Whanganui River Catchment: eDNA Survey 2023–2024

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Prepared for Department of Conservation

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SCIENCE + ENGAGEMENT

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FOREWORD

This mahi represents the collective effort of many hands and hearts working together in accordance with Tupua te Kawa, the intrinsic values that express the essence of Te Awa Tupua as a living and indivisible whole.

The eDNA survey undertaken across the upper Whanganui catchment represents a collaboration between Ngāti Hāua Iwi Trust and the Department of Conservation's Ngā Awa Programme. Over two summer seasons, Te Rōpū Awa Kaitiaki worked alongside DOC Rangers Jane Taylor and Aroha Greenhalgh, and Technical Advisor Rosemary Miller, to collect eDNA samples and deepen understanding of the biodiversity and ecological health of Te Awa Tupua and its tributaries. This mahi embodies the value of working together – sharing expertise, relationships, and commitment – to enhance the mana and mouri of the river.

We extend our special acknowledgement to Te Rōpū Awa Kaitiaki – Mihikeita Tawhara, Maki Ngarongo, Arthur Tane, Nicole Taiaroa, and Kuru Ketu – whose diverse experience, deep connections across the rohe, and passion for the environment have driven this kaupapa forward. Their leadership and dedication have provided a strong foundation for the ongoing implementation of the wider taiao strategy for Ngāti Hāua.

The Ngāti Hāua Iwi Trust (NHIT), established in 2001, is responsible for advancing the interests of Ngāti Hāua iwi, hapū, and whānau within its customary rohe and beyond. Recognising the importance of caring for the awa and the taiao, NHIT established the Awa Kaitiaki Programme to actively implement its environmental strategy through kaitiakitanga, mātauranga, and partnership.

We also acknowledge the generosity of landowners who granted access to their properties, and the hapū and whānau at place who offered guidance, support, and hospitality during the survey. Your contributions and manaakitanga were vital to the success of this work.

This kaupapa aligns naturally with the intent of the Te Awa Tupua (Whanganui River Claims Settlement) Act 2017, which recognises Te Awa Tupua as a living and indivisible whole – comprising all its physical and metaphysical elements – and acknowledges the inalienable relationship of Whanganui iwi with the river. Through this joint effort, we take another step towards fulfilling our shared responsibilities as tāngata tiaki, enhancing both the wellbeing of Te Awa Tupua and the relationships that connect people to it.

Wehea te muka, he taura whati. Whiria kia mau, kia ita, he taura mau waka.
Separated flax strands create weak links. Bound tightly together, they can meet any challenge.

In this spirit of unity and collaboration, Ngāti Hāua Iwi Trust and the Department of Conservation (Ngā Awa Programme) acknowledge all those who have contributed to this mahi – ngā ringa raupā, ngā ngākau mahaki, ngā reo o te awa – whose collective efforts continue to uphold the wellbeing of Te Awa Tupua and the enduring relationship between people and the river.

Ngāti Hāua Iwi Trust

Department of Conservation
Te Papa Atawhai

1 INTRODUCTION

The Whanganui River originates on the western slopes of Mount Tongariro and Mount Ruapehu, in the Central Plateau of Te Ika-a-Māui/North Island, Aotearoa/New Zealand. The river flows more than 290 kilometres from its headwaters to the Tasman Sea at Whanganui. The entire Whanganui River catchment covers an area of 7,118 km^2 and includes several major subcatchments, such as the Ōngarue (1,100 km^2), Ōhura (780 km^2), Retaruke (466 km^2), Manganui o te Ao (643 km^2), Tāngarākau (624 km^2), and Whangamōmona (231 km^2) rivers (Figure 1).

A recent review of fisheries and aquatic biodiversity in the Whanganui River catchment highlighted several knowledge gaps (Dewson, 2021). While many fish and macroinvertebrate surveys have been carried out over the years, many are now more than 20 years old, and updated data is needed. The review recommended using environmental DNA (eDNA) techniques to refresh fish biodiversity knowledge, as this method is practical, cost-effective, and well suited to large and hard-to-access catchments like the Whanganui. Several rivers within the catchment were also flagged as priorities for targeted fish surveys – either because they represent nationally important ecosystem types or because they have never been surveyed (Dewson, 2021). For instance, the Tangarākau River, Kakahi Stream, and Ōngarue River were recommended because of a lack of previous fish data.

An additional benefit of using eDNA sampling to enhance knowledge of fish species within the Whanganui catchment is its capacity to detect a broad range of other taxa. This technique is not limited to fish, but also provides information on the presence of mammals, birds, invertebrates, and plants. The most recent comprehensive macroinvertebrate survey of the catchment was completed in 1998 (Horrox, 1998), and Dewson (2021) has recommended that a resurvey of these sites is now warranted. Although six State of the Environment monitoring sites within the catchment are sampled annually for macroinvertebrates, this limited spatial coverage does not provide a comprehensive understanding of biodiversity across such a large and diverse catchment. Therefore, the current eDNA survey contributes not only to updated knowledge of fish distributions but also offers a more current snapshot of macroinvertebrates and other species present at these sites, including those of conservation concern.

Figure 1 *…Map over page…* Overview map of the Whanganui River catchment, showing subcatchments and environmental DNA (eDNA) sampling sites (sampled by Department of Conservation between March 2023 and April 2024). Also shown are the locations of publicly available eDNA records that exist on the Wilderlab database as of May 2025.

eDNA sampling site (DOC)

- 4. Ōhura
- 18. Kakahi
- 22. Pungapunga
- 23. Ruatiti
- 24. Waimiha
- 28. Ōngarue
- 29. Taringamotu
- 34. Matarawa
- 35. Makirikiri
- 36. Whangamōmona
- 37. Te Maire
- 39. Kokakonui
- 51. Heao
- 59. Mangakara West
- 62. Morgans
- 63. Upper Retaruke

Subcatchment

1. Whanganui mainstem
2. Ōngarue
3. Ōhura
4. Pungapunga
5. Whanganui headwaters
6. Tāngarākau
7. Retaruke
8. Whakapapa
9. Whangamōmona
10. Manganui o te Ao
11. Upokongaro
12. Matarawa

Whanganui River & Subcatchments

eDNA Sampling Sites

▭ Whanganui catchment
▭ Subcatchment
— Waterways (stream order >2)

eDNA SAMPLING SITES:
● Wilderlab
☐ Department of Conservation

0 10 20 Kilometres

Map © EOS Ecology, 2025 / www.eosecology.co.nz

Layer source: Whanganui catchment (EOS Ecology, REC2 (NIWA)), Whanganui subcatchments: based on surface water management zones from Horizons Regional Council, waterways (REC2 (NIWA)), hill shade (8M DEM (LINZ)).

Image source: NZ Imagery Eagle Technology, LINZ

2 METHODS

2.1 Field Data Collection

As part of a catchment-wide baseline ecological health survey conducted by the Department of Conservation (DOC), eDNA samples were collected from sixteen sites within the Whanganui River catchment (Figure 1). Eight sites were sampled in March 2023, and the remaining eight between January and April 2024 (Table 1). These locations were previously surveyed for macroinvertebrates by Horrox (1998), as part of a catchment-wide macroinvertebrate survey. The sampled sites span elevations from 20 to 330 metres above sea level and are situated between 17 and 320 kilometres from the Whanganui River mouth (Table 1).

eDNA is a method that measures the presence of fish and other organisms by detecting traces of genetic material these leave in the environment. To sample eDNA, replicate water samples are typically filtered on site and returned to an eDNA laboratory for processing. This is called active sampling or syringe sampling, since a large plastic syringe is used to filter the river water through a specialised filter which collects the eDNA from the water. In this study, six replicate water samples were collected at each site, and active sampling was completed with syringe sampling kits supplied by Wilderlab and following Wilderlab sampling protocols (Wilderlab sampling instructions). Samples were preserved and transported to Wilderlab NZ Ltd. (Wellington) for analysis.

During eDNA sample collection, site locations were recorded using a handheld GPS, and photographs were taken at each site. Physico-chemical parameters were also measured, using a YSI ProDSS multiparameter water quality meter (YSI Inc., Yellow Springs, OH, USA). Measurements included temperature, pH, conductivity, specific conductivity, dissolved oxygen, and turbidity. Water clarity was assessed using a clarity tube and water velocity and discharge were also measured for each site. The date of last flow exceeding three times the median flow (FRE3) and the last major rainfall event were recorded for each sampling location to provide context for the results.

At each site, mesohabitat was visually assessed based on the proportion of different channel units (e.g., pools, riffles, runs) across the reach. Additional assessments included Wolman substrate size analysis and the Pfankuch streambed stability index. Ecological stream health was visually evaluated using the ‘Stream Health Check’ sheet developed by Dr Russell Death. Benthic macroinvertebrates were also sampled; however, those results are reported elsewhere. Spatial attributes for each site were derived from the New Zealand River Environment Classification (REC), which provides data on physical factors such as climate, topography, geology, land cover, network position, and valley landform. This information complemented the field-based measurements and assessments conducted at each site.

2.2 Laboratory Analysis

At the laboratory, each sample underwent multi-species DNA metabarcoding to detect fish, insects, birds, and mammals. Four samples were processed using the basic analysis package, which includes eight assays targeting fish, mammals, birds, reptiles, amphibians, and macroinvertebrates. Samples from the remaining 12 sites were analysed using the comprehensive package, which incorporates additional assays for detecting land and aquatic plants, algae, zooplankton, and microorganisms. This level of analysis also allows for the calculation of the riverine Taxon-Independent Community Index (TICI), a metric used to assess the ecological health of the sampled stream (Wilkinson *et al.,* 2024).

2.3 Data Analysis & Reporting

The sampling sites in this study were located within ten different subcatchments of the Whanganui River catchment (Figure 1). For the presentation of results, individual sites have been ordered by subcatchment, to make within and between subcatchment comparisons easier. Results are presented both as catchment-wide summary tables (Section 3.1) and as site-specific results (Section 3.2).

It is important to note that eDNA sampling does come with limitations. While eDNA results do indicate the presence of genetic material, they do not distinguish between living and dead organisms, and they may detect species that are present some distance upstream of the sampling location. The absence of a species in an eDNA sample does not confirm its true absence from a site and not all species have the same likelihood of detection. Similarly, it is not currently possible to determine the abundance of organisms present at a site based on eDNA sample results.

The eDNA species level results were used to collate a summary of fish diversity for all sites in the catchment, with the proportion of threatened or at-risk species identified for each site (Dunn *et al.*, 2018). Further, the TICI scores provided for the 12 sites analysed with the Wilderlab comprehensive analysis option were tabulated to allow between site comparisons. The TICI score is interpreted on a scale from <80 to >120 in the following categories: very poor (<80); poor (80–90); average (90–100); good (100–110); excellent (110–120); pristine (>120).

The eDNA species level results were also used to list the bird, mammal, and fish species present at each site. The threat classifications of the New Zealand Threat Classification system (NZTCS) (Dunn *et al.*, 2018; Grainger *et al.*, 2018; Robertson *et al.*, 2021; O'Donnell *et al.*, 2022) were used to identify and list species of conservation concern. Invertebrate eDNA data was filtered to examine freshwater species in more detail and to classify these by Order. Using this data, the number of Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies) (EPT) taxa were counted and tabulated for each site. EPT refers to three Orders of invertebrates that are generally regarded as clean water taxa. EPT taxa are generally more diverse in non-impacted stream systems, although there is a small set of EPT taxa able to persist in degraded waterways. While not directly comparable to EPT metrics that are typically calculated from traditional macroinvertebrate sampling methods, the eDNA EPT count is suitable for comparisons between sites in this study.

Further to the eDNA data collected as part of this study, the publicly available data from the Wilderlab database was downloaded and added to the fish diversity map (Figure 2) to provide a more comprehensive overview of current knowledge.

Many of New Zealand's native fish species are migratory, meaning that they need to move both upstream and downstream within catchments to complete their life cycle. Many of the native fish species found in the Whanganui catchment are migratory, including longfin and shortfin eel, common and redfin bully, shortjaw and banded kōkopu, īnanga, piharau, and torrentfish. For these species, unimpeded passage upstream and downstream is crucial to their distribution in the catchment. Barriers to fish passage are known to limit fish migration, especially for species that have poorer swimming or climbing ability. The Fish Passage Assessment Tool (FPAT; https://fishpassage.niwa.co.nz) provides an online resource for recording the nature of instream structures and the likely impact of these structures on fish passage. The instream structures recorded in the FPAT for the Whanganui catchment have been summarised and mapped to facilitate further prioritisation for remediation and to highlight those fish barriers that are known to be protecting native species.

3 RESULTS

3.1 Catchment Overview

The physicochemical characteristics of the 16 sites where eDNA samples were collected were measured at the time of sampling (Table 1). All sites were sampled during the summer and early autumn, with water temperatures ranging from 12°C to 22°C. Conductivity varied widely across sites, from as low as 58 µS/cm at the Ōngarue site to as high as 540 µS/cm at the Matarawa site, which may be subject to tidal influence. pH levels across all sites were circumneutral to slightly alkaline, with recorded values ranging from 7.2 to 7.9. Water clarity was generally measured between 0.69 and 0.87 metres, although one site exhibited clarity exceeding 1 metre.

Table 1 Physicochemical characteristics of the sixteen sites in the Whanganui River catchment sampled for eDNA between March 2023 & April 2024. NA indicates that no measurements were collected for that site.

Site Subcatchment	Sampling Date	Site Number	Physicochemical Characteristics			
			Temperature °C	Conductivity µS/cm	pH	Clarity m
Pungapunga (Whanganui headwaters)	3 March 2023	22	14.3	113	7.7	0.80
Ōngarue (Ōngarue)	14 February 2024	28	12.0	58	7.2	>1.00
Waimiha (Ōngarue)	13 April 2024	24	14.0	69	7.3	0.76
Taringamotu (Ōngarue)	24 March 2023	29	16.6	81	7.7	0.78
Ōhura (Ōhura)	22 February 2024	4	17.1	184	7.4	0.75
Mangakara West (Ōhura)	7 March 2023	59	14.6	73	7.5	0.87
Kakahi (Whanganui mainstem)	4 April 2024	18	12.5	123	7.6	0.82
Te Maire (Whanganui mainstem)	2 March 2023	37	17.8	330	7.9	0.75
Kokakonui (Whanganui mainstem)	8 March 2023	39	15.1	279	7.8	0.85
Heao (Tāngarākau)	2 March 2023	51	16.5	116	7.2	0.80
Morgans (Tāngarākau)	1 March 2023	62	14.1	101	7.6	0.75
Upper Retaruke (Retaruke)	28 March 2023	63	15.3	116	NA	0.80
Whangamōmona (Whangamōmona)	8 January 2024	36	NA	NA	NA	NA
Ruatiti (Manganui o te Ao)	29 February 2024	23	16.2	117	7.5	0.79
Makirikiri (Ūpokongaro)	26 January 2024	35	14.4	NA	NA	0.69
Matarawa (Matarawa)	19 January 2024	34	22.3	540	NA	0.78

The taxon independent community index (TICI) is an index score developed by Wilderlab to provide an assessment of the ecological health of river sites, based on the sequences detected in freshwater samples (Wilkinson *et al.,* 2024). The TICI is included with the report on all comprehensive freshwater assay panels completed by Wilderlab. For the current sampling, comprehensive analysis was undertaken for samples from 12 sites in the Whanganui River catchment. The remaining four sites had basic analysis completed and thus they do not have a TICI score. The TICI scores varied widely across the catchment, from an average of 89 at the Whangamōmona and Heao sites to an average of 119 at the Morgans site in the Tāngarākau subcatchment (Table 2). In general, the sites in the headwaters of each subcatchment received higher TICI scores than those in the mainstem, indicating that there is a decline in ecological health down the catchment. The contrasting TICI scores recorded for the two sites in the Tāngarākau subcatchment – excellent-pristine for the Morgans site compared to poor-average for the Heao site – suggests that the two major tributaries in this subcatchment are experiencing different levels of stress. A count of EPT taxa detected in eDNA samples shows a similar pattern, with the number of EPT taxa detected ranging from seven at the Matarawa site in the lower catchment, to 39 at the Ōngarue site in the upper catchment.

Table 2 Taxon independent community index (TICI) values for the 12 sites in the Whanganui River catchment which were sampled for eDNA between March 2023 & April 2024 and analysed using Wilderlab's comprehensive analysis option, which includes calculation of the TICI. Sites where eDNA samples were analysed using basic analysis have no TICI values calculated and are denoted by NA. The TICI score is interpreted on a scale from <80 to >120 in the following categories: very poor (<80); poor (80–90); average (90–100); good (100–110); excellent (110–120); pristine (>120). Also included are counts of species from the Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) Orders, known as EPT taxa.

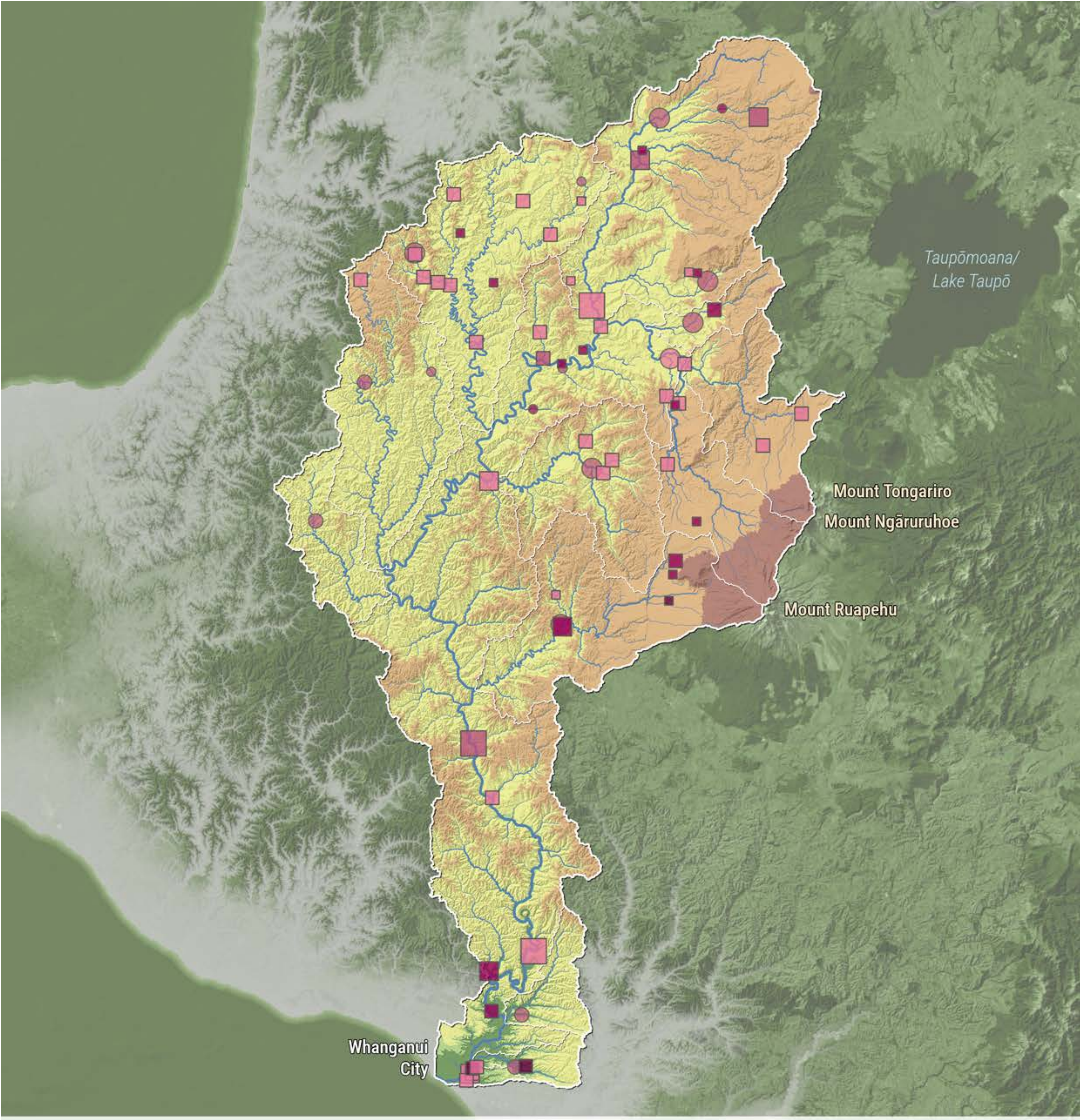
Site Subcatchment	Site Number	Taxon Independent Community Index (TICI) Scores			Count of EPT Taxa Recorded in eDNA
		Score Mean	Rating Range	Reliability Range	
Pungapunga (Whanganui headwaters)	22	110	Good–Excellent	Very high	24
Ōngarue (Ōngarue)	28	NA	NA	NA	39
Waimiha (Ōngarue)	24	NA	NA	NA	33
Taringamotu (Ōngarue)	29	112	Excellent	High–Very high	26
Ōhura (Ōhura)	4	91	Average	Very high	18
Mangakara West (Ōhura)	59	113	Good–Excellent	Very high	28
Kakahi (Whanganui mainstem)	18	102	Good	Very high	26
Te Maire (Whanganui mainstem)	37	91	Average	Very high	17
Kokakonui (Whanganui mainstem)	39	97	Average	Very high	20
Heao (Tāngarākau)	51	89	Poor–Average	High–Very high	17
Morgans (Tāngarākau)	62	119	Excellent–Pristine	High–Very high	21
Upper Retaruke (Retaruke)	63	110	Good–Excellent	Very high	30
Whangamōmona (Whangamōmona)	36	89	Poor–Average	Average–High	14
Ruatiti (Manganui o te Ao)	23	100	Average–Good	Very high	22
Makirikiri (Ūpokongaro)	35	NA	NA	NA	11
Matarawa (Matarawa)	34	NA	NA	NA	7

The number of fish species detected at each site ranged from ten species at the Ruatiti site to two species at the Ōngarue and Kokakonui sites (Table 3). The very high fish diversity at the Ruatiti site included four species with threatened or at-risk conservation status, and eight diadromous species. A look at the fish diversity recorded in publicly available eDNA samples from this catchment shows that there are hotspots of fish diversity throughout the mainstem and in the upper catchment, with several sites in the Ōngarue subcatchment showing especially high diversity (Figure 2). Making use of this data from Wilderlab introduces information from 53 additional eDNA sampling sites, significantly expanding the spatial coverage of the catchment. The eDNA results from the current study build on this existing dataset and align well with previously recorded patterns of fish diversity in the catchment (Figure 2).

Table 3 Summary of fish species results from eDNA sampling at 16 sites in the Whanganui River catchment, sampled by Department of Conservation between March 2023 & April 2024. The number of species detected, number of threatened or at-risk species (based on the New Zealand Threat Classification system (NZTCS); Dunn *et al.*, 2018), and the number of diadromous species are shown for each eDNA sampling site.

Site Subcatchment	Site Number	Summary of Fish Species Results from eDNA Sampling		
		Number of Species	Number of Threatened/At-risk Species	Number of Diadromous Species
Pungapunga (Whanganui headwaters)	22	8	2	5
Ōngarue (Ōngarue)	28	2	1	1
Waimiha (Ōngarue)	24	6	2	4
Taringamotu (Ōngarue)	29	8	2	5
Ōhura (Ōhura)	4	3	1	3
Mangakara West (Ōhura)	59	7	2	5
Kakahi (Whanganui mainstem)	18	6	1	3
Te Maire (Whanganui mainstem)	37	3	1	3
Kokakonui (Whanganui mainstem)	39	2	1	2
Heao (Tāngarākau)	51	3	1	3
Morgans (Tāngarākau)	62	4	1	2
Upper Retaruke (Retaruke)	63	7	3	5
Whangamōmona (Whangamōmona)	36	5	2	5
Ruatiti (Manganui o te Ao)	23	10	4	8
Makirikiri (Ūpokongaro)	35	4	1	4
Matarawa (Matarawa)	34	5	2	5

Figure 2 *…Map over page…* Map of the Whanganui River catchment, showing fish diversity and the proportion of threatened or at-risk fish species recorded in environmental DNA (eDNA) sampling completed by Department of Conservation between March 2023 and April 2024, as well as for publicly available eDNA records that exist on the Wilderlab database as of May 2025.



Whanganui River & Subcatchments

Fish Diversity (Wilderlab & the Department of Conservation)

▭ Whanganui catchment
▭ Subcatchment
— Waterways (stream order >2)

ELEVATION BANDS: (m ASL)

- 🟩 Very low (<60)
- 🟩 Low (60–100)
- 🟨 Moderately low (100–400)
- 🟧 Hill (400–1,000)
- 🟫 Mountain (>1,000)

THREATENED SPECIES:

<25% | 25–50% | 50–75% | >75%

SPECIES DIVERSITY:

Wilderlab		Department of Conservation	
□	>10	○	>10
□	6–10	○	6–10
□	1–5	○	1–5
□	0	○	0

0 10 20 Kilometres

N

Map © EOS Ecology, 2025 / www.eosecology.co.nz

Layer source: Whanganui catchment and waterways (EOS Ecology, REC2 (NIWA)), % threatened species and fish diversity (EOS Ecology based on New Zealand Freshwater Fish Database (NZFFD) and Wilderlab DiscoverDNA database), elevation bands (EOS Ecology based on NZ topographic contour layer, LAND Information New Zealand (LINZ), hill shade (8M DEM (LINZ)).

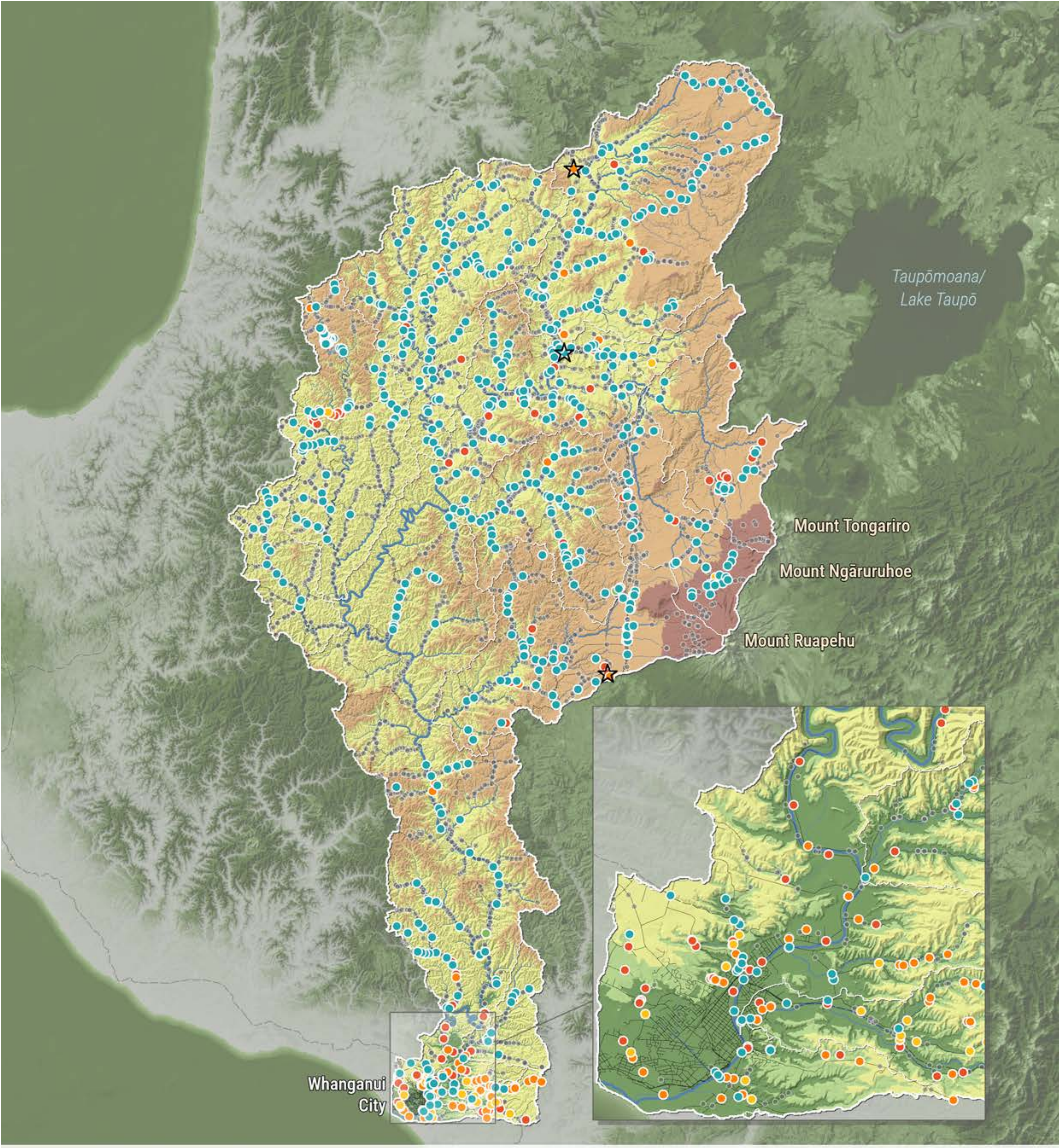
Image source: NZ Imagery Eagle Technology, LINZ

The Fish Passage Assessment Tool (FPAT; https://fishpassage.niwa.co.nz) provides an online tool for recording the nature of instream structures and the likely impact of these structures on fish passage. The FPAT records that there are at least 4750 structures with the potential to be a barrier to fish passage within the Whanganui catchment (Table 4; Figure 4). Many of these will be artificial structures, such as culverts, dams, fords, or weirs. However, natural barriers like waterfalls are also included in the FPAT records, with 162 of these recorded for the Whanganui catchment. Most of the potential barriers recorded in the FPAT have not been assessed regarding their actual risk to fish passage, but of the 978 that have been assessed, there are 224 that are rated as having a high or very high risk to fish passage (Table 4, Figure 3). Around 65% of the potential fish barriers in the catchment are located within the moderately low elevation band, which represents land at elevations of between 100–400 metres above sea level (Figure 3). However, the highest proportion of high and very high-risk barriers are located at very low elevations, where the largest diversity of migratory fish is also present (Table 4). Three barriers in the catchment are recorded in the FPAT as having a function for protecting threatened non-migratory endemic fish species.

Table 4 Summary of fish passage barrier assessments for the Whanganui catchment by elevation band. Risk categories are as recorded in the Fish Passage Assessment Tool (FPAT; https://fishpassage.niwa.co.nz) as of May 2025.

Elevation Metres Above Sea Level m ASL	Number of FPAT Records in Each Risk Category			
	High/Very High Risk	Moderate Risk	Low/Very Low Risk	Not Assessed
Mountain (>1000)	1	1	15	100
Hill (400–1000)	27	2	162	706
Moderately Low (100–400)	74	2	485	2,529
Low (60–100)	23	3	18	140
Very Low (<60)	99	17	49	297
OVERALL	**224**	**25**	**729**	**3,772**

Figure 3 *…Map over page…* Location of fish barriers within the Whanganui River catchment that are recorded on the New Zealand Fish Passage Assessment Tool (FPAT) as of June 2025. Elevation bands are also shown to provide a visual representation of the height above sea level for the land within the catchment.



Whanganui River & Subcatchments

Fish Passage

- ▭ Whanganui catchment
- ▭ Subcatchment
- - - - Railways
- — Roads
- ☆ Barriers protecting native fish

ELEVATION BANDS: (m ASL)

- 🟩 Very low (<60)
- 🟩 Low (60–100)
- 🟨 Moderately low (100–400)
- 🟧 Hill (400–1,000)
- 🟫 Mountain (>1,000)

FISH PASSAGE RISK:

Using Fish Passage Tool (FPAT) interpretation bands

- ● Very low
- ● Low
- ● Moderate
- ● High
- ● Very high
- ● Not assessed

0 10 20 Kilometres

N

Map © EOS Ecology, 2025 / www.eosecology.co.nz

Layer source: Whanganui catchment and waterways (EOS Ecology, REC2 (NIWA)), Risk to fish passage and barrier protecting native fish (EOS Ecology based on New Zealand Freshwater Fish Database (NZFFD) data), elevation bands (EOS Ecology based on NZ topographic contour layer, LAND Information New Zealand (LINZ), hill shade (8M DEM (LINZ)).

Image source: NZ Imagery Eagle Technology, LINZ

3.2 Site 22 eDNA Results – Pungapunga (Whanganui Headwaters Subcatchment)

The Pungapunga sampling site within the Whanganui headwaters subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 5). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 6), invertebrates (Table 7), and fish (Table 8) detected as sequences in the eDNA samples from this site.

For the Pungapunga site in the Whanganui headwaters subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Torrentfish – *Cheimarrichthys fosteri* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 5 **eDNA methods, site characteristics, and site photo for the Pungapunga site (site 22) in the Whanganui headwaters subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	3/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	14.3	
Conductivity (µS/cm)	113	
pH	7.7	
Clarity (m)	0.8	

Table 6 List of birds and mammals detected in eDNA samples from the Pungapunga site in the Whanganui headwaters subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Greylag goose/Kuihi (*Anser anser*)	Cattle (*Bos taurus*)
Pūkeko (*Porphyrio melanotus*)	Norway rat (*Rattus norvegicus*)
Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Pig (*Sus scrofa*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	Sheep (*Ovis aries*)
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Red deer (*Cervus elaphus*)
Silvereye/Tauhou (*Zosterops lateralis*)	Domestic water buffalo (*Bubalus bubalis*)
Fantail/Pīwakawaka (*Rhipidura fuliginosa*)	Goat (*Capra hircus*)
Black shag/Māpunga (*Phalacrocorax carbo*)	Black rat (*Rattus rattus*)
Australian magpie/Makipai (*Gymnorhina tibicen*)	House mouse (*Mus musculus*)

Table 7 Summary of freshwater invertebrate species detected in eDNA samples from the Pungapunga site in the Whanganui headwaters subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm the absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
6	1	17	Not detected	Present

Table 8 Fish detected in eDNA samples collected from the Pungapunga site (site 22) in the Whanganui headwaters subcatchment on 3 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Kaharore bully/toitoi	*Gobiomorphus mataraerore*	Not Threatened	Non-diadromous	
Redfin bully/toitoi	*Gobiomorphus huttoni*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Brown trout	*Salmo trutta*	Introduced & Naturalised	Anadromous-capable	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Torrentfish/panoko, panokonoko, panuku, papanoko	*Cheimarrichthys fosteri*	At Risk–Declining	Diadromous	

3.3 Site 28 eDNA Results – Ōngarue (Ōngarue Subcatchment)

The Ōngarue sampling site within the Ōngarue subcatchment was sampled during February 2024 using six replicate eDNA sampling kits (Table 9). Basic eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 10), invertebrates (Table 11), and fish (Table 12) detected as sequences in the eDNA samples from this site.

For the Ōngarue sampling site within the Ōngarue subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Blue duck/whio – *Hymenolaimus malacorhynchos* – Threatened–Nationally Vulnerable
- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon
- Mayfly – *Mauiulus aquilus* – At Risk–Naturally Uncommon

Table 9 eDNA methods, site characteristics, and site photo for the Ōngarue site (site 28) in the Ōngarue subcatchment.
Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	3/3/2023	
eDNA analysis type	Basic	
Number of replicates	6	
Temperature (°C)	12.0	
Conductivity (µS/cm)	57.9	
pH	7.2	
Clarity (m)	>1.0	

Table 10 List of birds and mammals detected in eDNA samples from the Ōngarue site in the Ōngarue subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Blue duck/whio (*Hymenolaimus malacorhynchos*)	Cattle (*Bos taurus*)
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Red deer (*Cervus elaphus*)
Little shag/Kawaupaka (*Microcarbo melanoleucos*)	Common brushtail possum (*Trichosurus vulpecula*)
Silvereye/Tauhou (*Zosterops lateralis*)	Black rat (*Rattus rattus*)
New Zealand pigeon/Kererū (*Hemiphaga novaeseelandiae*)	European rabbit (*Oryctolagus cuniculus*)
Bellbird/Korimako (*Anthornis melanura*)	Norway rat (*Rattus norvegicus*)
Fantail/Pīwakawaka (*Rhipidura fuliginosa*)	Sheep (*Ovis aries*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	European hedgehog (*Erinaceus europaeus*)
Blackbird/Manu pango (*Turdus merula*)	
Common starling/Tāringi (*Sturnus vulgaris*)	
Tūī (*Prosthemadera novaeseelandiae*)	

Table 11 Summary of freshwater invertebrate species detected in eDNA samples from the Ōngarue site in the Ōngarue subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
10	5	24	Not detected	Present

Table 12 Fish detected in eDNA samples collected from the Ōngarue site (site 28) in the Ōngarue subcatchment on 4 February 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	

3.4 Site 24 eDNA Results – Waimiha (Ōngarue Subcatchment)

The Waimiha sampling site within the Ōngarue subcatchment was sampled during April 2024 using six replicate eDNA sampling kits (Table 13). Basic eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 14), invertebrates (Table 15), and fish (Table 16) detected as sequences in the eDNA samples from this site.

For the Waimiha sampling site within the Ōngarue subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Blue duck/whio – *Hymenolaimus malacorhynchos* – Threatened–Nationally Vulnerable
- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Torrentfish – *Cheimarrichthys fosteri* – At Risk–Declining
- Freshwater mussel/Kākahi –*Echyridella menziesi* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon
- Mayfly – *Mauiulus aquilus* – At Risk–Naturally Uncommon
- Mayfly – *Zephlebia tuberculata* – At Risk–Naturally Uncommon

Table 13 eDNA methods, site characteristics, and site photo for the Waimiha site (site 24) in the Ōngarue subcatchment. Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	13/4/2024	
eDNA analysis type	Basic	
Number of replicates	Six	
Temperature (°C)	14.0	
Conductivity (µS/cm)	69.3	
pH	7.3	
Clarity (m)	0.76	

Table 14 List of birds and mammals detected in eDNA samples from the Waimiha site in the Ōngarue subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Cattle (*Bos taurus*)
Black shag/Māpunga (*Phalacrocorax carbo*)	Sheep (*Ovis aries*)
Little shag/Kawaupaka (*Microcarbo melanoleucos*)	Common brushtail possum (*Trichosurus vulpecula*)
Silvereye/Tauhou (*Zosterops lateralis*)	House mouse (*Mus musculus*)
Common starling/Tāringi (*Sturnus vulgaris*)	Norway rat (*Rattus norvegicus*)
Pūkeko (*Porphyrio melanotus*)	Black rat (*Rattus rattus*)
Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Goat (*Capra hircus*)
Blue duck/whio (*Hymenolaimus malacorhynchos*)	European hedgehog (*Erinaceus europaeus*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	
House sparrow/Tiu (*Passer domesticus*)	
Welcome swallow/Warou (*Hirundo neoxena*)	
Blackbird/Manu pango (*Turdus merula*)	

Table 15 Summary of freshwater invertebrate species detected in eDNA samples from the Waimiha site in the Ōngarue subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura.
Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	2	23	Present	Present

Table 16 Fish detected in eDNA samples collected from the Waimiha site (site 24) in the Ōngarue subcatchment on 13 April 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	
Brown trout	*Salmo trutta*	Introduced & Naturalised	Anadromous-capable	
Torrentfish/panoko, panokonoko, panuku, papanoko	*Cheimarrichthys fosteri*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	

3.5 Site 29 eDNA Results – Taringamotu (Ōngarue Subcatchment)

The Taringamotu sampling site within the Ōngarue subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 17). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 18), invertebrates (Table 19), and fish (Table 20) detected as sequences in the eDNA samples from this site.

For the Taringamotu sampling site within the Ōngarue subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

» Blue duck/whio – *Hymenolaimus malacorhynchos* – Threatened–Nationally Vulnerable

» Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining

» Torrentfish – *Cheimarrichthys fosteri* – At Risk–Declining

» Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 17 **eDNA methods, site characteristics, and site photo for the Taringamotu site (site 29) in the Ōngarue subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	24/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	16.6	
Conductivity (µS/cm)	81.0	
pH	7.7	
Clarity (m)	0.78	

Table 18 List of birds and mammals detected in eDNA samples from the Taringamotu site in the Ōngarue subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	**Mammal**
Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Red deer (*Cervus elaphus*)
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Pig (*Sus scrofa*)
Silvereye/Tauhou (*Zosterops lateralis*)	Cattle (*Bos taurus*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	Norway rat (*Rattus norvegicus*)
Blue duck/whio (*Hymenolaimus malacorhynchos*)	Goat (*Capra hircus*)
Black shag/Māpunga (*Phalacrocorax carbo*)	Black rat (*Rattus rattus*)
House sparrow/Tiu (*Passer domesticus*)	Sheep (*Ovis aries*)
White-faced heron/Matuku moana (*Egretta novaehollandiae*)	

Table 19 Summary of freshwater invertebrate species detected in eDNA samples from the Taringamotu site in the Ōngarue subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
7	4	15	Not detected	Present

Table 20 Fish detected in eDNA samples collected from the Taringamotu site (site 29) in the Ōngarue subcatchment on 24 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Kaharore bully/toitoi	*Gobiomorphus mataraerore*	Not Threatened	Non-diadromous	
Brown trout	*Salmo trutta*	Introduced & Naturalised	Anadromous-capable	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	
Torrentfish/panoko, panokonoko, panuku, papanoko	*Cheimarrichthys fosteri*	At Risk–Declining	Diadromous	
Redfin bully/toitoi	*Gobiomorphus huttoni*	Not Threatened	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	

3.6 Site 4 eDNA Results – Ōhura (Ōhura Subcatchment)

The Ōhura sampling site within the Ōhura subcatchment was sampled during February 2024 using six replicate eDNA sampling kits (Table 21). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 22), invertebrates (Table 23), and fish (Table 24) detected as sequences in the eDNA samples from this site.

For the Ōhura site in the Ōhura subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- New Zealand long-tailed bat – *Chalinolobus tuberculatus* – Threatened–Nationally Critical
- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Freshwater mussel/Kākahi –*Echyridella menziesi* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon
- Mayfly – *Zephlebia tuberculatus* – At Risk–Naturally Uncommon

Table 21 eDNA methods, site characteristics, and site photo for the Ōhura site (site 4) in the Ōhura subcatchment.
Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	22/2/2024	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	17.1	
Conductivity (µS/cm)	184	
pH	7.4	
Clarity (m)	0.75	

Table 22 List of birds and mammals detected in eDNA samples from the Ōhura site in the Ōhura subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Cattle (*Bos taurus*)
Little shag/Kawaupaka (*Microcarbo melanoleucos*)	Norway rat (*Rattus norvegicus*)
Yellowhammer/Hurukōwhai (*Emberiza citrinella*)	Goat (*Capra hircus*)
Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Common brushtail possum (*Trichosurus vulpecula*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	Sheep (*Ovis aries*)
Dunnock (*Prunella modularis*)	Brown hare (*Lepus europaeus*)
Welcome swallow/Warou (*Hirundo neoxena*)	Red deer (*Cervus elaphus*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	European hedgehog (*Erinaceus europaeus*)
Tūī (*Prosthemadera novaeseelandiae*)	House mouse (*Mus musculus*)
New Zealand pigeon/Kererū (*Hemiphaga novaeseelandiae*)	Black rat (*Rattus rattus*)
European goldfinch/Kōurarini (*Carduelis carduelis*)	New Zealand long-tailed bat (*Chalinolobus tuberculatus*)

Table 23 Summary of freshwater invertebrate species detected in eDNA samples from the Ōhura site in the Ōhura subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	1	9	Present	Present

Table 24 Fish detected in eDNA samples collected from the Ōhura site (site 4) in the Ōhura subcatchment on 22 February 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	

3.7 Site 59 eDNA Results – Mangakara West (Ōhura Subcatchment)

The Mangakara West sampling site within the Ōhura subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 25). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 26), invertebrates (Table 27), and fish (Table 28) detected as sequences in the eDNA samples from this site.

For the Mangakara West site in the Ōhura subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

» Blue duck/whio – *Hymenolaimus malacorhynchos* – Threatened–Nationally Vulnerable

» Shortjaw kōkopu – *Galaxias postvectis* – Threatened–Nationally Vulnerable

» Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining

» Mayfly – *Mauiulus aquilus* – At Risk–Naturally Uncommon

» Caddisfly – *Ecnomina zealandica* – At Risk–Naturally Uncommon

Table 25 **eDNA methods, site characteristics, and site photo for the Mangakara West site (site 59) in the Ōhura subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	7/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	14.6	
Conductivity (µS/cm)	73	
pH	7.5	
Clarity (m)	0.87	

Table 26 List of birds and mammals detected in eDNA samples from the Mangakara West site in the Ōhura subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Tūī (*Prosthemadera novaeseelandiae*) Black shag/Māpunga (*Phalacrocorax carbo*) Silvereye/Tauhou (*Zosterops lateralis*) Blue duck/whio (*Hymenolaimus malacorhynchos*)	Goat (*Capra hircus*) Red deer (*Cervus elaphus*) Sheep (*Ovis aries*) Black rat (*Rattus rattus*) European rabbit (*Oryctolagus cuniculus*) Common brushtail possum (*Trichosurus vulpecula*) Pig (*Sus scrofa*) Norway rat (*Rattus norvegicus*) Cattle (*Bos taurus*)

Table 27 Summary of freshwater invertebrate species detected in eDNA samples from the Mangakara West site in the Ōhura subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
10	0	18	Not detected	Present

Table 28 Fish detected in eDNA samples collected from the Mangakara West site (site 59) in the Ōhura subcatchment on 7 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Kaharore bully/toitoi	*Gobiomorphus mataraerore*	Not Threatened	Non-diadromous	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Redfin bully/toitoi	*Gobiomorphus huttoni*	Not Threatened	Diadromous	
Shortjaw kōkopu	*Galaxias postvectis*	Threatened–Nationally Vulnerable	Diadromous	

3.8 Site 18 eDNA Results – Kakahi (Whanganui Mainstem Subcatchment)

The Kakahi sampling site within the Whanganui mainstem subcatchment was sampled during April 2024 using six replicate eDNA sampling kits (Table 29). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 30), invertebrates (Table 31), and fish (Table 32) detected as sequences in the eDNA samples from this site.

For the Kakahi site in the Whanganui mainstem subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

» Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining

» Freshwater mussel/Kākahi –*Echyridella menziesi* – At Risk–Declining

» Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 29 eDNA methods, site characteristics, and site photo for the Kakahi site (site 18) in the Whanganui mainstem subcatchment. Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	4/4/2024	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	12.5	
Conductivity (µS/cm)	123	
pH	7.6	
Clarity (m)	0.82	

Table 30 List of birds and mammals detected in eDNA samples from the Kakahi site in the Whanganui mainstem subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Norway rat (*Rattus norvegicus*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	Cattle (*Bos taurus*)
Common starling/Tāringi (*Sturnus vulgaris*)	Common brushtail possum (*Trichosurus vulpecula*)
Silvereye/Tauhou (*Zosterops lateralis*)	Fallow deer (*Dama dama*)
Pūkeko (*Porphyrio melanotus*)	Black rat (*Rattus rattus*)
New Zealand pigeon/Kererū (*Hemiphaga novaeseelandiae*)	Red deer (*Cervus elaphus*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	Sheep (*Ovis aries*)
Blackbird/Manu pango (*Turdus merula*)	House mouse (*Mus musculus*)
Fantail/Pīwakawaka (*Rhipidura fuliginosa*)	

Table 31 Summary of freshwater invertebrate species detected in eDNA samples from the Kakahi site in the Whanganui mainstem subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
4	1	21	Present	Present

Table 32 Fish detected in eDNA samples collected from the Kakahi site (site 18) in the Whanganui mainstem subcatchment on 4 April 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Brown trout	*Salmo trutta*	Introduced & Naturalised	Anadromous-capable	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Black carp	*Mylopharyngodon piceus*	Not know to be in New Zealand – potential sample contamination – widely cultivated for food and medicine in Asia		

3.9 Site 37 eDNA Results – Te Maire (Whanganui Mainstem Subcatchment)

The Te Maire sampling site within the Whanganui mainstem subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 33). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 34), invertebrates (Table 35), and fish (Table 36) detected as sequences in the eDNA samples from this site.

For the Te Maire site in the Whanganui mainstem subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 33 **eDNA methods, site characteristics, and site photo for the Te Maire site (site 37) in the Whanganui mainstem subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	2/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	17.8	
Conductivity (µS/cm)	330	
pH	7.9	
Clarity (m)	0.75	

Table 34 List of birds and mammals detected in eDNA samples from the Te Maire site in the Whanganui mainstem subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*) Pūkeko (*Porphyrio melanotus*) Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Cattle (*Bos taurus*) Norway rat (*Rattus norvegicus*) Pig (*Sus scrofa*) Sheep (*Ovis aries*) Common brushtail possum (*Trichosurus vulpecula*) Black rat (*Rattus rattus*) Fallow deer (*Dama dama*)

Table 35 Summary of freshwater invertebrate species detected in eDNA samples from the Te Maire site in the Whanganui mainstem subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
7	0	10	Not detected	Present

Table 36 Fish detected in eDNA samples collected from the Te Maire site (site 37) in the Whanganui mainstem subcatchment on 2 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	

3.10 Site 39 eDNA Results – Kokakonui (Whanganui Mainstem Subcatchment)

The Kokakonui sampling site within the Whanganui mainstem subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 37). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 38), invertebrates (Table 39), and fish (Table 40) detected as sequences in the eDNA samples from this site.

For the Kokakonui site in the Whanganui mainstem subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 37 **eDNA methods, site characteristics, and site photo for the Kokakonui site (site 39) in the Whanganui mainstem subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	8/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	15.1	
Conductivity (µS/cm)	279	
pH	7.8	
Clarity (m)	0.85	

Table 38 List of birds and mammals detected in eDNA samples from the Kokakonui site in the Whanganui mainstem subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*) Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*) Pūkeko (*Porphyrio melanotus*) California quail/Tikaokao (*Callipepla californica*) Common chaffinch/Pahirini (*Fringilla coelebs*)	Cattle (*Bos taurus*) Norway rat (*Rattus norvegicus*) Sheep (*Ovis aries*) Common brushtail possum (*Trichosurus vulpecula*) Black rat (*Rattus rattus*)

Table 39 Summary of freshwater invertebrate species detected in eDNA samples from the Kokakonui site in the Whanganui mainstem subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	0	12	Not detected	Not detected

Table 40 Fish detected in eDNA samples collected from the Kokakonui site (site 39) in the Whanganui mainstem subcatchment on 8 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	

3.11 Site 51 eDNA Results – Heao (Tāngarākau Subcatchment)

The Heao sampling site within the Tāngarākau subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 41). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 42), invertebrates (Table 43), and fish (Table 44) detected as sequences in the eDNA samples from this site.

For the Heao site in the Tāngarākau subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

» New Zealand long-tailed bat – *Chalinolobus tuberculatus* – Threatened–Nationally Critical
» Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
» Freshwater mussel/Kākahi –*Echyridella menziesi* – At Risk–Declining
» Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon
» Mayfly – *Zephlebia tuberculata* – At Risk–Naturally Uncommon
» Freshwater snail – *Sororipyrgus raki* – At Risk–Naturally Uncommon

Table 41 eDNA methods, site characteristics, and site photo for the Heao site (site 51) in the Tāngarākau subcatchment.
Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	2/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	16.5	
Conductivity (µS/cm)	116	
pH	7.2	
Clarity (m)	0.80	

Table 42 List of birds and mammals detected in eDNA samples from the Heao site in the Tāngarākau subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	**Mammal**
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Cattle (*Bos taurus*)
Black shag/Māpunga (*Phalacrocorax carbo*)	Sheep (*Ovis aries*)
Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Norway rat (*Rattus norvegicus*)
Pūkeko (*Porphyrio melanotus*)	Common brushtail possum (*Trichosurus vulpecula*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	New Zealand long-tailed bat (*Chalinolobus tuberculatus*)
Wild turkey/Korukoru (*Meleagris gallopavo*)	Pig (*Sus scrofa*)
	Black rat (*Rattus rattus*)

Table 43 Summary of freshwater invertebrate species detected in eDNA samples from the Heao site in the Tāngarākau subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	0	9	Present	Present

Table 44 Fish detected in eDNA samples collected from the Heao site (site 51) in the Tāngarākau subcatchment on 2 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	

3.12 Site 62 eDNA Results – Morgans (Tāngarākau Subcatchment)

The Morgans sampling site within the Tāngarākau subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 45). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 46), invertebrates (Table 47), and fish (Table 48) detected as sequences in the eDNA samples from this site.

For the Morgans site in the Tāngarākau subcatchment, eDNA has detected the presence of one species that has a threat status in the New Zealand Threat Classifications System (NZTCS):

» Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining

Table 45 **eDNA methods, site characteristics, and site photo for the Morgans site (site 62) in the Tāngarākau subcatchment.** Photo by Department of Conservation

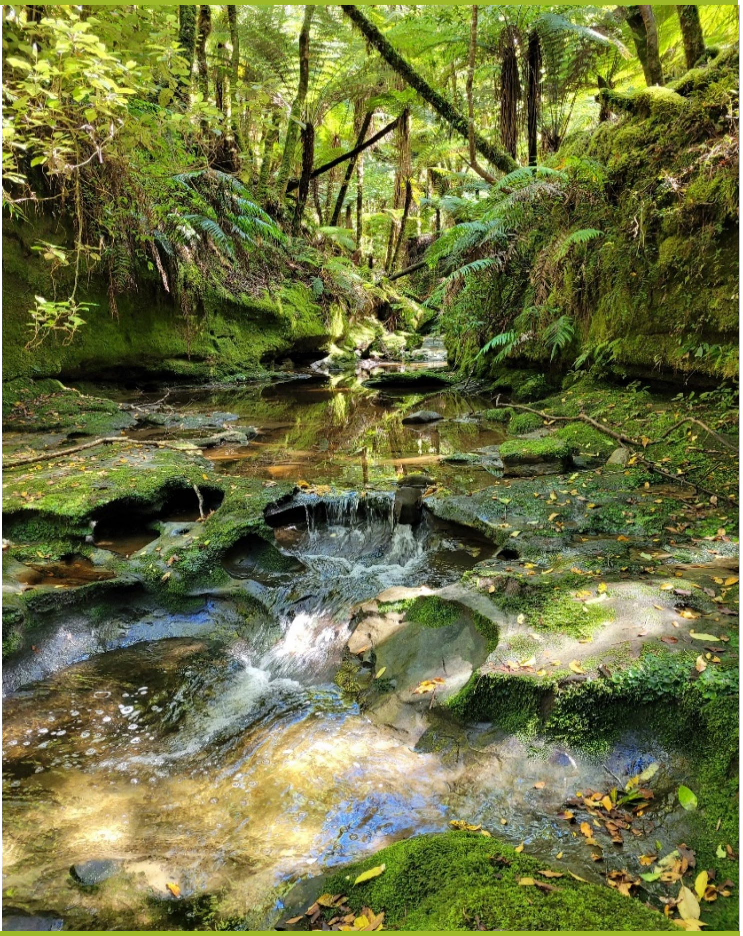
eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	1/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	14.1	
Conductivity (µS/cm)	101	
pH	7.6	
Clarity (m)	0.75	

Table 46 List of birds and mammals detected in eDNA samples from the Morgans site in the Tāngarākau subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*) Tūī (*Prosthemadera novaeseelandiae*)	Black rat (*Rattus rattus*) Sheep (*Ovis aries*) Fallow deer (*Dama dama*) Red deer (*Cervus elaphus*)

Table 47 Summary of freshwater invertebrate species detected in eDNA samples from the Morgans site in the Tāngarākau subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	1	12	Not detected	Present

Table 48 Fish detected in eDNA samples collected from the Morgans site (site 62) in the Tāngarākau subcatchment on 1 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Snapper	*Pagrus auratus*	Marine species not expected in this location – possible sample contamination, perhaps used as bait		
Kahawai	*Arripis trutta*	Marine species not expected in this location – possible sample contamination, perhaps used as bait		

3.13 Site 63 eDNA Results – Upper Retaruke (Retaruke Subcatchment)

The Upper Retaruke sampling site within the Retaruke subcatchment was sampled during March 2023 using six replicate eDNA sampling kits (Table 49). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 50), invertebrates (Table 51), and fish (Table 52) detected as sequences in the eDNA samples from this site.

For the Upper Retaruke site in the Retaruke subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Shortjaw kōkopu – *Galaxias postvectis* – Threatened–Nationally Vulnerable
- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Torrentfish – *Cheimarrichthys fosteri* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 49 **eDNA methods, site characteristics, and site photo for the Upper Retaruke site (site 63) in the Retaruke subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	28/3/2023	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	15.3	
Conductivity (µS/cm)	116	
pH	Not recorded	
Clarity (m)	0.80	

Table 50 List of birds and mammals detected in eDNA samples from the Upper Retaruke site in the Retaruke subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	**Mammal**
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Goat (*Capra hircus*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	Cattle (*Bos taurus*)
Paradise shelduck/Pūtangitangi (*Tadorna variegata*)	Red deer (*Cervus elaphus*)
Little shag/Kawaupaka (*Microcarbo melanoleucos*)	Pig (*Sus scrofa*)
Pūkeko (*Porphyrio melanotus*)	House mouse (*Mus musculus*)
Common starling/Tāringi (*Sturnus vulgaris*)	Sheep (*Ovis aries*)
Black shag/Māpunga (*Phalacrocorax carbo*)	Common brushtail possum (*Trichosurus vulpecula*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	Fallow deer (*Dama dama*)
Yellowhammer/Hurukōwhai (*Emberiza citrinella*)	Black rat (*Rattus rattus*)

Table 51 Summary of freshwater invertebrate species detected in eDNA samples from the Upper Retaruke site in the Retaruke subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	1	21	Not detected	Not detected

Table 52 Fish detected in eDNA samples collected from the Upper Retaruke site (site 63) in the Retaruke subcatchment on 28 March 2023. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Brown trout	*Salmo trutta*	Introduced & Naturalised	Anadromous-capable	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	
Torrentfish/panoko, panokonoko, panuku, papanoko	*Cheimarrichthys fosteri*	At Risk–Declining	Diadromous	
Shortjaw kōkopu	*Galaxias postvectis*	Threatened–Nationally Vulnerable	Diadromous	

3.14 Site 36 eDNA Results – Whangamōmona (Whangamōmona Subcatchment)

The Whangamōmona sampling site within the Whangamōmona subcatchment was sampled during January 2024 using six replicate eDNA sampling kits (Table 53). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 54), invertebrates (Table 55), and fish (Table 56) detected as sequences in the eDNA samples from this site.

For the Whangamōmona site in the Whangamōmona subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Īnanga – *Galaxias maculatus* – At Risk–Declining
- Freshwater mussel/Kākahi –*Echyridella menziesi* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon
- Mayfly – *Zephlebia tuberculata* – At Risk–Naturally Uncommon

Table 53 eDNA methods, site characteristics, and site photo for the Whangamōmona site (site 36) in the Whangamōmona subcatchment. Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	8/1/2024	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	Not recorded	
Conductivity (µS/cm)	Not recorded	
pH	Not recorded	
Clarity (m)	Not recorded	

Table 54 List of birds and mammals detected in eDNA samples from the Whangamōmona site in the Whangamōmona subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	**Mammal**
Mallard duck/Rakiraki (*Anas platyrhynchos*) Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*) Pūkeko (*Porphyrio melanotus*)	Cattle (*Bos taurus*) Common brushtail possum (*Trichosurus vulpecula*) Norway rat (*Rattus norvegicus*) Sheep (*Ovis aries*) Goat (*Capra hircus*)

Table 55 Summary of freshwater invertebrate species detected in eDNA samples from the Whangamōmona site in the Whangamōmona subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
7	0	7	Present	Present

Table 56 Fish detected in eDNA samples collected from the Whangamōmona site (site 36) in the Whangamōmona subcatchment on 8 January 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Common smelt/ngaore	*Retropinna retropinna*	Not Threatened	Diadromous	
Īnanga/atutahi, atutai, karohi, karohe	*Galaxias maculatus*	At Risk–Declining	Diadromous	

3.15 Site 23 eDNA Results – Ruatiti (Manganui O Te Ao Subcatchment)

The Ruatiti sampling site within the Manganui o te Ao subcatchment was sampled during February 2024 using six replicate eDNA sampling kits (Table 57). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 58), invertebrates (Table 59), and fish (Table 60) detected as sequences in the eDNA samples from this site.

For the Ruatiti site in the Manganui o te Ao subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Piharau – *Geotria australis* – Threatened–Nationally Vulnerable
- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Torrentfish – *Cheimarrichthys fosteri* – At Risk–Declining
- Īnanga – *Galaxias maculatus* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon
- Mayfly – *Zephlebia tuberculata* – At Risk–Naturally Uncommon

Table 57 **eDNA methods, site characteristics, and site photo for the Ruatiti site (site 23) in the Manganui o te Ao subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	29/2/2024	
eDNA analysis type	Comprehensive	
Number of replicates	6	
Temperature (°C)	16.2	
Conductivity (µS/cm)	117	
pH	7.5	
Clarity (m)	0.79	

Table 58 List of birds and mammals detected in eDNA samples from the Ruatiti site in the Manganui o te Ao subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Red deer (*Cervus elaphus*)
New Zealand pigeon/Kererū (*Hemiphaga novaeseelandiae*)	Fallow deer (*Dama dama*)
Tūī (*Prosthemadera novaeseelandiae*)	Cattle (*Bos taurus*)
Common starling/Tāringi (*Sturnus vulgaris*)	Norway rat (*Rattus norvegicus*)
Muscovy duck (*Cairina moschata*)	Black rat (*Rattus rattus*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	Goat (*Capra hircus*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	Sheep (*Ovis aries*)
Bellbird/Korimako (*Anthornis melanura*)	Common brushtail possum (*Trichosurus vulpecula*)
Blackbird/Manu pango (*Turdus merula*)	House mouse (*Mus musculus*)

Table 59 Summary of freshwater invertebrate species detected in eDNA samples from the Ruatiti site in the Manganui o te Ao subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
8	0	14	Not detected	Present

Table 60 Fish detected in eDNA samples collected from the Ruatiti site (site 23) in the Manganui o te Ao subcatchment on 29 February 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Brown trout	*Salmo trutta*	Introduced & Naturalised	Anadromous-capable	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Redfin bully/toitoi	*Gobiomorphus huttoni*	Not Threatened	Diadromous	
Torrentfish/panoko, panokonoko, panuku, papanoko	*Cheimarrichthys fosteri*	At Risk–Declining	Diadromous	
Īnanga/atutahi, atutai, karohi, karohe	*Galaxias maculatus*	At Risk–Declining	Diadromous	
Lamprey, piharau	*Geotria australis*	Threatened–Nationally Vulnerable	Diadromous	
Common smelt/ngaore	*Retropinna retropinna*	Not Threatened	Diadromous	
Rainbow trout	*Oncorhynchus mykiss*	Introduced & Naturalised	Anadromous-capable	

3.16 Site 35 eDNA Results – Makirikiri (Ūpokongaro Subcatchment)

The Makirikiri sampling site within the Ūpokongaro subcatchment was sampled during January 2024 using six replicate eDNA sampling kits (Table 61). Basic eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 62), invertebrates (Table 63), and fish (Table 64) detected as sequences in the eDNA samples from this site.

For the Makirikiri site in the Ūpokongaro subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 61 **eDNA methods, site characteristics, and site photo for the Makirikiri site (site 35) in the Ūpokongaro subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	26/1/2024	
eDNA analysis type	Basic	
Number of replicates	6	
Temperature (°C)	14.4	
Conductivity (µS/cm)	Not recorded	
pH	Not recorded	
Clarity (m)	0.69	

Table 62 List of birds and mammals detected in eDNA samples from the Makirikiri site in the Ūpokongaro subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	Mammal
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Cattle (*Bos taurus*)
House sparrow/Tiu (*Passer domesticus*)	Norway rat (*Rattus norvegicus*)
New Zealand pigeon/Kererū (*Hemiphaga novaeseelandiae*)	Fallow deer (*Dama dama*)
Common starling/Tāringi (*Sturnus vulgaris*)	Sheep (*Ovis aries*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	European rabbit (*Oryctolagus cuniculus*)
European goldfinch/Kōurarini (*Carduelis carduelis*)	Common brushtail possum (*Trichosurus vulpecula*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	House mouse (*Mus musculus*)
Pūkeko (*Porphyrio melanotus*)	Black rat (*Rattus rattus*)
Welcome swallow/Warou (*Hirundo neoxena*)	Cat (*Felis catus*)
Silvereye/Tauhou (*Zosterops lateralis*)	
Yellowhammer/Hurukōwhai (*Emberiza citrinella*)	

Table 63 Summary of freshwater invertebrate species detected in eDNA samples from the Makirikiri site in the Ūpokongaro subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
4	0	7	Not detected	Present

Table 64 Fish detected in eDNA samples collected from the Makirikiri site (site 35) in the Ūpokongaro subcatchment on 26 January 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Banded kōkopu	Galaxias fasciatus	Not Threatened	Diadromous	

3.17 Site 34 eDNA Results – Matarawa (Matarawa Subcatchment)

The Matarawa sampling site within the Matarawa subcatchment was sampled during January 2024 using six replicate eDNA sampling kits (Table 65). Comprehensive eDNA analysis was completed at Wilderlab and data have been analysed to examine the birds and mammals (Table 66), invertebrates (Table 67), and fish (Table 68) detected as sequences in the eDNA samples from this site.

For the Matarawa site in the Matarawa subcatchment, eDNA has detected the presence of several species that have a threat status in the New Zealand Threat Classifications System (NZTCS):

- Īnanga – *Galaxias maculatus* – At Risk–Declining
- Longfin eel – *Anguilla dieffenbachii* – At Risk–Declining
- Mayfly – *Zephlebia pirongia* – At Risk–Naturally Uncommon

Table 65 **eDNA methods, site characteristics, and site photo for the Matarawa site (site 34) in the Matarawa subcatchment.** Photo by Department of Conservation

eDNA Methods & Measured Site Characteristics		Site Photo
Date sampled	19/1/2024	
eDNA analysis type	Basic	
Number of replicates	6	
Temperature (°C)	22.3	
Conductivity (µS/cm)	540	
pH	Not recorded	
Clarity (m)	0.78	

Table 66 List of birds and mammals detected in eDNA samples from the Matarawa site in the Matarawa subcatchment. Note that non-detection does not confirm absence of a species. Bird and mammal species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list.

Species Recorded in eDNA	
Bird	**Mammal**
Mallard duck/Rakiraki (*Anas platyrhynchos*)	Cattle (*Bos taurus*)
Common starling/Tāringi (*Sturnus vulgaris*)	Red deer (*Cervus elaphus*)
Song thrush/Manu-kai-hua-rakau (*Turdus philomelos*)	Sheep (*Ovis aries*)
European goldfinch/Kōurarini (*Carduelis carduelis*)	European rabbit (*Oryctolagus cuniculus*)
Common chaffinch/Pahirini (*Fringilla coelebs*)	Norway rat (*Rattus norvegicus*)
Australian magpie/Makipai (*Gymnorhina tibicen*)	Stoat (*Mustela erminea*)
House sparrow/Tiu (*Passer domesticus*)	
Silvereye/Tauhou (*Zosterops lateralis*)	

Table 67 Summary of freshwater invertebrate species detected in eDNA samples from the Matarawa site in the Matarawa subcatchment. The number of sensitive Ephemeroptera (E), Plecoptera (P), and Trichoptera (T) species detected in the samples is indicated, as is the detection or non-detection of mega-invertebrates kākahi and kōura. Note that non-detection does not confirm absence of a species.

Number of Taxa			Kākahi *Echyridella menziesi*	Kōura *Paranephrops planifrons*
E	P	T		
2	0	5	Not detected	Present

Table 68 Fish detected in eDNA samples collected from the Matarawa site (site 34) in the Matarawa subcatchment on 19 January 2024. Fish species are listed in order of decreasing number of eDNA sequence counts at this site, with species having the most eDNA sequence counts found at the top of the list. Note that eDNA sequence counts do not provide a reliable prediction of fish abundance, as there are many factors that affect the number of sequences recorded at any site, including the distance of the animal from the sampling point and the amount of eDNA that is shed by different species.

Common/ Māori Names	Species Name	Threat Classification	Migratory Status	Photo
Common bully/toitoi	*Gobiomorphus cotidianus*	Not Threatened	Diadromous	
Īnanga/atutahi, atutai, karohi, karohe	*Galaxias maculatus*	At Risk–Declining	Diadromous	
Longfin eel/tuna	*Anguilla dieffenbachii*	At Risk–Declining	Diadromous	
Shortfin eel/tuna	*Anguilla australis*	Not Threatened	Diadromous	
Common smelt/ngaore	*Retropinna retropinna*	Not Threatened	Diadromous	

4 DISCUSSION & RECOMMENDATIONS

The eDNA sampling detailed in this report was carried out as part of a catchment-wide baseline ecological health survey led by the Department of Conservation (DOC). By collecting and analysing eDNA samples from sixteen sites across the Whanganui River catchment, the study has provided valuable insights into the presence of fish and invertebrate species within the river. Additionally, it has enhanced understanding of the biodiversity of the wider catchment, including mammals, birds, invertebrates, and plants. This work has also contributed to understanding the distribution of species of conservation interest within the catchment (e.g., blue duck/whio).

While site-specific summaries provide detailed insights into each eDNA sampling location, several broader patterns emerge across the dataset. One example involves the Taxon Independent Community Index (TICI), an index developed by Wilderlab to assess the ecological health of river sites based on DNA sequences detected in freshwater samples (Wilkinson *et al.,* 2024). Although TICI scores varied widely across the study sites, the general pattern was that sites in the headwaters of each subcatchment received higher TICI scores than those in the mainstem and lower tributaries, indicating a decline in ecological health down the catchment. However, the Tāngarākau subcatchment does not conform to this pattern. The contrasting TICI scores recorded for its two sites – excellent–pristine for the Morgans site and poor–average for the Heao site – suggest that the two major tributaries are experiencing different levels of stress, despite being located at similar positions within the catchment. The difference in these sites is well illustrated by the site photos for the two sampling locations (Table 41; Table 45).

The three sites sampled in the Ōngarue subcatchment also reveal notable differences. The Ōngarue site (site 28) is characterized by high water clarity, a rich diversity of EPT taxa, and the presence of blue duck/whio, indicating good ecological condition. However, it recorded lower fish diversity compared to the other sites in the subcatchment. Only longfin eel and rainbow trout were detected at this site, whereas samples from the Waimiha (site 24) and Taringamotu (site 29) sites in the same subcatchment also identified common bully, torrentfish, shortfin eel, and redfin bully (the latter only at Taringamotu). The absence (non-detection) of these additional diadromous species at the Ōngarue site may point to potential barriers to fish passage, which would warrant further investigation.

Another site with relatively low fish diversity compared to others in the upper catchment is the Ōhura site (site 4). Three fish species were detected here, including common bully, longfin eel, and shortfin eel, indicating that the site is accessible to migratory fish. However, it lacks species such as redfin bully and shortjaw kōkopu, which were detected at the Mangakara West site within the same subcatchment. The Ōhura site also recorded lower EPT taxa diversity than Mangakara West, suggesting that site-specific environmental factors may be influencing the reduced fish diversity.

The Ruatiti site (site 23) stands out for its high fish diversity relative to other parts of the Whanganui catchment. Ten fish species were detected at this site with eDNA sampling, including eight diadromous species and four classified as threatened or at-risk, highlighting the ecological value of this subcatchment. Notably, Ruatiti was the only site in the study where piharau/lamprey was detected, further reinforcing its importance within the catchment.

The eDNA sampling undertaken in this study has expanded the spatial coverage of sampling sites within the Whanganui catchment, particularly in its western areas, where publicly available data have been limited. This is especially true for the Tāngarākau and Whangamōmona subcatchments, which were previously underrepresented. Figure 2 shows the distribution of eDNA sites from both this and earlier studies, highlighting current coverage and identifying gaps across the catchment. This information will be valuable for guiding the planning of future monitoring efforts.

Recommendations to gain further value from this eDNA work in the catchment:

» Use the comprehensive analysis option for all future eDNA surveys since this includes the calculation of the TICI score for each sample. The TICI score appears to be a valuable indicator of ecological condition, particularly for summarising site health where traditional macroinvertebrate-based metrics are unavailable.

» Develop a searchable map or GIS-based system to store and visualise DOC’s eDNA data, including information on species with conservation threat status. This could provide more targeted and accessible insights for DOC’s conservation priorities than the existing Wilderlab database. For example, although these samples were collected from the river and tributaries, they have detected the presence of long-tailed bat and therefore have wider interest beyond the freshwater or catchment focus.

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