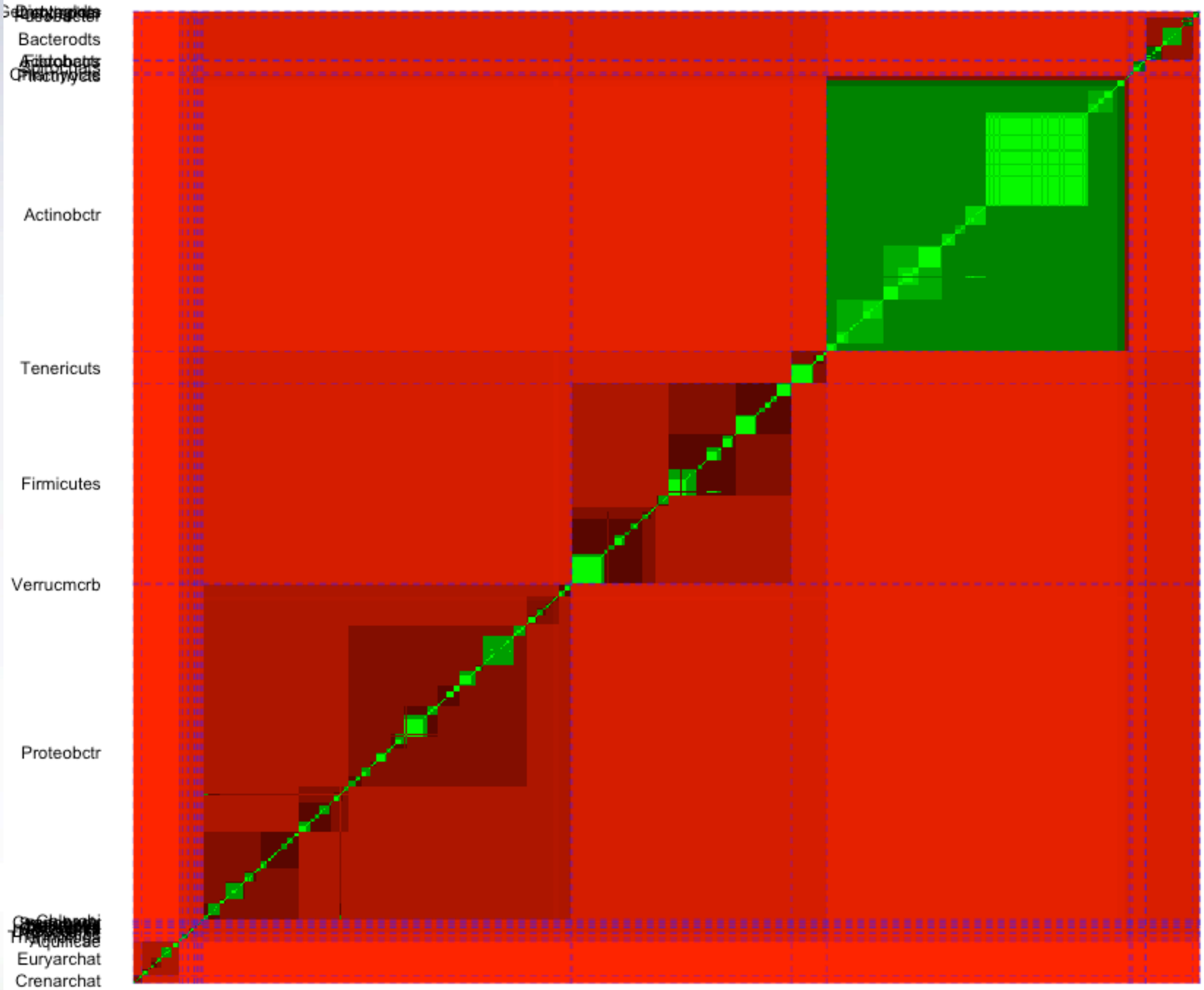
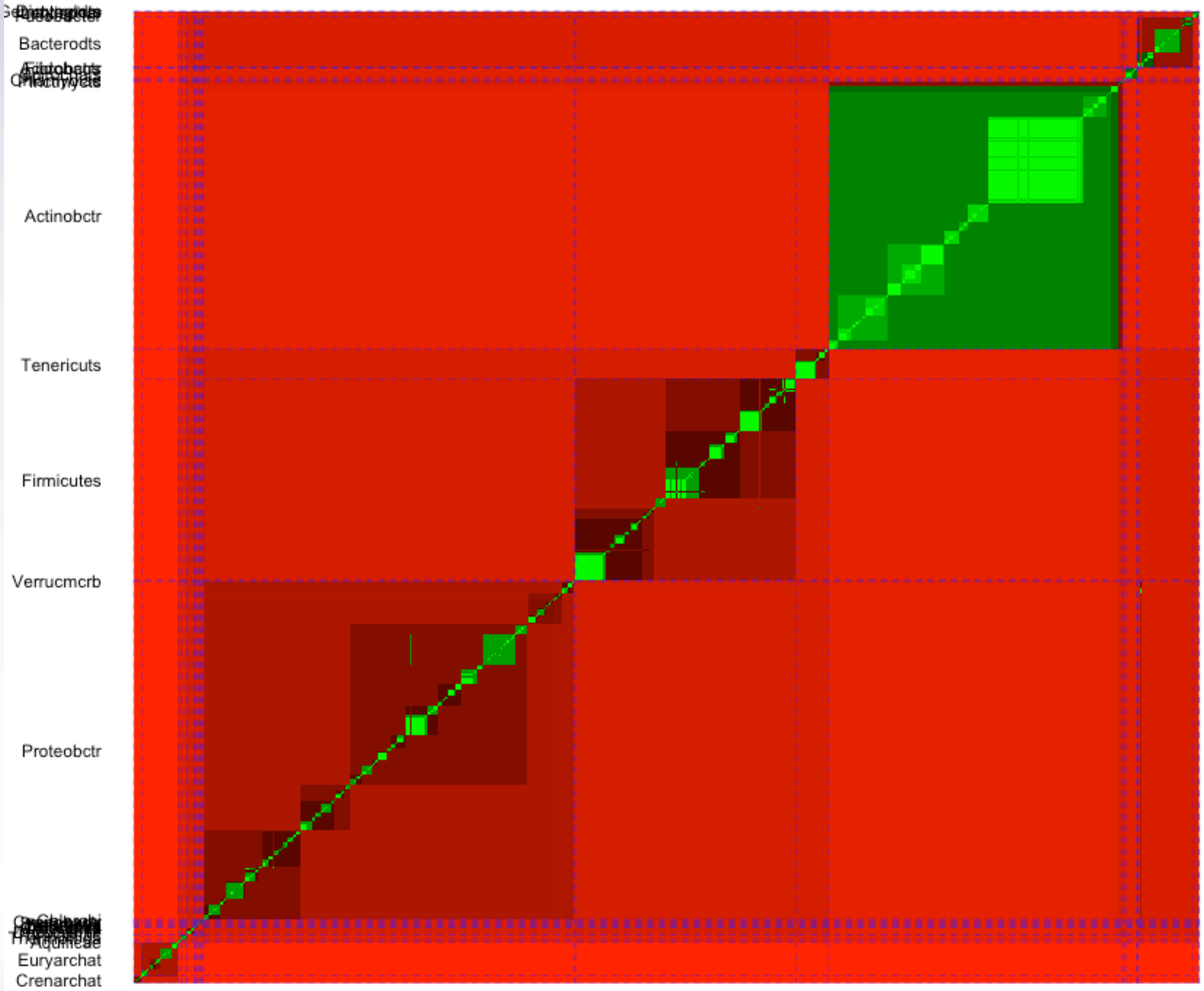
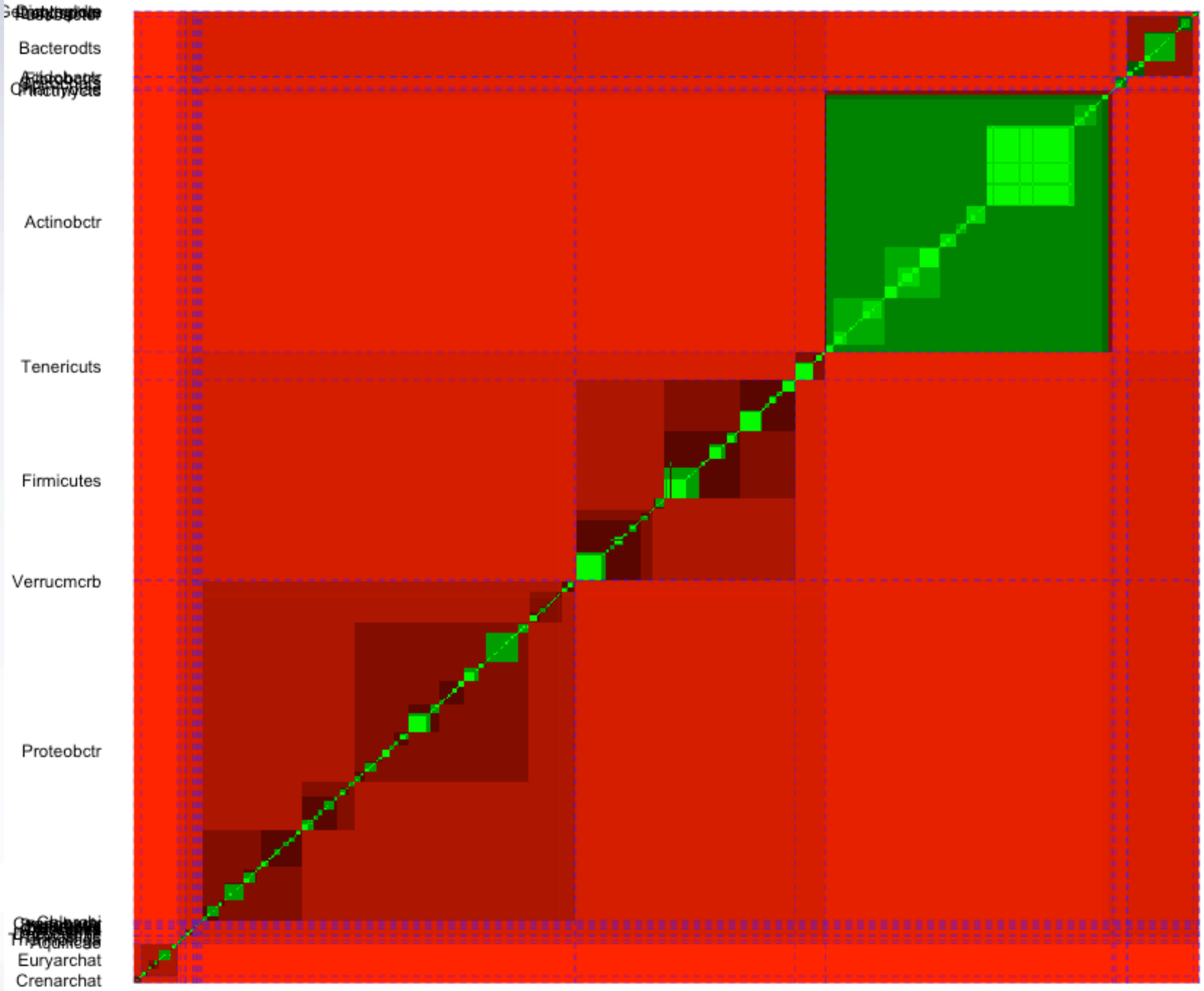


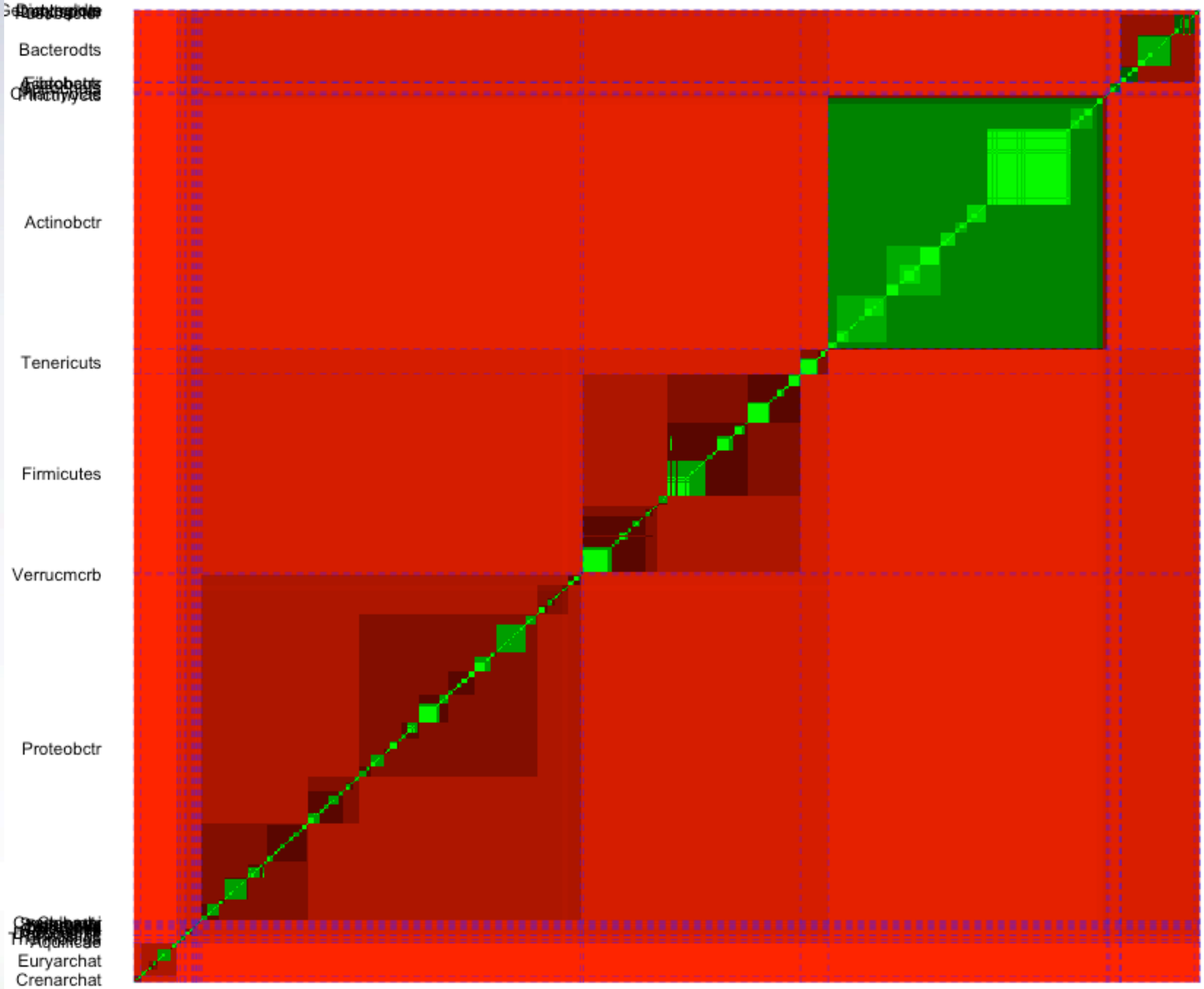
Taxonomy of type strains of Bacteria and Archaea 2006



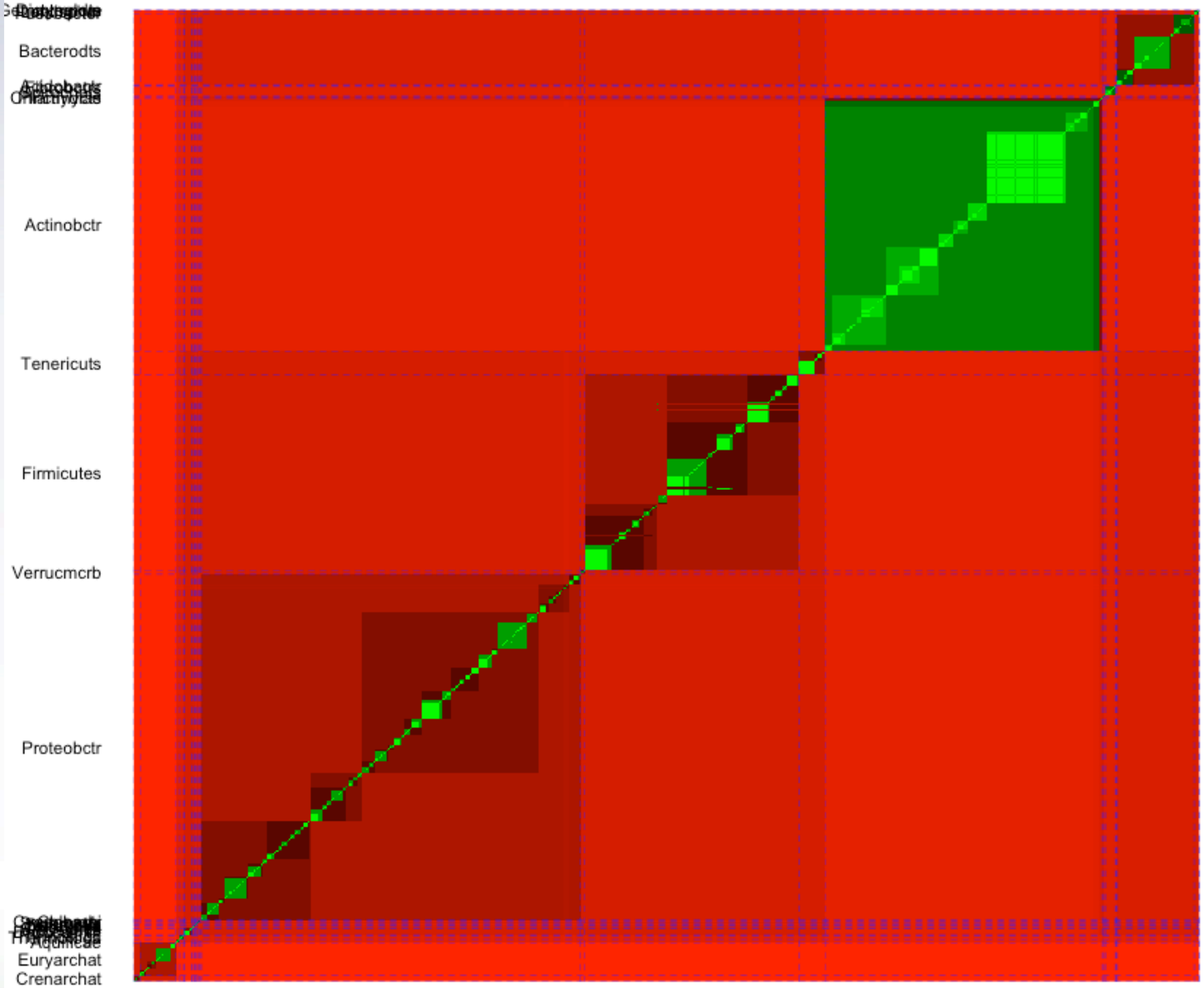
Taxonomy of type strains of Bacteria and Archaea 2007



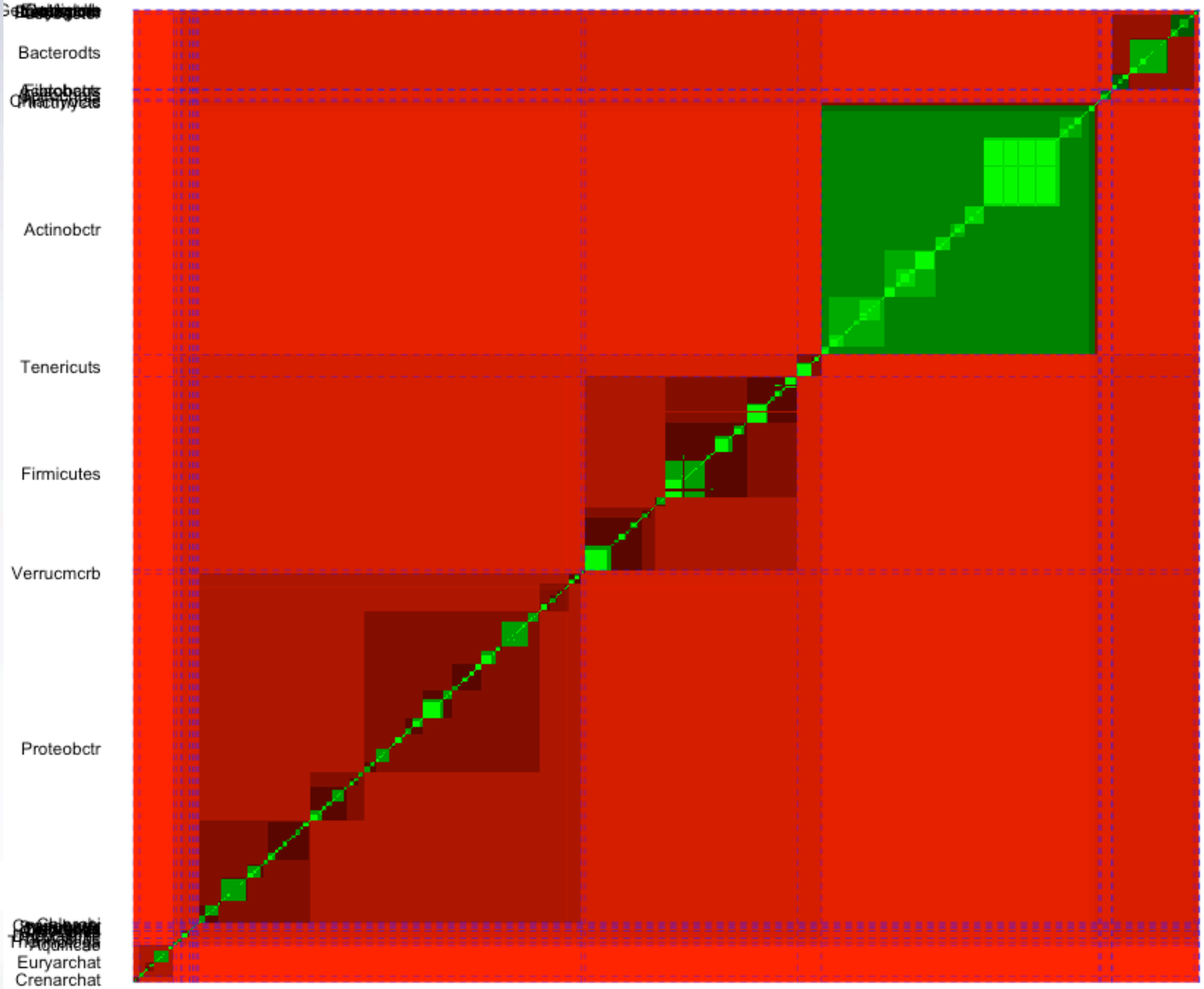
Taxonomy of type strains of Bacteria and Archaea 2008



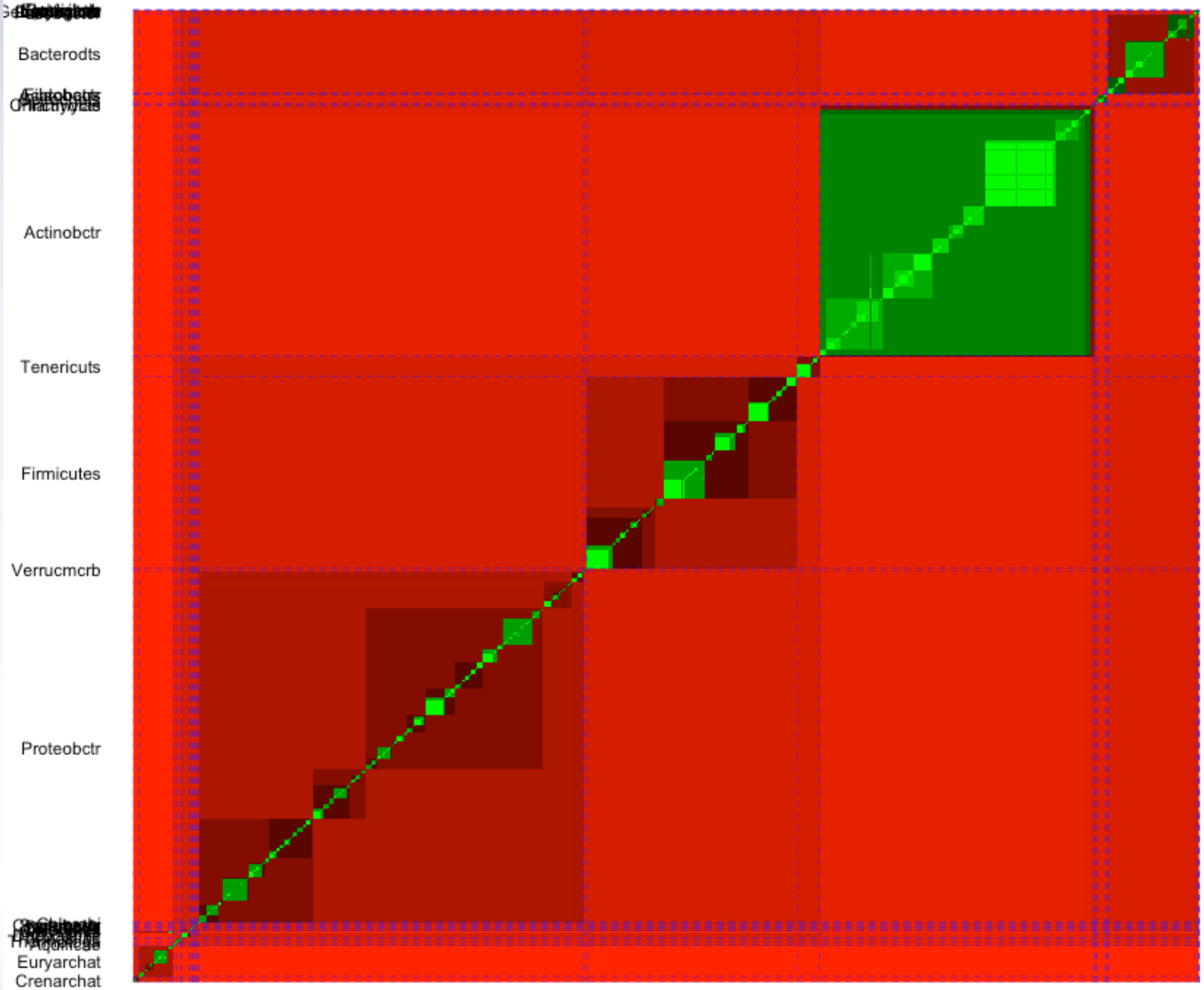
Taxonomy of type strains of Bacteria and Archaea 2009



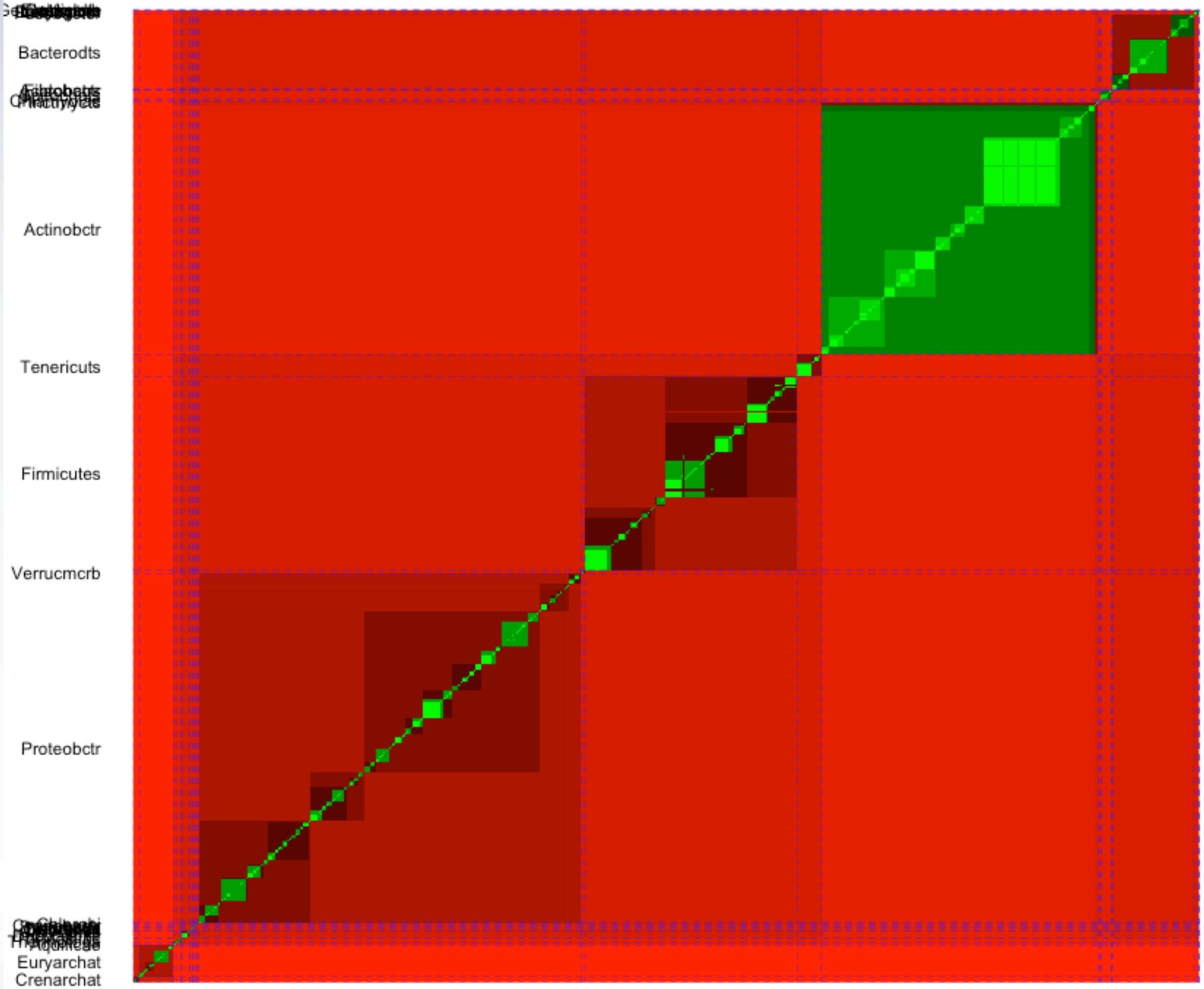
Taxonomy of type strains of Bacteria and Archaea 2010



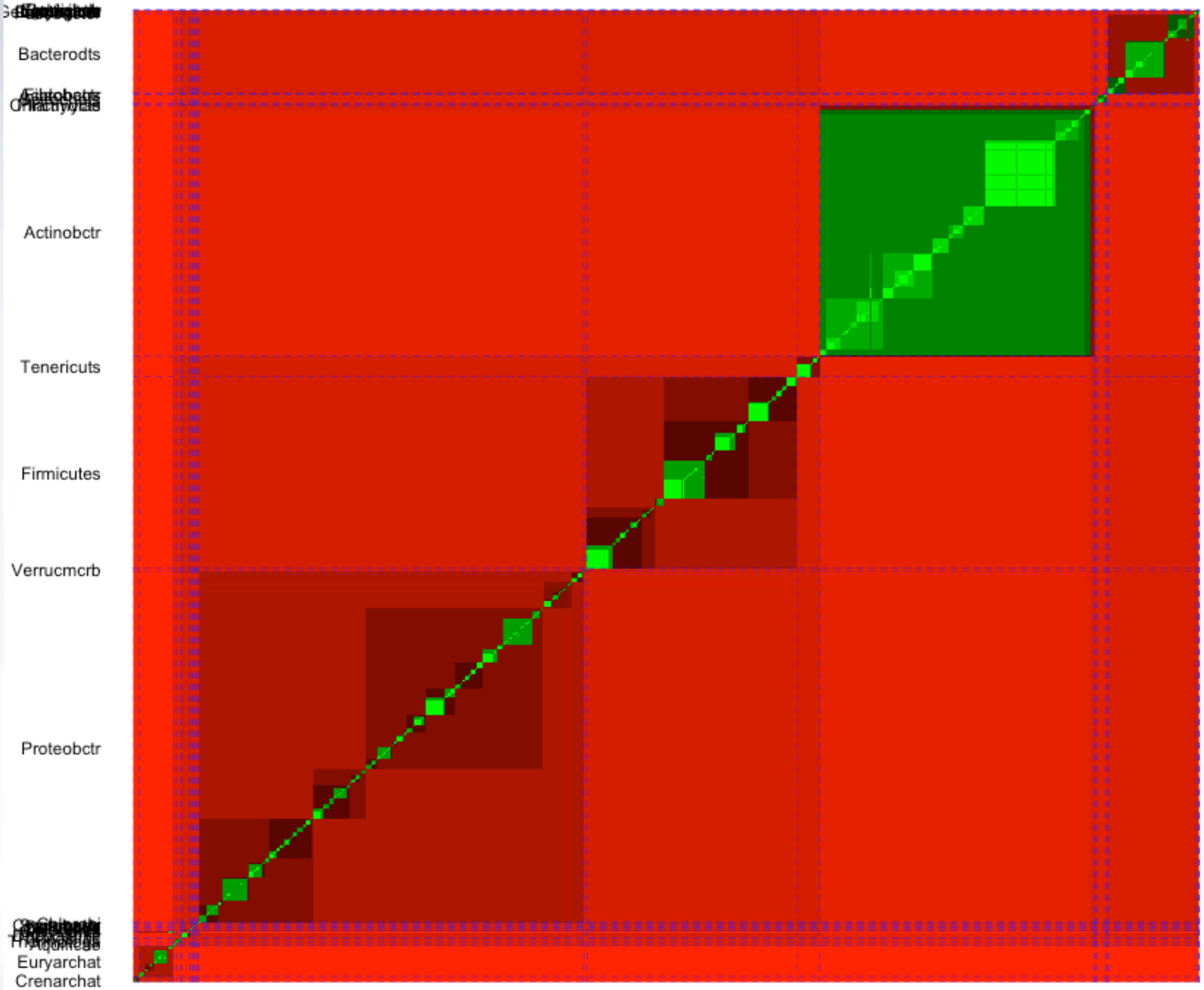
Taxonomy of type strains of Bacteria and Archaea 2011



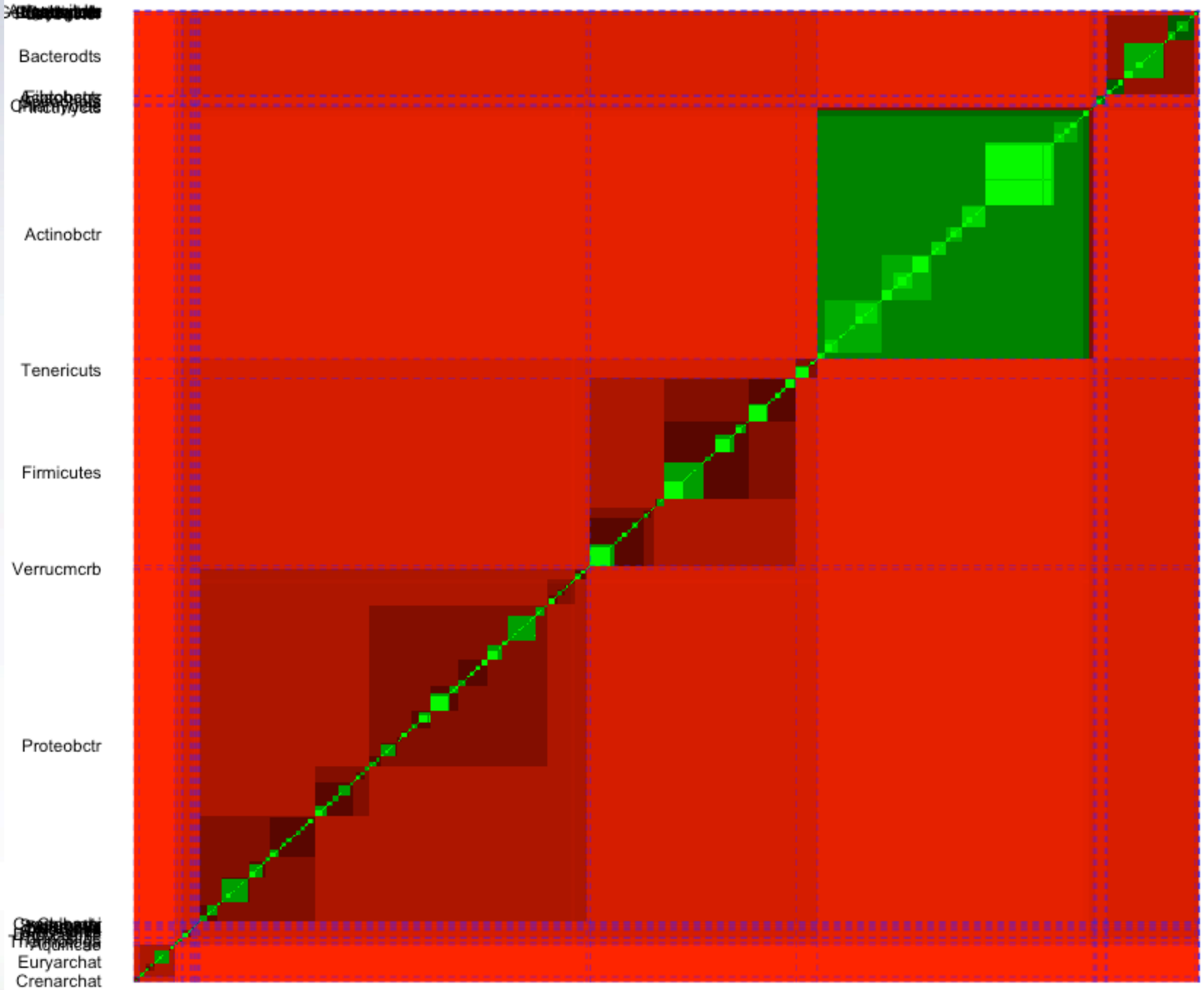
Taxonomy of type strains of Bacteria and Archaea 2010



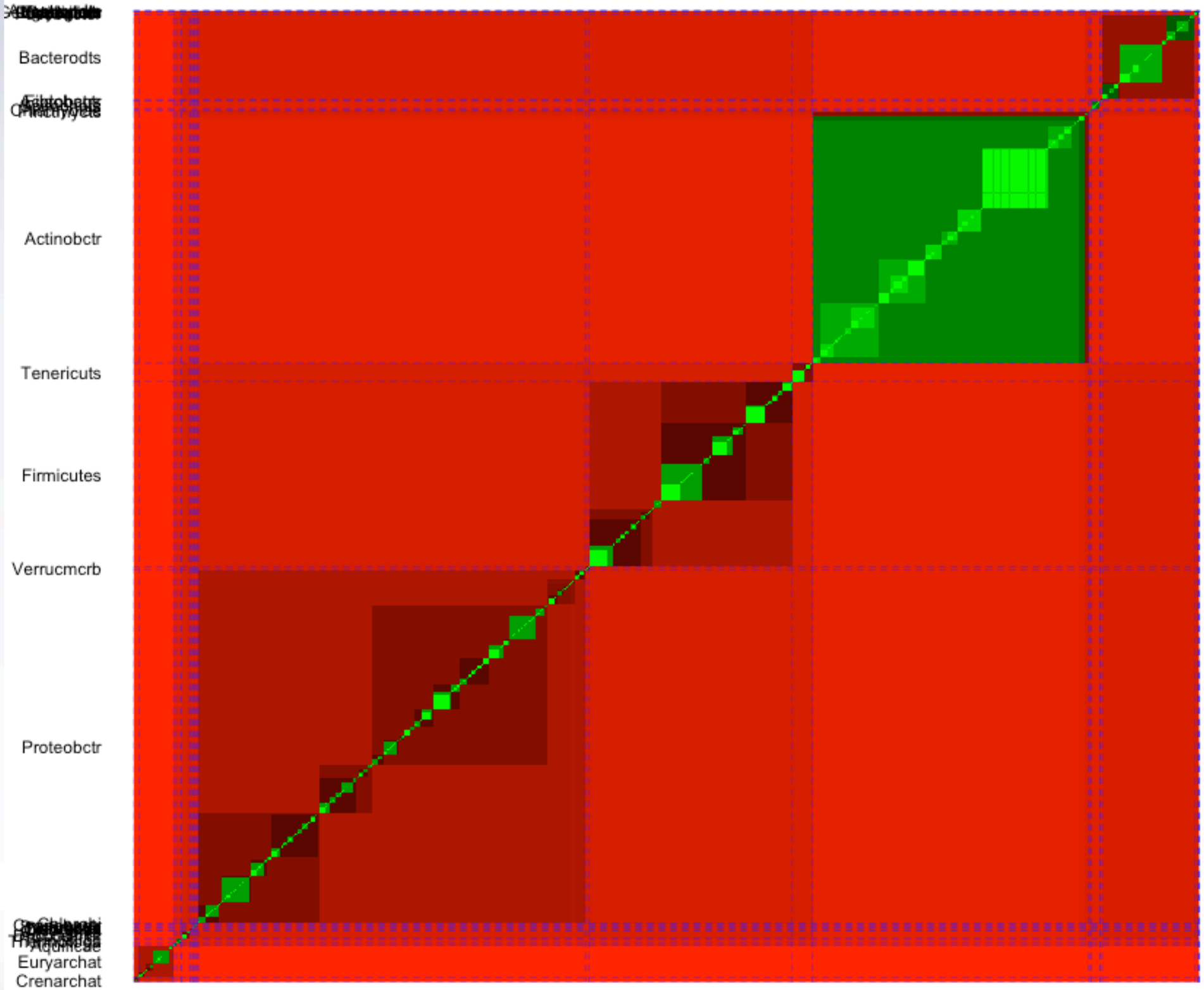
Taxonomy of type strains of Bacteria and Archaea 2011



Taxonomy of type strains of Bacteria and Archaea 2012

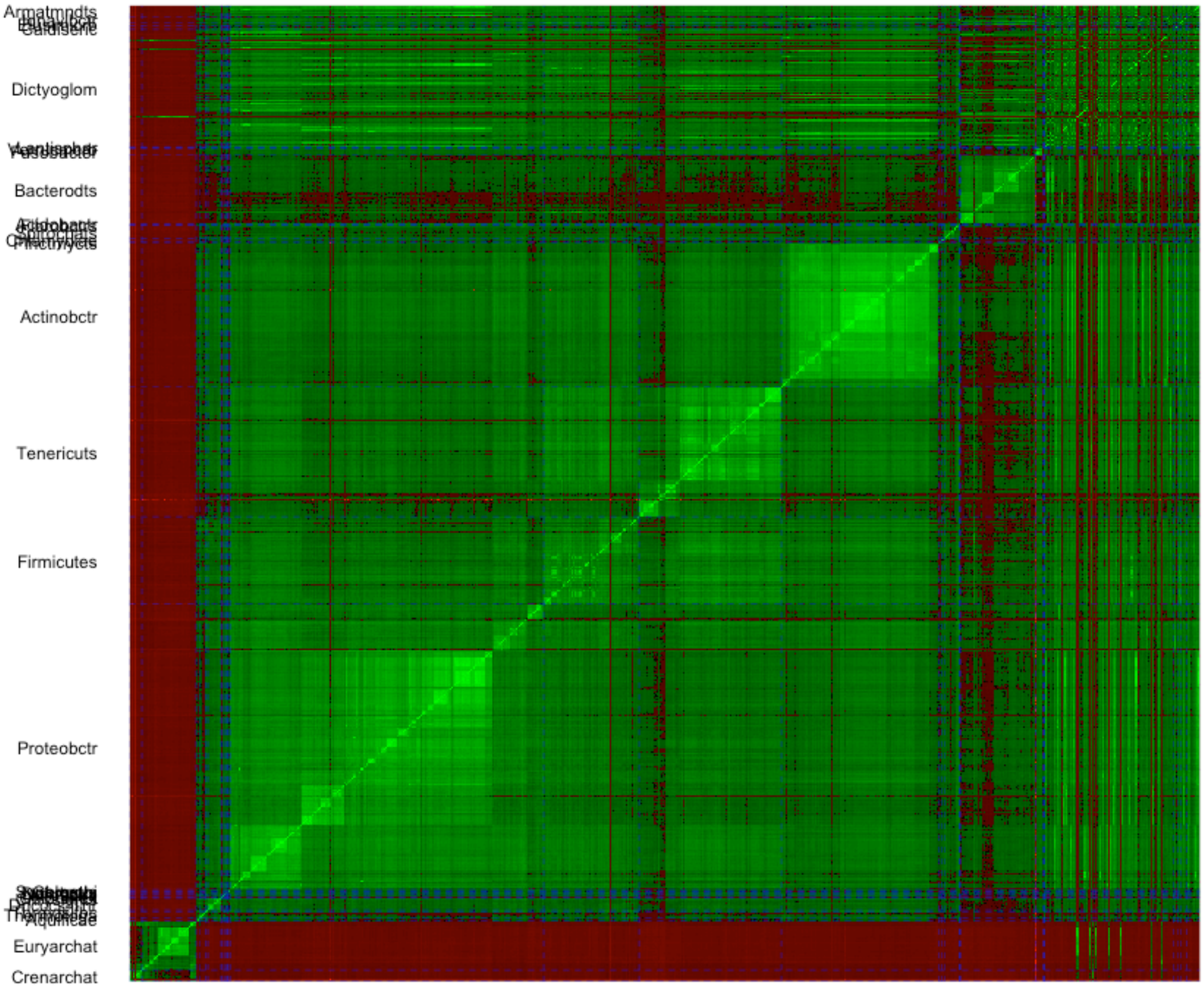


Taxonomy of type strains of Bacteria and Archaea 2013

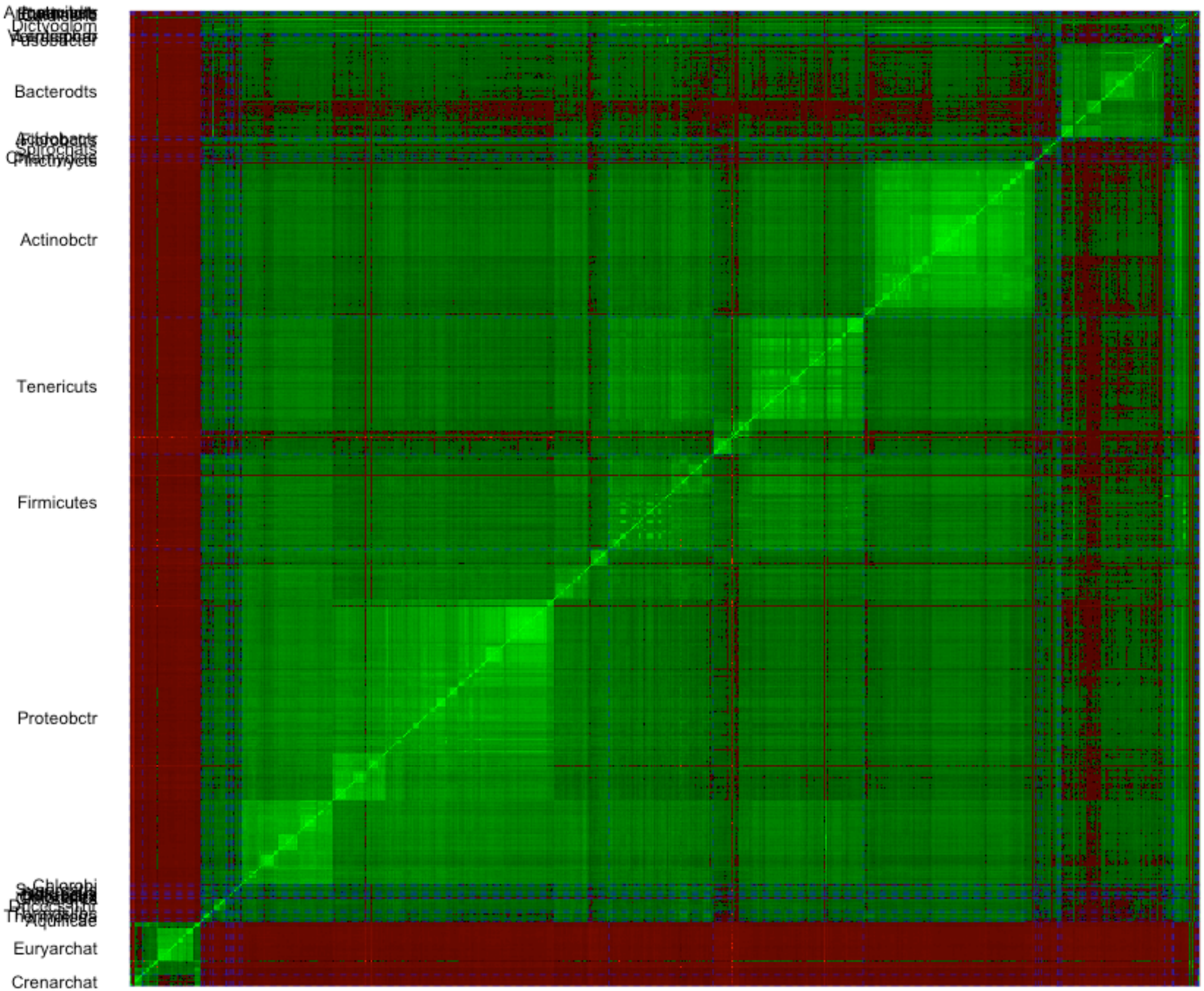


The Microbial Earth/GEBA genomes

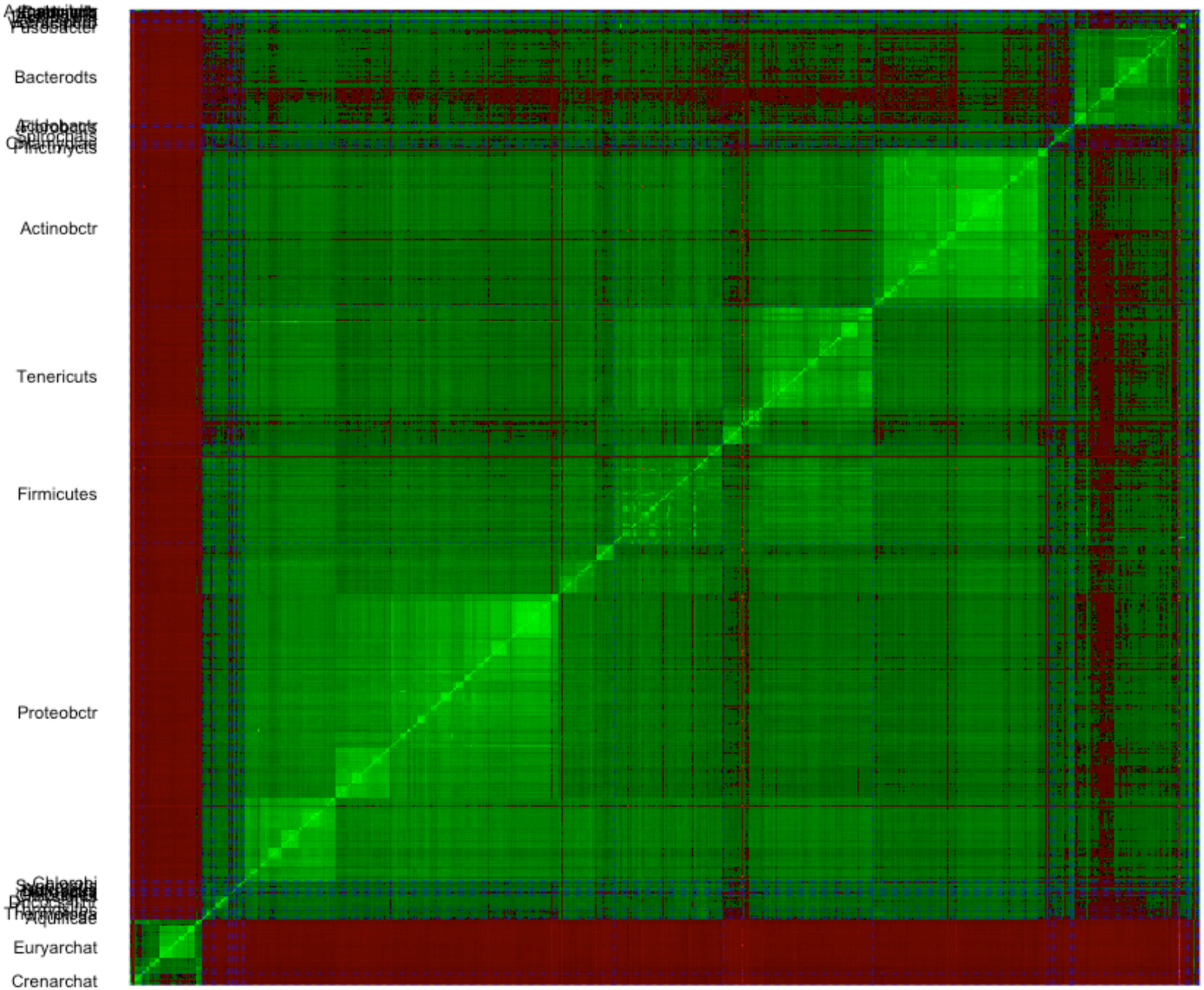
Input ordering based on TOBA 7.7



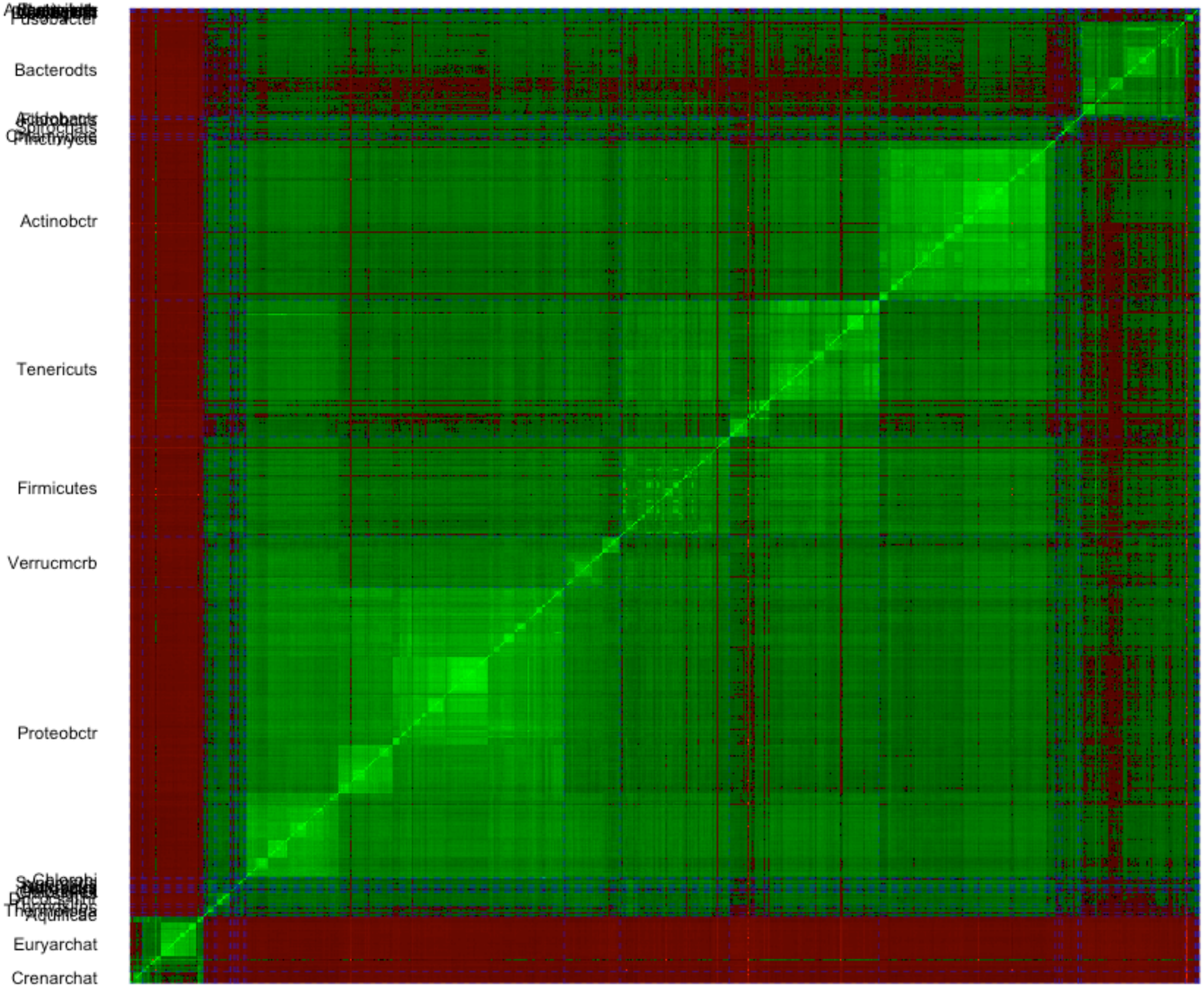
Rearranged at genus level



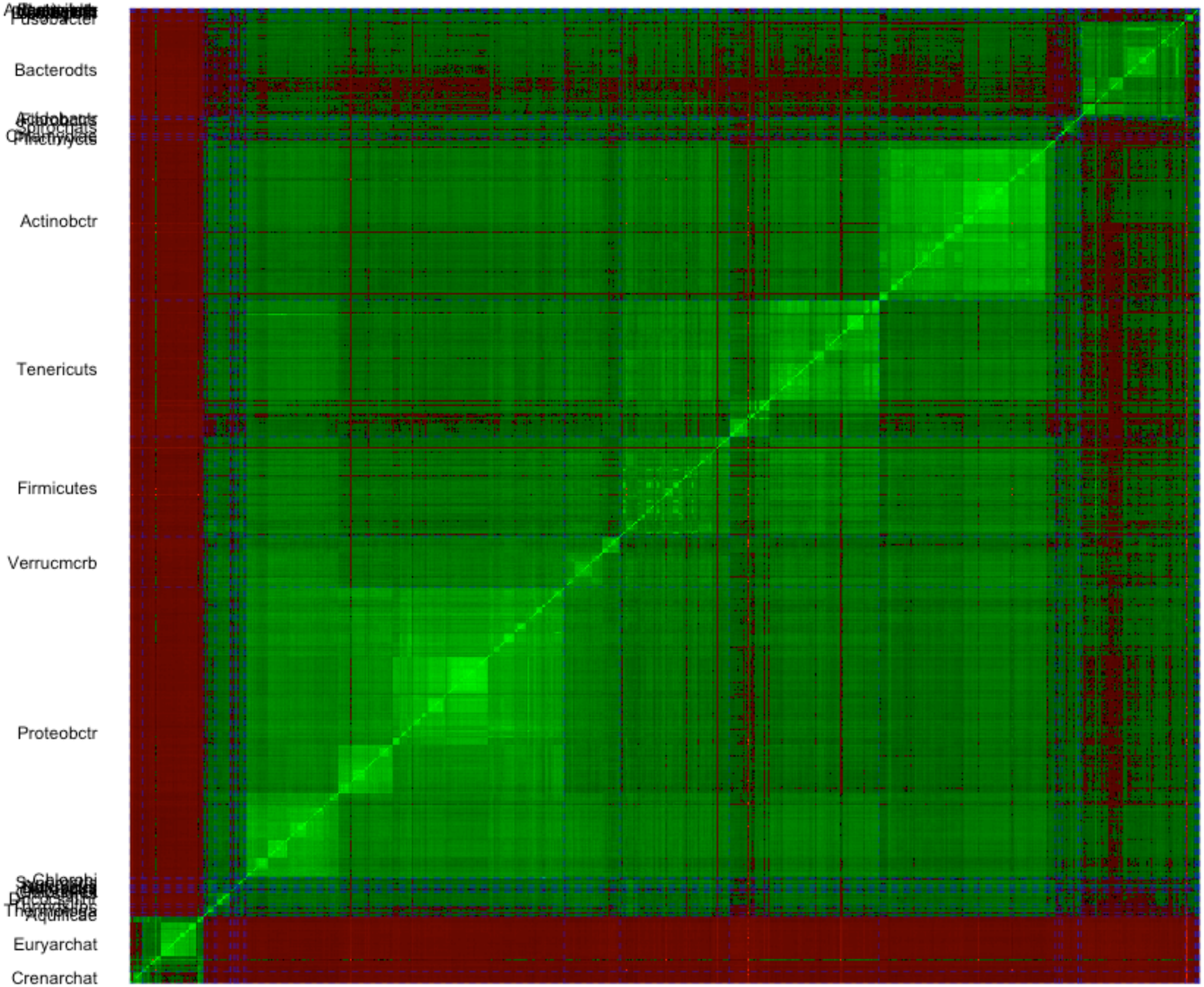
Rearranged at family level



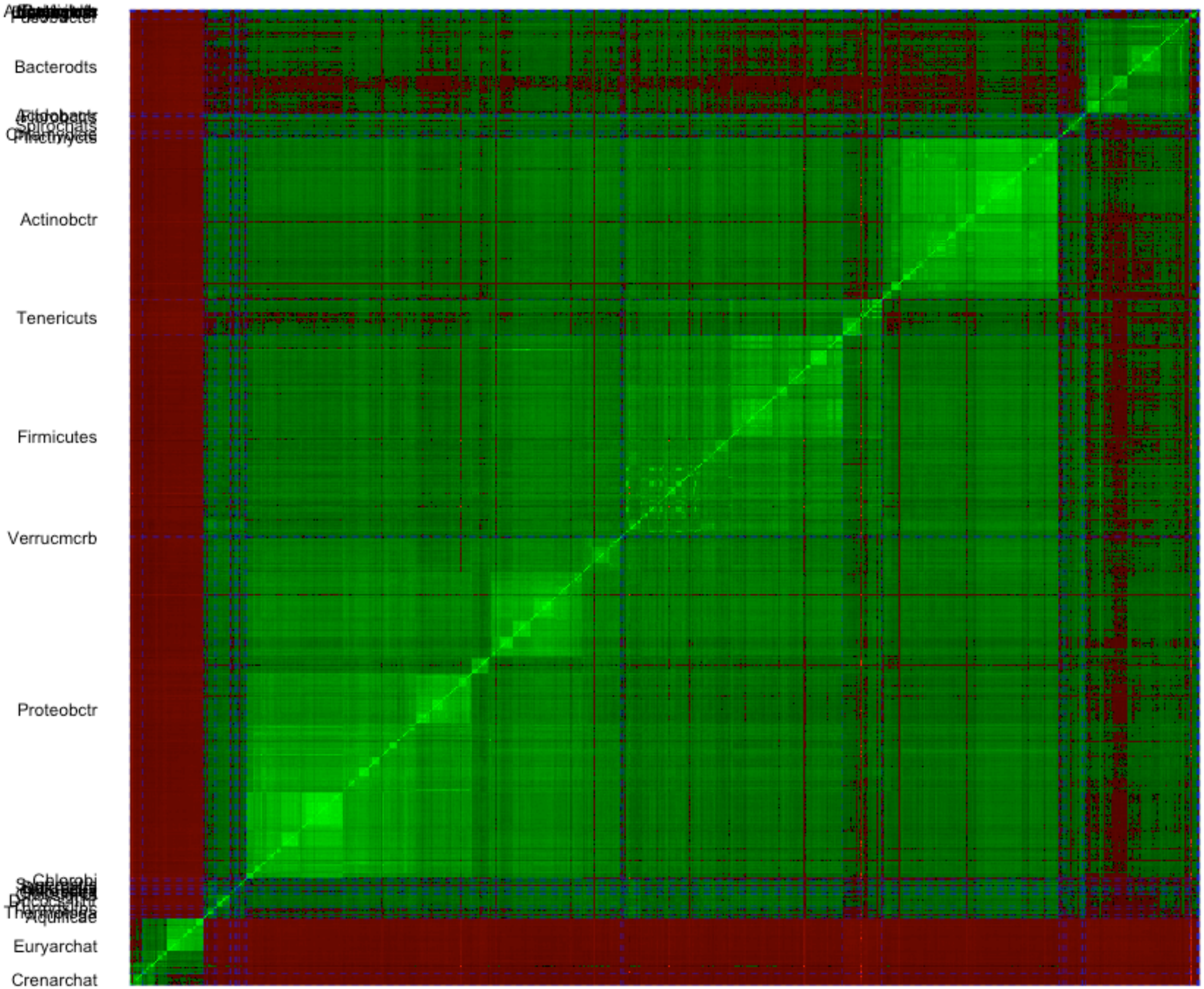
Rearranged at order level



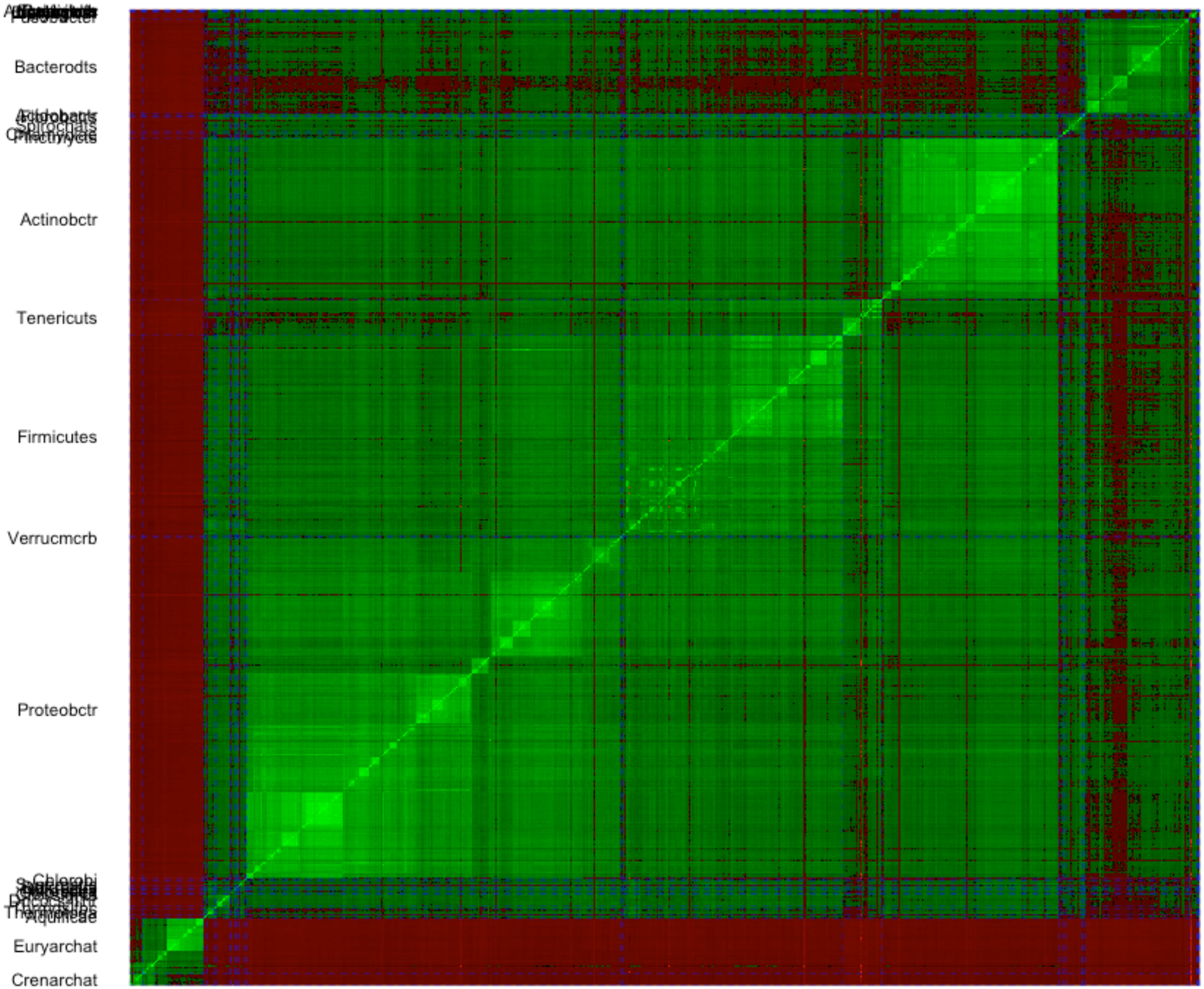
Rearranged at order level



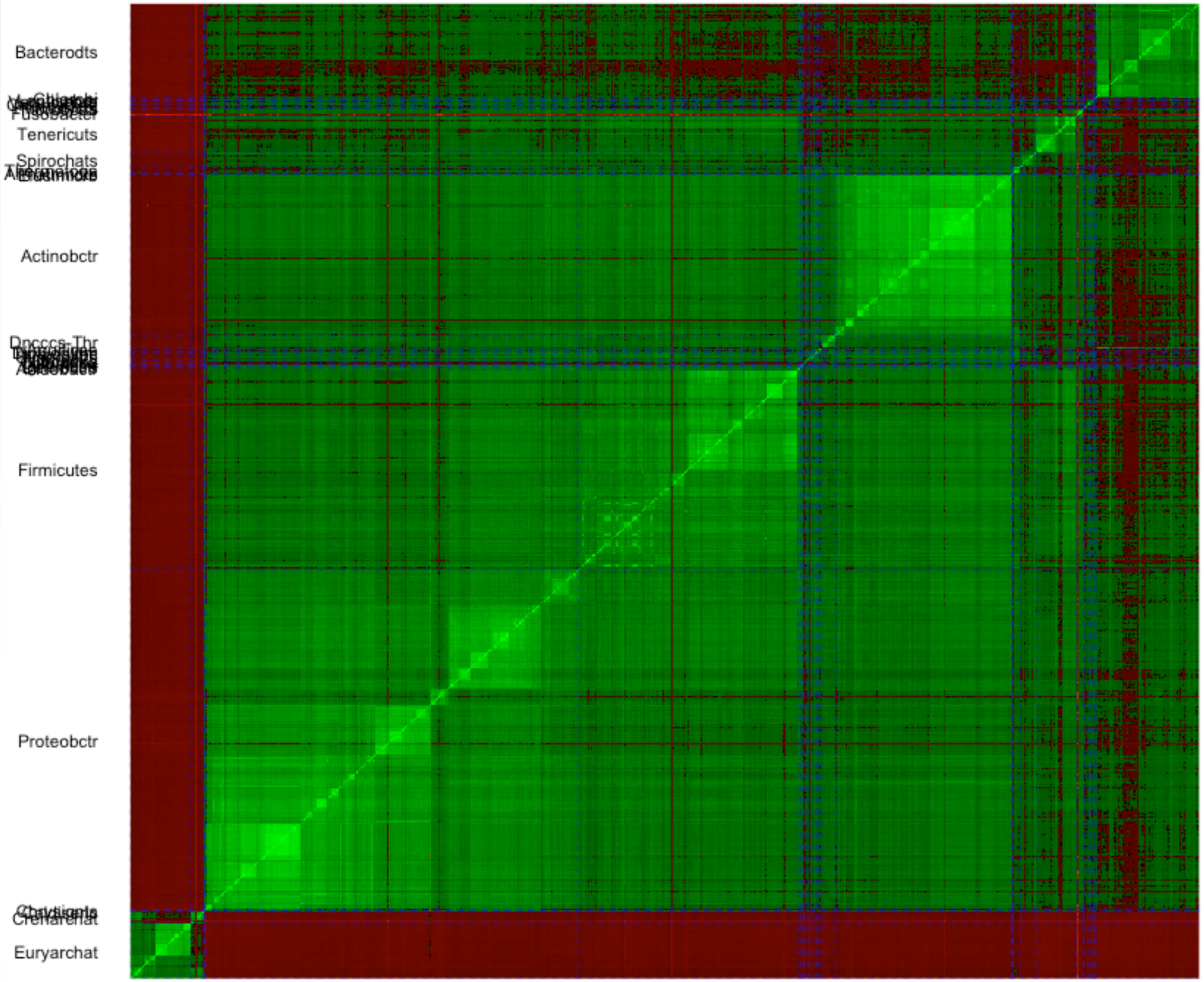
Rearranged at class level



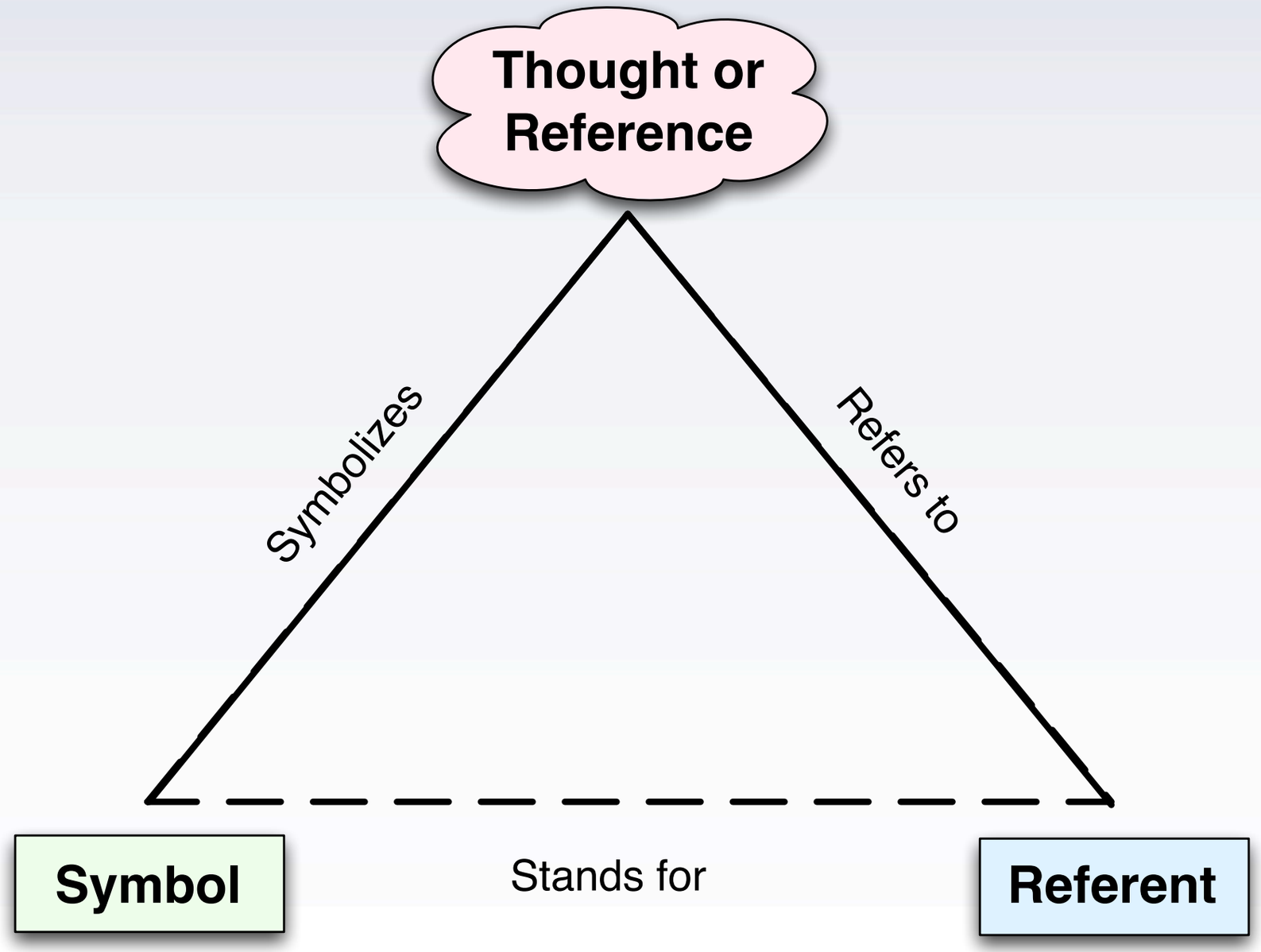
Rearranged at class level



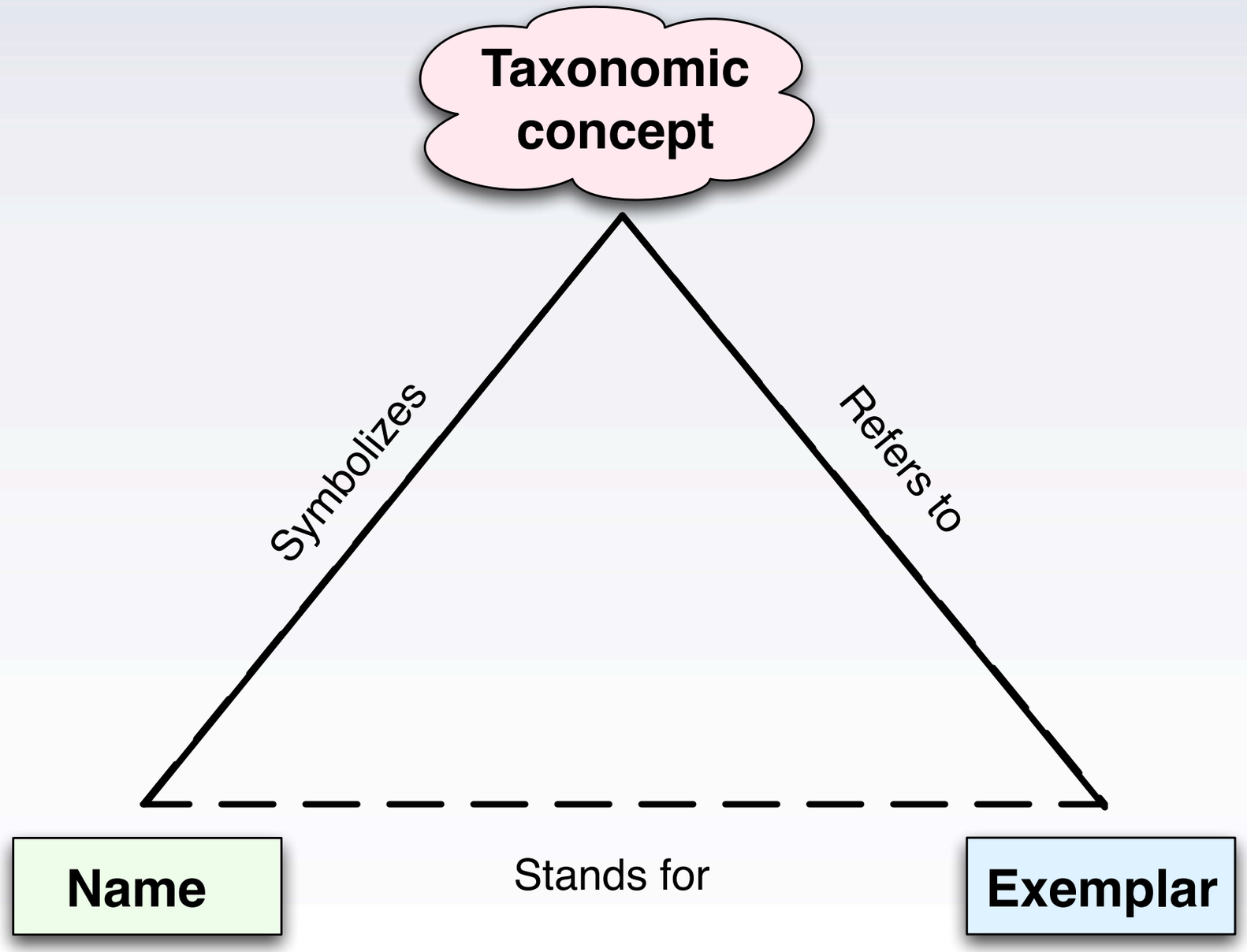
Rearranged at phylum level



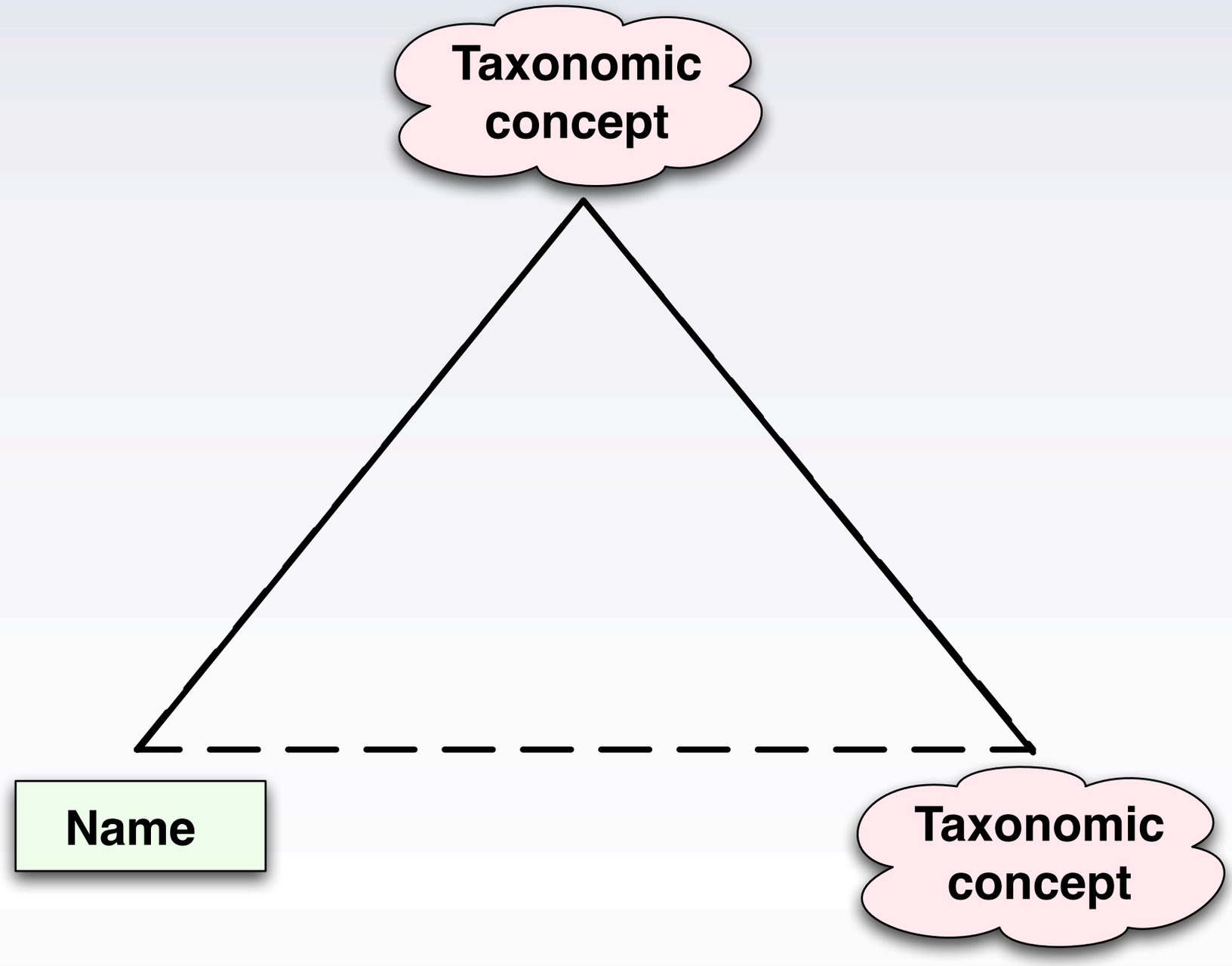
Disambiguating bacterial and archaeal names



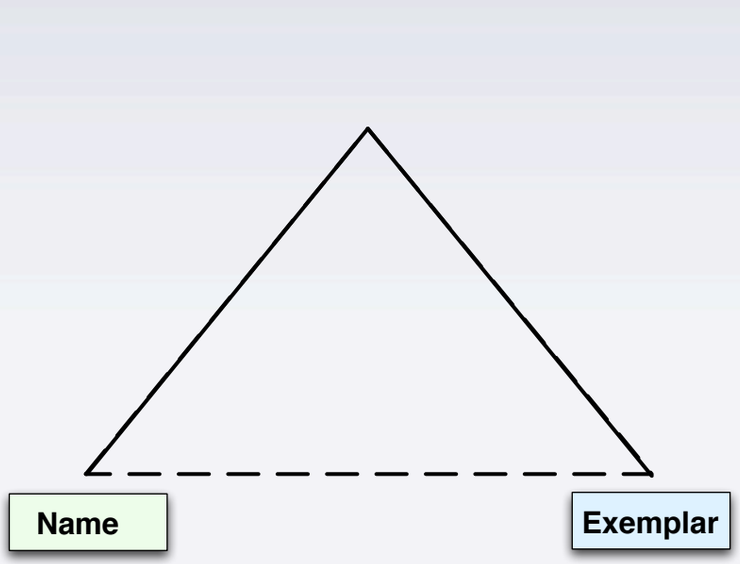
Ogden and Richard, The Meaning of Meaning 1923

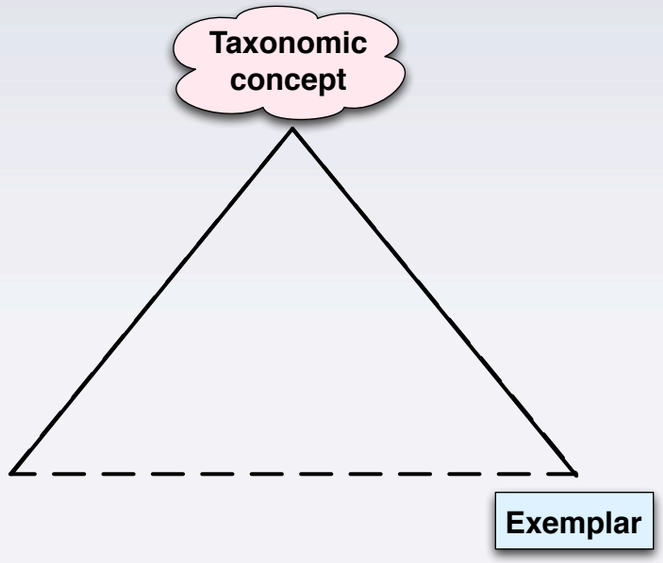


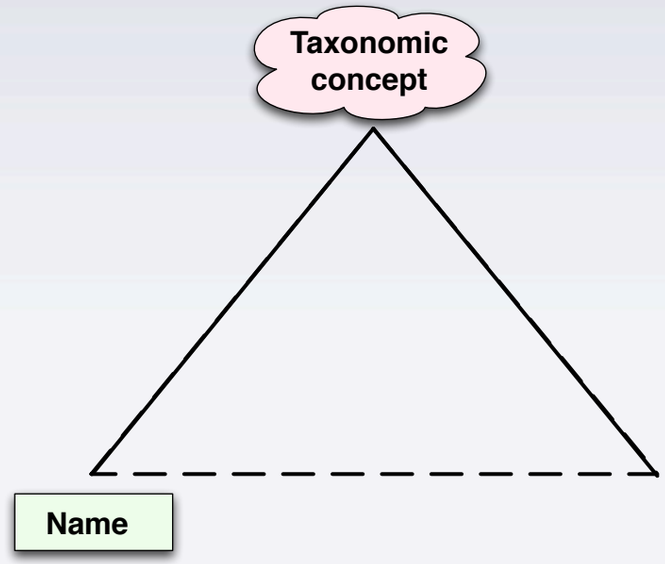
Garrity and Lyons, 2003,
2011 US Pat 7,925,444

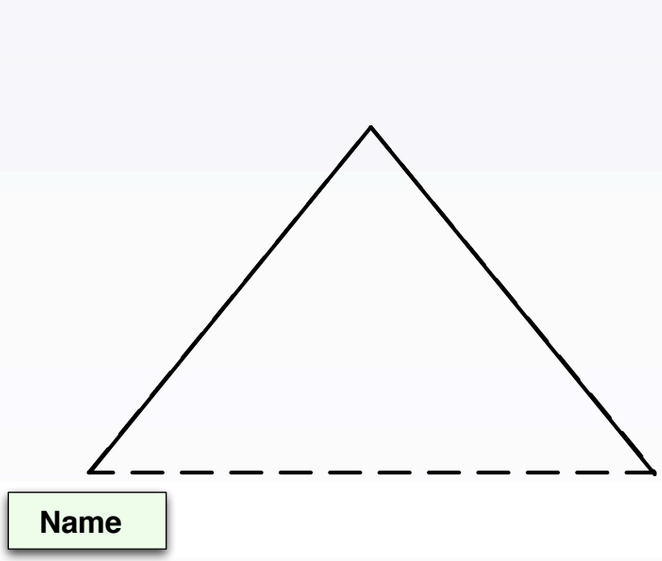


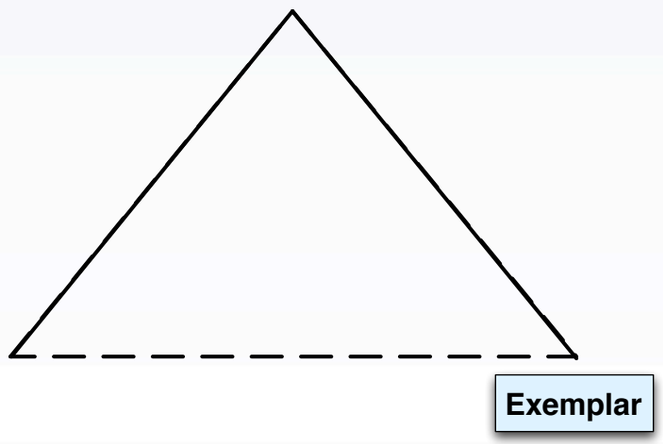
Garrity and Lyons, 2003,
2011 US Pat 7,925,444

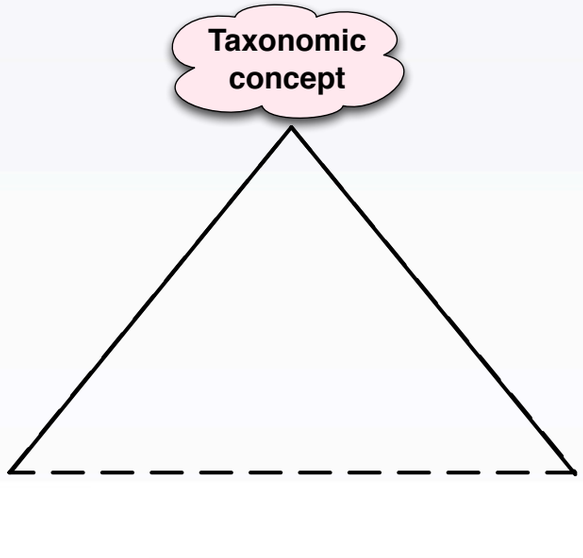








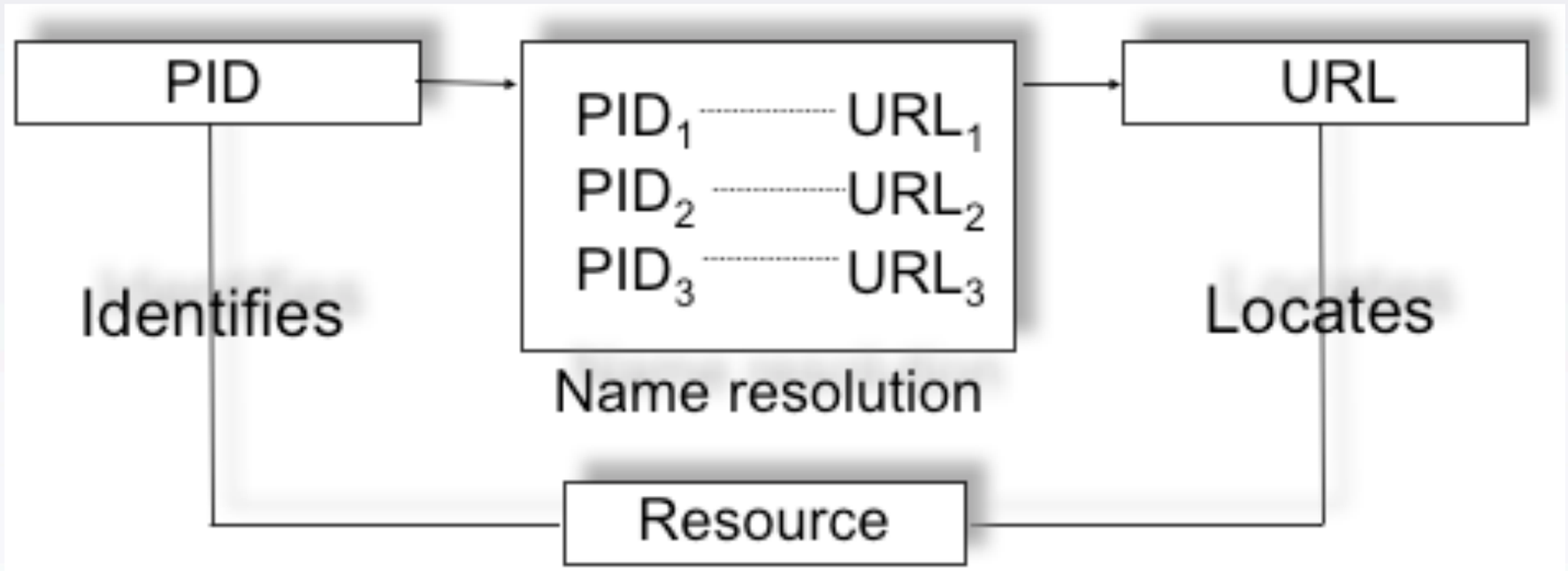


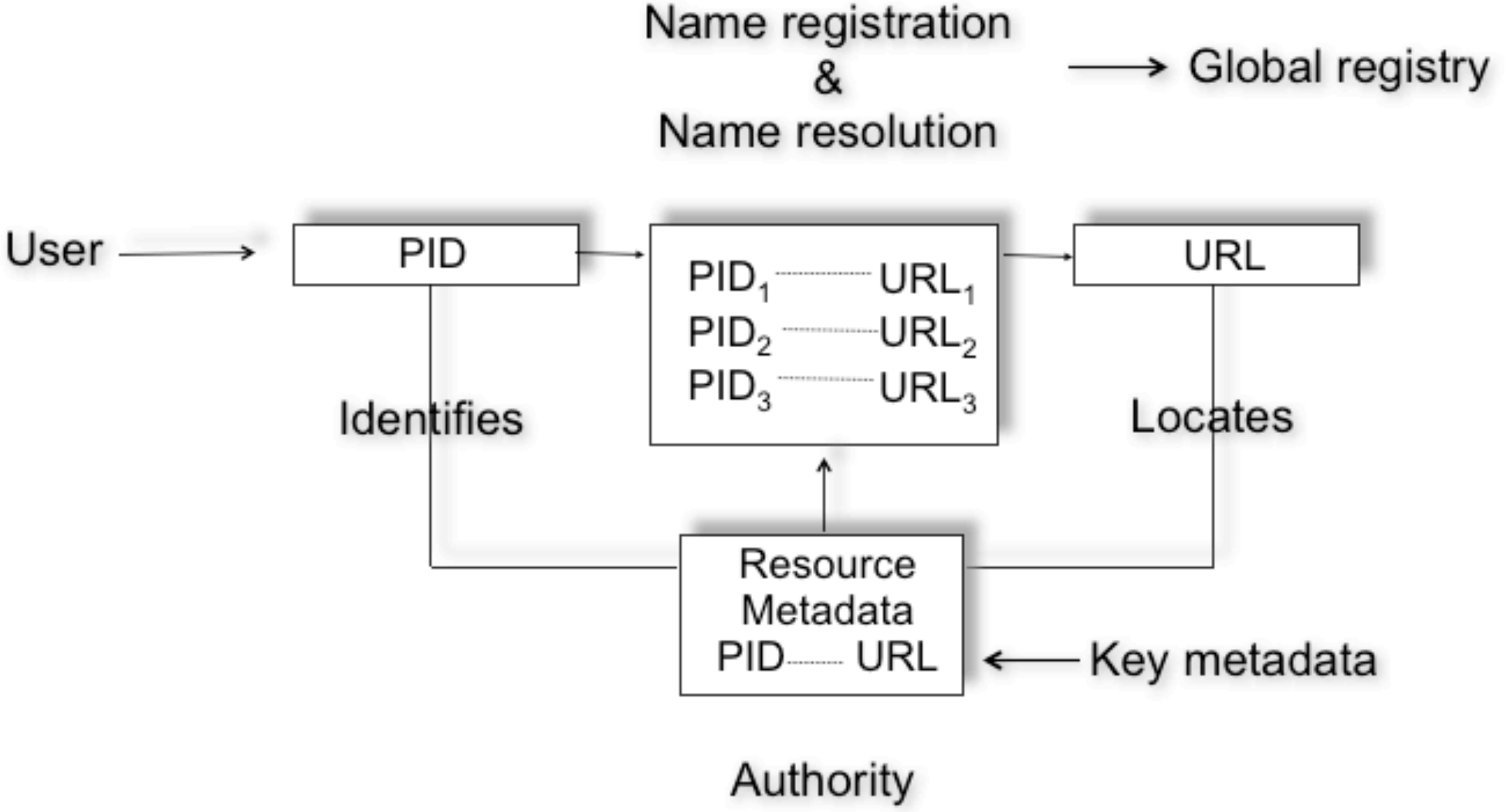


Garrity and Lyons, 2003,
2011 US Pat 7,925,444

	Names	Taxa	Exemplars
phylum	39	38	0
class	77	69	0
subclass	7	7	0
order	140	136	0
suborder	23	22	0
family	349	344	0
genus	2,437	2,406	0
species	13,042	12,637	11,230
subspecies	587	551	301

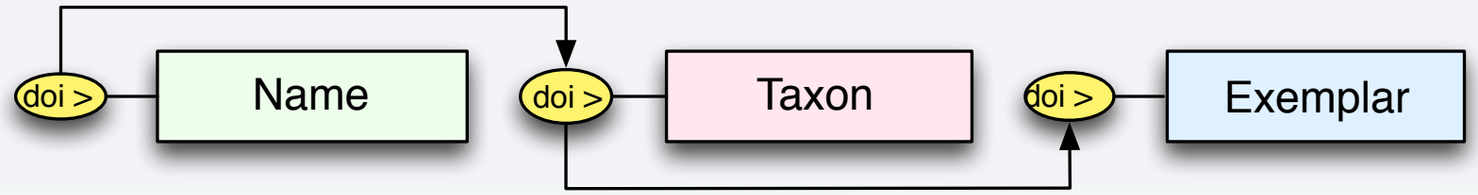
The importance of redirection


PID
PID1 URL1
PID2 URL2
PID3 URL3
URL
Identifies
Locates
Name resolution
Resource

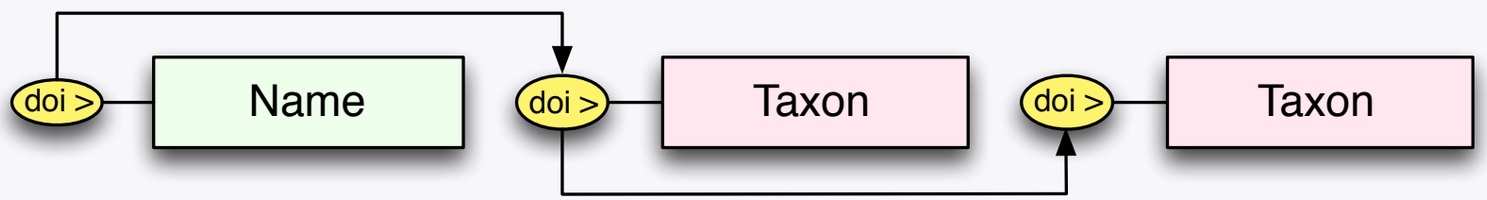

Name registration
&
Name resolution
Global registry
User
PID
PID1 URL1
PID2 URL2
PID3 URL3
URL
Identifies
Locates
Resource
Metadata
PID URL
Key metadata
Authority

The N4L model

New species

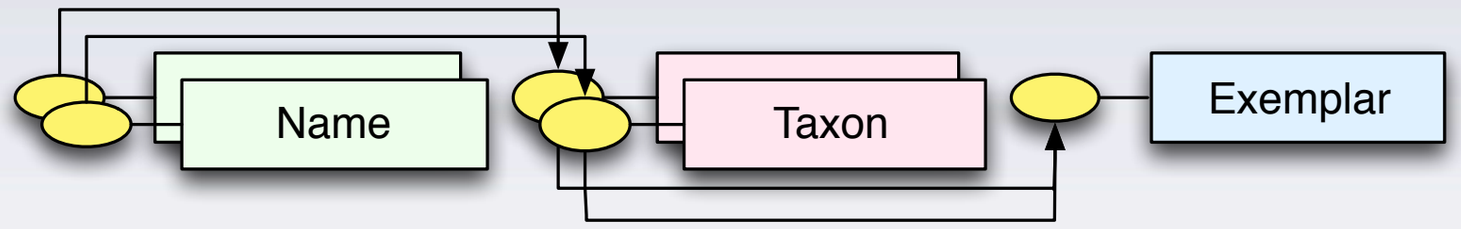


New higher taxon

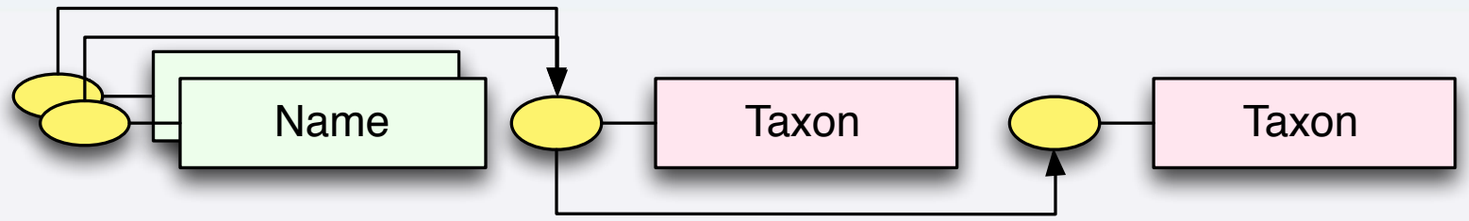


Garrity and Lyons, 2003,
2011 US Pat 7,925,444

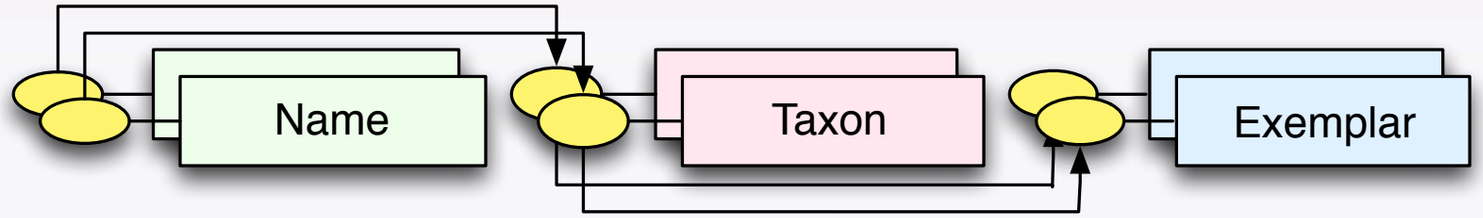
New combination or homotypic synonym



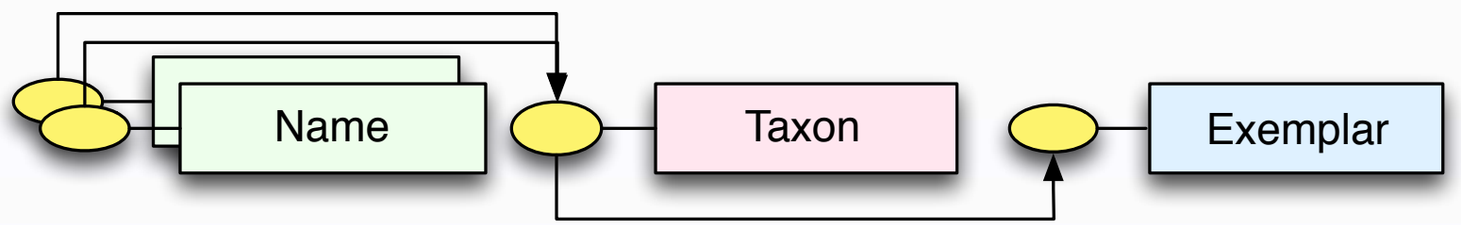
Unified higher taxon



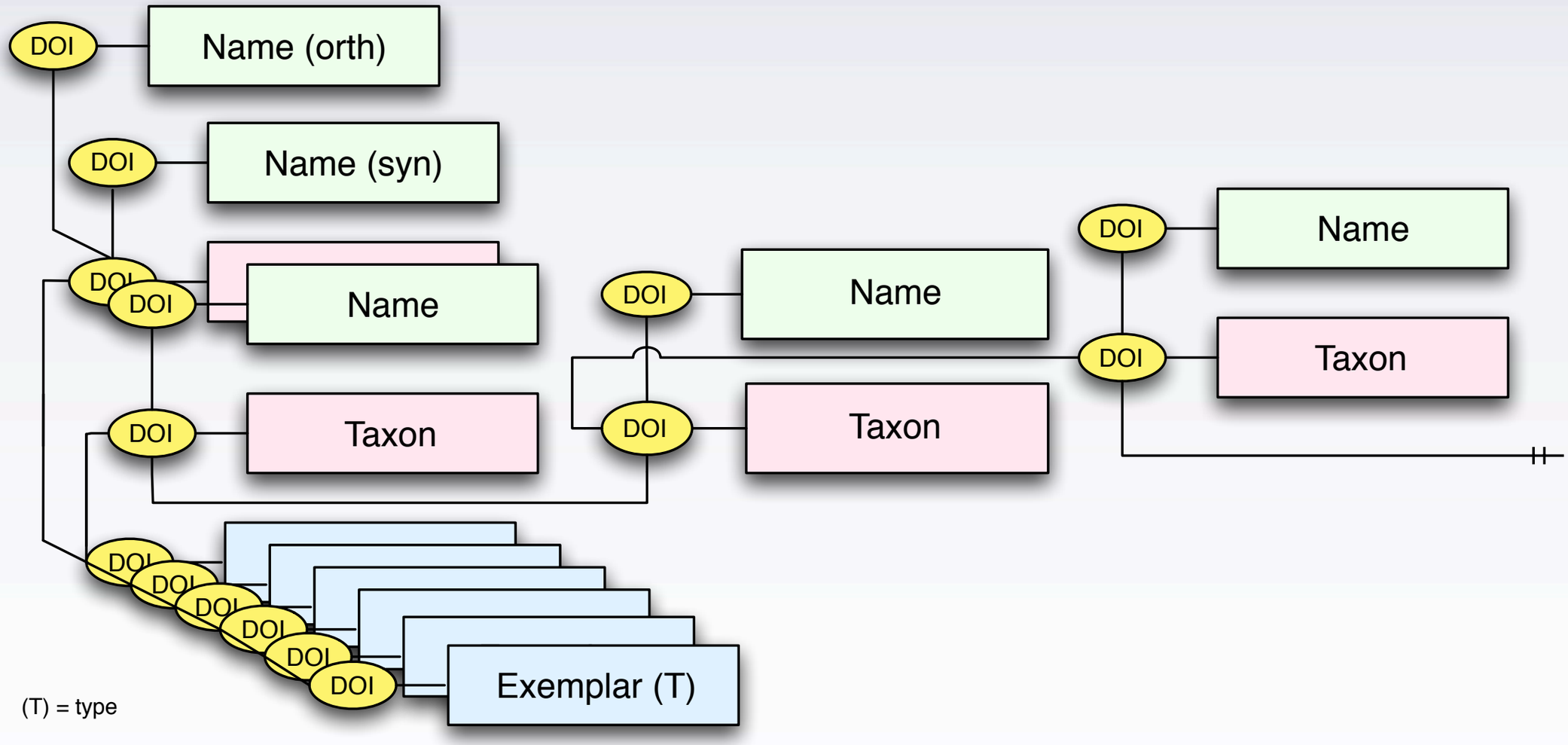
Heterotypic synonym



Orthographic correction



Garrity and Lyons, 2003,
2011 US Pat 7,925,444



Garrity and Lyons, 2003,
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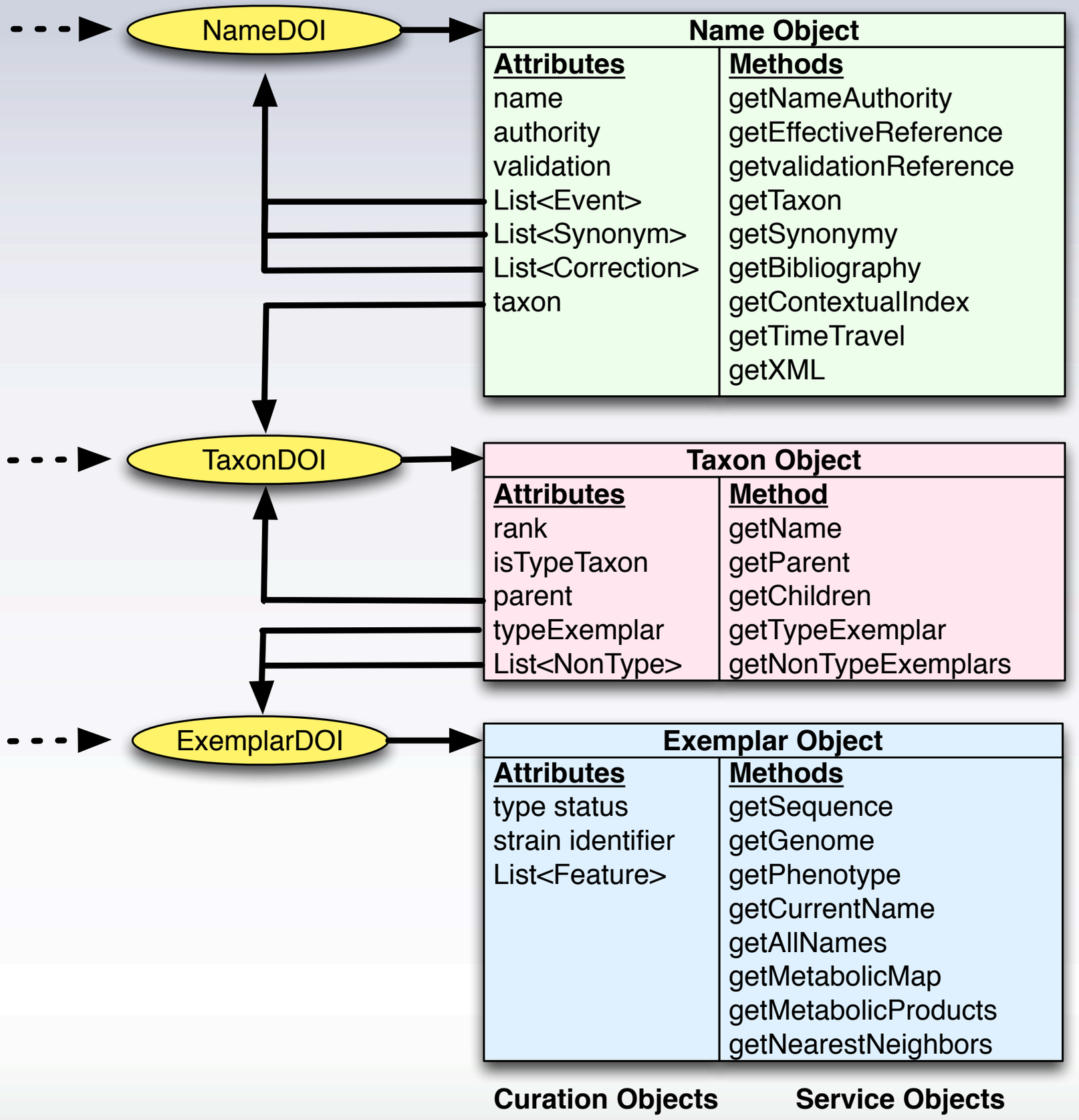


Parker et al 2010

The N4L model as an ontology

Curated Nomenclatural and Taxonomic Events

Taxonomic events are harvested and curated from the original literature

Prokaryotic Code of Nomenclature

The events are interpreted by business logic according to the Rules of Nomenclature

Ordered list of Operations on N4L Model

Prokaryotic N4L Model

N4L Core Model

SKOS XL

SKOS Core Model

A reasoner over the N4L ontology infers appropriate SKOS relations, allowing direct mapping into SKOS.

N4L Model Example

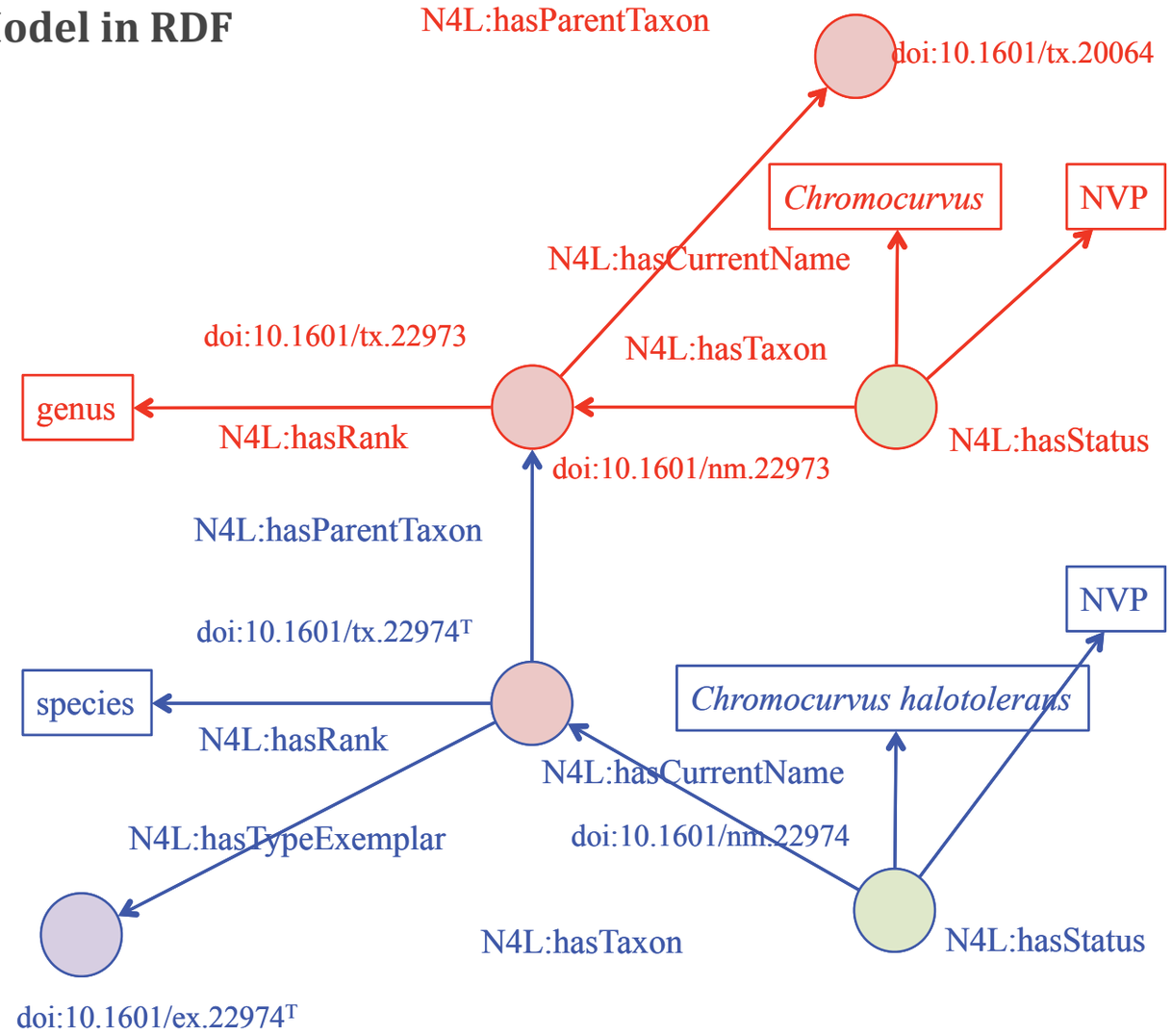
Event: *Chromocurvus halotolerans* gen. nov., sp. nov.

1. *Chromocurvus* gen. nov.
   a) ID = N4LID.NEXT_ID [22973]
   b) model.createTaxon(tx.22973, rank=genus)
   c) model.createName(nm.22973, "Chromocurvus")
   d) [tx.22973].addName(nm.22973)
   e) [tx.22973].setParentTaxon(tx.20064,isType=FALSE)
   f) [nm.22973].setStatus(NVP)
2. *Chromocurvus halotolerans* sp. nov.
   a) ID = N4LID.NEXT_ID [22974]
   b) model.createTaxon(tx.22974, rank=species)
   c) model.createExemplar(ex.22974)
   d) [tx.22974].setExemplar(ex.22974,isType=TRUE)
   e) model.createName(nm.22974, "Chromocurvus halotolerans")
   f) [tx.22974].addName(nm.22974)
   g) [tx.22974].setParentTaxon(tx.22973,isType=TRUE)

To infer N4L model we use:

- SPIN framework is used for mapping from Event ontology to N4L ontology. To perform that mapping we use SPIN reasoner.
- RDF(S) is used to represent N4L model.
- An ontology reasoner (such as Jena reasoner) to check consistency of N4L model.

N4L Model in RDF



N4L Model Example

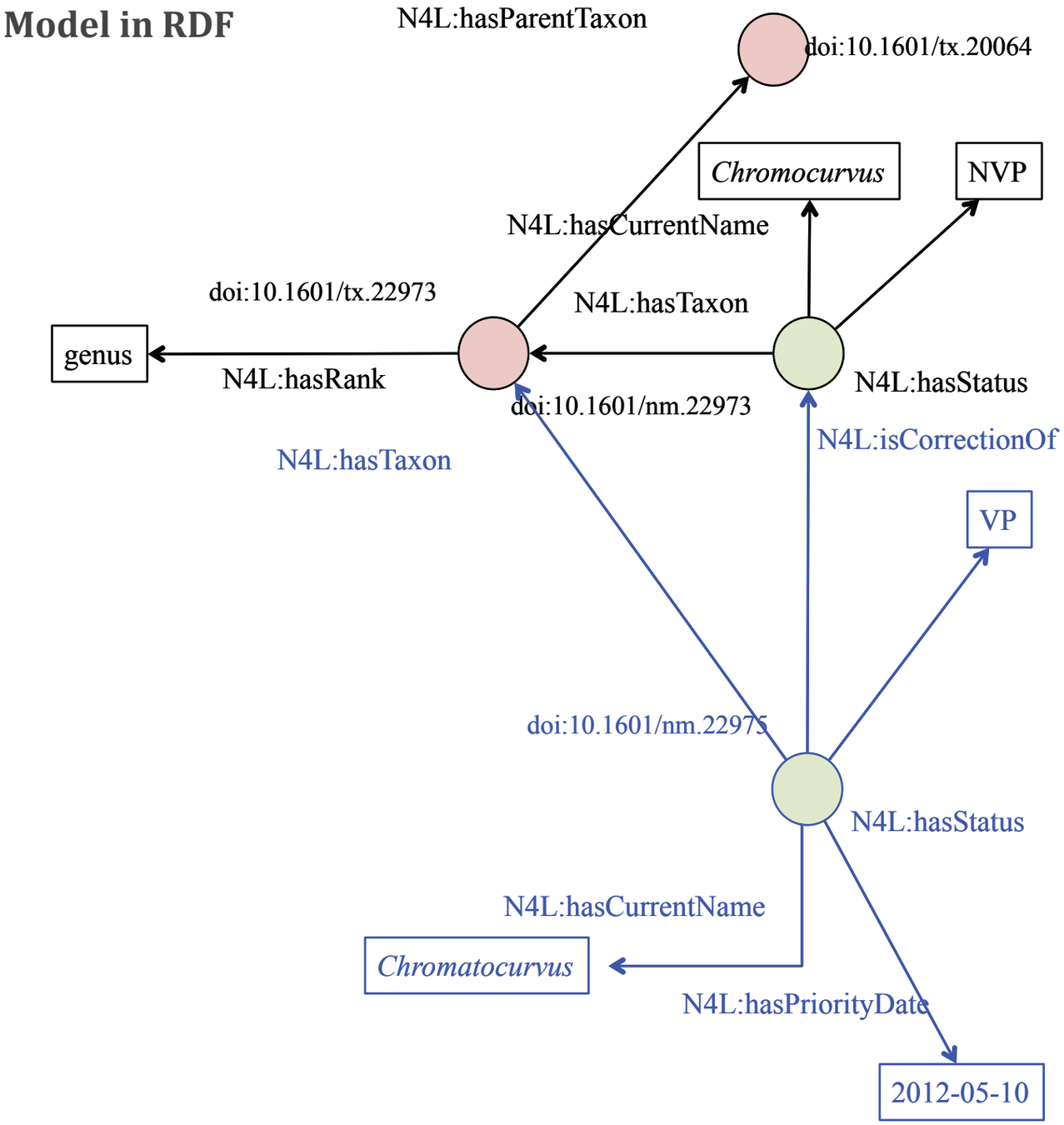
Event: Valid Publication of *Chromatocurvus* corrig.

1.) Chromatocurvus corrig.
   a) ID = N4LID.NEXT_ID [22975]
   b) model.createName(nm.22975, “Chromatocurvus”)
   c) [nm.22973].correctTo(nm.22975)
   d) [tx.22973].addName(nm.22975)
   e) [nm.22975].validate(VL, 2012-10-05)
   f) [nm.22975].setPriorityDate(2012-10-05)
   g) [nm.22975].setStatus(VP)

To infer N4L model we use:

- SPIN framework is used for mapping from Event ontology to N4L ontology. To perform that mapping we use SPIN reasoner.
- RDF(S) is used to represent N4L model.
- An ontology reasoner (such as Jena reasoner) to check consistency of N4L model.

N4L Model in RDF



N4L Model Example

Event: Valid Publication of *Chromatocurvus halotolerans* corrig.

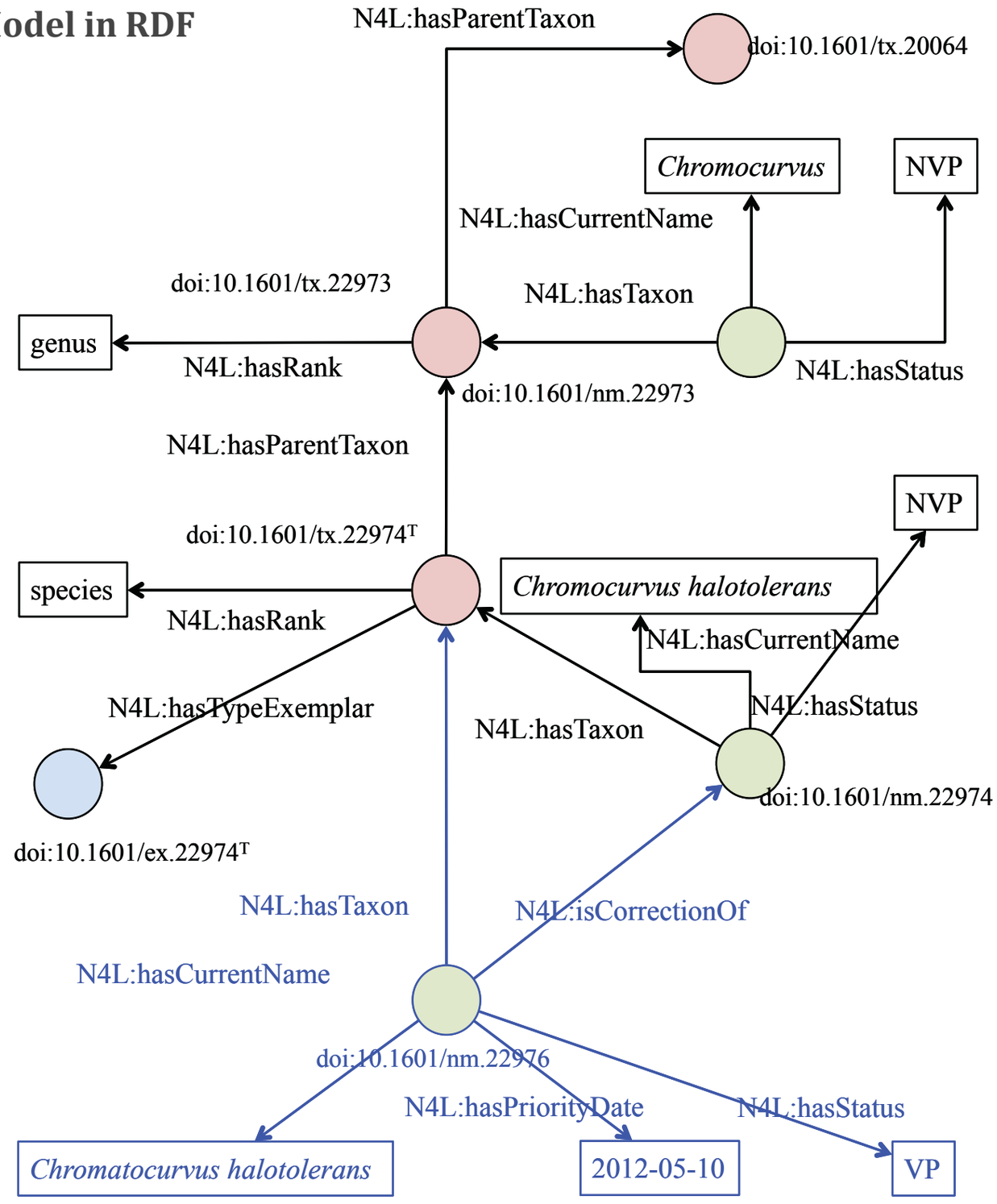
Chromatocurvus halotolerans corrig.

a) ID = N4LID.NEXT_ID [22976]
b) model.createName(nm.22976, "Chromatocurvus halotolerans")
c) [nm.22974].correctTo(nm.22976)
d) [tx.22974].addName(nm.22976)
e) [nm.22976].validate(VL, 2012-10-05)
   a) [nm22976].setPriorityDate(2012-10-05)
   b) [nm.22976].setStatus(VP)

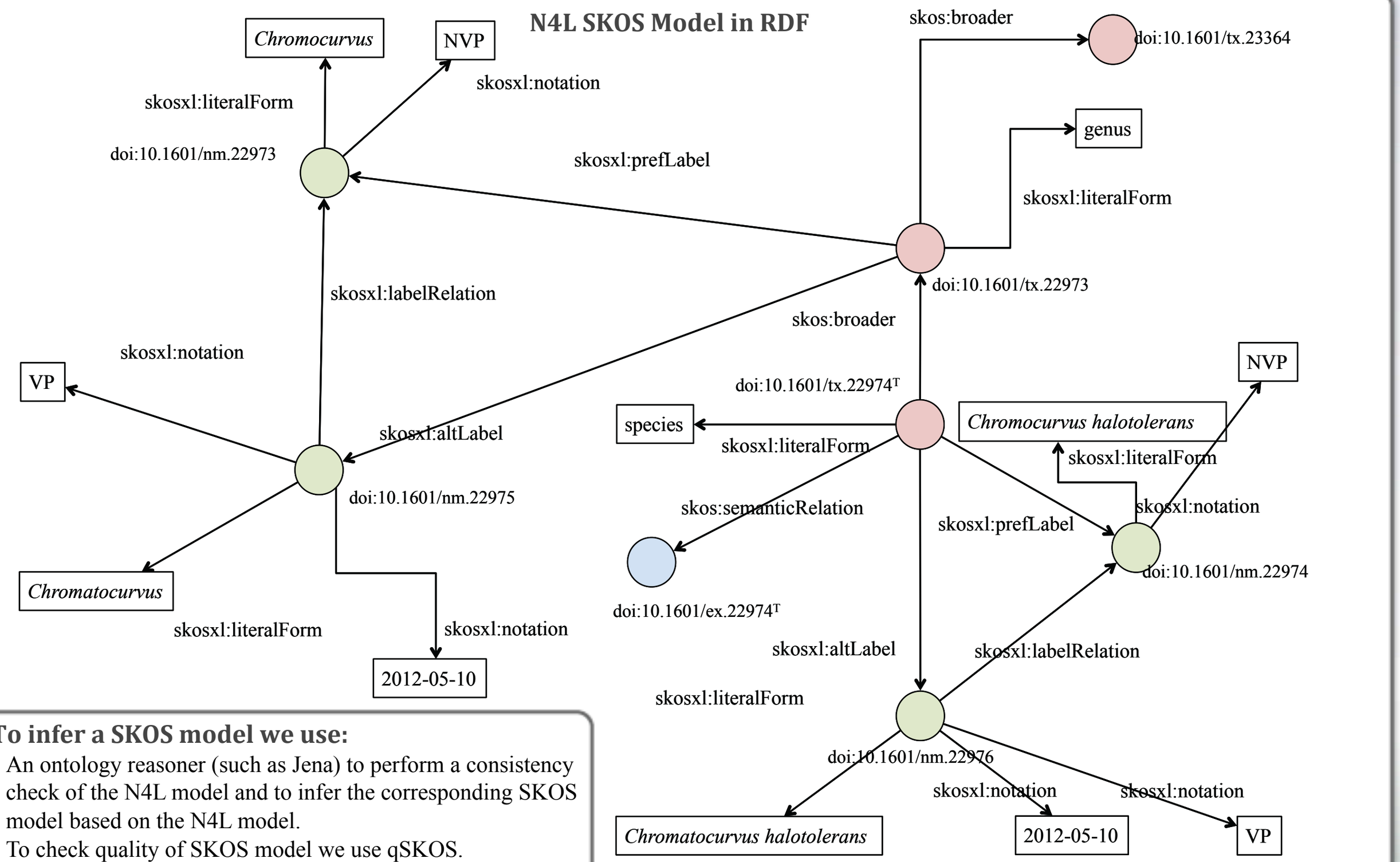
To infer N4L model we use:

- SPIN framework is used for mapping from Event ontology to N4L ontology. To perform that mapping we use SPIN reasoner.
- RDF(S) is used to represent N4L model.
- An ontology reasoner (such as Jena reasoner) to check consistency of N4L model.

N4L Model in RDF



N4L Model Example



To infer a SKOS model we use:

- An ontology reasoner (such as Jena) to perform a consistency check of the N4L model and to infer the corresponding SKOS model based on the N4L model.
- To check quality of SKOS model we use qSKOS.

Some final thoughts

Problems in taxonomy and nomenclature need to be solved independently

Need for precision and accuracy

Process not static

- Taxonomies are in constant state of flux
- Revise knowledge over time without a loss of prior knowledge

Standards, work practices and social issues

Prepare for the forthcoming changes

Lecture slides available at:

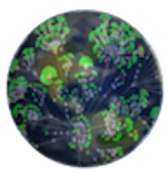
http://services.namesforlife.com/announcements

NamesforLife™
Bringing meaning to life ...

Catherine Lyons
Charles T. Parker
Dorothea Taylor
Sarah Wigley
Nicole Osier
Grace Rodriguez
Amber Roberts

INTERNATIONAL COMMITTEE ON SYSTEMATICS OF PROKARYOTES

Brian Tindall
Aharon Oren



Nikos Kyrpides
Hans-Peter Klenk
Barney Whitman

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Gerry Roston
Kurt Riegger

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