Vertebrate Diversity Profiling (vDNA)

Customer Sample Description	Scat Sample C
Sampling Point	N/A
Sampled Date	N/A
Sample ID	N/A

Key Vertebrate DNA Diversity Profile Evaluation

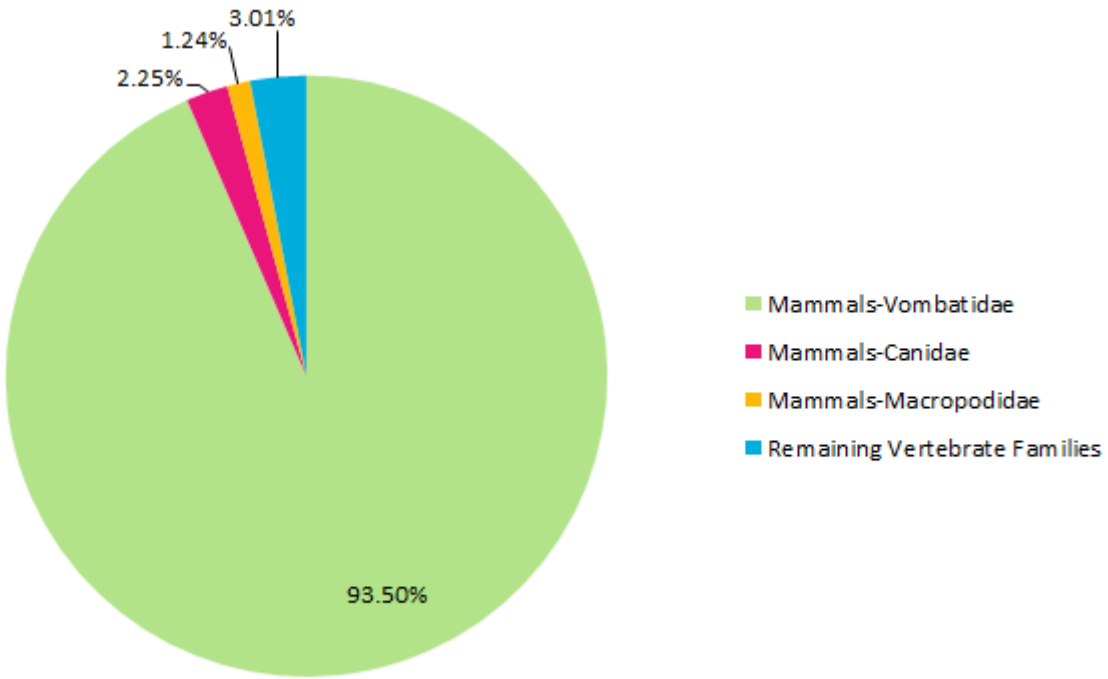
The vDNA data is used to make assessments over time, based on sample baseline data. We recommend this test being conducted in parallel with the bDNA test for bacterial profiles.

The vertebrate DNA detected in a sample can be monitored to determine if the different vertebrate groups are contributing to eDNA (environmental DNA) found in samples. The vertebrate DNA diversity profile represents the current status of the sample and should remain relatively static, depending on the source, volume and (if applicable) disinfection protocols.

The diversity profile consists of the following main taxonomic groups

Note: Only taxa representing >1% of the total DNA extracted from the sample has been interpreted in this report.

Diversity Profile – Top 3 Vertebrate Families



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Diversity Profile – Family Level

Vombatidae (94%) were the main vertebrates detected.

Family	Common Name	
Vombatidae	Wombat	93.5
Canidae	Fox	2.25
Macropodidae	Wallaby	1.24
Remaining Vertebrate Families		3.01

FAMILY	COMMENT
Canidae	• Canid mammals including domestic dogs, foxes and dingoes.
Macropodidae	• Marsupial family including kangaroos, wallabies, tree kangaroos, pademelons and quokkas.
Vombatidae	• Marsupial family consisting of the wombat.

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Notes

1. DNA extraction performed using the DNeasy (MoBio) PowerSoil® kit as per manufacturer's instructions. DNA extraction processes and sampling techniques can influence the types of vertebrates detected and reported. Standardisation of these practices is required for consistent and reliable results. Vertebrate DNA can have varied degradation rates in environmental samples and matrices which may affect the sensitivity of detection.
2. The AWQC report is an interpretation of the raw data output. The determination(s) and interpretative report produced have been based on the taxonomic hierarchy detected from the mapped reads. The mapped reads are an interpretation based on a 90% match to the DNA detected and a bit score of 150 to allow for inherent sequencing errors, degradation of environmental DNA and vertebrates that might have close homology but are in fact unique species for an area of interest. The complete data files can be supplied upon request.
3. Understanding the phylogenetic and ecological relationship of different vertebrates for an area is important. Some species may not have genetic divergence across the area of the 12S primers selected. Additional 12S primers or targeted primers should be considered if 100% of Taxa or specific species are required to be identified.
4. The relative amplification efficiency for each species is a nonlinear function of the fraction that each of those taxa represent within a community or multispecies DNA template. Vertebrate inputs detected by 12S mitochondrial primers may saturate NGS amplification of taxa present in lower proportion. It is also possible with low abundance in the sample that contamination can become more apparent.
5. The AWQC has a fish specific amplicon to identify Australian freshwater fish at the species level and an expert sampling team for habitat knowledge and sampling protocols.
6. Strict adherence to the AWQC DNA sampling protocol is required to avoid contamination. It is recommended that five (5) 1L samples are taken according to the AWQC DNA sampling criteria. The size of the water body, habitat of the defined species, month and period of collection, water flow and other hydrological factors needs to be considered for the sampling and biodiversity estimations to be effective.

References

1. Altschul et al, 1990. Basic local alignment search tool.
2. Hardy et al, 2011, DNA barcoding to support conservation: species identification, genetic structure and biogeography of fishes in the Murray-Darling River Basin, Australia.
3. Kelly et al, 2014. Using Environmental DNA to census marine fishes in a large mesocosm.
4. Shaw et al, 2015 Ground-truthing environmental DNA.
5. Yang et al, 2014. Species identification through mitochondrial rRNA genetic analysis.