

¹ICAR-National Dairy Research Institute, Karnal, Haryana, 132001

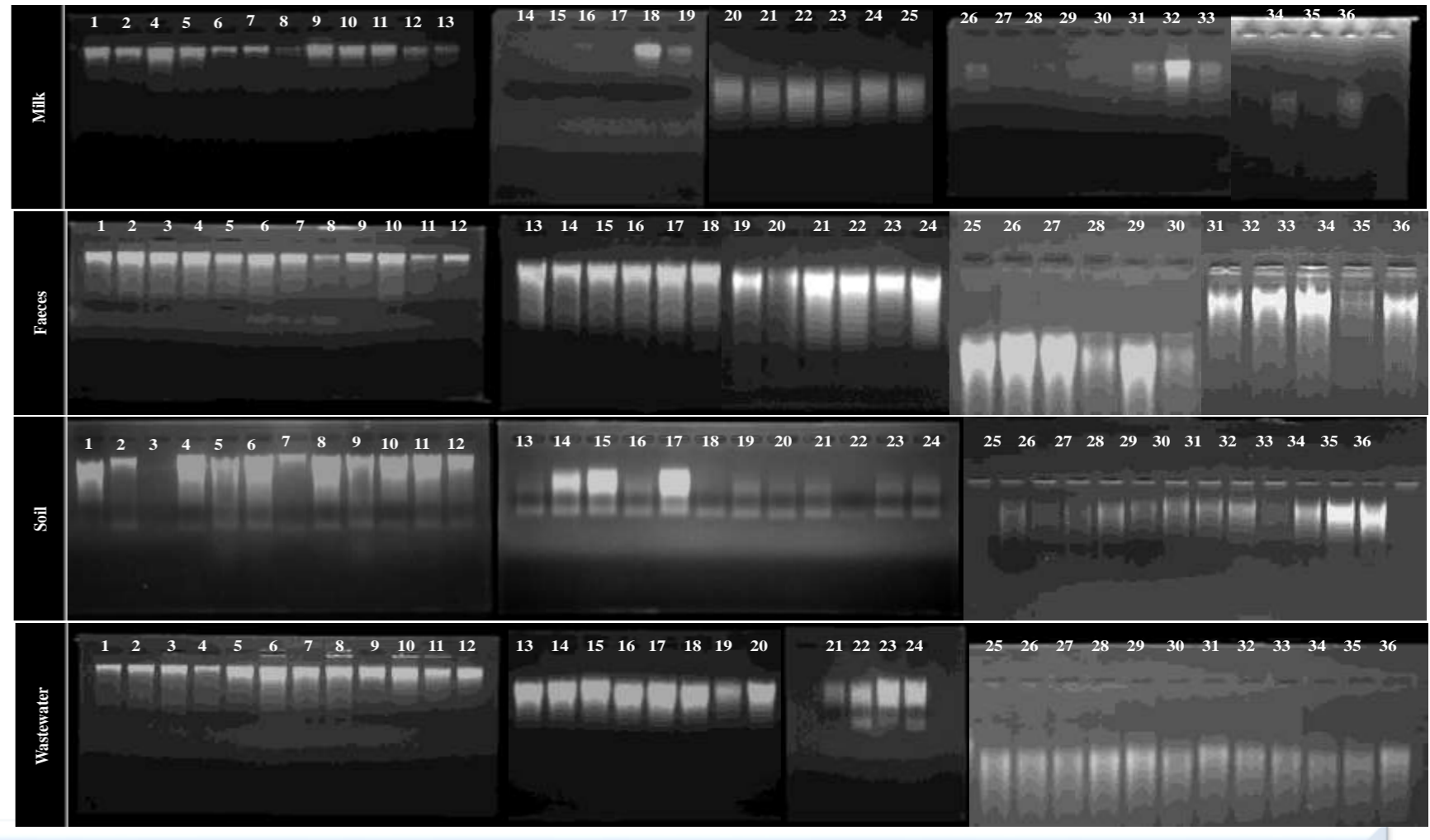
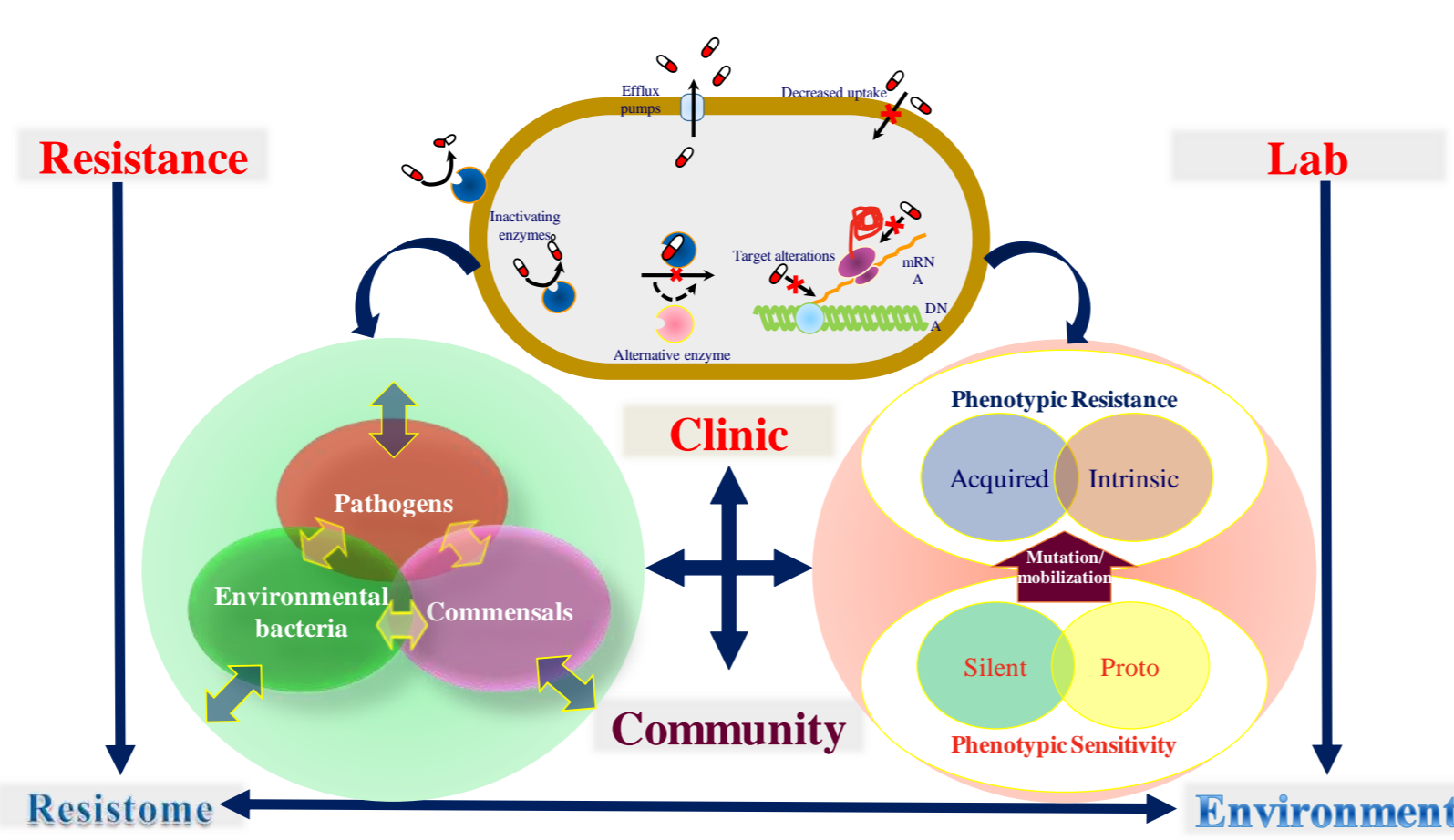
²Southern Regional Station, ICAR-National Dairy Research Institute, Bengaluru, Karnataka, 560030.

³Department of Animal Husbandry and Dairying, Central University of Odisha, Koraput, Odisha, 763004

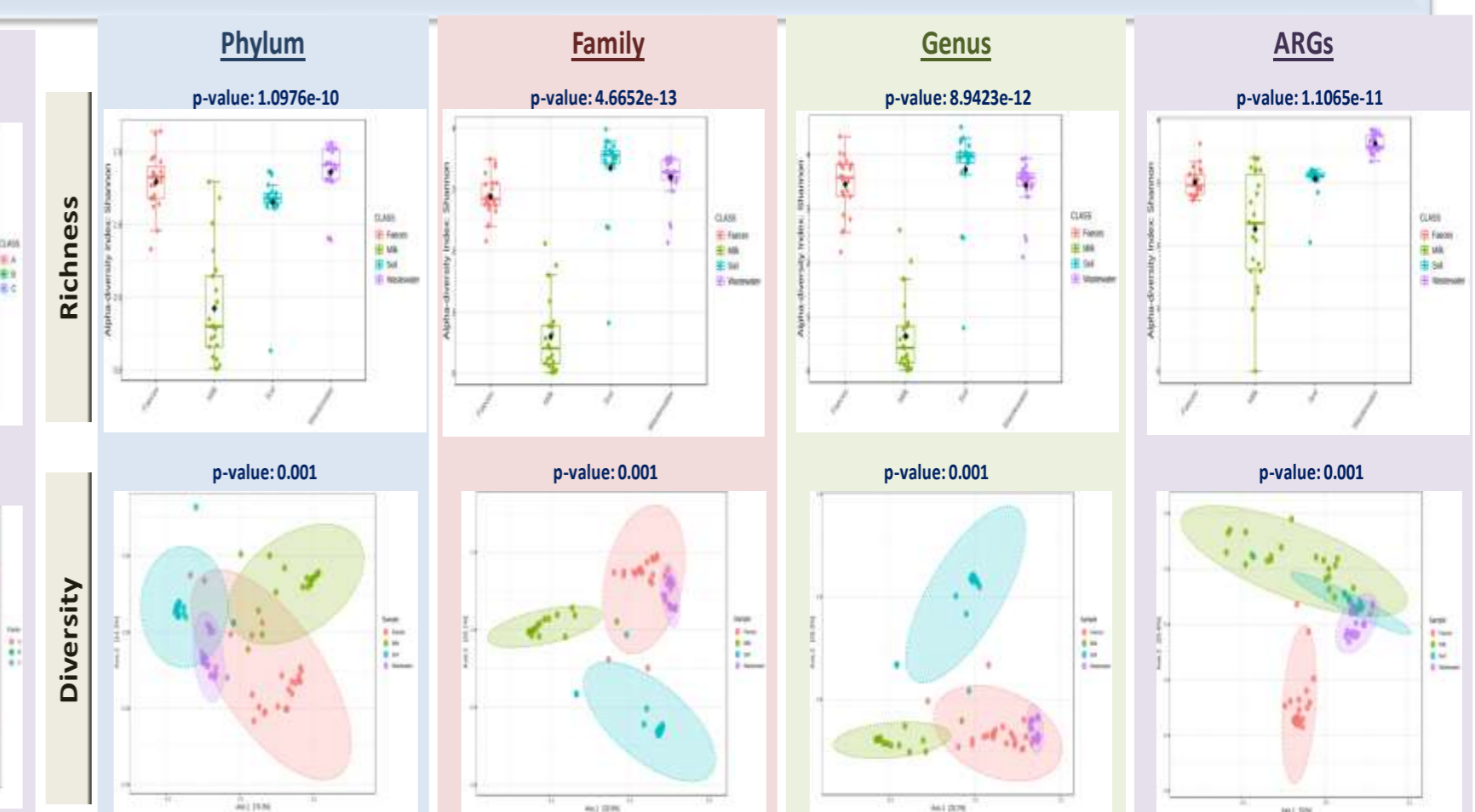
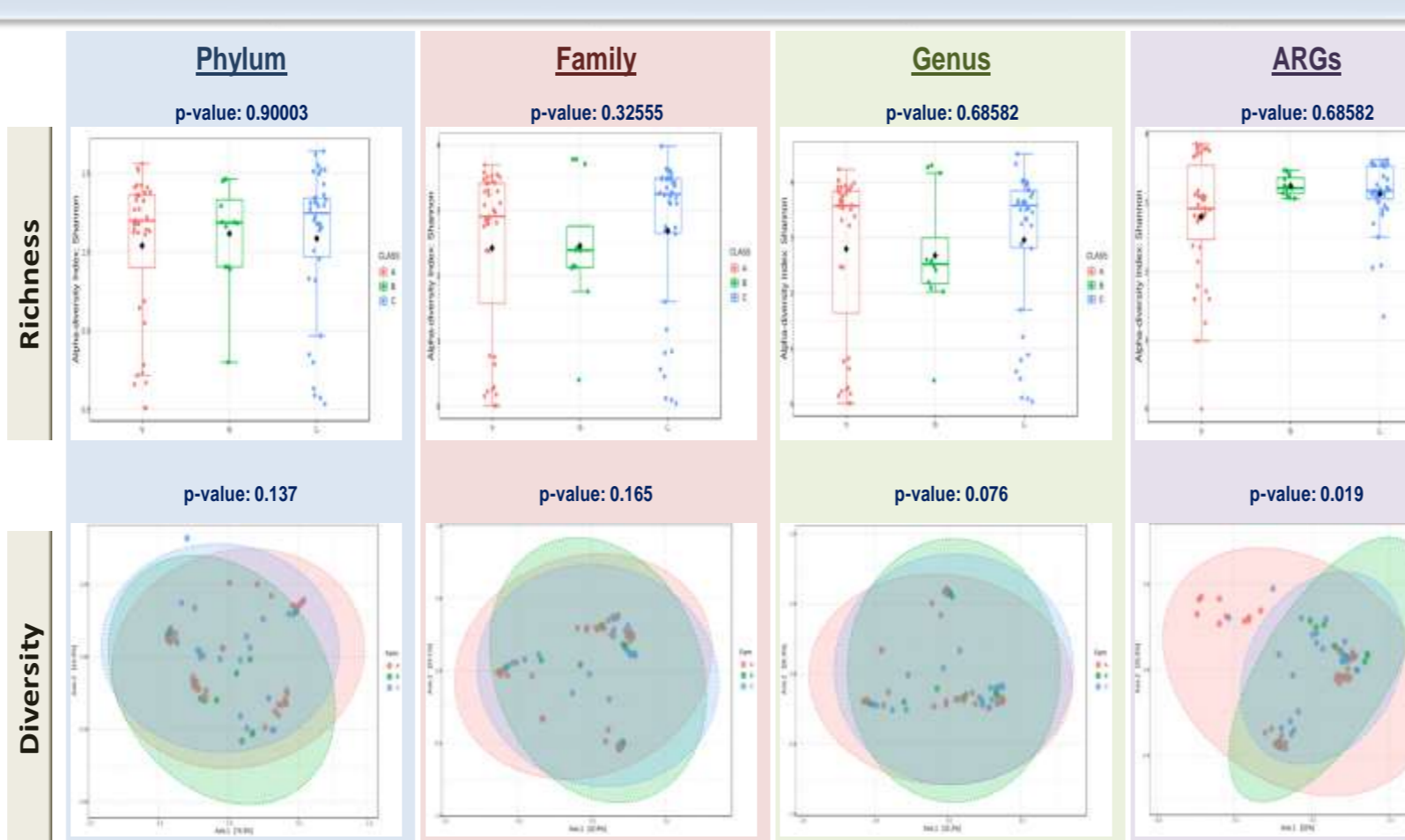
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⁵ICAR-National Institute of Animal Nutrition and Physiology, Bengaluru, Karnataka, 560030

Study Overview

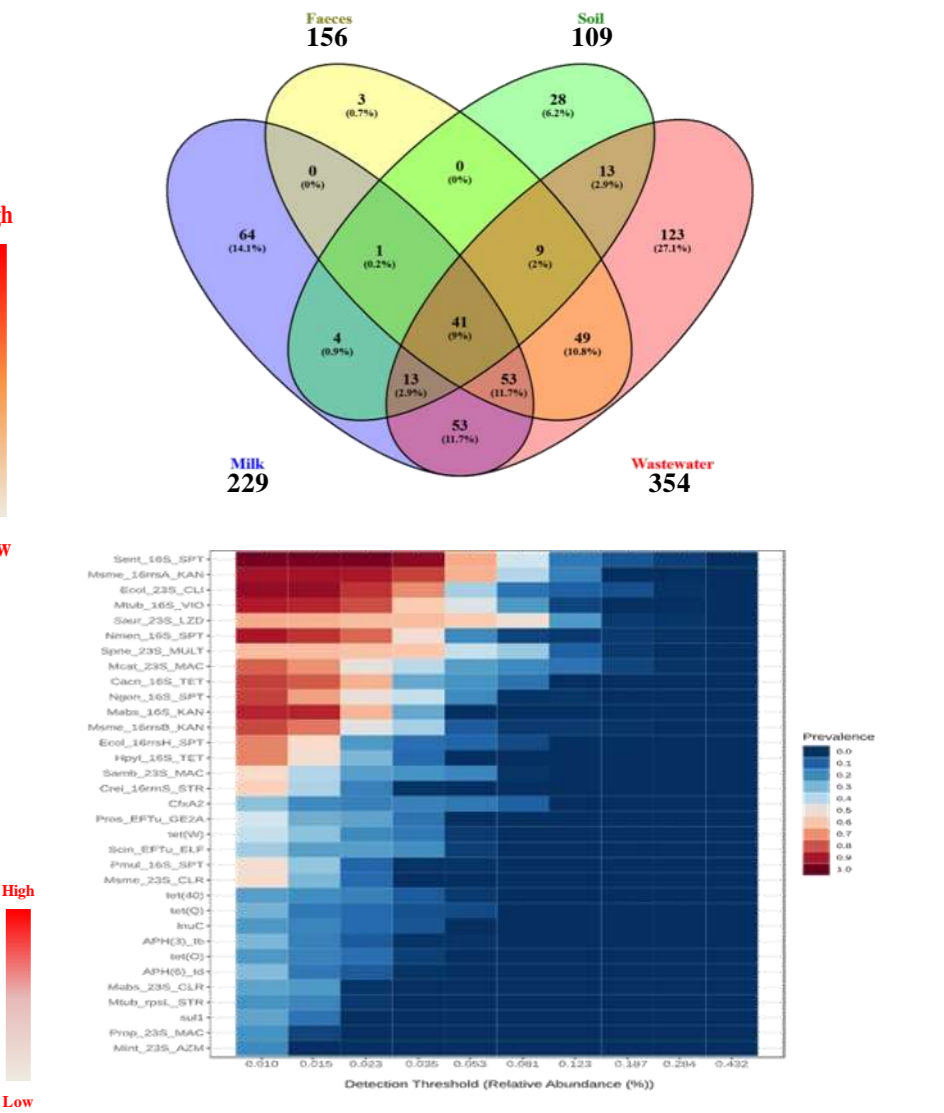
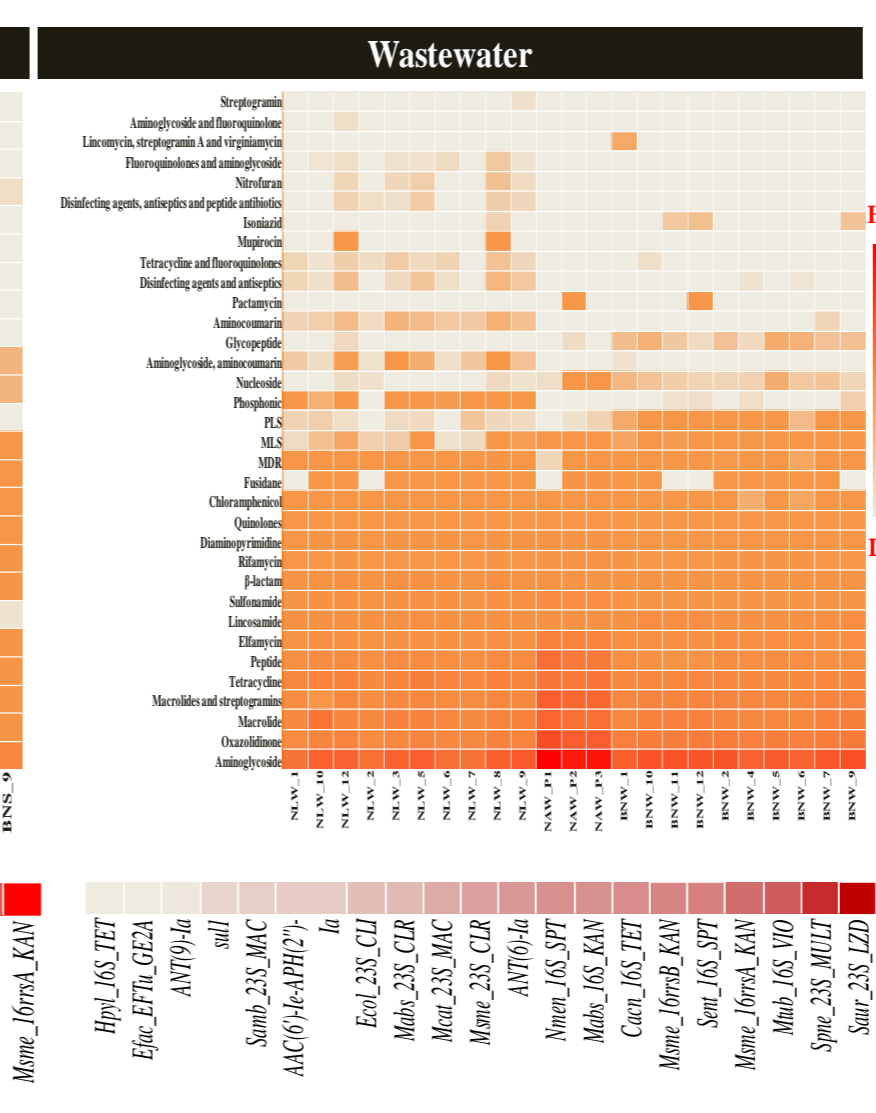
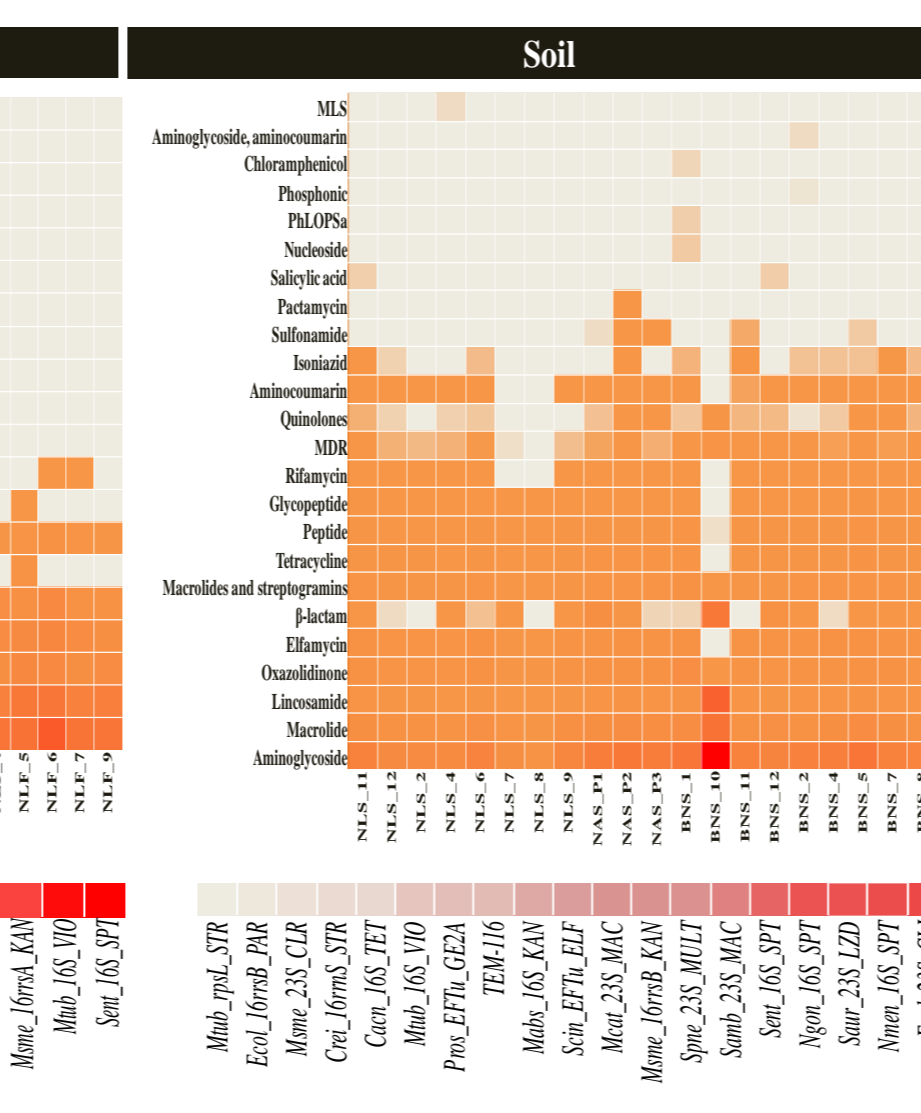
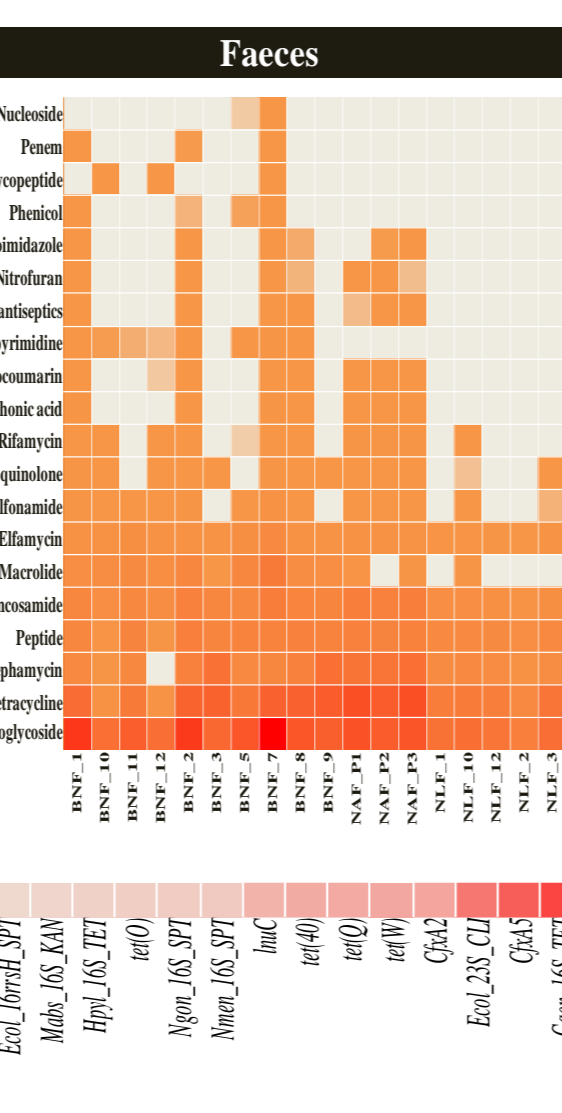
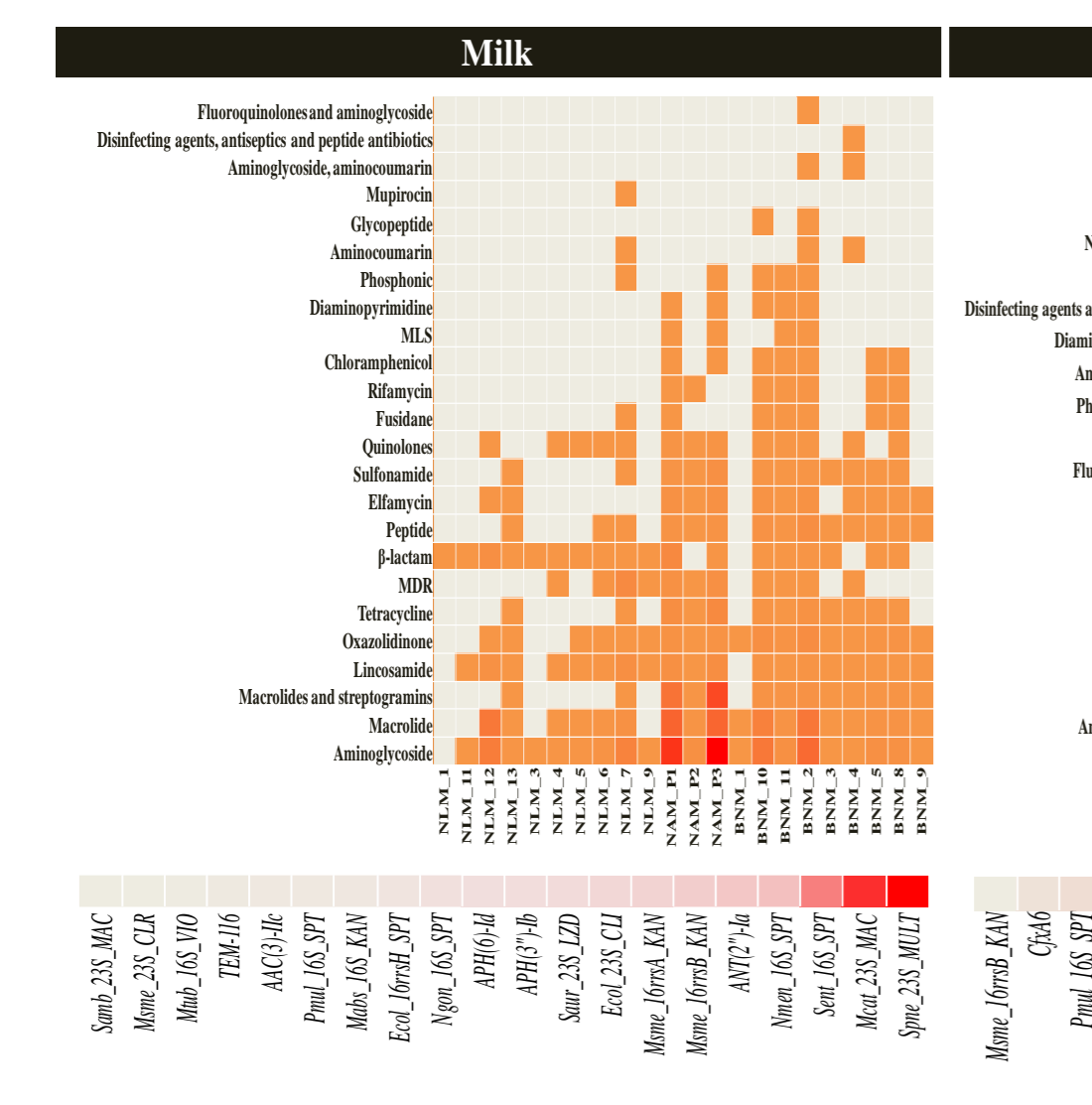
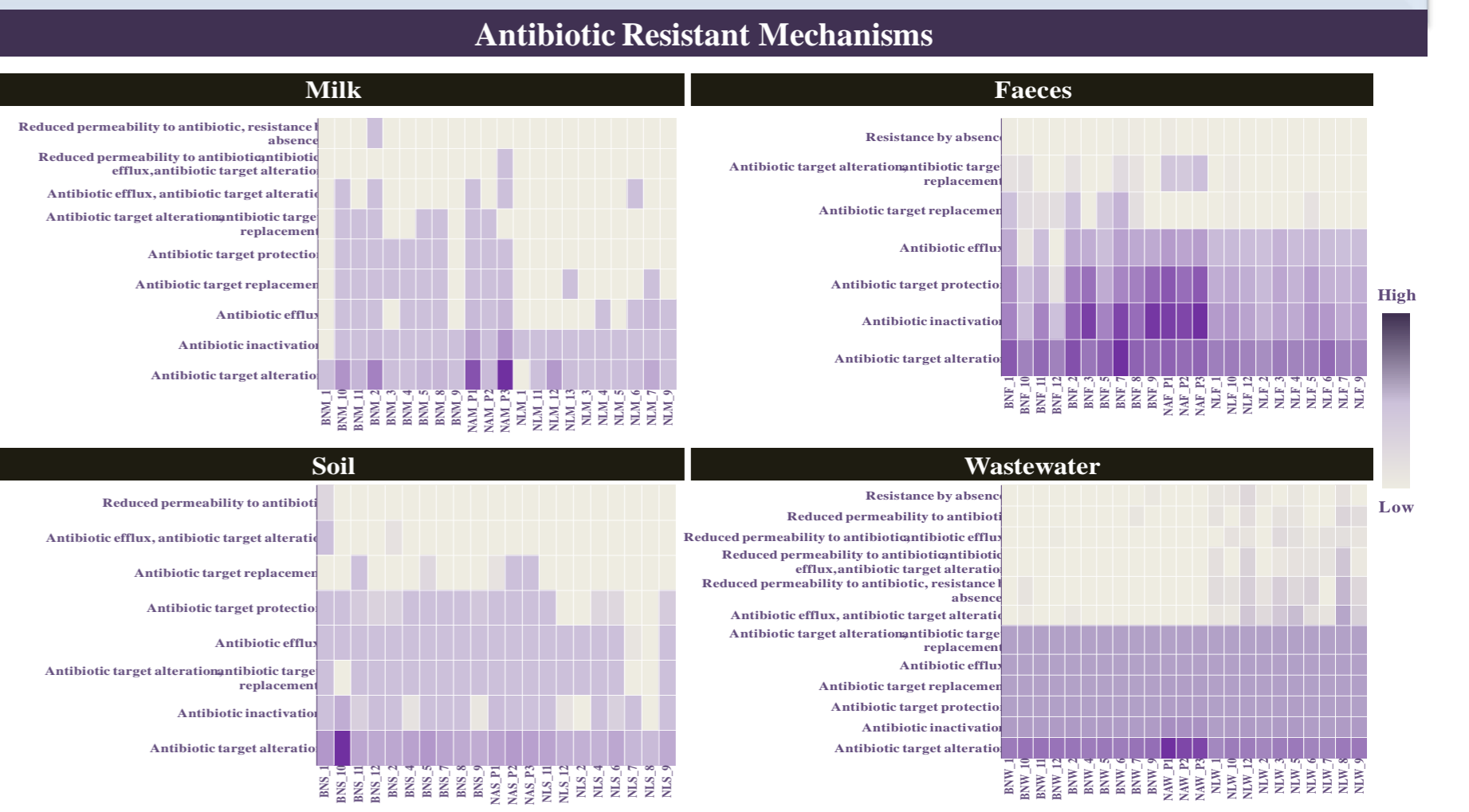
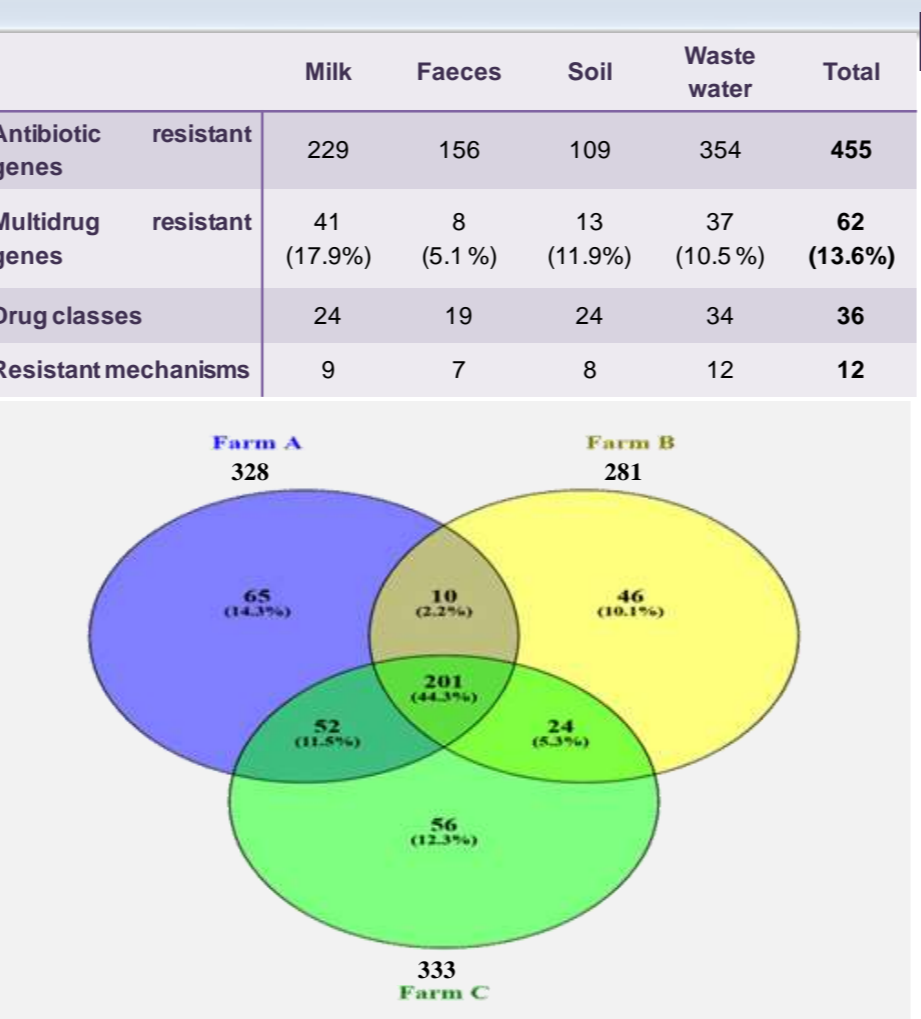
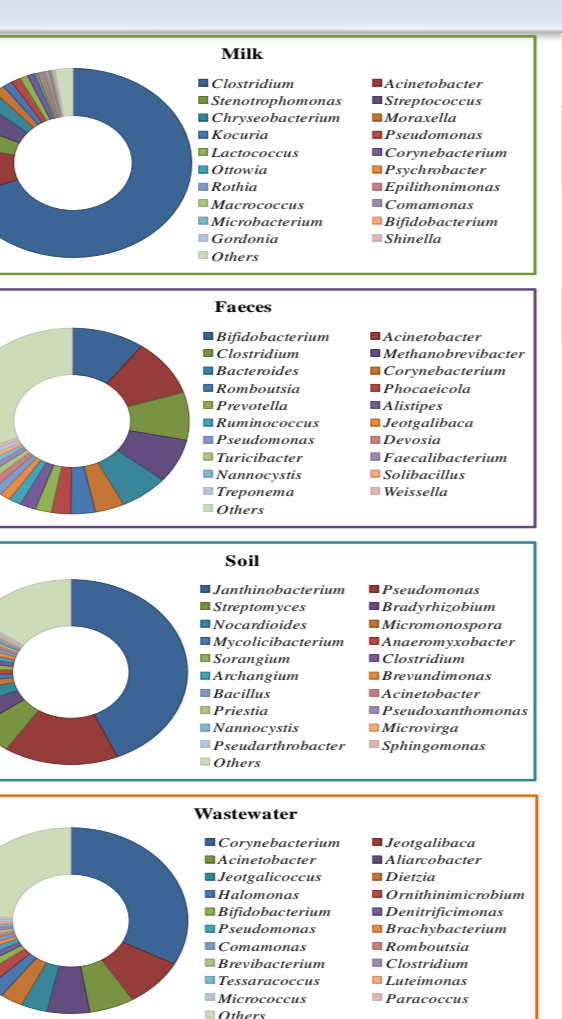
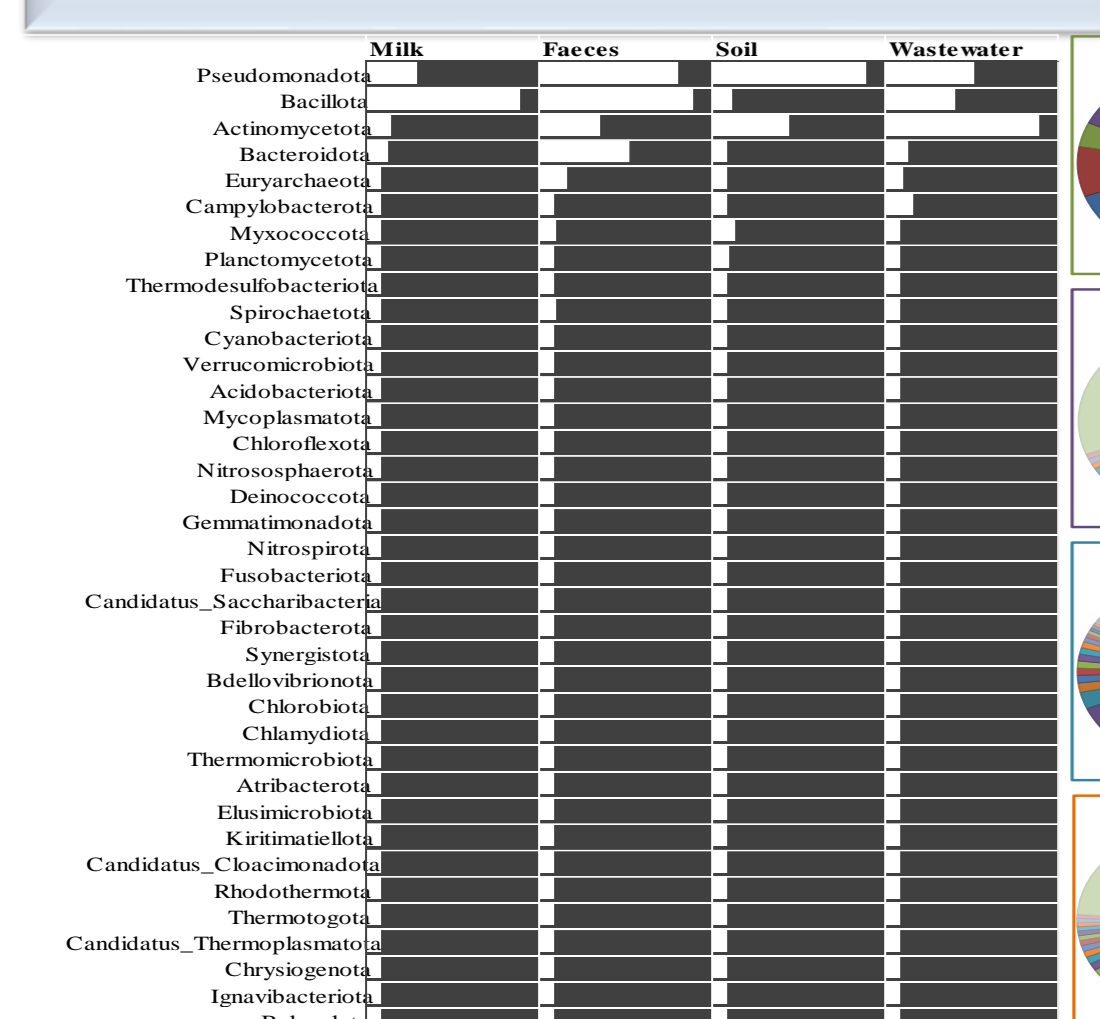


Microbiome and Resistome Ecological Indexes of Dairy Production System



Sample	Number of reads (Billion)				
	Input	Both surviving	Forward only surviving	Reverse only surviving	Dropped
Milk	2.58	1.96	0.34	0.06	0.23
Faeces	2.81	2.24	0.29	0.07	0.21
Soil	3.48	2.48	0.50	0.13	0.36
Wastewater	2.81	2.21	0.31	0.08	0.22
Total	11.68	8.89	1.44	0.34	1.01

Microbiome and Resistome of Dairy Production System



Conclusions

- ✓ Aminoglycoside resistant genes were most abundant and common among all the sample types
- ✓ Antibiotic target alteration was the most predominant antibiotic resistant mechanism
- ✓ The most abundant antibiotic resistant genes were present in wastewater, followed by faeces, soil and milk
- ✓ In dairy production system, wastewater is the reservoir of antibiotic resistant genes

Acknowledgement



Declaration

There is no conflict of interest for authors in poster publication