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RAFTS

River Trusts

Eric Verspoor (Marine Scotland)

Mark Coulson (RAFTS)

Focusing

Atlantic Salmon Management

on

Populations

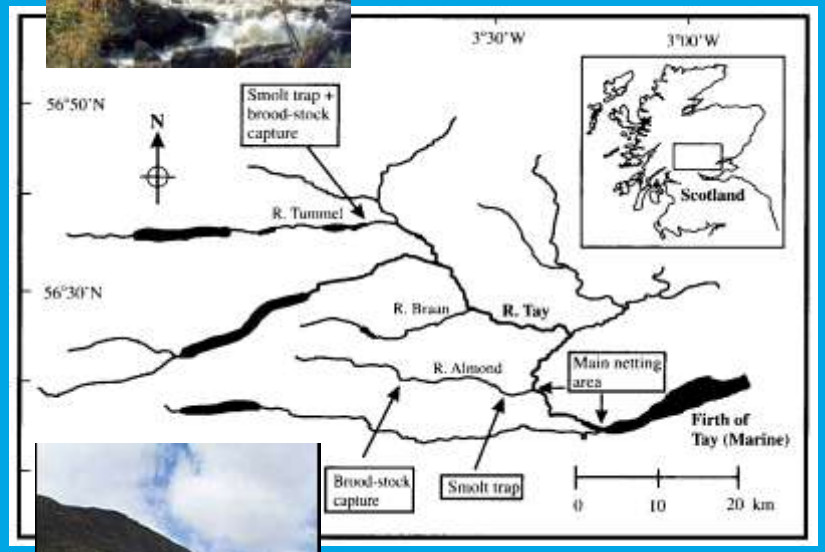
FASMOP

Emerging results and prospects and potential for the future

Within River Stock Variation in Scotland

River Tay

High altitude



Low altitude

Adult Run Timing

Stewart et al. 2002

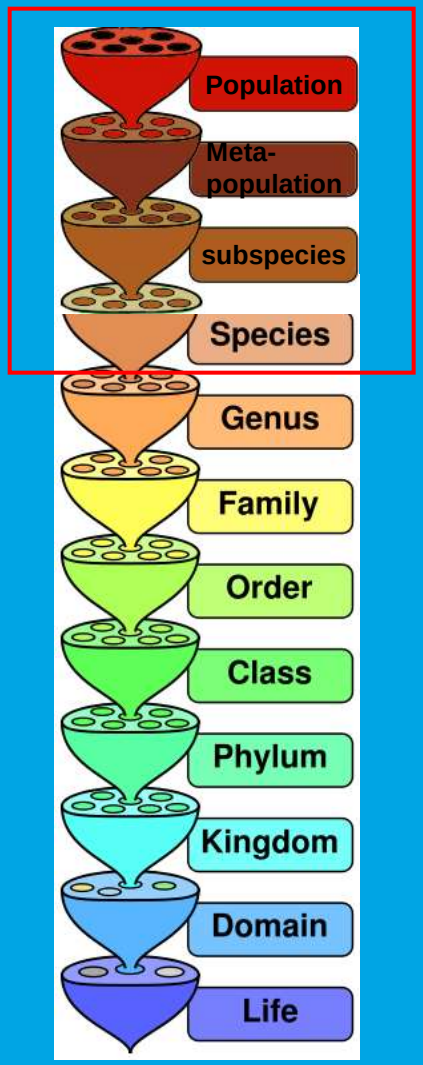
Smolt run timing

Stewart et al. 2006

Other traits!?

Only possible if river stocks are subdivided into multiple, reproductively distinct breeding populations!

Within River Stock Variation in Scotland



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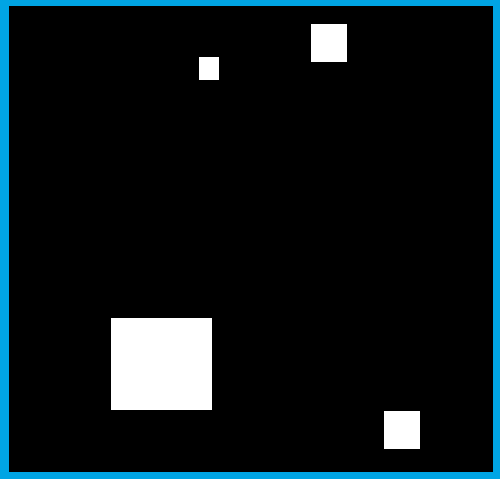
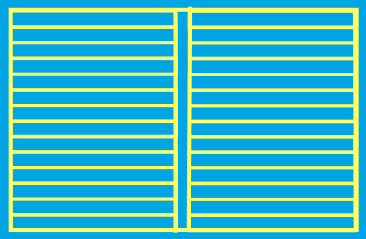
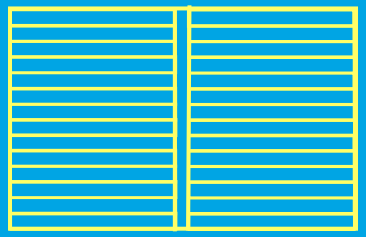


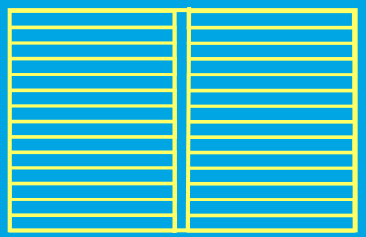
What kind of population structuring exists within Atlantic salmon river stocks in Scotland?

Marker Resolution – what you see may depend on what markers you use



Different sampling locations

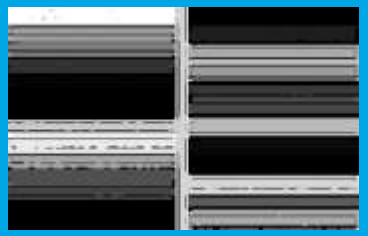


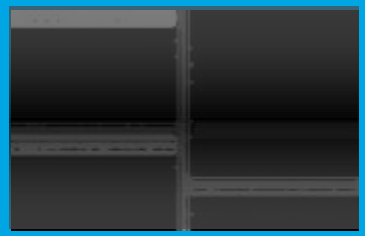


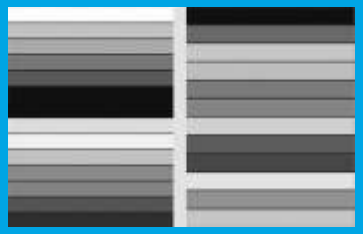
Differentiation with

allozymes

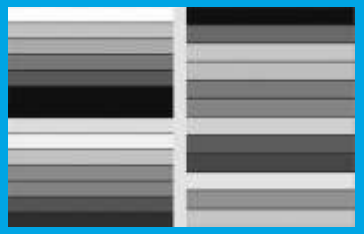
microsatellites

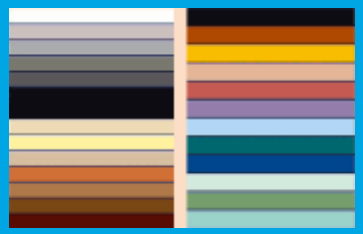




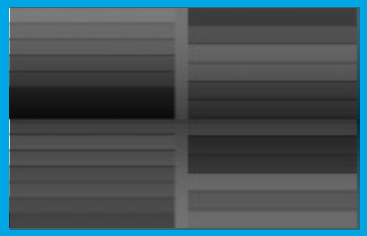


random SNPs





adaptive SNPs



FASMOP

1. Identify structure
2. Determine population of origin of individual fish
3. Understand differences between and impacts on individual populations

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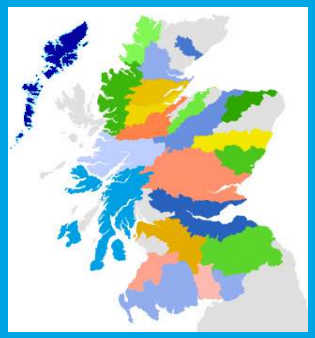

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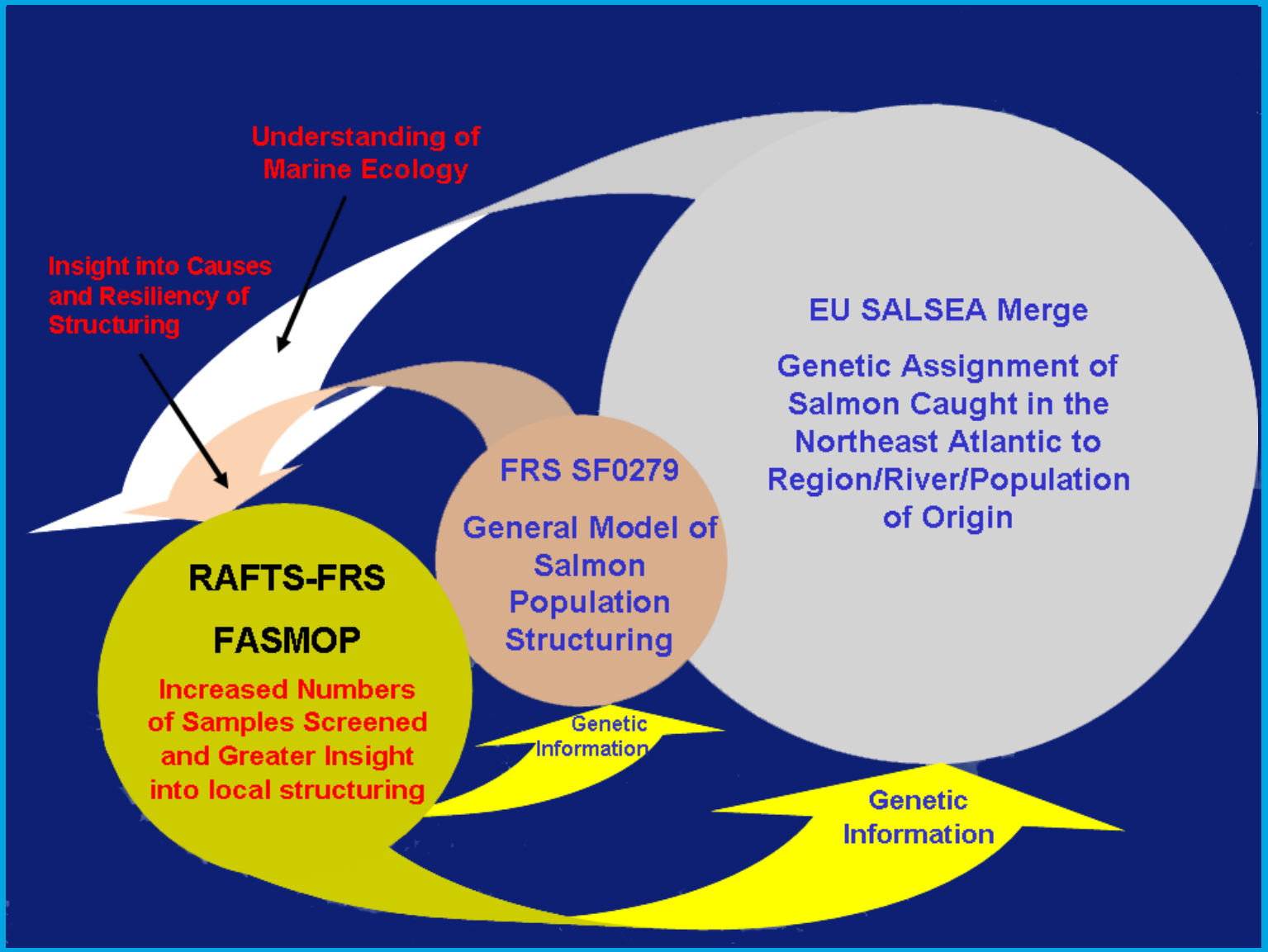
Partnership

~~1 May 2009 to 30 November 2011~~

1 May 2009 to 31 March 2012

Partnership



Population Modelling

Marine Scotland

Is population structure a function of:

- colonisation history
- branching
- habitat discontinuities
- Distance between habitat patches
- water quality heterogeneity (e.g. pH)
- physical heterogeneity (e.g. altitude, ^{o}C)

Without FASMOP:

- three small rivers
- three medium rivers
- three large rivers
- three test rivers
- 120 sites – 6,000 fish

With FASMOP:

- five small rivers
- five medium rivers
- five large rivers
- five test rivers
- 240+ sites – 12,000+ fish

- **Increased model robustness**
- **Better general understanding**
- **More sites screened for local insight**
- **Extended analysis of within and among river SNP variation**

SALSEA-MERGE

NASCO, EU, Marine Scotland, other European partners

With FASMOP:

- Higher quality Scottish baseline
- more river assignments of marine fish
- robust picture of regional differentiation at national level

- More accurate stock assignment
- Finer scale assignments
- Understanding of uniqueness of Scottish stocks

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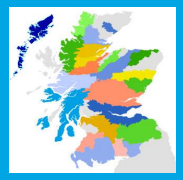

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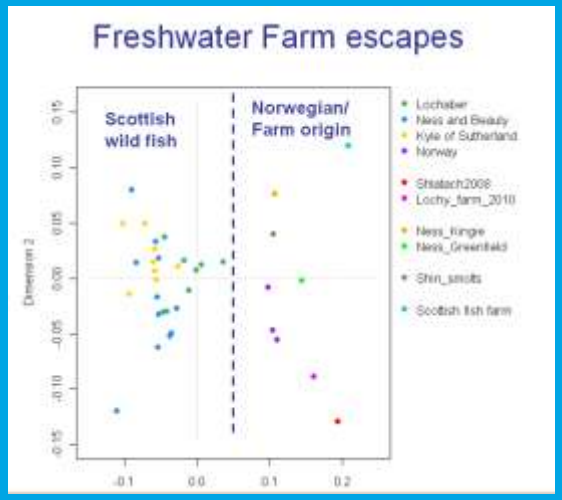
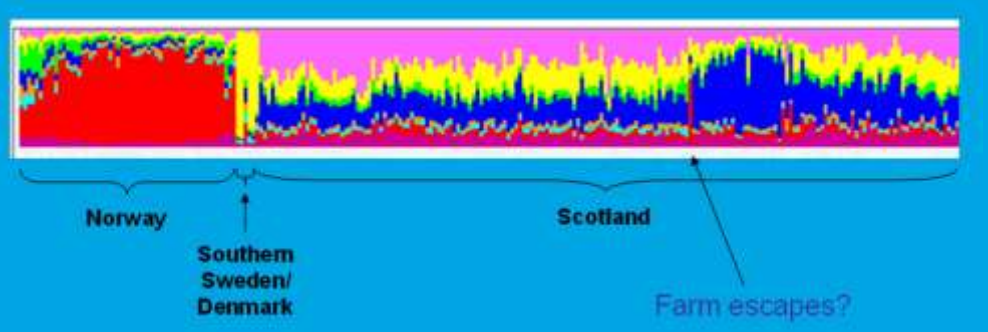
With POPMOD and SALSEA Merge:

- exploit existing state of the art genetic screening programme
- Exploit existing data base and GIS systems
- results placed in national/ international context
- ~ 30% more sites and fish screened
- a general framework of population structuring within which to interpret local results
- access to new SNP technology through existing Marine Scotland- CIGENE collaboration



- **more robust inferences about local population structure**
- **rapid adoption of new higher resolution SNP technology**
- **Understanding of uniqueness of individual stocks in a national perspective**
- **Insight to advance understanding of effects farm escapes**



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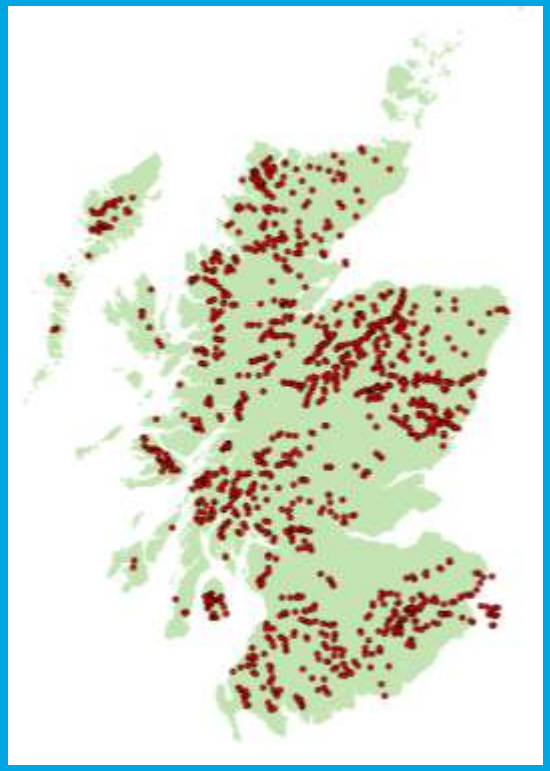

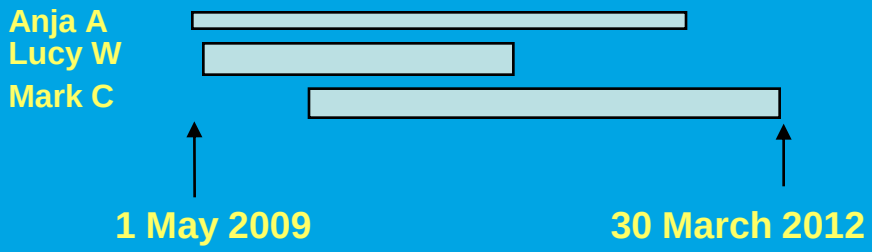

Tasks

- consult and design sampling programmes
- field collection of samples
- genotying of samples
- preliminary analysis of first year results
- discussion with Trusts of first year results
- planning of 2nd years sampling
- genotyping of 2nd years samples
- final analysis of microsatellite data
- collection, preparation, genotyping, and analysis of SNP samples
- production of final reports

Microsatellites

- 17 marker loci
- 24 Fisheries Trusts & Boards
- ~18,500 salmon genotypes
- ~750 sites
- ~300 rivers

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SNPs – the Future

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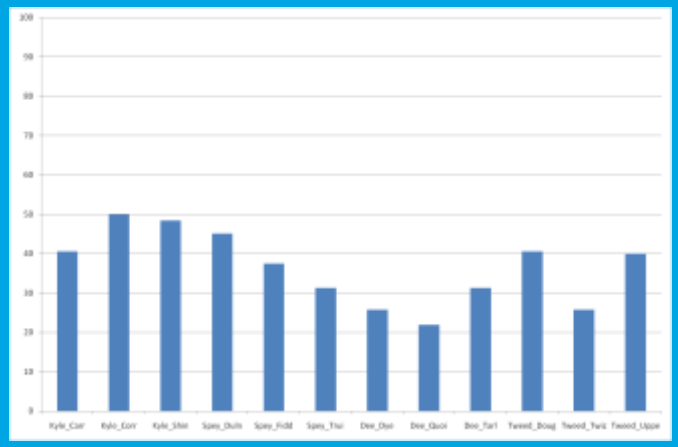
+

CIGENE
Centre for Integrative Genetics

Microsatellite loci

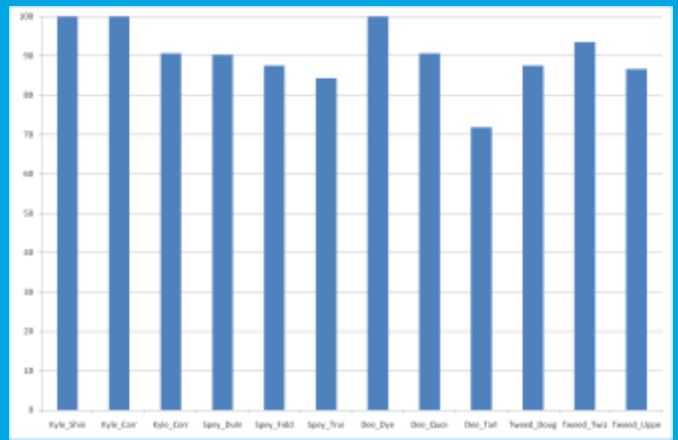


SNP loci

…ACTTGGCAGTC…

|

…ACTTGTCAGTC…



Trusts involved in SNP work

~1,200 salmon genotypes

~40 sites

~10 rivers

2 sites on the Dionard

7 sites from the Kyle of Sutherland

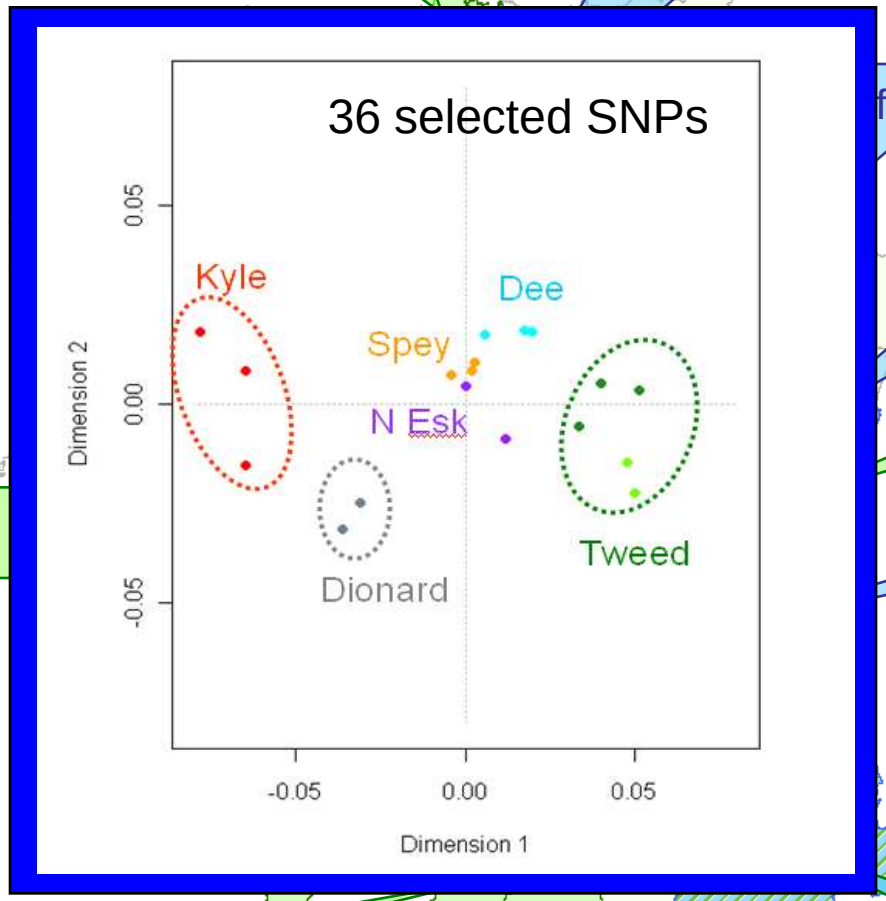
from the Spey

8 sites from the Dee

2 sites on the North Esk

3 sites from the Tay

2 sites in Argyll



2 sites in Ayrshire

8 sites on the Tweed

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2 sites on the Nith

SNPs - the Future for FASMOP

- Farm vs. wild individual identification & interbreeding
  - getting started
- Increase resolution of breeding groups
  - under development
- Identification of candidate genes underlying ‘adaptive’ traits?
  - develop collaborations?

…ACTTGGCAGTC…

…ACTTGTCAGTC…

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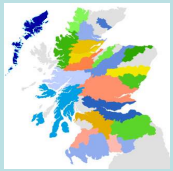


River Trusts

Output

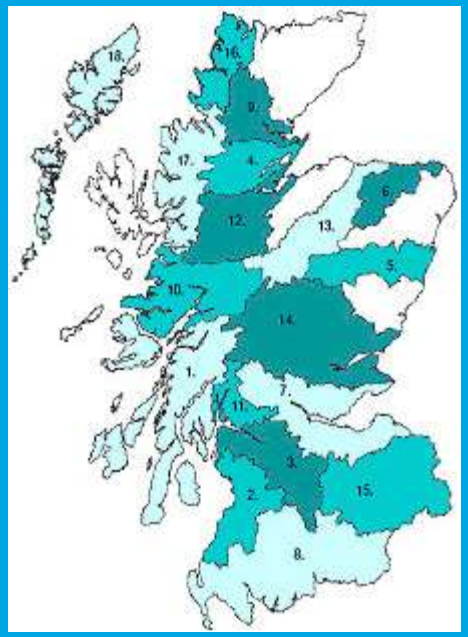
Reports cover:

- nature of population structuring with each river
- capacity of markers for individual assignment to population
- presence of farm escapes
- presence of stocked fish in angled catch (some Trusts)
- Potential for increased resolution with SNPs (some Trusts)

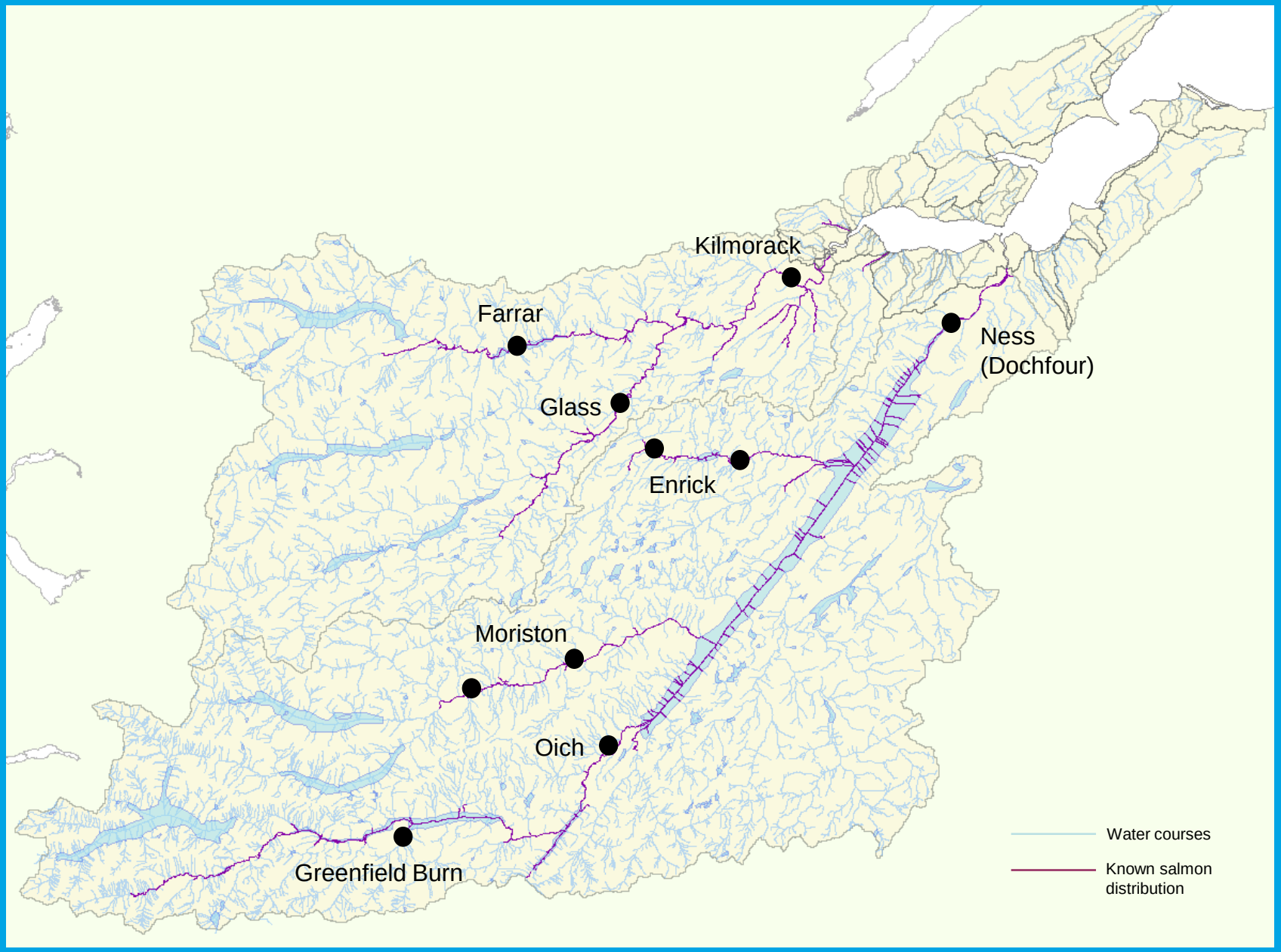
24 reports for individual Trusts starting delivery summer 2011

Example of Genetic Analysis

Ness and Beauly River Systems



1. Mapping of ‘breeding populations’



Ness & Beauly Fisheries Trust

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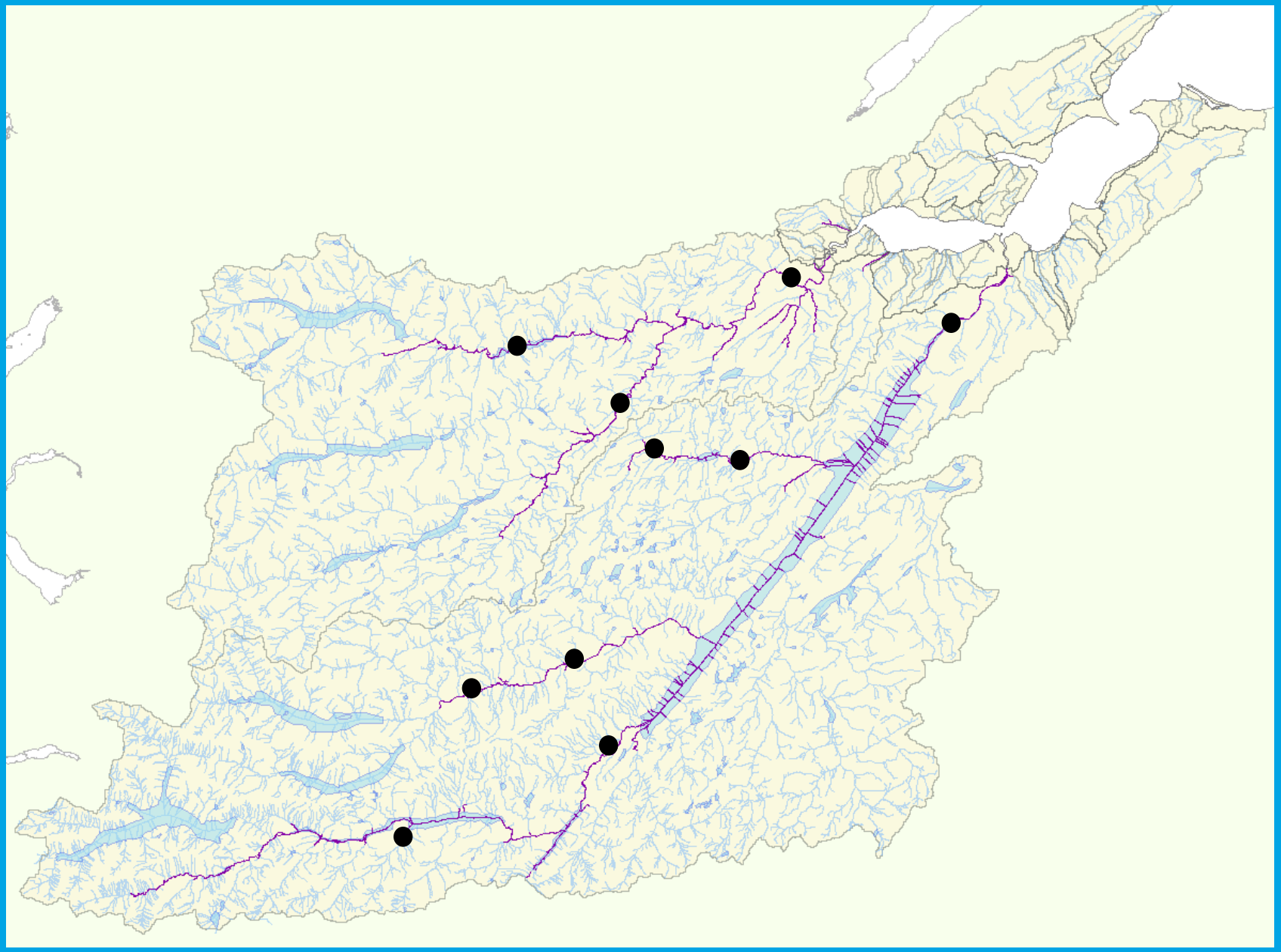

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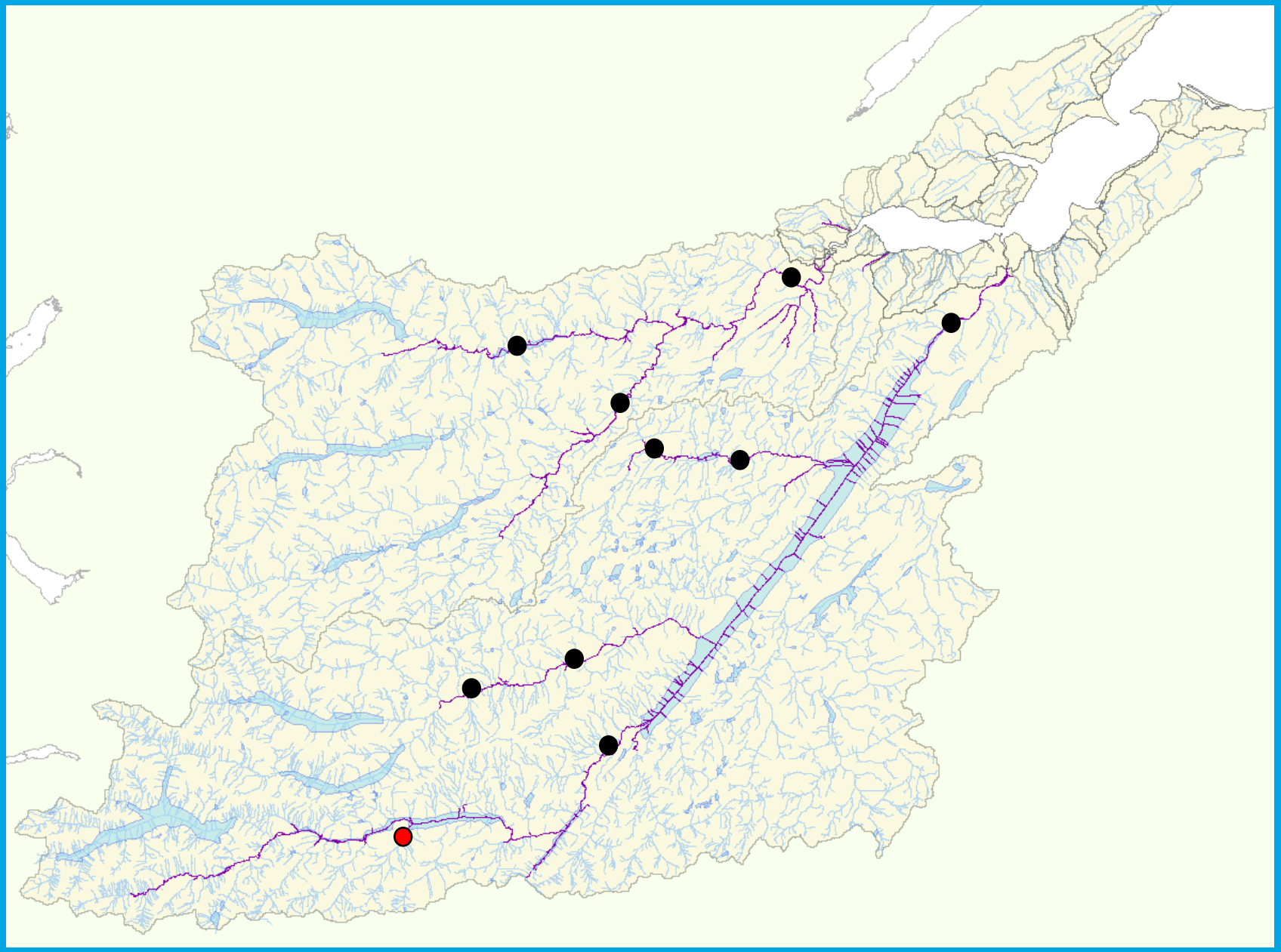

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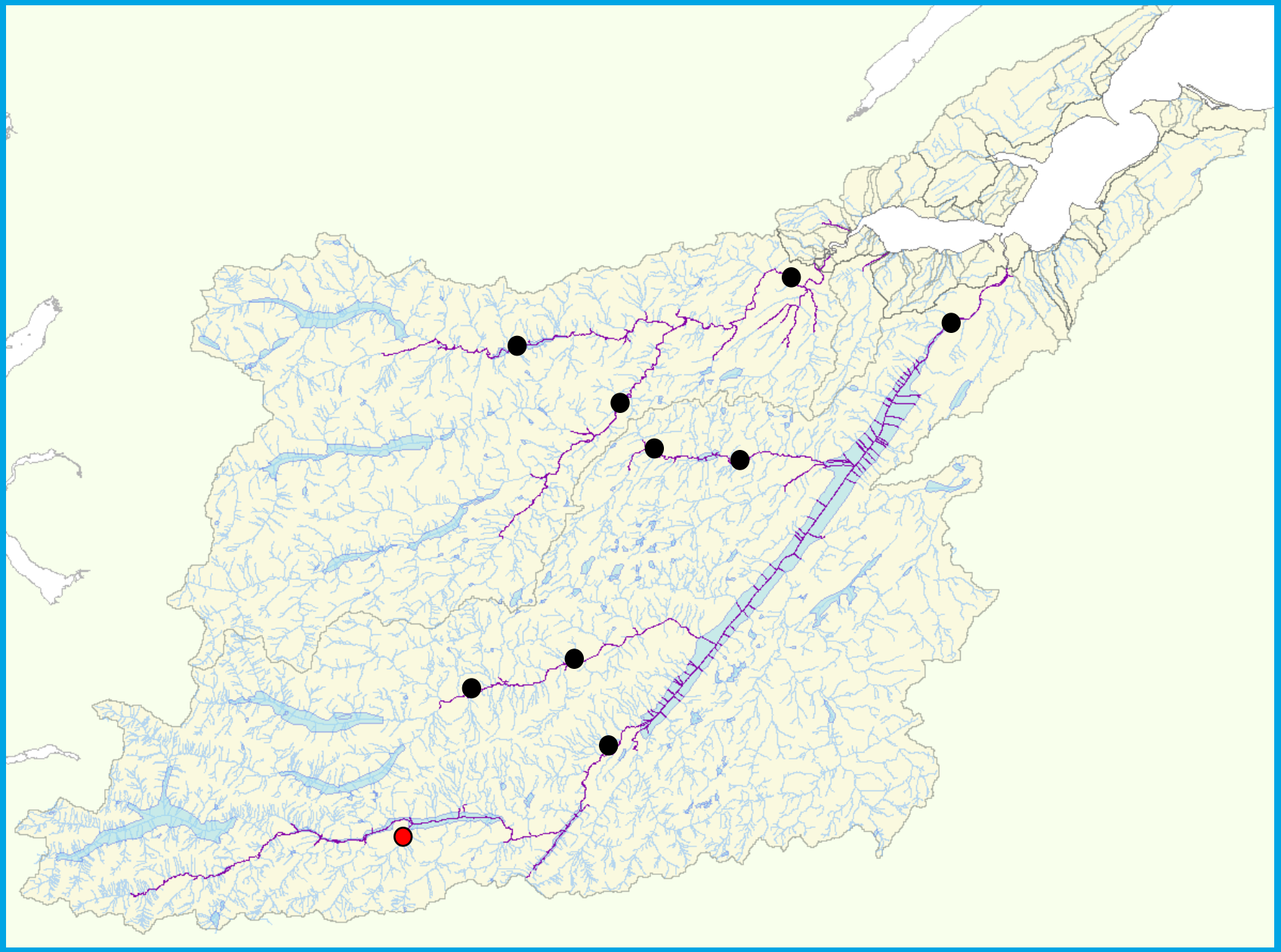

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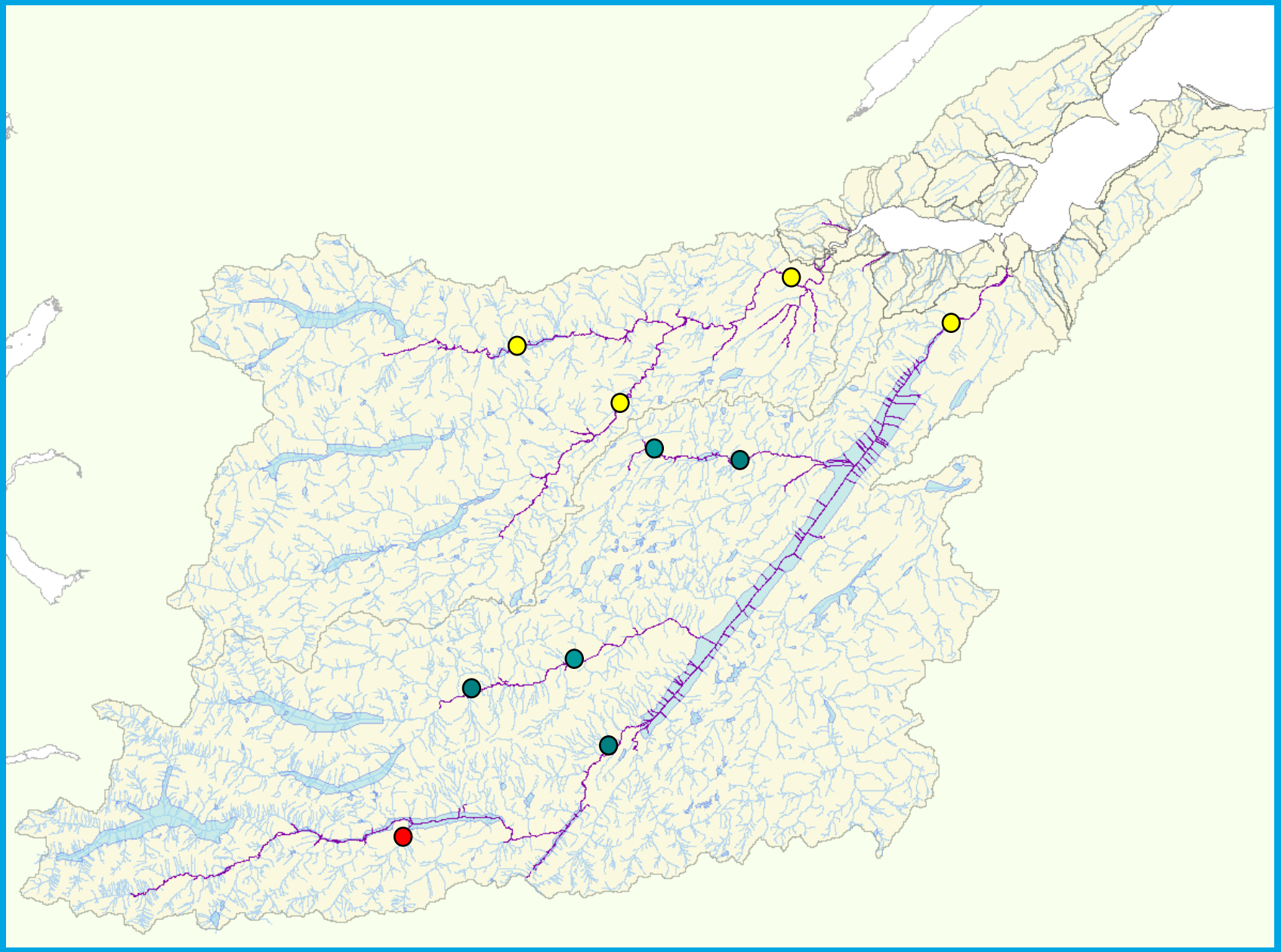

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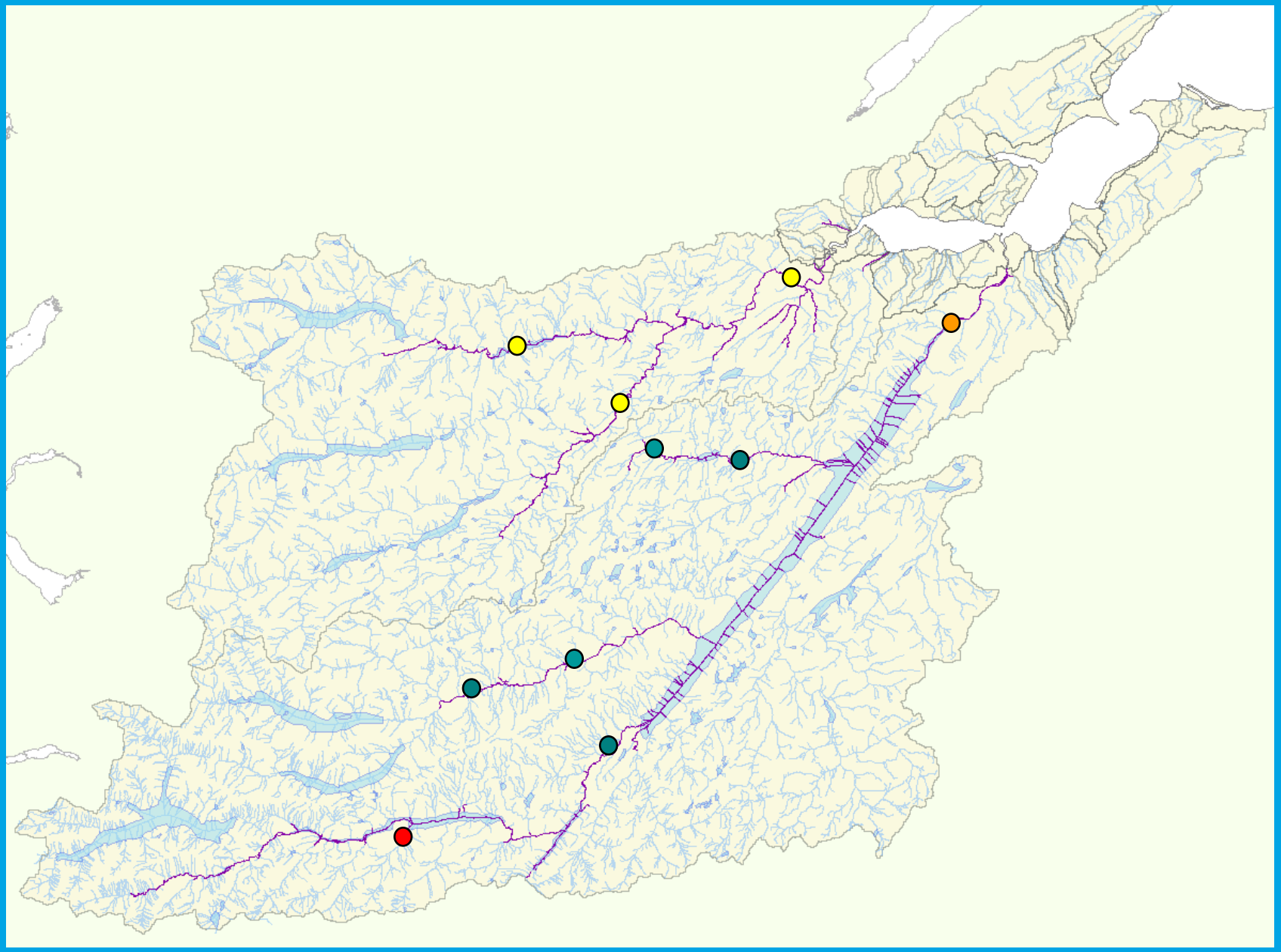

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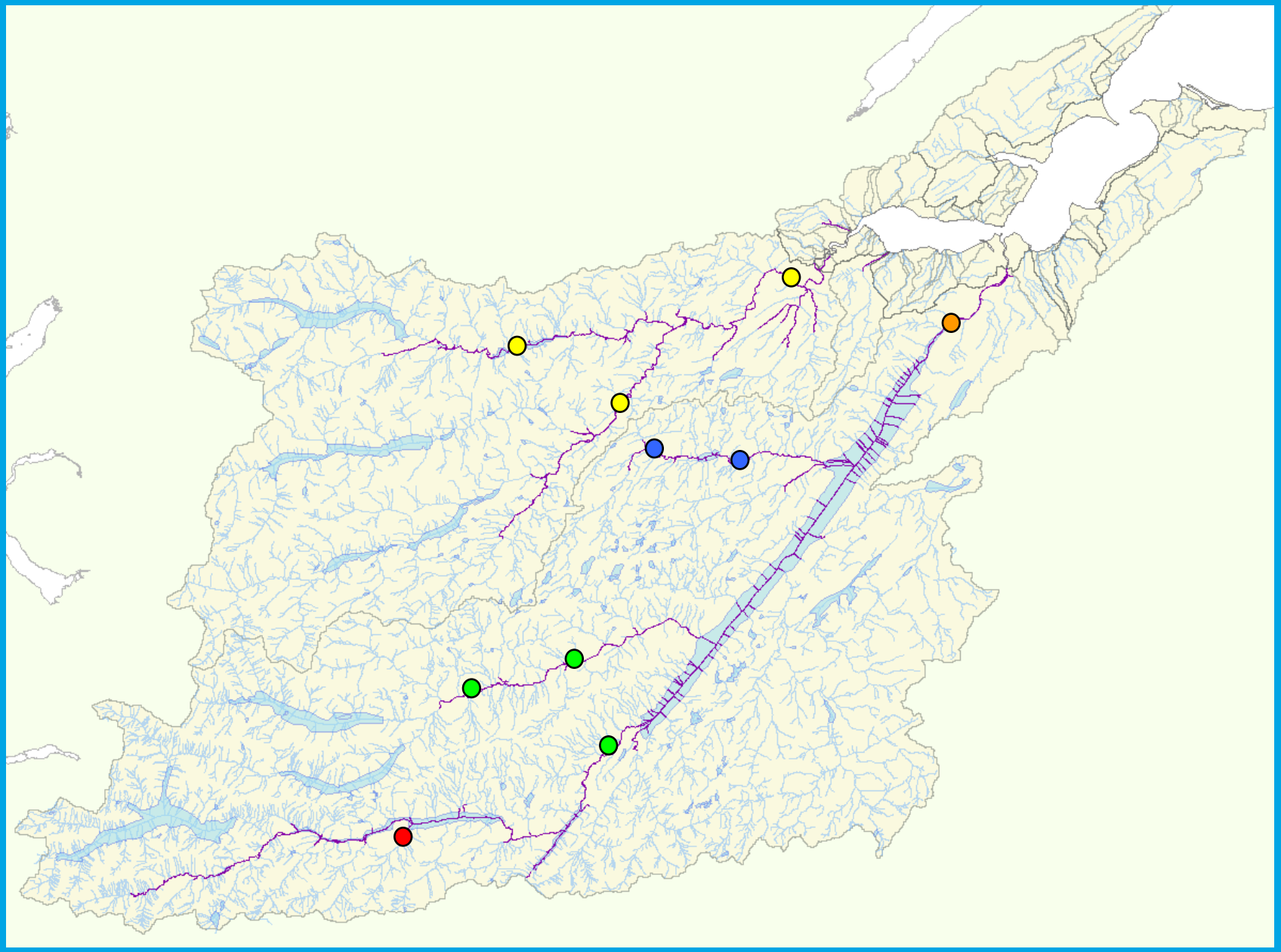

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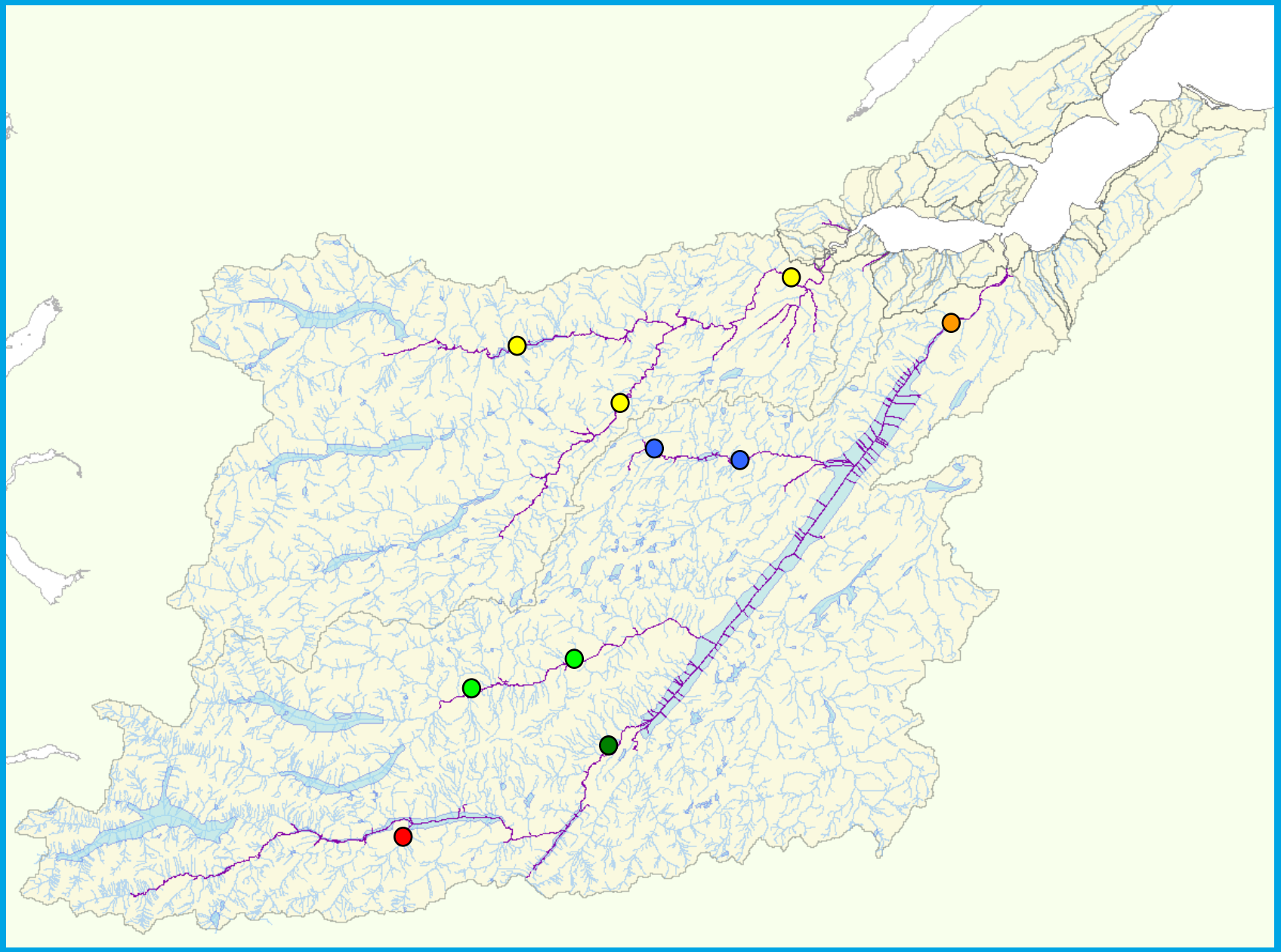

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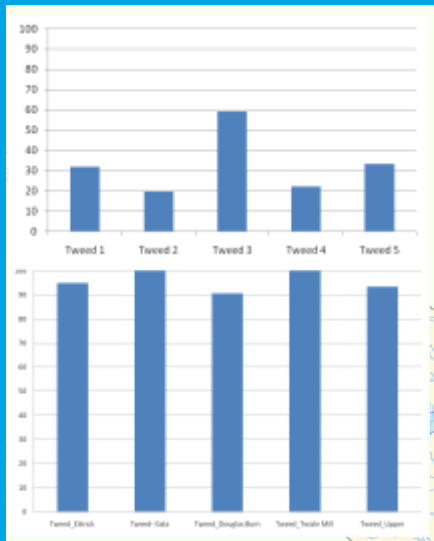
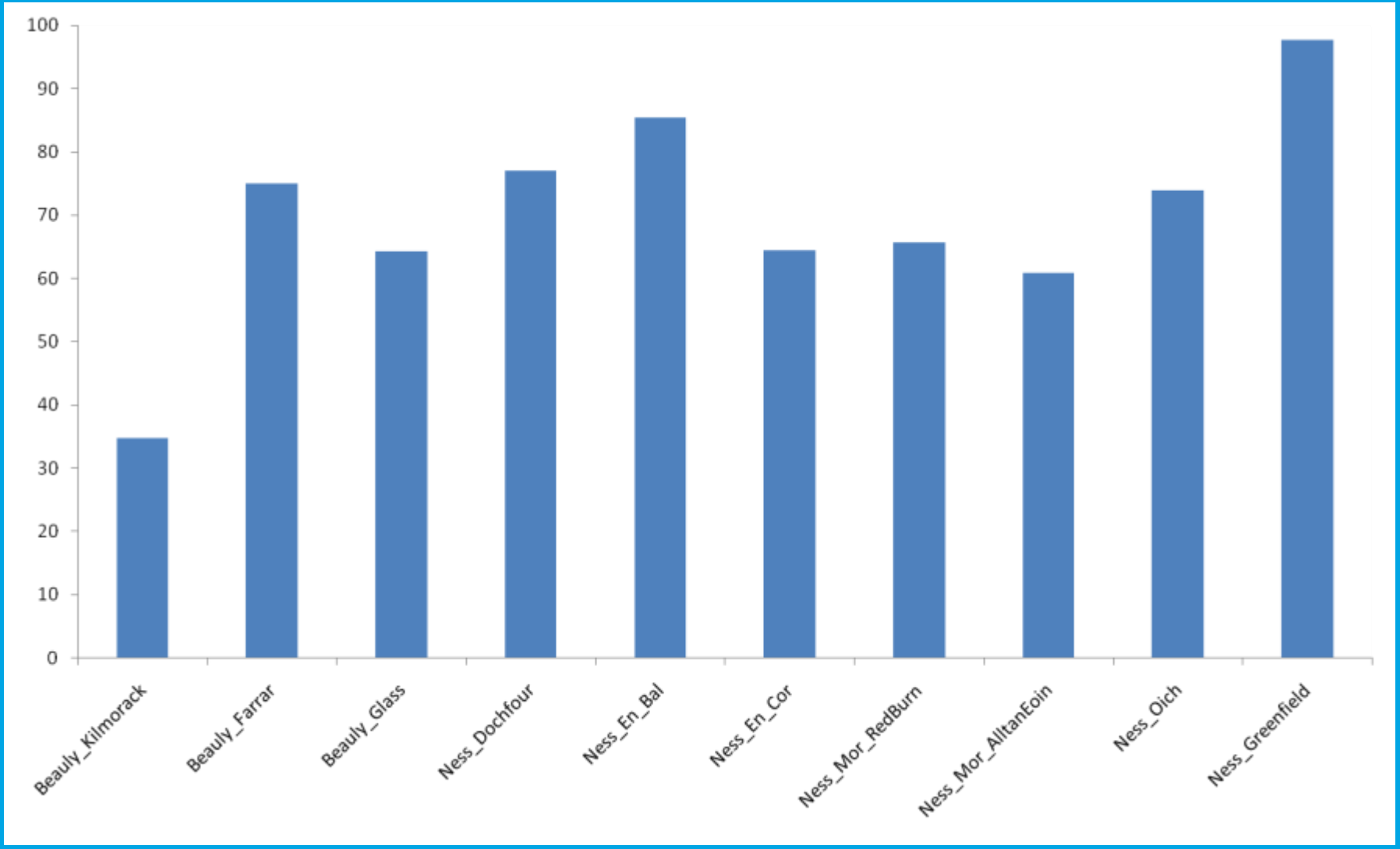


microsatellites

SNPs

2. Genetic assignment to source population



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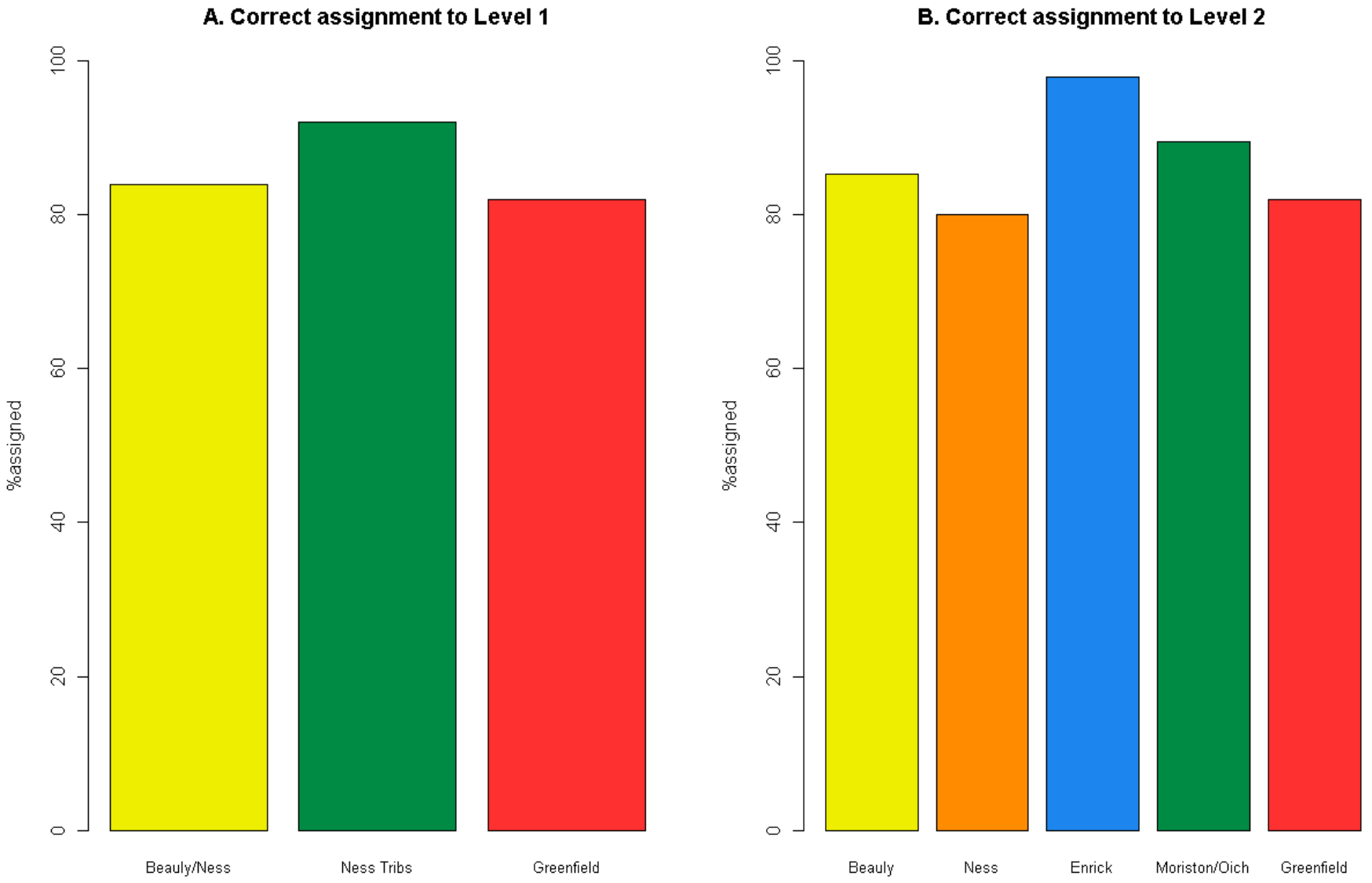
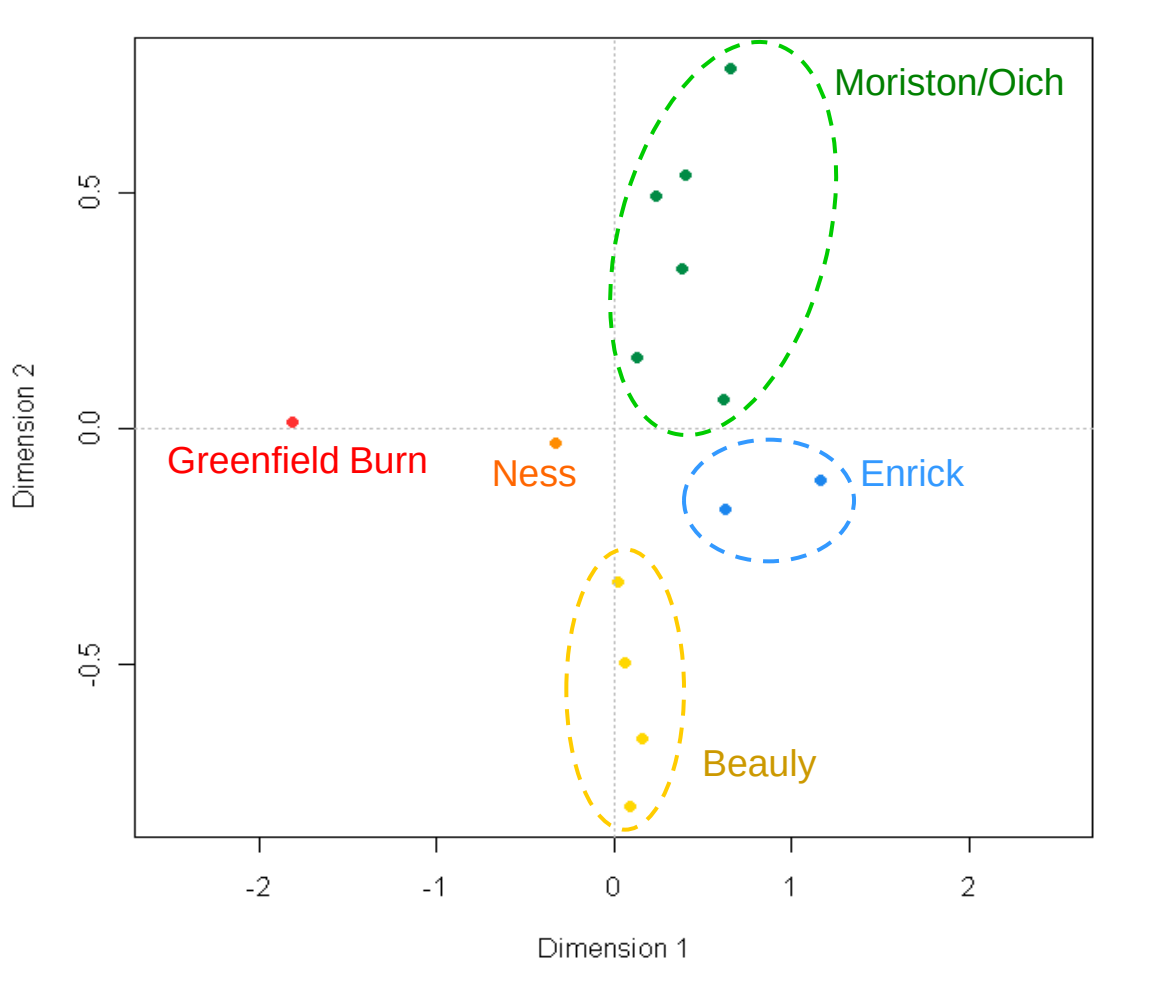
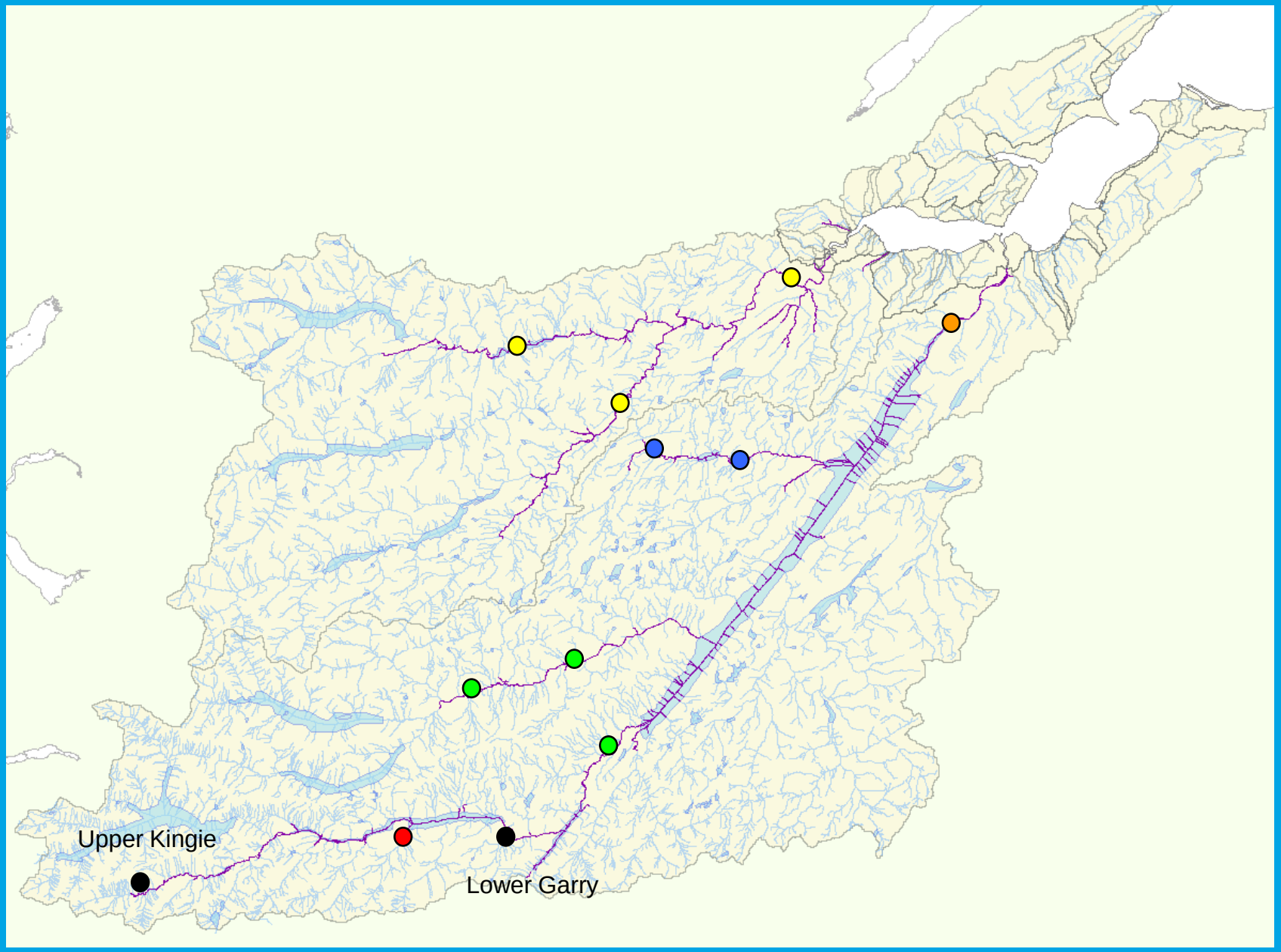


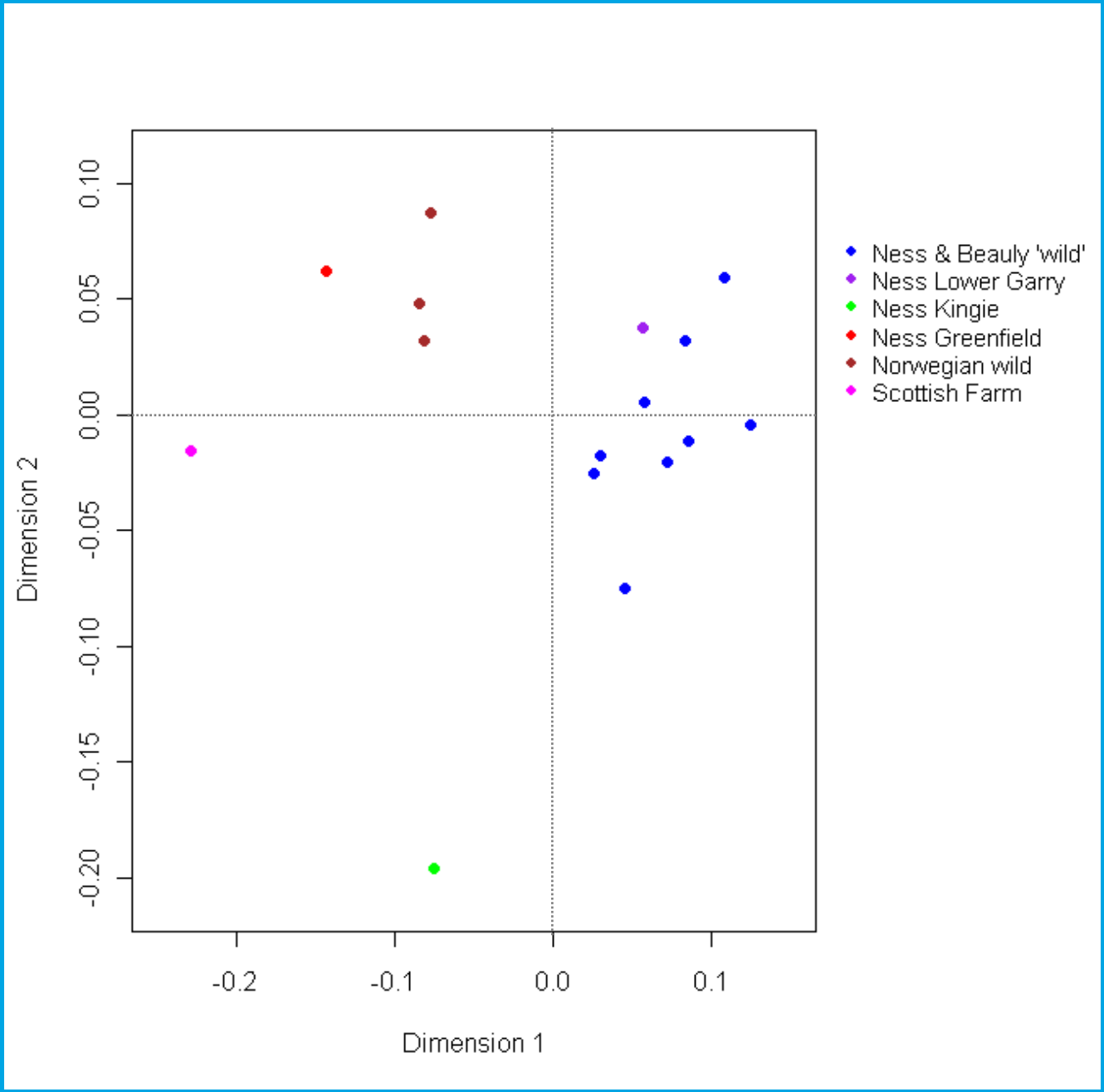
MDS plot


Moriston/Oich
Greenfield Burn
Ness
Enrick
Beauly
Dimension 2
0.5
0.0
-0.5
-2
-1
0
1
2
Dimension 1

3. Fish farm impacts?



MDS Plot – Fish farm impacts



Take home messages – Ness & Beauly

- Virtually all sites distinct from one another
- Smaller differences within the Beauly vs. within the Ness (most tributaries are clearly distinct)
- Greenfield Burn & Kingie site most distinct (fish farm effects?)
- Assignment to tributary is quite high

TO DO

- New Farm/Wild SNP panel (~60 SNPs)
- Assess other locations which may have had impacts from farm escapes (above Lochs etc)
- Write up in 2011

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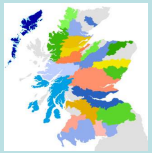

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