Thank you for your support for our research!

How to read the survey:

Your survey has two charts, the first is at the Phylum level and the second is at the Species level.

The Phyla level is a very broad level identification of the bacteria found in your horse's gut. The Species level is a more specific level of identification (see Figure 1).

The charts demonstrate your horse's microbiome composition against the average microbiome composition of all horses in the EMP database.

The bacteria name in the Species level chart lists the taxonomic level prior to the name of taxonomic rank.

Example:
p___Firmicutes**; o**___Clostridiales; **f**___Ruminococcaceae; **g**___Ruminococcaceae NK4A214 group; **s**__

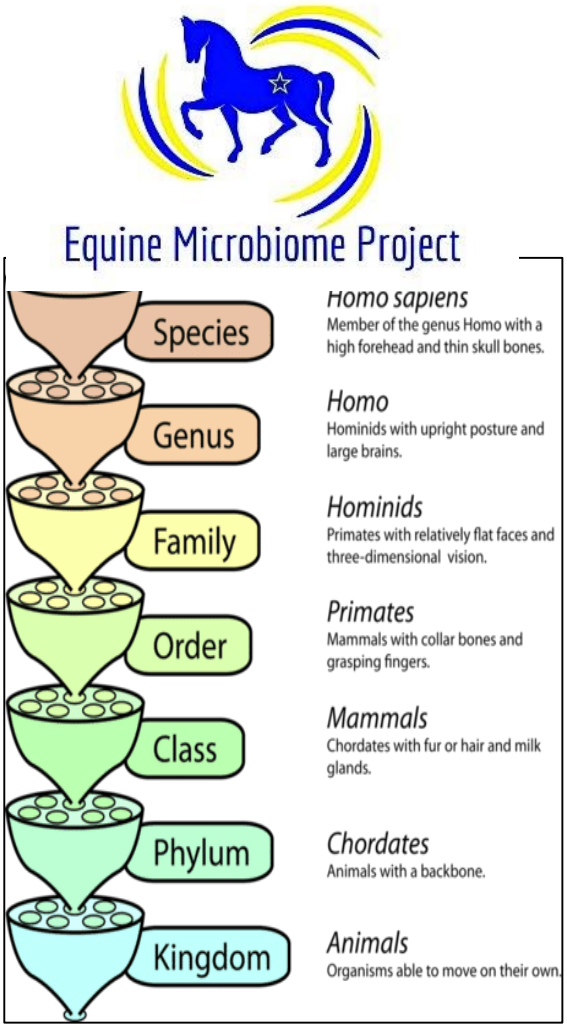
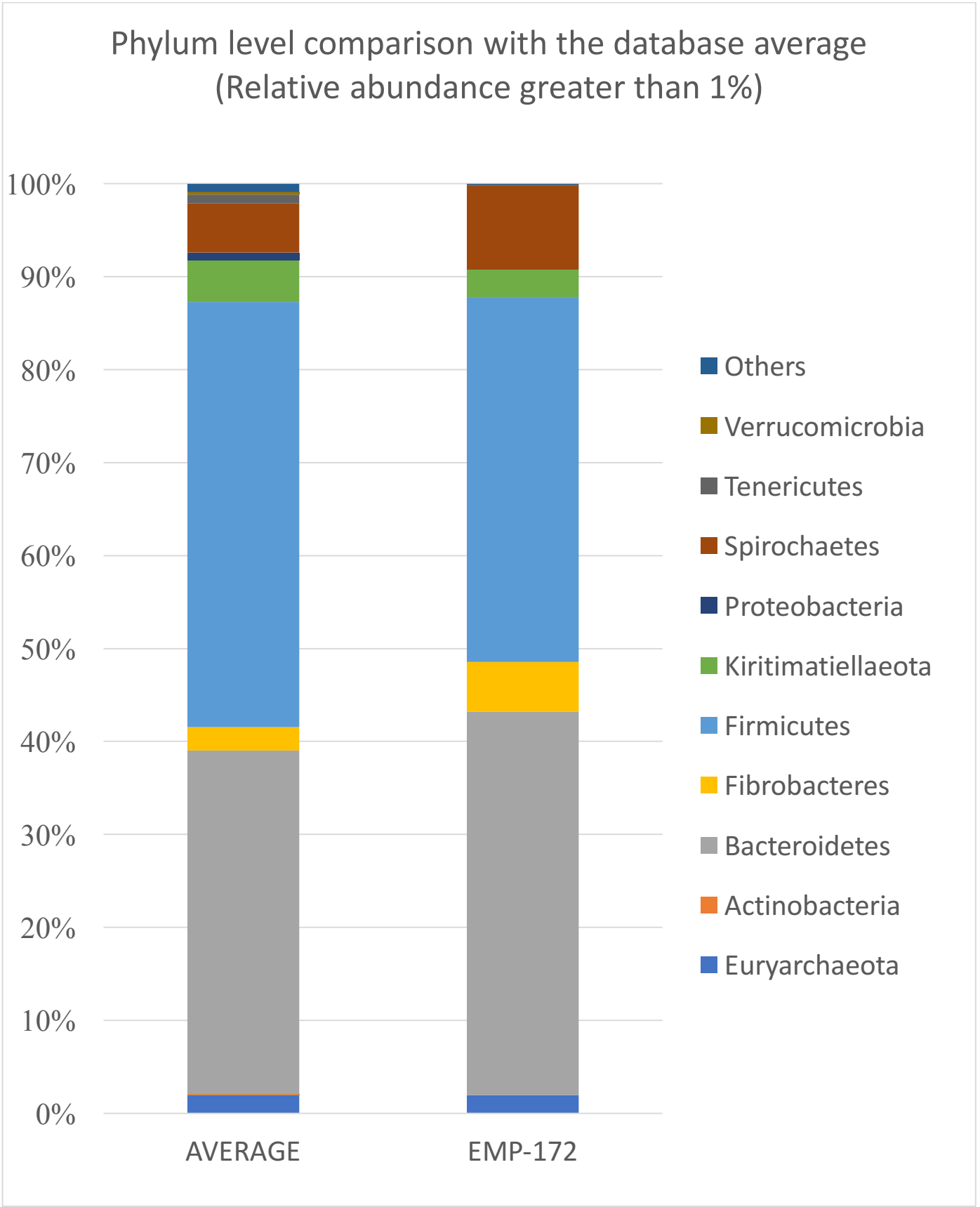
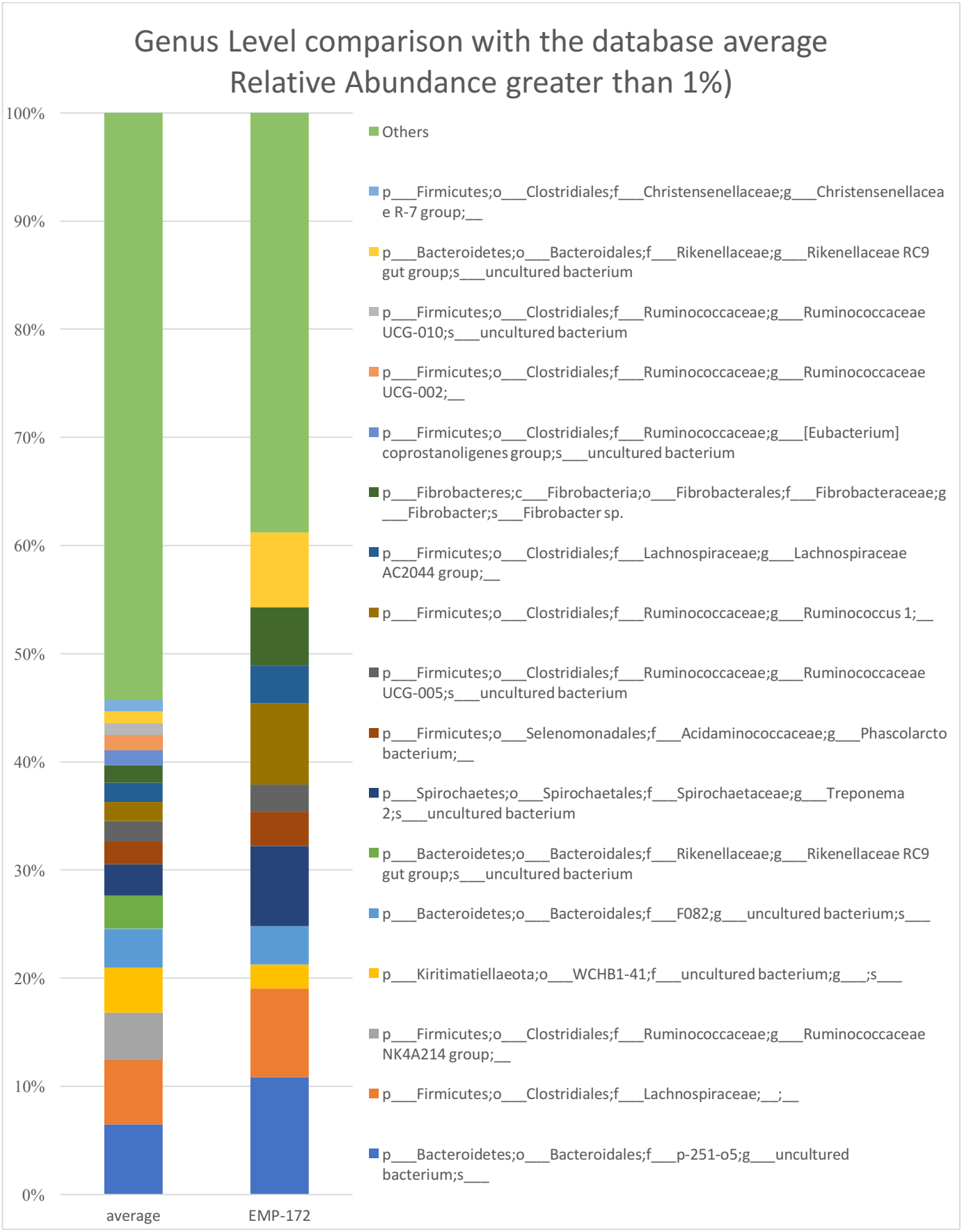


Figure 1. Taxonomic Levels

The example bacteria is an unidentified species, from the Ruminococcaceae NK4A214 group genus, from the Ruminococcaceae family, from the Clostridiales order, and of the Firmicutes phyla.


Phylum level comparison with the database average
(Relative abundance greater than 1%)
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
AVERAGE
EMP-172
Others
Verrucomicrobia
Tenericutes
Spirochaetes
Proteobacteria
Kiritimatiellaeota
Firmicutes
Fibrobacteres
Bacteroidetes
Actinobacteria
Euryarchaeota


Genus Level comparison with the database average
Relative Abundance greater than 1%)
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
average
EMP-172
Others
p___Firmicutes;o___Clostridiales;f___Christensenellaceae;g___Christensenellacea e R-7 group;__
p___Bacteroidetes;o___Bacteroidales;f___Rikenellaceae;g___Rikenellaceae RC9 gut group;s___uncultured bacterium
p___Firmicutes;o___Clostridiales;f___Ruminococcaceae;g___Ruminococcaceae UCG-010;s___uncultured bacterium
p___Firmicutes;o___Clostridiales;f___Ruminococcaceae;g___Ruminococcaceae UCG-002;__
p___Firmicutes;o___Clostridiales;f___Ruminococcaceae;g___[Eubacterium] coprostanoligenes group;s___uncultured bacterium
p___Fibrobacteres;c___Fibrobacteria;o___Fibrobacterales;f___Fibrobacteraceae;g ___Fibrobacter;s___Fibrobacter sp.
p___Firmicutes;o___Clostridiales;f___Lachnospiraceae;g___Lachnospiraceae AC2044 group;__
p___Firmicutes;o___Clostridiales;f___Ruminococcaceae;g___Ruminococcus 1;__
p___Firmicutes;o___Clostridiales;f___Ruminococcaceae;g___Ruminococcaceae UCG-005;s___uncultured bacterium
p___Firmicutes;o___Selenomonadales;f___Acidaminococcaceae;g___Phascolarcto bacterium;__
p___Spirochaetes;o___Spirochaetales;f___Spirochaetaceae;g___Treponema 2;s___uncultured bacterium
p___Bacteroidetes;o___Bacteroidales;f___Rikenellaceae;g___Rikenellaceae RC9 gut group;s___uncultured bacterium
p___Bacteroidetes;o___Bacteroidales;f___F082;g___uncultured bacterium;s___
p___Kiritimatiellaeota;o___WCHB1-41;f___uncultured bacterium;g___;s___
p___Firmicutes;o___Clostridiales;f___Ruminococcaceae;g___Ruminococcaceae NK4A214 group;__
p___Firmicutes;o___Clostridiales;f___Lachnospiraceae;__;__
p___Bacteroidetes;o___Bacteroidales;f___p-251-o5;g___uncultured bacterium;s___

What do we know about these bacteria?

Actinobacteria

Bifidobacteria have potential probiotic properties such as protection against pathogens through competitive exclusion, bile salt hydrolase activity, immune modulation, and the ability to adhere to mucus or the intestinal epithelium.

Bacteroidetes

Bacteroidetes are specialists for the degradation of complex organic matter, i.e., proteins and carbohydrates, and other substrates found in the diet.

Euryarchaeota

Archaea like *Methanomicrobiales* produce methane and recycle short chain fatty acids like acetate.

Fibrobacteres

There are two cultured species of this group, *Fibrobacter succinogenes* and *Fibrobacter intestinalis*, that are recognized as major degraders of lignocellulosic material in the herbivore gut.

Firmicutes

Firmicutes are better at extracting energy from food than Bacteroidetes. When there are more Firmicutes in the gut, more of the plant material can be converted to energy for the body to use or storage. Lachnospiraceae and Ruminococcaceae are two families with many cellulose degraders. Lactobacillales is a group containing Lactobacillaceae and Streptococcaceae, two families of bacteria that ferment sugars to lactic acid.

Proteobacteria

Proteobacteria show extreme metabolic diversity and include a wide variety of commensals, such as Enterobacter, Enterococcus, Vibrio, Helicobacter, and others.

Spirochaetes

Treponema are spiral-shaped bacteria that are commonly found in anaerobic liquid environments, such as the equine digestive system. They digest simple carbohydrates.

Tenericutes

RF39 is the most abundant Tenericute in the horse gut. These are largely uncategorized.

Verrucomicrobia.

Akkermansia muciniphila, isolated from a human fecal sample, can use gastric mucin (constituent of mucus) as carbon, energy and nitrogen source. Verruco-5 and Verruco-6 are the most common members of this group in the equine gut.

Please note, the Equine Microbiome Project personnel are microbiologists and not veterinarians. The Equine Microbiome Project personnel are not licensed to provide medical advice for your horse based on your horse's results.

While your horse's microbiome may look different from the "Average" horse, it is still yet to be discovered the subtle differences in the equine microbiome that are attributed to health status or disease states. Your contribution to the EMP will further improve equine research so we may be able to provide more distinctive answers to you in the near future.