



Western Washington University  
Western CEDAR

---

Salish Sea Ecosystem Conference

2022 Salish Sea Ecosystem Conference  
(Online)

---

Apr 27th, 4:30 PM - 5:00 PM

## Investigating contaminant-related health effects in killer whales in British Columbia using omics

Dr. Bethany DeCourten  
*Ocean Wise*

Follow this and additional works at: <https://cedar.wwu.edu/ssec>

---

DeCourten, Dr. Bethany, "Investigating contaminant-related health effects in killer whales in British Columbia using omics" (2022). *Salish Sea Ecosystem Conference*. 231.  
<https://cedar.wwu.edu/ssec/2022ssec/allsessions/231>

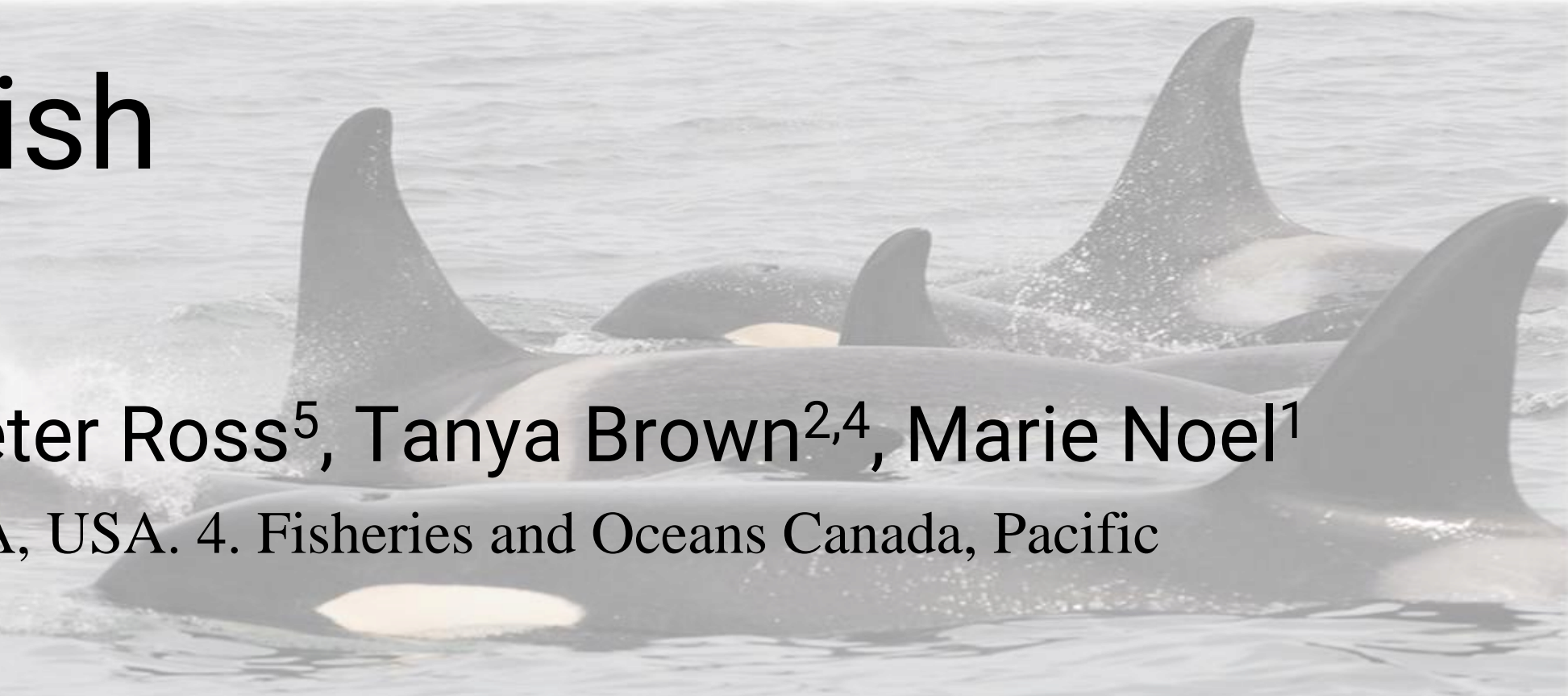
This Event is brought to you for free and open access by the Conferences and Events at Western CEDAR. It has been accepted for inclusion in Salish Sea Ecosystem Conference by an authorized administrator of Western CEDAR. For more information, please contact [westerncedar@wwu.edu](mailto:westerncedar@wwu.edu).



# Investigating contaminant-related health effects in killer whales in British Columbia using molecular "omics" approach

Bethany DeCourten<sup>1,2</sup>, Adam Warner<sup>1</sup>, Gina Ylitalo<sup>3</sup>, M. Bradley Hanson<sup>3</sup>, Candi Emmons<sup>3</sup>, Jared R. Towers<sup>4</sup>, Lance Barrett-Lennard<sup>5</sup>, Peter Ross<sup>5</sup>, Tanya Brown<sup>2,4</sup>, Marie Noel<sup>1</sup>

1. Ocean Wise Conservation Association, Vancouver, BC, Canada 2. Simon Fraser University, Burnaby, BC, Canada, 3. NOAA/NMFS Northwest Fisheries Science Center, Seattle, WA, USA. 4. Fisheries and Oceans Canada, Pacific Biological Station, Nanaimo, BC, Canada 5. Raincoast Conservation Foundation, Sidney, BC, Canada



## Introduction

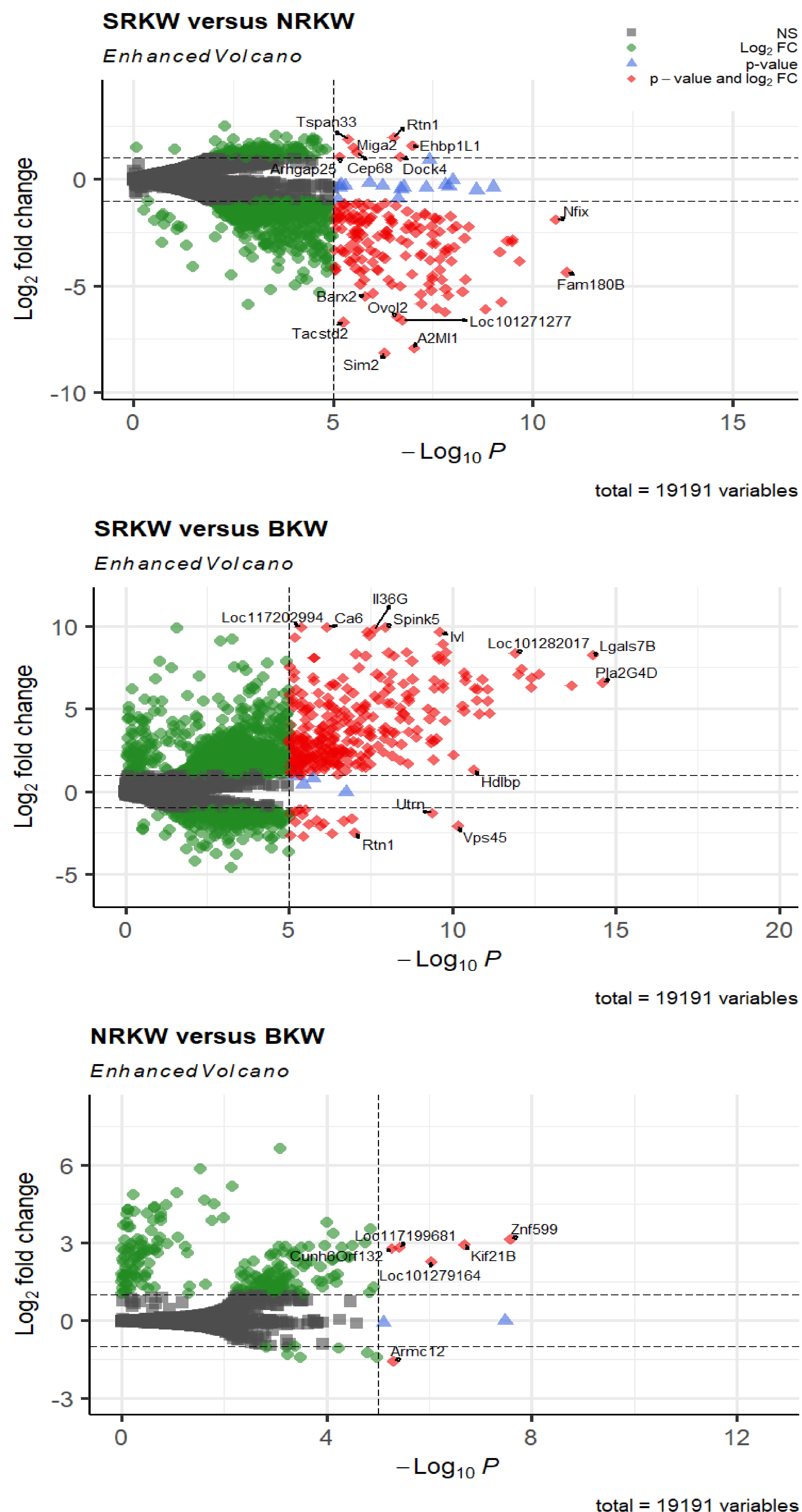
Killer whales (*Orcinus orca*) are an iconic species in the Salish Sea with three populations inhabiting the area: the Northern Resident (NRKW), Southern Resident (SRKW), and Bigg's (BKW) populations. Complementing contaminant profiles presented elsewhere (refer to snapshot presentation by Marie Noel), we present differences in gene expression measured using RNAseq. Building upon decades of research, these findings will provide a clearer understanding of health effects associated with contaminants in killer whales that can be used to inform risk-based prioritization of conservation efforts.

## Methods

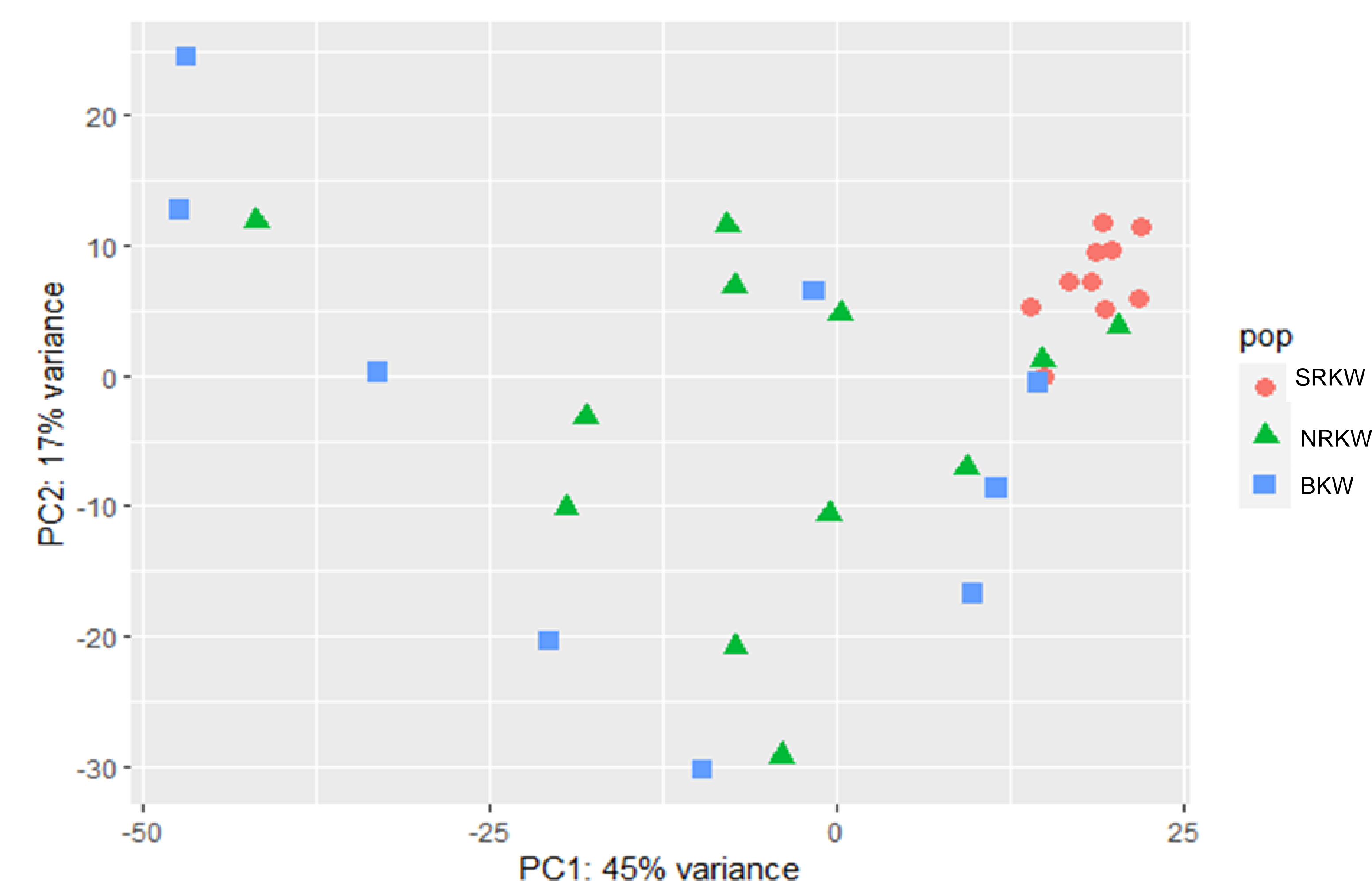
Blubber biopsies were collected using pneumatic darts from NRKW (n=12) and BKW (n=9) populations in British Columbia in collaboration with Bay Cetology/DFO. SRKW samples (SRKW, n=10) included in this study came from Ocean Wise's archive (collected by NOAA, 2016). RNA was extracted using QIAzol-chloroform protocols. RNA was sequenced at UBC's Sequencing and Bioinformatics Core using ribodepletion prepared libraries. Samples with abundant read percentage >10% were excluded from analysis. Gene expression was quantified using Salmon, and DESeq2 was used to test for statistically different gene expression (p<0.05) between populations. Gene Ontology (GO) term enrichment was analyzed via [www.webgestalt.org](http://www.webgestalt.org), mapped to the *Bos taurus* genome.

## Results & Conclusions

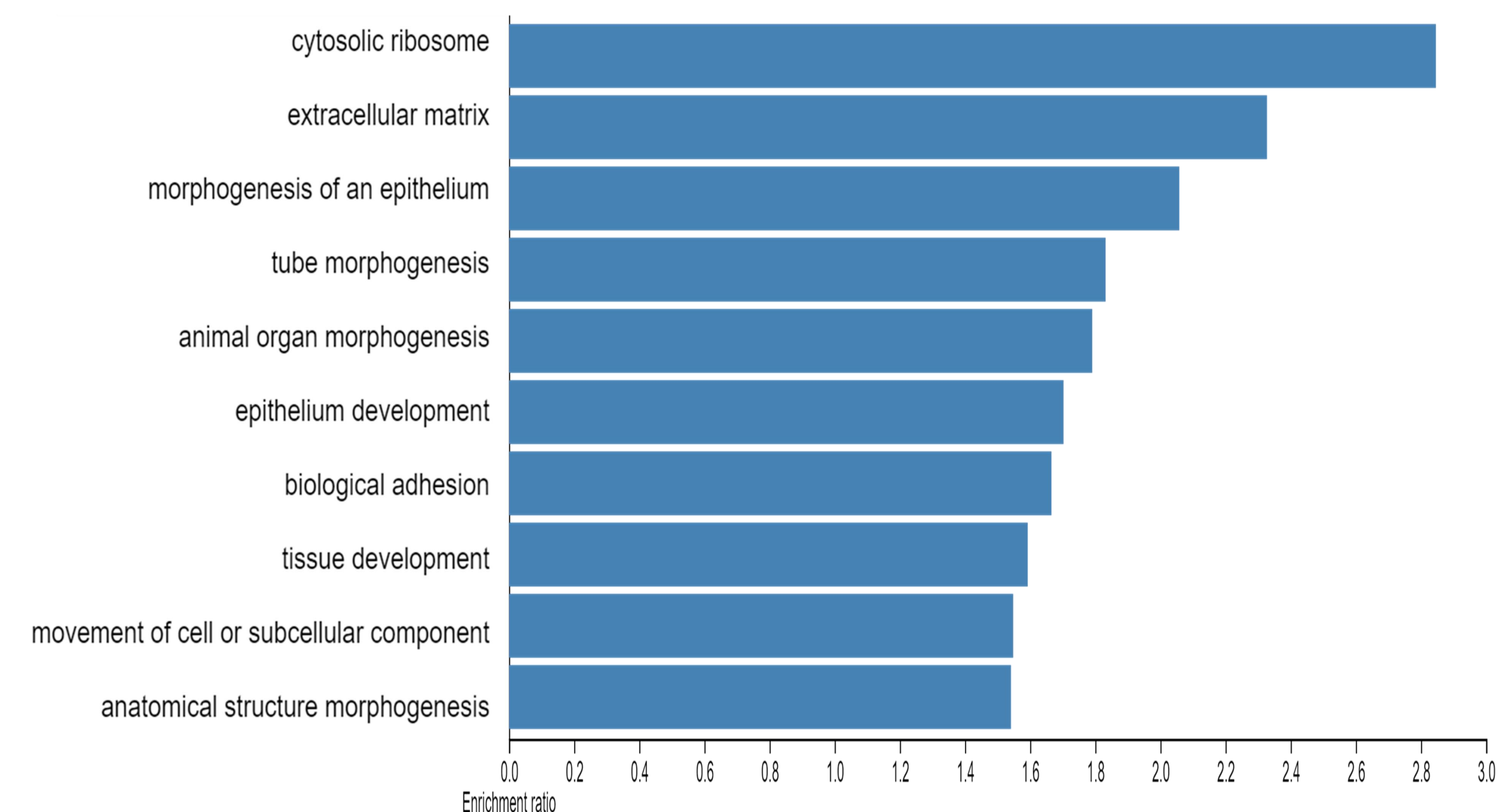
Differential gene expression was observed when comparing the SRKW to the NRKW (1509 genes) and BKW (2351 genes; Figure 1.) Fewer genes were found to differ between the NRKW and the BKW (34 genes; Figure 1). Principal components analysis shows greater variance within the NRKW and BKW populations, than within the SRKW population (Figure 2). GO term enrichment analysis shows over-represented pathways involved in biological processes, molecular function, and cellular components (Figure 3). These findings illustrate differences in gene expression in the SRKW compared to the NRKW and BKW, suggesting that specialized management strategies may help optimize conservation efforts of killer whale populations.



**Figure 1.** Enhanced volcano plots comparing  $\log_2$  shrunken (apeglm) fold change (FC) and p-values between 3 populations of killer whales (pairwise).  $\log_2$ FC cutoff was set to 1.0 and p-value cutoff was set to  $10e^{-6}$ . Grey square markers indicate non-significance, green circle markers indicate values that fall above the FC cutoff, blue triangle markers indicate points that fall above the p-value cutoff, red diamond markers represent points that fall above both the p-value and fold change cutoffs.



**Figure 2.** Principal components analysis displaying variance-stabilizing transformed values. Markers represent samples in the SRKW (red circles), NRKW (green triangles) and BKW (blue squares).



**Figure 3.** Enriched gene sets analyzed with WebGestalt (FDR p-value < 0.05). Analysis included GO terms from the *Bos taurus* genome in the biological processes, molecular function, and cellular components categories.

### Next steps

- Further analyses will incorporate measured contaminant levels
- Key genes responsive to contaminant levels will be identified
- Metabolic profiles will be analyzed to provide a more complete estimate of organismal health

### Acknowledgments

Funding provided by National Fish and Wildlife Foundation, Fisheries and Oceans Canada, National Oceanic and Atmospheric Administration, SeaWorld and Busch Gardens Conservation Funds. The views and conclusions presented are those of the authors and not endorsed by funding agencies. We thank SGS-AXYS for analysis of chemical contaminants. We thank the Biomedical Research Centre Sequencing Core at the University of British Columbia for their assistance with RNAseq. We thank the Ocean Wise Photogrammetry team for assistance in identification. Title photo provided by Lance Barrett-Lennard.