

Unveiling the Endangered St. Lawrence Estuary Beluga's Skin Microbiome and It's Potential Utility in Halogenated Flame Retardant Exposure Monitoring

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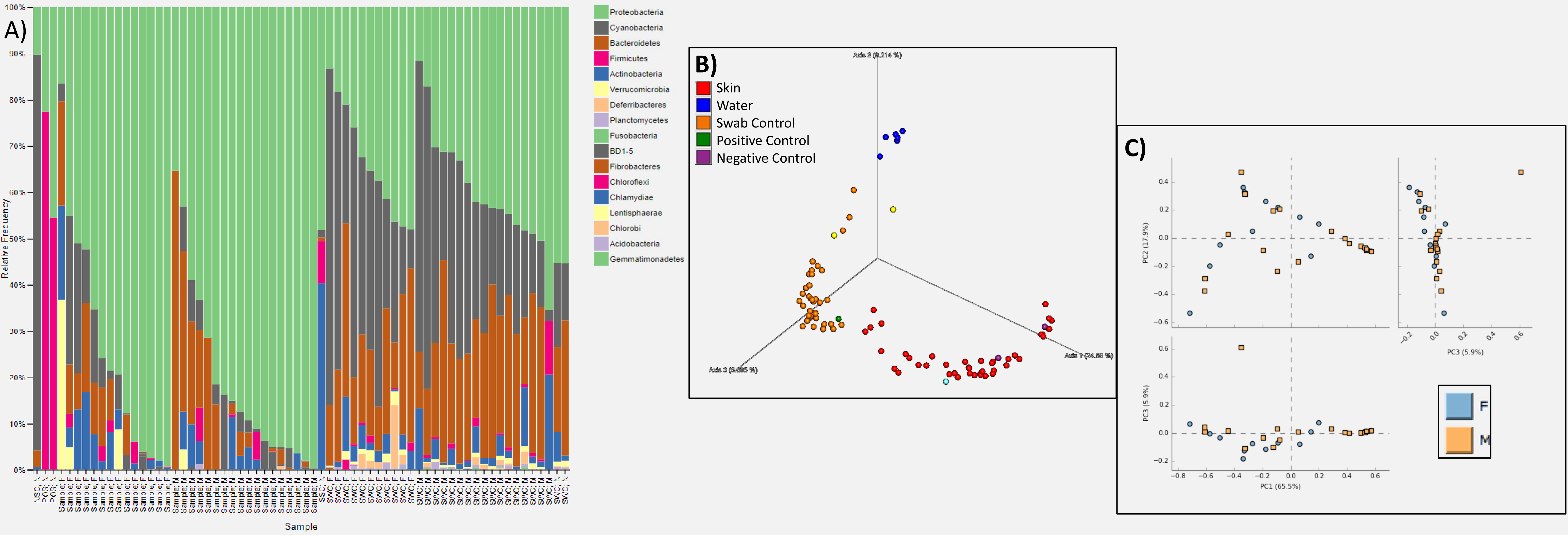
INTRODUCTION

- Marine mammals are integral part of the food web and an important socioeconomic benefit for coastal communities.
- St. Lawrence Estuary (SLE) beluga (*Delphinapterus leucas*) population is thought to be endangered by, among other stressors, elevated tissue concentrations of environmental contaminants (e.g. halogenated flame retardants)¹. Flame retardants (FRs) like PBDEs and emerging FRs have been found to be a risk factor for dystocia in beluga females².
- Current contaminant monitoring relies on skin biopsies using a series a challenging and highly invasive procedures.
- The beluga skin microbiome has been uncharacterized, and represents an innovative and less destructive biomarker to monitor environmental contaminants and animal health.

Hypothesis:

The beluga skin microbiome changes as a function of beluga tissue contaminant concentrations, and will act as biomarkers of contaminant exposure for the non-invasive detection of altered ecosystem health.

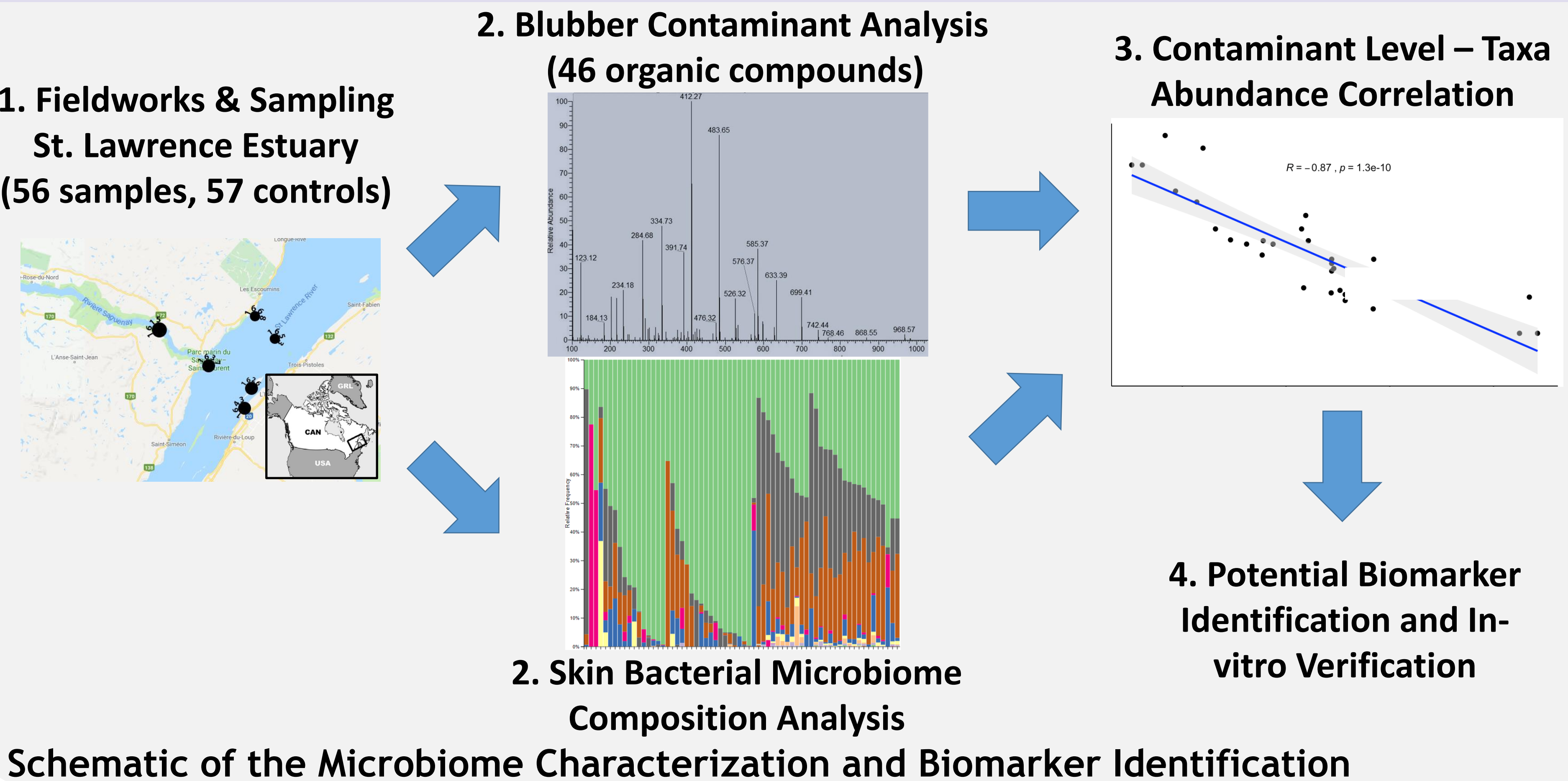
RESULTS – Skin Microbiome of Belugas



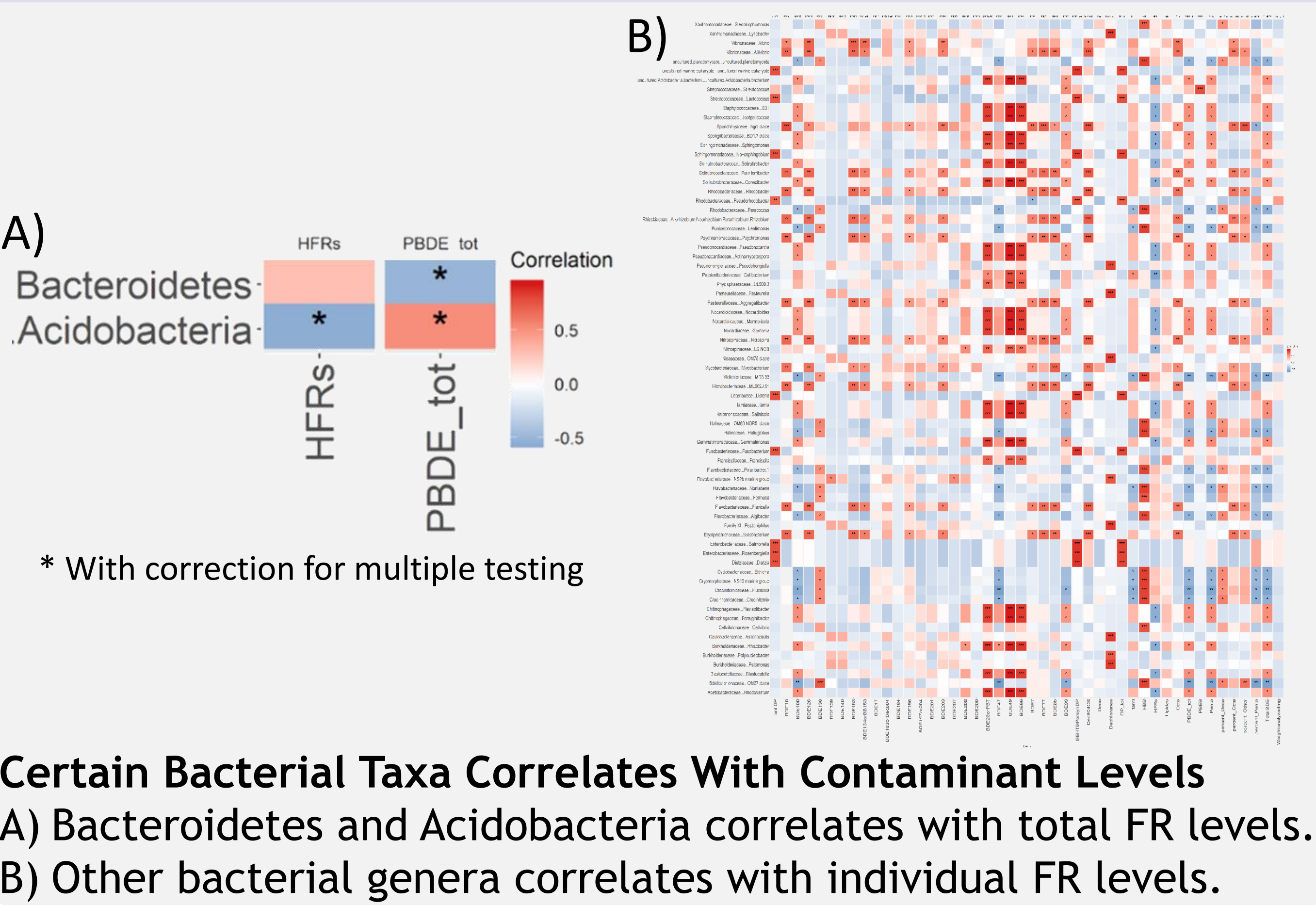
The Skin Microbiome of Belugas

- A) Relative abundance of bacterial phylum organized by sample source, sex and sample type (POS = positive control, NSC = negative control).
- B) Principal component analysis (PCA) showing the distinct beluga skin (red) and surrounding water (blue) microbiomes.
- C) PCA of the beluga skin microbiomes between males (orange) and females (blue) show no differences in microbiome between sexes.

METHOD



RESULTS – Biomarker Identification



SUMMARY & FUTURE DIRECTIONS

- The beluga skin microbiome warrants further investigation as a non-invasive approach for monitoring of beluga and ecosystem health.
- The beluga skin microbiome is distinct from their environment/sea water. It does not appear to vary as a function of beluga sex or location.
- Two bacterial phyla, and additional genera, significantly correlated with PBDE or emerging FR concentrations in their blubber.
- Metagenomics could reveal microbial metabolic pathways associated with contaminant levels.

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References

- 1. Covaci A, et al. 2011. Environ. Int. 37, 532-556
- 2. Lair, S. et al. 2014. DFO Can. Sci. Advis. Sec.Res. Doc. 2013/119. iv + 37 p.

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