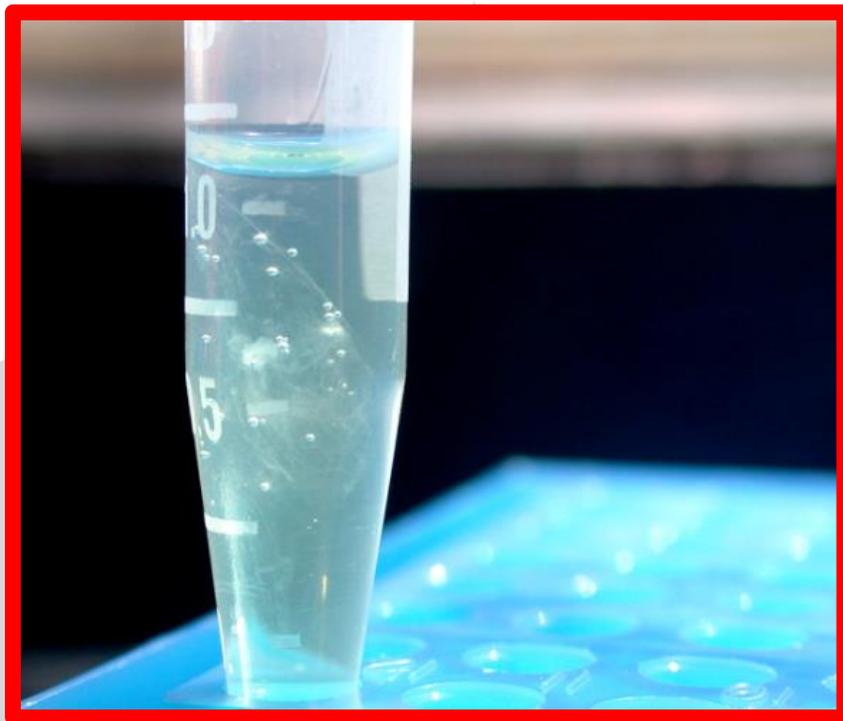


FishGen

User Manual v2.3

July 21st, 2015



FishGen.net is a final repository for genetic information of fish species that are of conservation and management importance to federal, state and tribal agencies in the United States and Canada. The repository currently houses salmon and steelhead genetic data as part of Genetic Stock Identification and Parentage Based Tagging projects in the Columbia River basin and throughout the Pacific Coast of North America. FishGen.net was developed by Resource Data, Inc. (RDI) for the Idaho Department of Fish and Game with funding from the Pacific Coast Salmon Recovery Fund and the Bonneville Power Administration.

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Questions/Help

Please contact Jesse McCane or Matt Campbell if you have any questions about FishGen or need any assistance:

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Home Page

You can browse the database and learn about collaborating labs without logging in. To learn about fish genetics labs that contribute to conservation and management of steelhead and salmon, click [Learn about collaborating labs](#). If you are interested in uploading or downloading data you need to be a registered user and *Log In* with your username and password. If you are not registered, click **Register** in the upper right corner of the screen.

Welcome, Guest. Home | Log In | Register | User Manual | Contact

Home Search Data Sets

FishGen

FishGen.Net

FishGen.net is a final repository for salmon and steelhead genetic data as part of Genetic Stock Identification and Parentage Based Tagging projects in the Columbia River basin and throughout the Pacific Coast of North America. FishGen.net was developed by Resource Data, Inc. (RDI) for the Idaho Department of Fish and Game with funding from the Pacific Coast Salmon Recovery Fund.

Register

Learn about collaborating labs

NOAA PACIFIC COASTAL SALMON RECOVERY FUND PROJECT DATABASE NOAA FISHERIES

IDAHO Idaho Governor's Office of Species Conservation

GENIDAQS Canada Department of Fisheries & Oceans

Northwest Fisheries Science Center Southwest Fisheries Science Center

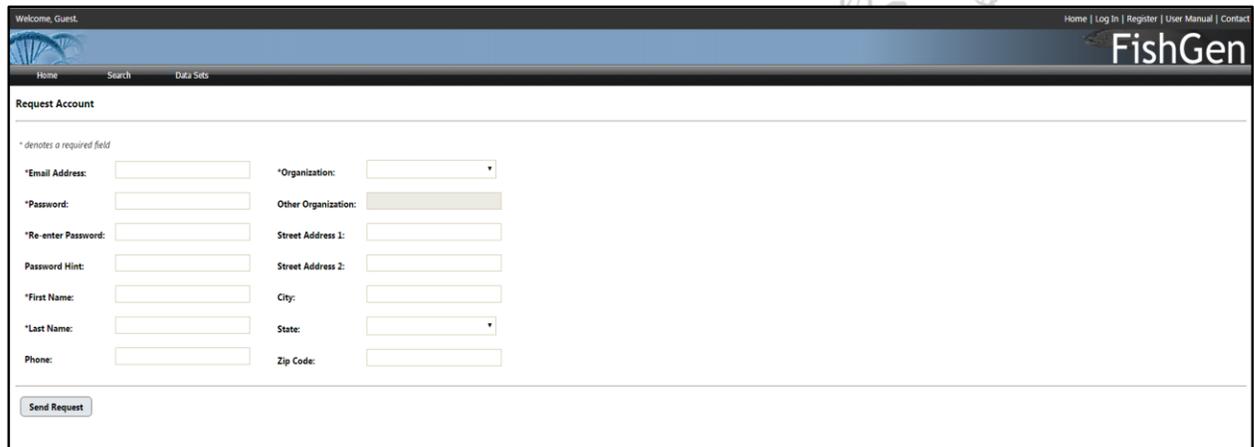
Figure 1. Home Page. In this example the user is a guest.

From this page, you may login or register for an account. To complete registration, click the **Register** heading.

Request Account Page

The **Request Account** page opens.

Required fields are denoted with an asterisk (*). After filling in the form with all required information, click the *Send Request* button. An e-mail will be sent to the FishGen curator who will verify the data and approve the account. A return e-mail will be sent from the curator notifying you that the login is ready to use.



Welcome, Guest. Home | Log In | Register | User Manual | Contact

Home Search Data Sets

Request Account

* denotes a required field

*Email Address:	<input type="text"/>	*Organization:	<input type="text"/>
*Password:	<input type="text"/>	Other Organization:	<input type="text"/>
*Re-enter Password:	<input type="text"/>	Street Address 1:	<input type="text"/>
Password Hint:	<input type="text"/>	Street Address 2:	<input type="text"/>
*First Name:	<input type="text"/>	City:	<input type="text"/>
*Last Name:	<input type="text"/>	State:	<input type="text"/>
Phone:	<input type="text"/>	Zip Code:	<input type="text"/>

Figure 2. Request Account page.

Uploading Genetic Markers

Before genetic data can be successfully uploaded on FishGen, the genetic markers in your dataset must be defined and uploaded in to the database. FishGen currently accepts definitions for both microsatellite markers and single nucleotide polymorphic markers (SNPs). For SNP markers, the database accepts three sub-types: Taqman, RAD-tag, and GTSeq. To define markers in FishGen, a text file needs to be uploaded that provides the name of the marker as well as the necessary DNA sequences, primer/probe sequences, and allelic information. This information is necessary to ensure that genetic markers used in FishGen are both standardized and unique (not duplicated within the database).

The first time that a marker (whether a microsatellite locus or SNP locus) is uploaded into the database, two things happen – a unique locus is created, and an initial marker definition for that locus is created (as described by the user’s upload file). If a user is uploading new definitions for loci/markers that already exist in FishGen, the user will identify their upload as containing marker synonyms. When this happens, no new loci are created in FishGen, but rather new marker definitions are created for existing loci. This new marker definition is described by the user’s upload file. When genetic data are uploaded to FishGen, the data are stored at the locus level – FishGen does not track which marker definition was used to generate the data. Details regarding marker synonyms and uploading procedures are described in more detail under [Creating Marker Synonyms](#).



Figure 3 - Selecting Upload Markers.

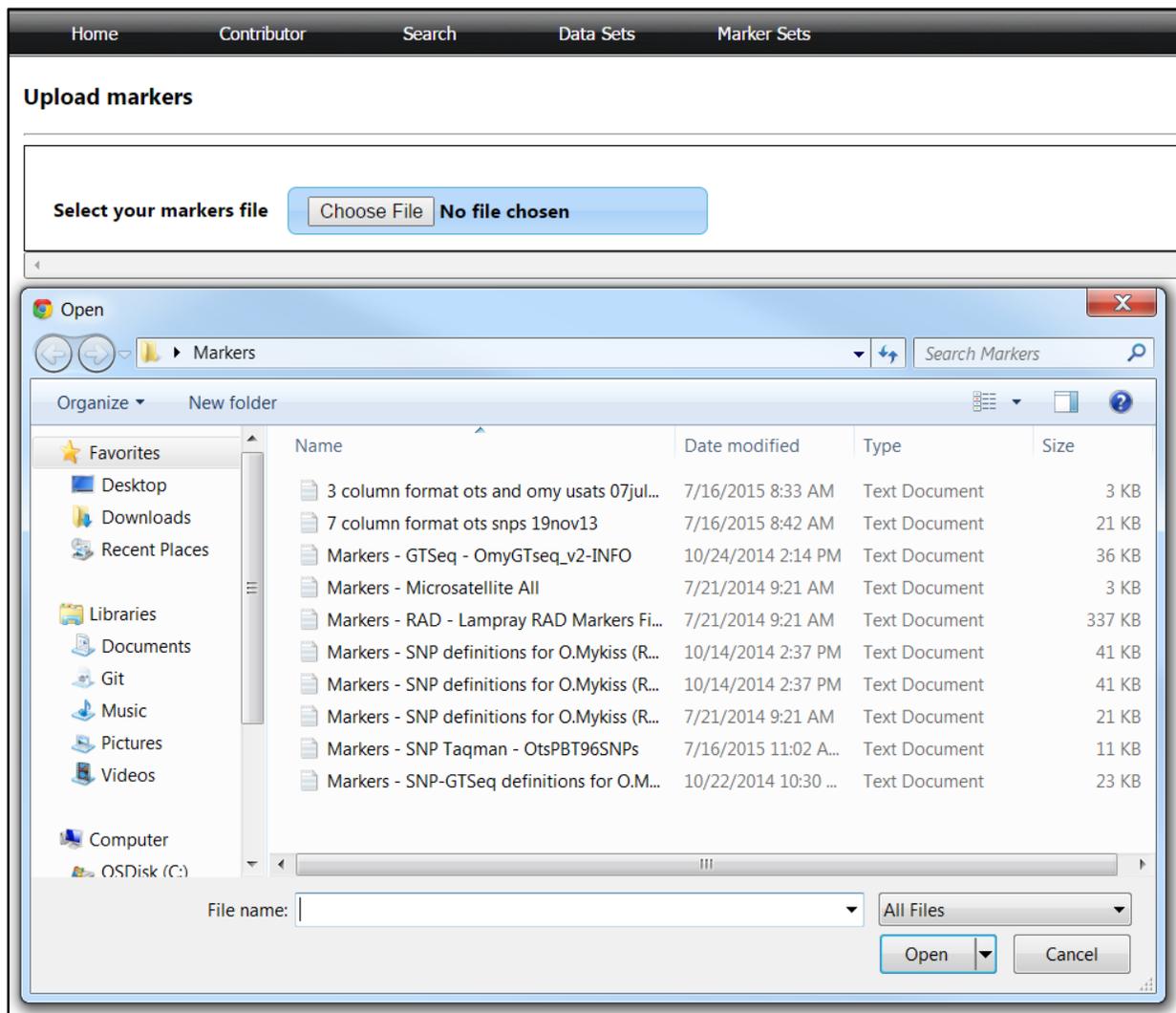


Figure 4 - Select Markers File.

Uploading Microsatellite Markers

Microsatellite markers are not species-specific in FishGen. The only information necessary to upload microsatellite markers in the database is the marker name and the forward and reverse primer sequences. This information can be saved in a tab delimited text file as shown below. Marker names must be unique - FishGen will reject marker uploads that contain markers whose names match markers that already exist in the database. FishGen will also check to ensure that the primer sequences provided have not already been assigned to a marker that exists in FishGen under a different name. Most labs using this database will be familiar with the GAPS (Chinook salmon) and SPAN (steelhead) microsatellite marker sets that have been standardized among PNW fish genetic labs. These microsatellite markers have already been uploaded into FishGen.

```

3 column format ots and omy usats 07jul15 - Notepad
File Edit Format View Help
MarkerName ForwardPrimerSequence ReversePrimerSequence
Ogo1a GATCTGGGCCTAAGGAAAC ACTAGCGGTTGGAGAACCC
Ogo2 ACATCGCACACCATAAGCAT GTTCTTCGACTGTTTCTCTGTGTTGAG
Ogo4 GTCGTCACCTGGCATCAGCTA GAGTGGAGATGCACCCAAAG
Oke4 AGGCCAAAGTCTGTAGTGAAGG GATGAATCGAGAGAATAGGGACTGAAT
Ok-i1 AGGATGGCAGAGCACCACCT CACCATAATCACATATTCAGA
Ok-i100 CCAGCACTCTCACATTTT CCAGAGTAGTCATCTCTG
Ok-i23 TGTGCTATAGGGTGAATGTGC AACACAGGCATCCCCACTAA
Omm1070 GACAGGTTGTGTCGAATGGA GGTGGGATTCAGTGTGTTAAAC
Omm1080 GAGACTGACACGGGTATTGA GTTATGTTGTCATGCCTAGGG
Omy1001 GATTCCATAACCTCGCCTTC GTCCCTGTGCTGCCTGCT
Omy1011 AACTTGCTATGTGAATGTGC GACAAAAGTGACTGGTTGGT
Omy27 TTTATGTCATGTCAGCCAGTG TTTATGGCTGGCAACTAATGT
Omy325 TGTGAGACTGTCAGATTTTGC CGGAGTCCGTATCCTTCCC
Omy7 TTAAGTTTTGCCTAGATAAGGG CAAGGAATGGCACAGCTTG
Omy77 CGTTCTCTACTGAGTCAT GGGTCTTTAAGGCTTCACTGCA
One103 AATGTTGAGAGCTATTTCAATCC GATTGATGAATGGGTGGG
One104 ATCTTTATGTTGGCAAGTCC ATCTGGTACTTCCCTGATGC
One106 TACCCTGCAAGACAGTGA GCTGTTTAGGAAGGAGGGTT
One108 TGCAGAGCCATACTAAACCA GTTTAAGAATTGAGAGATGCAGGG
One110 CCTCCATTTCAATCTCATCC ACAGAGAACAGTGAAGGGAGC
One111 ATGACCAAGGAGCTTCTGC TATCCAGGTACTCCACTGGC
One112 GTGACCCAGACTCAGAGGAC CACAAACCATCACATGAAAC
One114 TCATTAATCTAGGCTTGTACGC GTTTTGCAGGTAAGACAAGGTATCC
One115 CGTATACATTTTCCATTTTCC GTTTTTTTAAAGTGGGAGAACTTGC
One13 TCATACCCCATGCCTTCTGT GATGAGTGAAGAGAGGGAGCGA
Oneu10.2 TTTGGCACCATTTGTAAACAG CTGTAGGTGTGAAATGTATTTAAA
Oneu11 GTTTGGATGACTCAGATGGGACT TCTATCTTTCCTGTCAACTTCCA
Oneu14 AGAAACATGAGAACAGTCTAGGT CCTTATGAGTTTGGTCTCCATGT

```

Figure 5 - Example of a tab delimited text file needed to upload microsatellite marker information.

To upload the marker definition file, select the Upload Marker tab under Contributor. Next click “Choose File”. Then browse to the correct file and click “Open”.

After the text file has opened, you will need to provide the following information:

Data Formatting-

- Check the box if the first row in your marker definition file is a header row.
- Select the delimiter (tab or comma)

Marker Type-

- Select Microsatellite

Additional Upload Options-

- If you would like to save the markers that you are uploading as a unique marker set, one that you can select during data exporting, check the box labeled “Save Marker Set” and provide a name.
- If you would like to save the column mapping that you enter as a unique set, one that you can use when entering marker sets at a later time, check the box labeled “Save Column Mapping” and provide a name.

Upload markers

3 column format ots and omy usats 07jul15.txt

Data Formatting

First row is Header

Select Delimiter
Tab

Marker Configuration

New markers Marker synonyms

Marker Type

SNP

Microsatellite

SNP

Acipenser transmontanus

Additional Upload Options

Save Marker Set

Save Column Mapping

Use Saved Column Mapping:
[Select Mapping]

1	2	3
<Ignore Field>	<Ignore Field>	<Ignore Field>
MarkerName	ForwardPrimerSequence	ReversePrimerSequence
Ogo1a	GATCTGGCCCTAAGGAAAC	ACTAGCGGTTGGAGAACCC
Ogo2	ACATGGCACACCATAAGCAT	GTTTCTCGACTGTTCTCTGTGTGAG
Ogo4	GTCGCTACTGGCATCAGCTA	GAGTGGAGATGCAGCCAAAG
Oke4	AGGCCAAAGTCTGTAGTGAAGG	GATGAATCGAGAGAATAGGGACTGAAT
Ok11	AGGATGGCAGAGCACCCT	CACCCATAATCACATATTCAGA
Ok1100	CCAGCACTCTCACTATT	CCAGAGTAGTCATCTCTG

Figure 6 - Selecting Marker Type Microsatellite.

Selecting Fields-

Finally, select which columns contain the Marker Name, the Forward Primer and the Reverse Primer.

Upload markers

3 column format ots and omy usats 07jul15.txt

Data Formatting

First row is Header

Select Delimiter
Tab

Marker Configuration

New markers Marker synonyms

Marker Type

Microsatellite

Additional Upload Options

Save Marker Set

Save Column Mapping

Use Saved Column Mapping:
[Select Mapping]

1	2	3
Marker Name	Forward Primer	Reverse Primer
Marker Name	Forward Primer	<Ignore Field>
Ots1	AGATAGGTGTACATCCATA	Forward Primer
Ots2	AGTAATCGTATGCCGGTAT	Lab Synonym
Ots3	AGATAGGTGTACATCCATA	Marker Name
		Reverse Primer
		AGATAGGTGTACATCCATA

Figure 7 - Selecting Column Headers Microsatellite.

Once all necessary fields have been set and column headers entered click “Upload” to upload the markers to FishGen.

Uploading SNP Markers

The term “SNP” in this database describes a marker that interrogates a SNP using a forward and reverse primer and two allele-specific probes (i.e. Taqman SNP assays). The procedures for uploading SNP marker names and definitions are similar as those used for Microsatellite markers. However, SNPs are species-specific in FishGen, and the user must provide VIC and FAM probe sequences and VIC and FAM allele designations, along with forward and reverse primers in the marker definition text file. FishGen will check Marker Names, Primer and Probes sequences and allele designations to ensure Marker standardization. This prevents different SNPs from being uploaded into FishGen under the same name and prevents the same SNP being uploaded under different marker names.

SNPs are currently broken out in to three sub-types in FishGen, with the ability to add additional sub-types in the future as the need arises. The three sub-types currently supported are Taqman, RAD, and GTSeq. Each of these three sub-types has different required fields for upload and validation in FishGen.net, which are described below. All three SNP sub-types have a few requirements in common, such as a marker name, a VIC allele, and a FAM allele. For standardization purposes, *the VIC and FAM alleles are named based on the compliment to the probes*. If your lab follows the convention of naming alleles based on the probes themselves as opposed to the complements, you will need to adjust your genetic data accordingly in order to upload your data in to FishGen. This would involve converting between G <-> C and A <-> T in your genotypes upload.

After the text file has opened (see below), you will need to provide the following information:

Data Formatting-

- Check the box if the first row in your marker definition file is a header row.
- Select the delimiter (tab or comma)

Marker Type-

- Select appropriate SNP marker type (Taqman, RAD, or GTSeq)

Select Species-

- Select species that the SNP marker is screened on.

Selecting Fields-

- Select which columns contain the Marker Name, and the additional field values based on the SNP sub-type (see below).

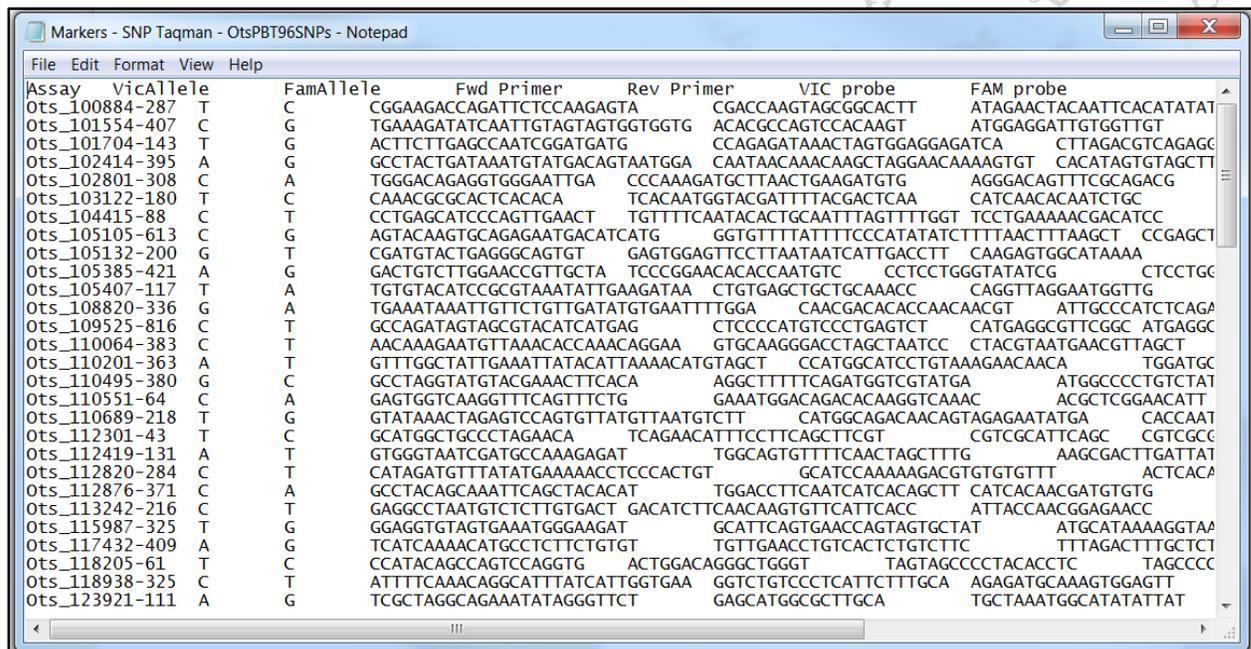
Additional Upload Options-

- If you would like to save the markers that you are uploading as a unique marker set, one that you can select during data exporting, check the box labeled “Save Marker Set” and provide a name.
- If you would like to save the column mapping that you enter as a unique set, one that you can use when entering marker sets at a later time, check the box labeled “Save Column Mapping” and provide a name.

Uploading Taqman SNP markers

Required Fields:

- Marker Name (Assay)
- VIC Allele
- FAM Allele
- Forward Primer
- Reverse Primer
- VIC Probe
- FAM Probe



```

Markers - SNP Taqman - OtsPBT96SNPs - Notepad
File Edit Format View Help
Assay  VicAllele  FamAllele  Fwd Primer  Rev Primer  VIC probe  FAM probe
Ots_100884-287  T  C  CGGAAGACCAGATTCTCCAAGAGTA  CGACCAAGTAGCGGCACTT  ATAGAACTACAATTCACATATAT
Ots_101554-407  C  G  TGAAAGATATCAATTGTAGTAGTGGTGGTG  ACACGCCAGTCCACAAGT  ATGGAGGATTGTGGTTGT
Ots_101704-143  T  G  ACTTCTTGAGCCAATCGGATGATG  CCAGAGATAAACTAGTGGAGGAGATCA  CTTAGACGTCAGAGC
Ots_102414-395  A  G  GCCTACTGATAAATGTATGACAGTAATGGA  CAATAACAACAAGCTAGGAACAAAAGTGT  CACATAGTGTAGCTT
Ots_102801-308  C  A  TGGGACAGAGGTGGGAATTGA  CCCAAAGATGCTTAACTGAAGATGTG  AGGGACAGTTTCGCAGACG
Ots_103122-180  T  C  CAAACCGCAGCTCACACA  TCACAATGGTACGATTTTACGACTCAA  CATCAACACAATCTGC
Ots_104415-88  C  T  CCTGAGCATCCAGTTGAACT  TGTTTTCAATACACTGCAATTTAGTTTTGGT  TCCTGAAAAACGACATCC
Ots_105105-613  C  G  AGTACAAGTCAGAGAATGACATCATG  GGTGTTTTATTTCCCATATATCTTTAACTTAAGCT  CCGAGCT
Ots_105132-200  G  T  CGATGACTGAGGGCAGTGT  GAGTGGAGTTCCCTAATAATCATTGACCTT  CAAGAGTGGCATAAAA
Ots_105385-421  A  G  GACTGTCTTGAACCGTTGCTA  TCCCGAACACACCAATGTC  CCTCTGGGTATATCG  CTCCTGC
Ots_105407-117  T  A  TGTGTACATCCGCTAAATATTGAAGATAA  CTGTGAGCTGCTGCAACC  CAGGTTAGGAATGGTTG
Ots_108820-336  G  A  TGAAATAAATTGTTCTGTGTGATATGTGAATTTTGGGA  CAACGACACACCAACAACGT  ATTGCCATCTCAGA
Ots_109525-816  C  T  GCCAGATAGTAGCGTACATCATGAG  CTCCCCATGTCCCTGAGTCT  CATGAGGCGTTCCGGC  ATGAGGC
Ots_110064-383  C  T  AACAAAGAATGTTAAACACCAAAACAGGAA  GTGCAAGGGACCTAGCTAATCC  CTAGCTAATGAACGTTAGCT
Ots_110201-363  A  T  GTTTGGCTATTGAAATATACATTAACATGAGCT  CCATGGCATCTGTAAAGAACAACA  TGGATGC
Ots_110495-380  G  C  GCCTAGGTATGTACGAAACTTCACA  AGGCTTTTTCAGATGGTGTATGA  ATGGCCCTGTCTAT
Ots_110551-64  C  A  GAGTGGTCAAGGTTTCAGTTTCTG  GAAATGGACAGACACAAGGTCAAC  ACGCTCGGAACATT
Ots_110689-218  T  G  GTATAAACTAGAGTCCAGTGTATGTTAATGTCTT  CATGGCAGACAACAGTAGAGAATATGA  CACCAAT
Ots_112301-43  T  C  GCATGGCTGCCCTAGAACA  TCAGAACAATTTCCCTCAGCTTCGT  CGTCGATTGAGC  CGTCGGC
Ots_112419-131  A  T  GTGGGTAATCGATGCCAAAGAGAT  TGGCAGTGTTTTCACTAGCTTTG  AAGCGACTTGATTA
Ots_112820-284  C  T  CATAGATGTTTATATGAAAAACCTCCCAGTGT  GCATCCAAAAGACGTGTGTGTTT  ACTCACA
Ots_112876-371  C  A  GCCTACAGCAAATTCAGCTACACAT  TGGACCTTCAATCATCACAGCTT  CATCACAACGATGTGTG
Ots_113242-216  C  T  GAGGCCAATGTCTCTTGTGACT  GACATCTTCAACAAGTGTTCATTACC  ATTACCAACGGGAACC
Ots_115987-325  T  G  GGAGGTGTAGTGAATGGGAAGAT  GCATTTCAGTGAACCAAGTGTGCTAT  ATGCATAAAAGGTA
Ots_117432-409  A  G  TCATCAAAACATGCCTCTCTGTGT  TGTGAACTGTCACTCTGTCTTC  TTTAGACTTTGTCT
Ots_118205-61  T  C  CCATACAGCCAGTCCAGGTG  ACTGGACAGGGCTGGGT  TAGTAGCCCTACACCTC  TAGCCCC
Ots_118938-325  C  T  ATTTTCAACAGGCATTTATCATTGGTGAA  GGCTGTCCCTCATTCTTTGCA  AGAGATGCAAAGTGGAGTT
Ots_123921-111  A  G  TCGCTAGGCAGAAATATAGGGTTCT  GAGCATGGCGCTTGCA  TGCTAAATGGCATATATTAT
  
```

Figure 8 - Example of a tab delimited text file needed to upload Taqman SNP marker information.

Upload markers

Upload Cancel Markers - SNP Taqman - OtsPBT96SNPs.txt

Data Formatting

First row is Header

Select Delimiter: Tab

Marker Configuration

New markers Marker synonyms

Marker Type: SNP

Marker Sub-type: SNP-Taqman

Additional Upload Options

Save Marker Set

Save Column Mapping

Use Saved Column Mapping: [Select Mapping]

Toggle fieldset View

1	2	3	4	5	6
<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>
Assay	VicAllele	FamAllele	Fwd Primer	Rev Primer	VIC probe
Ots_100884-287	T	C	CGGAAGACCAGATTCTCCAAGAGTA	CGACCAAGTAGGGGCACCT	ATAGAACTACAATTCACATATAT
Ots_101554-407	C	G	TGAAAGATATCAATTGTAGTAGTGGTGGTG	ACACGCCAGTCCACAAGT	ATGGAGGATTGTGGTTGT
Ots_101704-143	T	G	ACTTCTTGAGCCAATCGGATGATG	CCAGAGATAAACTAGTGGAGGAGATCA	CTTAGACGTGAGAGGTC
Ots_102414-395	A	G	GCCTACTGATAAATGTATGACAGTAATGGA	CAATAACAACAAGCTAGGAACAAGTGT	CACATAGTGTAGCTTACTAC
Ots_102801-308	C	A	TGGGACAGAGTGGGAATTGA	CCCAAGATGCTTAACTGAAGATGTG	AGGGACAGTTTCGAGACG
Ots_103122-180	T	C	CAACGCCACTCACACA	TCACAATGTACGATTTACGACTCAA	CATCAACAACATCTGC
Ots_104415-88	C	T	CCTGAGCATCCAGTTGAAC	TGTTTTCAATACACTGCAATTTAGTTTGGT	TCCTGAAAAGGACATCC

Figure 9 - Selecting Marker Type Taqman SNP.

Upload markers

Upload Cancel Markers - SNP Taqman - OtsPBT96SNPs.txt

Data Formatting

First row is Header

Select Delimiter: Tab

Marker Configuration

New markers Marker synonyms

Marker Type: SNP

Marker Sub-type: SNP-Taqman

Select Species: Oncorhynchus mykiss

Additional Upload Options

Save Marker Set

Save Column Mapping

Use Saved Column Mapping: [Select Mapping]

Toggle fieldset View

1	3	4	5	6
<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>
Assay	FamAllele	Fwd Primer	Rev Primer	VIC probe
Ots_100884-287	C	CGGAAGACCAGATTCTCCAAGAGTA	CGACCAAGTAGGGGCACCT	ATAGAACTACAATTCACATATAT
Ots_101554-407	G	TGAAAGATATCAATTGTAGTAGTGGTGGTG	ACACGCCAGTCCACAAGT	ATGGAGGATTGTGGTTGT
Ots_101704-143	G	ACTTCTTGAGCCAATCGGATGATG	CCAGAGATAAACTAGTGGAGGAGATCA	CTTAGACGTGAGAGGTC
Ots_102414-395	G	GCCTACTGATAAATGTATGACAGTAATGGA	CAATAACAACAAGCTAGGAACAAGTGT	CACATAGTGTAGCTTACTAC
Ots_102801-308	A	TGGGACAGAGTGGGAATTGA	CCCAAGATGCTTAACTGAAGATGTG	AGGGACAGTTTCGAGACG
Ots_103122-180	C	CAACGCCACTCACACA	TCACAATGTACGATTTACGACTCAA	CATCAACAACATCTGC
Ots_104415-88	T	CCTGAGCATCCAGTTGAAC	TGTTTTCAATACACTGCAATTTAGTTTGGT	TCCTGAAAAGGACATCC

Figure 10 - Selecting Species Taqman SNP.

Upload markers

Upload Cancel Markers - SNP Taqman - OtsPBT96SNPs.txt

Data Formatting

First row is Header

Select Delimiter
Tab

Marker Configuration

New markers Marker synonyms

Marker Type
SNP

Marker Sub-type
SNP-Taqman

Select Species
Oncorhynchus mykiss

Additional Upload Options

Save Marker Set

Save Column Mapping

Use Saved Column Mapping:
[Select Mapping]

Toggle fieldset View

1	2	3	4	5	6
Marker Name	VIC Allele	FAM Allele	Forward Primer	Reverse Primer	-Ignore Field-
Assay	VicAllele	FamAllele	Fwd Primer	<Ignore Field>	VIC probe
Ots_100884-287	T	C	CGGAAGACCAGATTCTCAAGAGTA	FAM Allele	ATAGAAGTACAATTCACATATAT
Ots_101554-407	C	G	TGAAGATATCAATTGTAGTAGTGGTGGTG	Forward Primer	ATGGAGGATTGTGGTTGT
Ots_101704-143	T	G	ACTTCTTGAGCCAATCGGATGATG	Lab Synonym	CTTAGACGTCAGAGGTC
Ots_102414-395	A	G	GCCTACTGATAAATGTATGACAGTAATGGA	Marker Name	GT CACATAGTGTAGCTTACTAG
Ots_102801-308	C	A	TGGGACAGAGGTGGGAATTGA	Reverse Primer	AGGGACAGTTTCGAGACG
Ots_103122-180	T	C	CAAACGCGACTCACACA	VIC Allele	CATCAACACAATCTGC
Ots_104415-88	C	T	CCTGAGCATCCAGTTGAACT	VIC Probe	TCCTGAAAAACGACATCC

Figure 11 - Selecting Column Headers Taqman SNP.

Uploading RAD SNP markers

Required Fields:

- Marker Name (Locus)
- Sequence A (e.g. Allele 1 5 3)
- Sequence B (e.g. Allele 2 5-3)
- Restriction Enzyme
- Recognition Site
- SNP Allele A
- SNP Allele B
- Sequence Length
- SNP Position

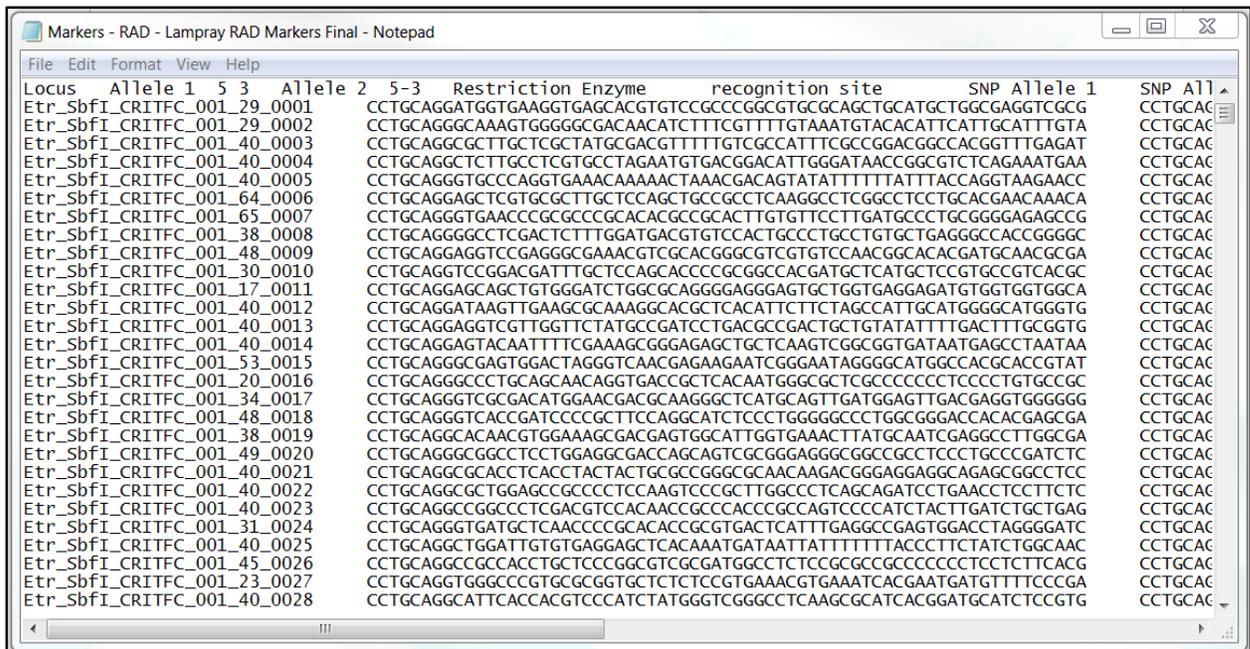


Figure 12 - Example of a tab delimited text file needed to upload RAD SNP marker information.

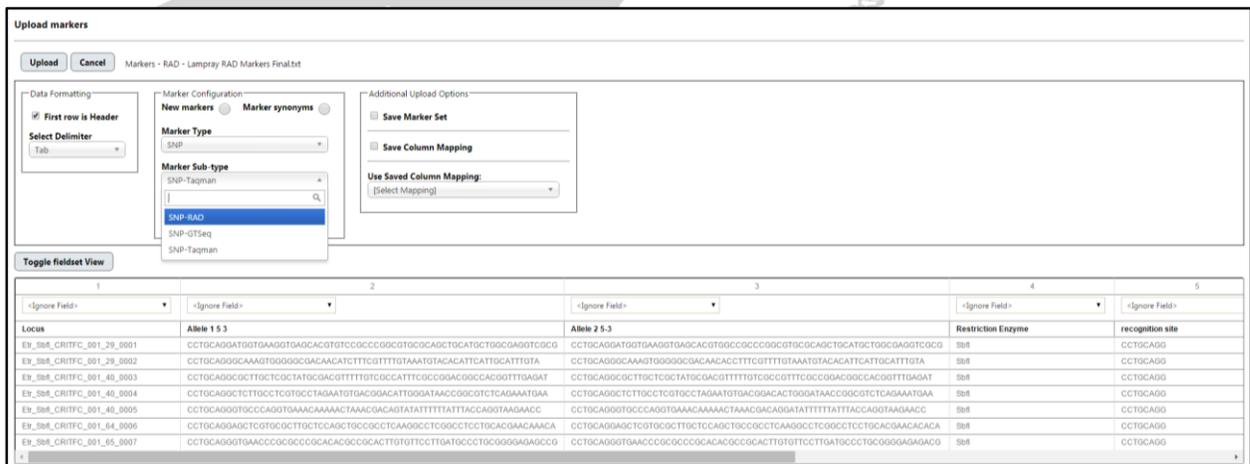


Figure 13 - Selecting Marker Type RAD SNP.

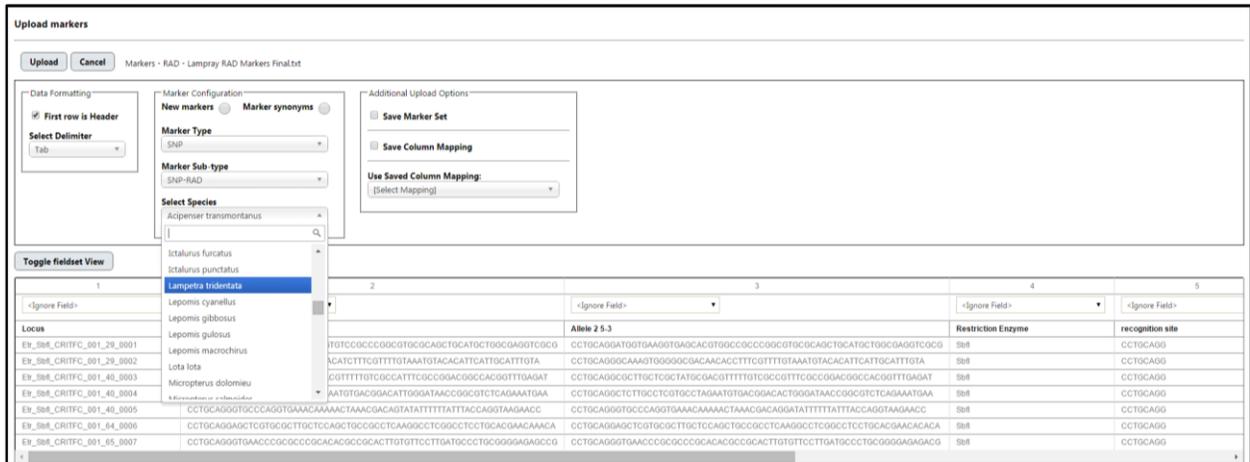


Figure 14 - Selecting Species RAD SNP



Figure 15 - Selecting Column Headers RAD SNP.

Uploading GTSeq SNP markers

Required Fields:

- Marker Name (Assay)
- VIC Allele
- FAM Allele
- Forward Primer
- Reverse Primer
- VIC Probe
- FAM Probe

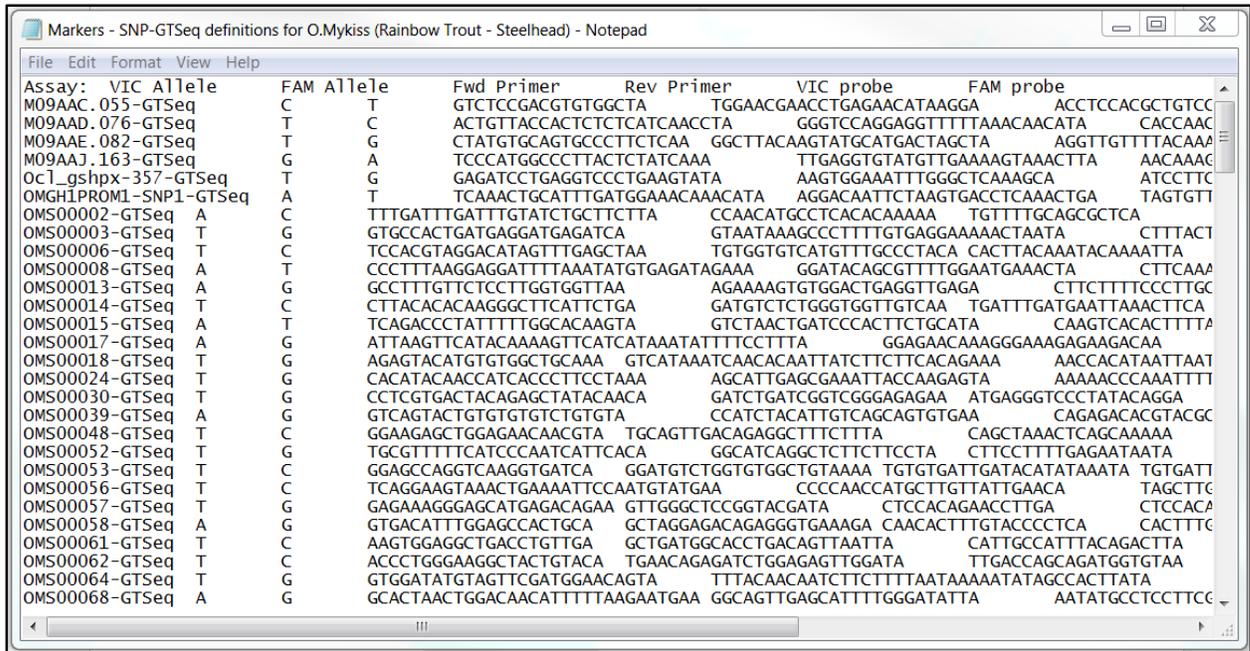


Figure 16 - Example of a tab delimited text file needed to upload GTSeq SNP marker information.

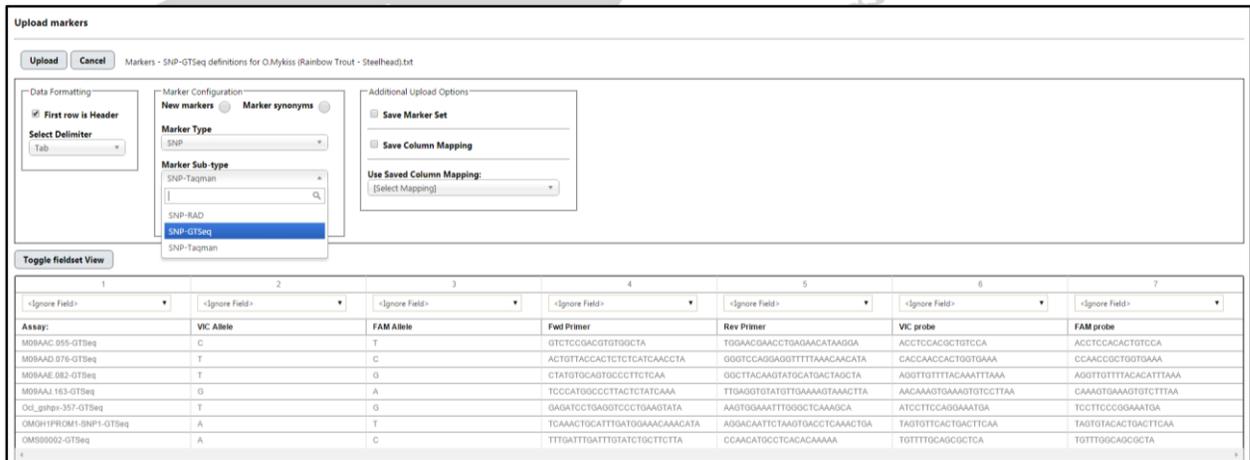


Figure 17 - Selecting Marker Type GTSeq SNP.

Upload markers

Markers - SNP-GTSeq definitions for O.Mykiss (Rainbow Trout - Steelhead).txt

Data Formatting: First row is Header
 Select Delimiter: Tab

Marker Configuration: New markers Marker synonyms
 Marker Type: SNP
 Marker Sub-type: SNP-GTSeq
 Select Species: **Oncorhynchus mykiss**

Additional Upload Options:
 Save Marker Set
 Save Column Mapping
 Use Saved Column Mapping: [Select Mapping]

1	2	3	4	5	6	7
Assay:	FAM Allele	Fwd Primer	Rev Primer	VIC probe	FAM probe	
M9BAAC-055-GTSeq	C	GTCTCCGACGTGTGGCTA	TG9AACGAACCTGAGAACATAAGGA	ACCTCCACGCTGTGCCA	ACCTCCACACTGTGCCA	
M9BAAD-076-GTSeq	T	ACTGTACCACCTCTCTCATCAACCTA	GGGTCCAGGAGGTTTTAAACAACATA	CACCACCACTGTGTGAAA	CCAACC-GCTGTGTGAAA	
M9BAAE-082-GTSeq	T	CTATGTGAGTGCCTCTCTCAA	GGCTACAAGTATGCATGACTAGCTA	AGGTTGTTTTACAAATTTAAA	AGGTTGTTTTACAGATTTAAA	
M9BAAJ-163-GTSeq	G	TCCATGGCCCTTACTCTATCAA	TTGAGGTGTATGTGAAAAGTAACTTA	AACAAGTGAAGTGTCTCTTAA	CAAAGTGAAGTGTCTTTAA	
Ocl_gfhrx-357-GTSeq	T	GAGATCTGAGTCCCTGAAAGTATA	AAGTGAAGTATGGGCTCAAAGCA	ATCCTCCAGGAATGA	TCCTCCCGAAGTGA	
OMGH1PROM1-SNP1-GTSeq	A	TCAAACGGATTGATGGAAACAACATA	AGGACAATCTAAGTGACCTCAAACTGA	TAGTGTCACTGACTCAA	TAGTGTACACTGACTCAA	
OMS90002-GTSeq	A	TTGATTGATTGTATGTGCTCTTA	CCAAGATGCTCACACAAA	TGTTTTGACGGCTCA	TGTTGGGAGCGCTA	

Figure 18 - Selecting Species GTSeq SNP.

Upload markers

Markers - SNP-GTSeq definitions for O.Mykiss (Rainbow Trout - Steelhead).txt

Data Formatting: First row is Header
 Select Delimiter: Tab

Marker Configuration: New markers Marker synonyms
 Marker Type: SNP
 Marker Sub-type: SNP-GTSeq
 Select Species: Oncorhynchus mykiss

Additional Upload Options:
 Save Marker Set
 Save Column Mapping
 Use Saved Column Mapping: [Select Mapping]

Toggle fieldset View: **VIC Probe**

1	2	3	4	5	6	7
Marker Name	VIC Allele	FAM Allele	Forward Primer	Reverse Primer	VIC Probe	-Ignore Field-
Assay:	VIC Allele	FAM Allele	Fwd Primer	Rev Primer	-Ignore Field- FAM Allele FAM Probe Forward Primer Lab Synonym Marker Name Reverse Primer VIC Allele	FAM probe
M9BAAC-055-GTSeq	C	T	GTCTCCGACGTGTGGCTA	TG9AACGAACCTGAGAACATAAGGA	ACCTCCACGCTGTGCCA	ACCTCCACACTGTGCCA
M9BAAD-076-GTSeq	T	C	ACTGTACCACCTCTCTCATCAACCTA	GGGTCCAGGAGGTTTTAAACAACATA	CACCACCACTGTGTGAAA	CCAACC-GCTGTGTGAAA
M9BAAE-082-GTSeq	T	G	CTATGTGAGTGCCTCTCTCAA	GGCTACAAGTATGCATGACTAGCTA	AGGTTGTTTTACAAATTTAAA	AGGTTGTTTTACAGATTTAAA
M9BAAJ-163-GTSeq	G	A	TCCATGGCCCTTACTCTATCAA	TTGAGGTGTATGTGAAAAGTAACTTA	AACAAGTGAAGTGTCTCTTAA	CAAAGTGAAGTGTCTTTAA
Ocl_gfhrx-357-GTSeq	T	G	GAGATCTGAGTCCCTGAAAGTATA	AAGTGAAGTATGGGCTCAAAGCA	ATCCTCCAGGAATGA	TCCTCCCGAAGTGA
OMGH1PROM1-SNP1-GTSeq	A	T	TCAAACGGATTGATGGAAACAACATA	AGGACAATCTAAGTGACCTCAAACTGA	TAGTGTCACTGACTCAA	TAGTGTACACTGACTCAA
OMS90002-GTSeq	A	C	TTGATTGATTGTATGTGCTCTTA	CCAAGATGCTCACACAAA	TGTTTTGACGGCTCA	TGTTGGGAGCGCTA

Figure 19 - Selecting Column Headers GTSeq SNP.

Creating Marker Synonyms

Marker “synonyms”, or new definitions for loci/markers that have already been defined in FishGen, can also be created. When uploading markers, a user has two options – uploading new loci and associated marker definitions, or uploading new marker definitions for existing loci. A marker definition upload cannot contain a mix of new markers and new definitions for existing markers. Thus, some initial work may be necessary to split your marker definitions file into two files – one that contains new markers not previously defined in FishGen, and one that contains new definitions for markers that *have* been previously defined in FishGen. The latter may result when a marker has already been uploaded into FishGen but has had a modification to the primer or probe sequence, or is being interrogated using a different platform/chemistry (e.g. Taqman versus GTSeq). It is important to note that the onus is on the user to export existing markers from FishGen to determine if there is any overlap between what is

currently in FishGen and what markers they wish to upload.

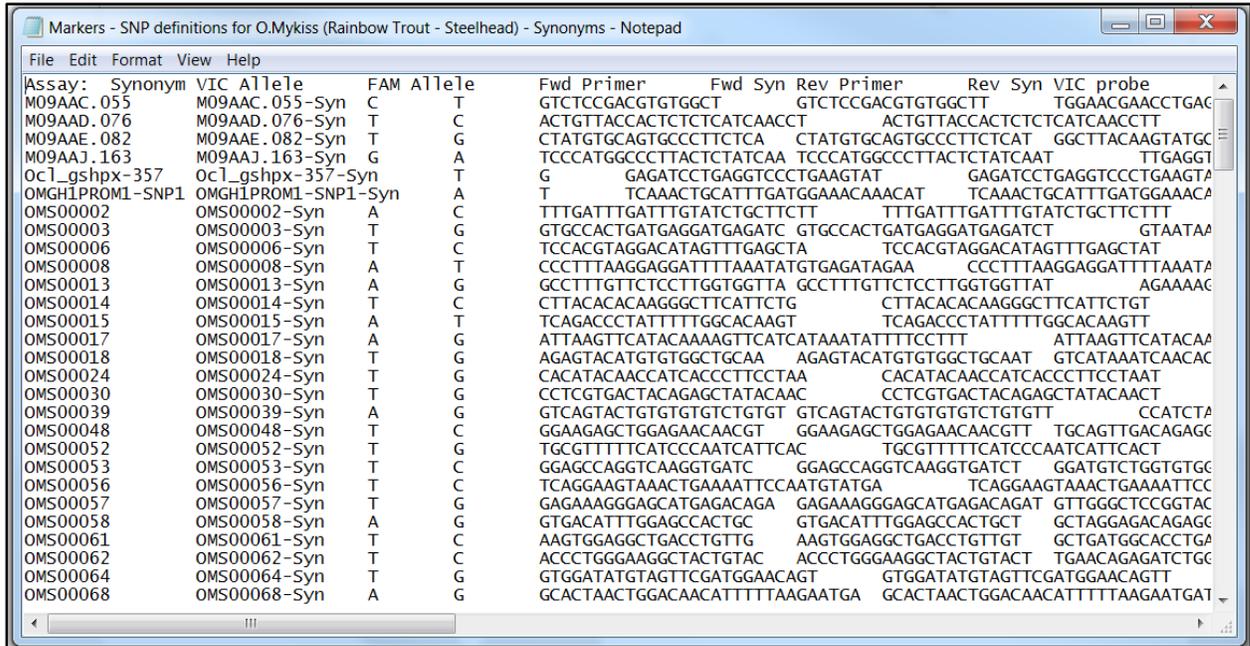


Figure 20 - Example of a tab delimited text file needed to upload marker synonym information.

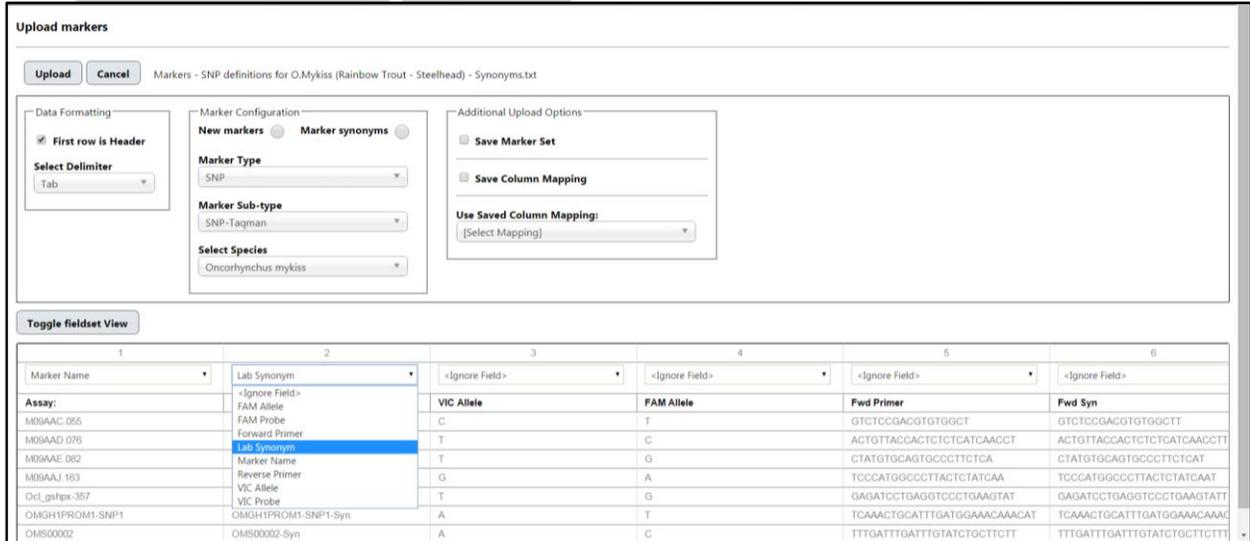


Figure 21 - Selecting Column Headers synonyms file.

Creating and Exporting marker sets

Creating custom marker sets

Sets of markers can be saved when uploading markers to FishGen, but custom marker sets can also be created and saved using the Marker Sets feature. To create a custom marker set, select “Marker Sets” and choose the dropdown: “Create”. This will bring you to the Custom Marker Set page where you can select markers using a dropdown list or upload a list of markers via a text file. The text file simply contains a list of the marker names you are interested in including in a set. The markers must have already been uploaded in FishGen and the marker name must match exactly. After the text file has opened (Figure 22), you will need to provide the name of your custom marker set and the marker type (Microsatellite, Taqman SNP, RAD SNP, or GTSeq SNP). Again, the advantage of custom marker sets is that the user can select these during data exporting.

Figure 22 - Selecting markers for a saved marker set.

Exporting custom marker sets

Once a marker set has been saved in FishGen, users can export a text file containing all of the information that defines the markers in that set (e.g. name, primer sequence, etc.).

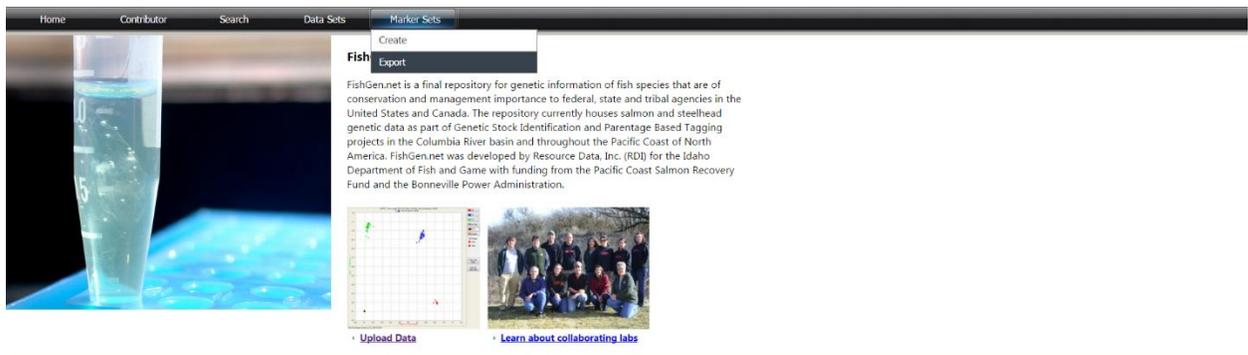


Figure 23 - Selecting Export Marker Set.

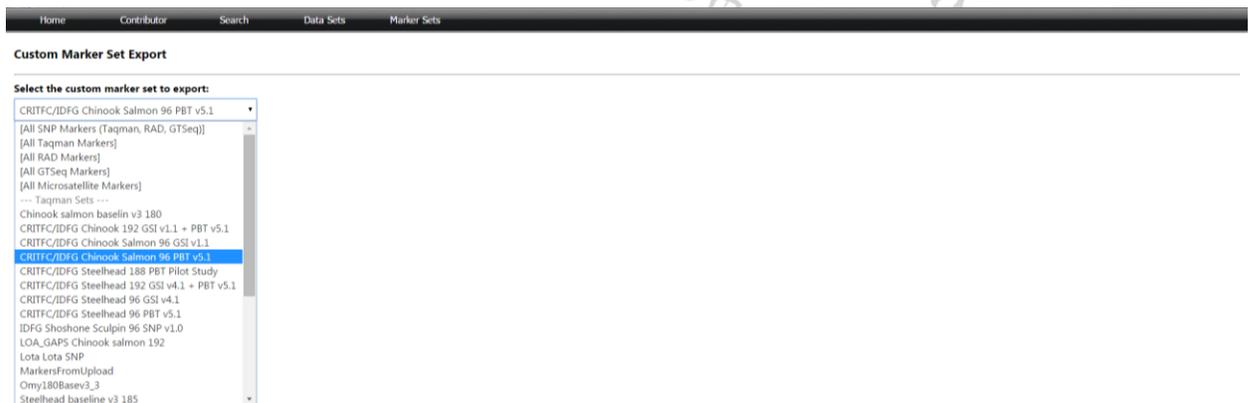


Figure 24 - Export Custom Marker Set

Uploading genetic data

Once the genetic markers in your dataset have been defined and uploaded in FishGen, you can upload a data file that contains metadata and genetic data from a dataset. Metadata is captured within Collection Fields and Individual Fields. Collection fields contain information that applies to all individuals within the collection. Within a collection field, all of the data must be the same for all rows. Individual fields contain information unique to an individual fish. FishGen only requires that seven collection fields are completed and three individual fields are completed. Complete lists of possible fields and valid entries for each field are available in [Appendix A](#) and [Appendix B](#) as well as at <https://www.fishgen.net/webpages/legalvalues.aspx>

Required Collection Fields-

Body of Water: The river, stream, creek, lake, pond, ditch, etc. that your sample came from.

FishGen will automatically calculate HUC8 designations, so additional details regarding drainage, basin,

etc. are not needed.

Hatchery: The hatchery your samples came from.

Collection Species: Genus species. Must be written out completely and spelled correctly. The term "Mixed" can be used for hybridization studies that involve sampling multiple species. However, Mixed is not intended to be used outside of hybridization studies (e.g. you wouldn't include a sample of steelhead and Chinook salmon under the same collection).

Collection Origin: Whether the collection consists of wild, hatchery or a mixture of wild and hatchery fish.

Sample Year: In what year (e.g. 2013) or range of years (e.g. 2013 – 2014) did the samples in your collection come from.

Collection Latitude and Longitude: Collection latitude and longitude are extremely important, since FishGen will calculate and autopopulate State/Province and USGS Hydrological Unit Code (HUC) information for your collection. Collection Latitude and Longitude must be the same for all individuals in the collection. In a situation where you have sampled multiple locations within a stream, individual latitude/longitude coordinates can be entered at the individual level. Please see section below titled: [Entering Latitude and Longitude coordinates for your dataset](#).

Collection Name: A name that describes each collection of samples. We recommend that these names are descriptive, since each collection name must be unique in FishGen and is limited to 30 characters. One example might be OmyOXBO08, which combines information on species, sample location, and sample year.

Required Individual Fields-

Individual Name: A name that describes each collection of samples. We recommend that these names are descriptive, since each name must be unique in FishGen and is limited to 30 characters. One example might be OmyOXBO08, which combines information on species, sample location, and sample year.

Phenotypic Sex: This information is useful for Parentage Based Tagging programs. Valid fields are: F = Female; M = Male; U = Unknown

Phenotypic Species: A list of valid species is provided in [Appendix D Valid Species List](#) as well as at www.fishgen.net/webpages/legalvalues.aspx

Valid Genetic Data-

Microsatellite data

- The allele values can be in 2-digit or 3-digit format: 01-99 or 001-999
- Alleles can't be >999
- X, Y for sex marker
- 0, 00, or 000 could be input for no data
- Can't have blank cells
- Can't have one allele with 0 and the other allele >0
- Can't have any other text than X, Y
- Text and numbers cannot go together (e.g. X, 0)

SNP data

- Alleles can be in numeric or alpha characters.
- For alpha characters, allele values are A, C, G, T, X, Y, 0, or -
- For numeric values we follow the HapMap standard: A = 1, C = 2, G = 3, T = 4, - = 5
- For sex markers, use X = 6 and Y=7
- 0 is no data

Entering Latitude and Longitude coordinates for your dataset

As mentioned above, entering accurate estimates of Latitude/Longitude coordinates for sample collections is important, because the database will map these collections and estimate Hydrological Unit Codes (United States) and/or Watershed Groups and Watershed names (Canada) for collections and auto-populate these values within the database. Although it is encouraged that users require samplers to measure latitude/longitude coordinates in the field with a GPS unit, the database does allow users to locate sample locations on ESRI map layers and cut and paste latitude/longitude values. The database also allows users to enter latitude/longitude coordinates and zoom in to see the point on an ESRI map for verification purposes.

Find latitude/longitude coordinates for a collection

To find latitude/longitude coordinates, simply use the available map layers on the search page and the coordinate widget (Figure 25) to place a pin on the map and obtain Latitude and Longitude coordinates that can be copied and pasted into a text file. To activate the pin, click your mouse once. This will place a pin on the map and show the latitude and longitude coordinates in the coordinate box. The coordinate box can also be used to help find a location by typing in an address or landmark name.

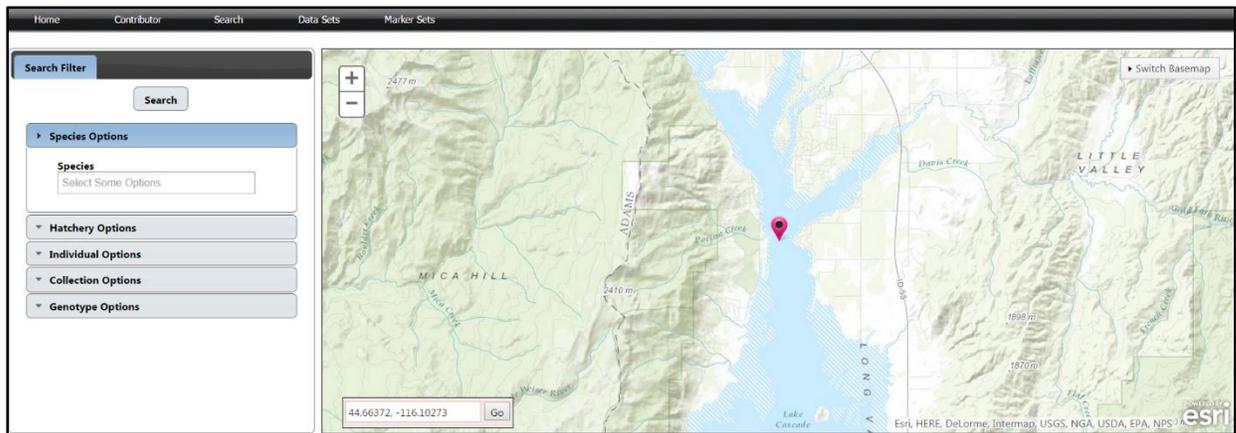


Figure 25. Coordinate widget for placing a point on the map. The pin is red (in Lake Cascade).

Verify latitude/longitude coordinates for a collection

To find verify that the latitude/longitude coordinates you have associated with a collection are accurate, simply cut and past the coordinates into search box in the bottom left of the screen (latitude, longitude) and press “Go” (Figure 26). Then use the map layers and the zoom (+ -) buttons to identify where coordinates currently map your collection.



Figure 26. Verifying latitude/longitude coordinates.

Uploading Collections

To upload a text file that contains meta- and genetic collection data you can either select “Upload Data” below the SNP plot picture on the home page or select “Contributor” from the header line and select “Upload Collections” from the drop-down (Figure 27).

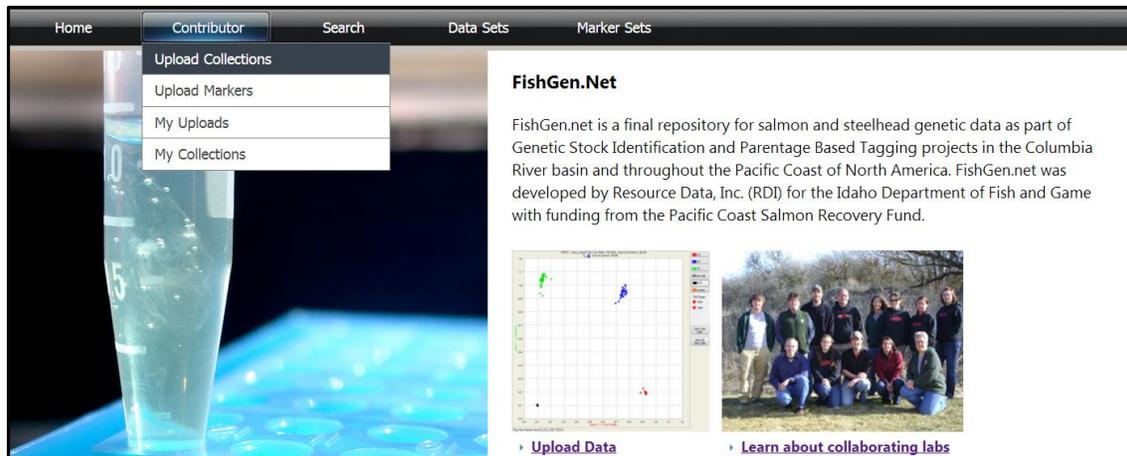


Figure 27. Upload collections from the Contributor dropdown.

This will bring you to the Upload Collection Page (Figure 28). Here you will choose “Standard” as the upload type and then the “Choose File” button, where you can browse for your text file saved on your computer.

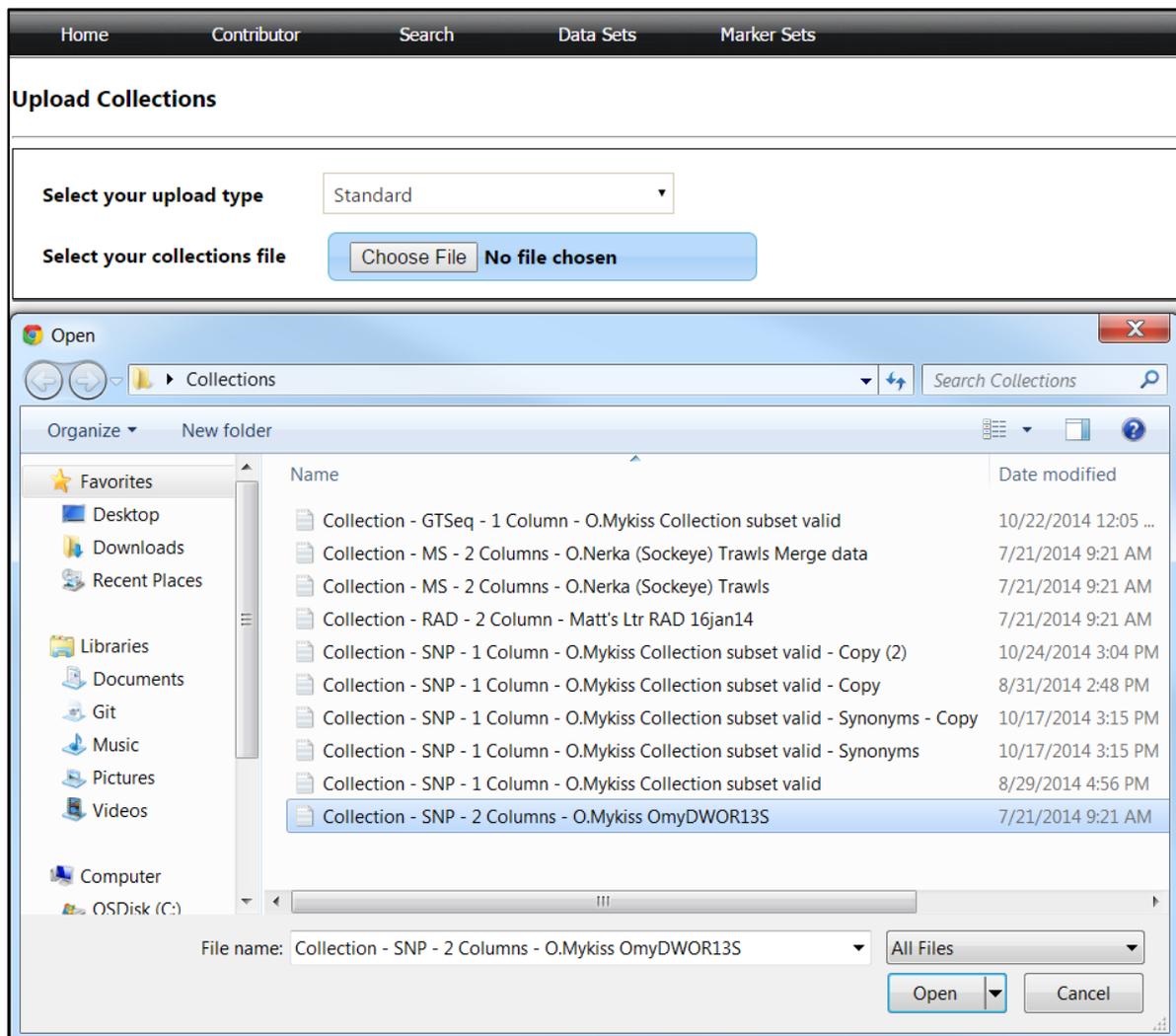


Figure 28. Browse for text file containing collection information - Standard.

After selecting your file and pressing “Open”, FishGen will bring up your file in the Upload Collections window (Figure 29).

1	2	3	4	5	6
<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>
Pedigree	Individual Name	Hatchery	Gender	Species	Latitude
OmyDWOR135	OmyDWOR135_0001	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR135	OmyDWOR135_0002	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR135	OmyDWOR135_0003	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR135	OmyDWOR135_0004	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR135	OmyDWOR135_0005	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR135	OmyDWOR135_0006	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR135	OmyDWOR135_0007	Dworshak NFH	M	Oncorhynchus mykiss	46.50225

Figure 29. Upload Collections Window - Standard

After the text file has opened, you will need to provide the following information:

Data Formatting

- Select the delimiter (tab or comma)
- Identify the column number where the genetic data begins. This would be the first column that follows metadata fields. Note that all columns containing genetic data must be to the right of all columns containing metadata.
- FishGen accepts genetic data in 1 or 2 column format. The default is 2 columns and the box is checked automatically. If your data is in 1 column format, uncheck the box.
- FishGen accepts genetic data in numeric or letter format: A = 1, C = 2, G = 3, T = 4, - = 5, X = 6, and Y = 7. The default is letter format. If your data is in numeric format, check the box.

Allele Suffix Configuration

- Marker names must include a suffix differentiating allele 1 from allele 2. Some examples include: _1/_2; -A/-B; L/R; etc. Please indicate what configuration is used. Pressing the “Preview Marker Name” button should show the marker name in the first column where the genetic data begins. The name shown will not include the allele suffix.

Additional Upload Options

- Genetic data that is uploaded to FishGen can either be made immediately available to the public or stored privately for up to 6 months. The 6 month time period is intended to allow the user to meet project/reporting requirements while preparing data for publication. If the “Data set is Private” box is checked, FishGen will withhold the release of the submission for up to 6 months. During this period, the user may delete the uploaded collections without contacting the curator. The user will be notified via e-mail 1 month prior to the release date, and again 1 week prior to the release date. After 6 months, the submission will be made public.
- The “Save Data Set” feature allows the user to save the collections that are being uploaded into

a separate stored file. **It is critical that the user understands that “Saved Datasets” are snapshots of collections (meta and genetic data) stored in the database. Any subsequent changes that might occur in the source database will not be reflected in “Saved Datasets”.** We envision that “Saved Datasets” will include such things as a completed PBT baseline that will be used for analyses and reporting purposes during a particular return year. In these situations, the uploader will likely email collaborators with the name and description of the saved dataset. Another example of a “Saved Dataset” may be a collection of samples and genetic data that are part of a published manuscript. For example, FishGen currently contains metadata and genetic data for all 15,658 individuals as part of the *Blankenship et al 2011* paper examining major steelhead lineages and metapopulations in Columbia River basin. Datasets can also be created manually using the “Create” option under the Data Sets heading (see [Creating Saved Datasets](#) below)

- “Column mapping” refers to association of column headings in the uploader’s text file with the appropriate collection and individual fields used in the database. This process will be somewhat time consuming, especially if you are new to the database and have many metadata fields. To make this process faster for future uploads, the user can save the column mapping configuration and then use that saved configuration to map additional collection uploads. To use this feature, check the “Save Column Mapping” box and name it. On future uploads, after the text file has been uploaded, select the appropriate Column Map from the “Use Saved Column Mapping:” dropdown and the database will automatically fill in the correct column headings.

Adding genetic data to existing collections/individuals

FishGen has the functionality to allow a user to add genetic data to collections/individuals that have already been uploaded to the database. To add genetic data to existing individuals, navigate to the “Contributor” tab and then to the “Upload Collections” dropdown. To add genetic data to collections and individuals that have already been uploaded in FishGen, select the “Merge” feature under the “Select your upload type” (Figure 30). From there, click “Choose File” to browse and select your text file for upload. The text file must contain Collection and Individual Names and then columns of genetic data. Similar to a standard upload, the user must fill in information for Data Formatting, Allele Suffix Configuration, and Additional Upload Options.

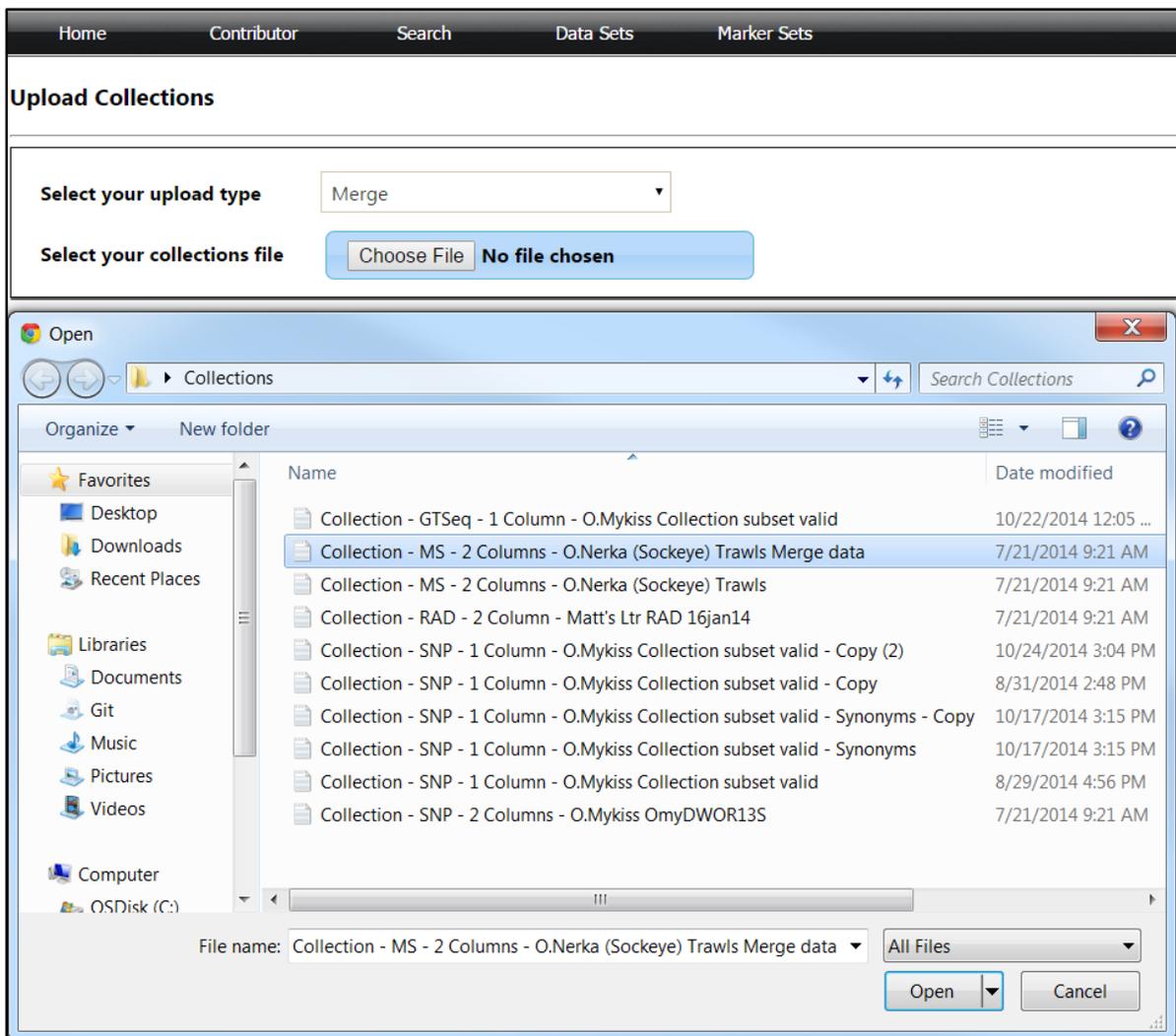


Figure 30 - Browse for text file containing collection information - Merge.

1	2	3	4	5	6
<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>
Collection Name	Individual Name	Ssa408-A1	Ssa408-A2	Ssa407-A1	Ssa407-A2
OneALTL12CTR	OneALTL12CTR_0001	256	300	160	160
OneALTL12CTR	OneALTL12CTR_0002	232	232	168	168
OneALTL12CTR	OneALTL12CTR_0003	232	236	168	208
OneALTL12CTR	OneALTL12CTR_0004	268	276	168	168
OneALTL12CTR	OneALTL12CTR_0005	272	276	168	204
OneALTL12CTR	OneALTL12CTR_0006	236	276	168	172
OneALTL12CTR	OneALTL12CTR_0007	232	268	160	160

Figure 31 - Upload Collections Window – Merge.

Creating Saved Datasets

As mentioned previously, “Saved Datasets” can be created during collection upload. In addition, “Saved Datasets” can be created using the “Create” dropdown under the “Data Sets” heading (Figure 32).

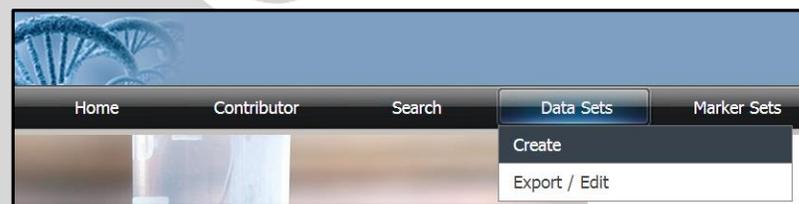


Figure 32 - Creating saved datasets.

This will take you to the “Create Data Set” page where you will be asked to choose a file. At minimum, this text file requires a list of Individual sample names and their corresponding Collection Name (Figure 33). These individuals must have already been uploaded to FishGen. The user can also add additional columns of information when creating a saved dataset. We envision using this functionality for things like adding a “group” identifier to collections. For example, an additional column of information can be added to identify reporting groups that could be used for GSI purposes (Figure 34). It is important to keep in mind that these additional columns of information are not saved within the FishGen database. This information is only included in the saved dataset.

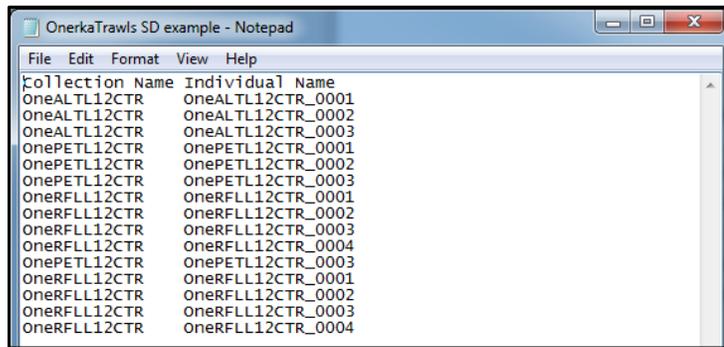


Figure 33 - Example of a text file that would be uploaded to create a saved dataset.

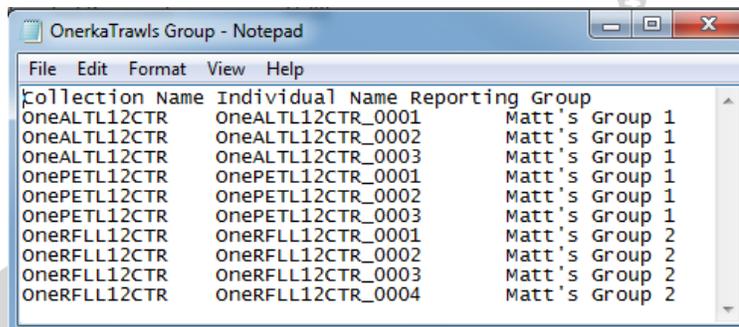


Figure 34 - Example of a text file that would be uploaded to create a saved dataset and add a column with group designations.

After selecting the text file from which to create the dataset the user will be taken to the Create Data Set page. Here the user will be required to provide a name for the dataset, designate whether the dataset should be kept private for six months ([see above](#)), specify a marker set for the dataset (required), and add any additional notes regarding the dataset. Clicking “Upload” adds the dataset to the FishGen database.

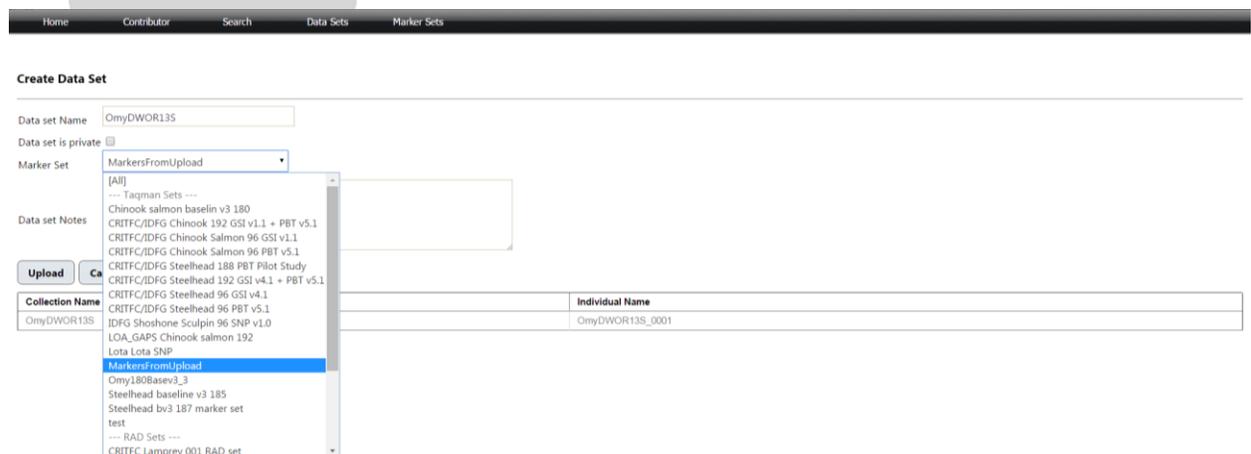


Figure 35 - Create Data Set

Searching for saved datasets and collections

Saved Datasets

The easiest way to search for genetic collections stored on FishGen is from the home page, under the heading “Data Sets” and then the dropdown “Export/Edit” (Figure 36).

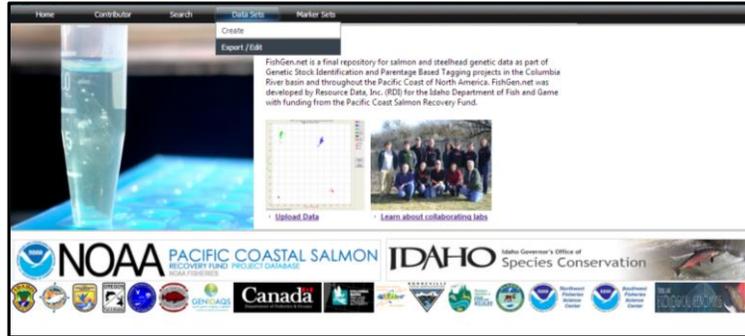


Figure 36. Find and export saved datasets.

This will take you to the “Data Set Find and Export” page (Figure 37). From here you can search by Dataset Name, Species, Organization, or BPA project number. If you know the name of the saved dataset in which you are interested (e.g. Blankenship et al 2011), typing this name into the “Name” box and clicking the Search button will bring the dataset up in the Search Results window. Clicking the “Map Datasets” link in the top right corner of the Search Results table will place an icon on the map for each result row in the table that has the “Map” checkbox checked. Once the icons have been placed on the map, you can press the “Notes” button to read a brief summary of the saved dataset, you can click the blue “Export” link to export the dataset, or you can click the blue “Delete” link to delete the dataset. Currently, collections and datasets in FishGen can be exported in GenePop format or FishGen format. Details of these formats are described below:

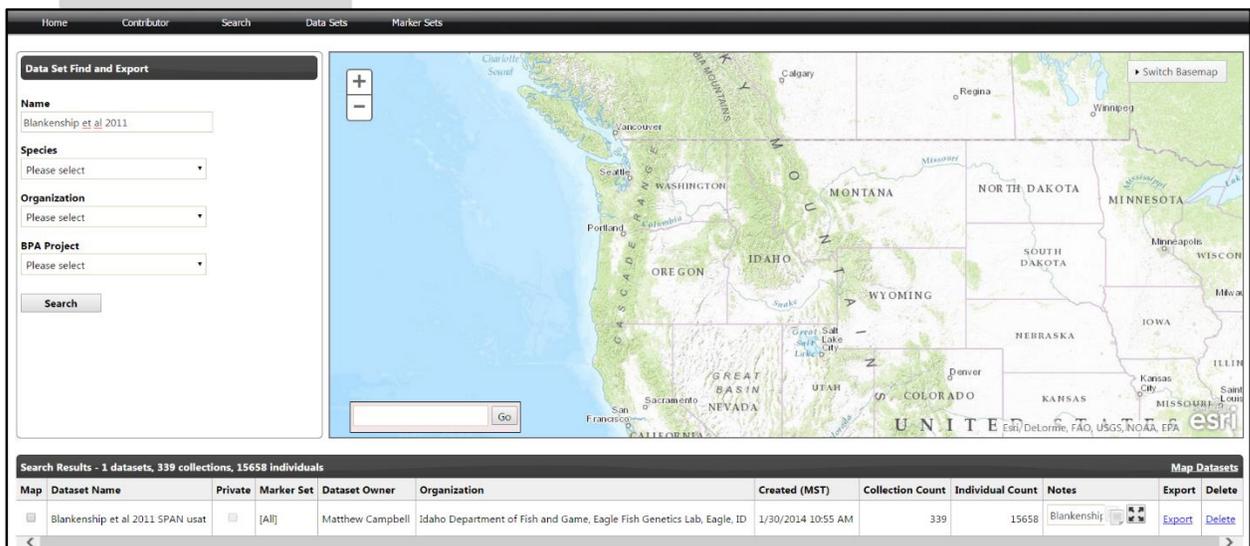


Figure 37. Data Set Find and Export page.

GenePop format details:

- Tab-delimited .txt file
- First row contains the title line or any use line
- The second row contains the names of loci, separated by commas
- The first row after locus names contains the word: Pop (no case sensitivity). This is also used as a header each time a new population is started.
- Rows following “Pop” include the sample name, alleles at each locus, separated by a space between loci (missing data should be indicated with 0, not a blank).
- The exported GenePop file can be cut and pasted directly into GenePop on the web for analyses or can be uploaded into Genalex for analysis or additional conversion to other software formats.

FishGen format details:

- Tab-delimited .txt file
- First row always contains column header names
- One row per individual
- First column always contains some sort of population/collection identifier
- Second column always contains some sort of unique individual identifier
- Columns 3 through # are collection/individual level fields, whichever are selected by the user for exporting. The number of fields exported is flexible.
- All columns after the last collection/individual level field contain genetic data:
- Two columns per marker (regardless of marker type)
- SNP (Taqman, RAD, GTSeq) data:
 - VIC/Allele A in the first column
 - FAM/Allele B in the second column
- uSAT data:
 - Three-digit numbers or 000 for no Call.
 - First Allele in the first column
 - Second allele in the second column

Searching for collections

When not looking for saved datasets, the database can be searched for available collections by selecting the “Search” tab from the toolbar. This will bring up the Search Page (Figure 38), where you can search for collections using several filters and sub-options. The primary filter options are Species, Hatchery, Individual, Collection, and Genotype. To search for collections select a filter option, select the appropriate parameters, then click the “Search” button.



Figure 38. Search page.

Under species, only species that have actually been uploaded into FishGen are shown (Figure 39).



Figure 39. Filtering by species.

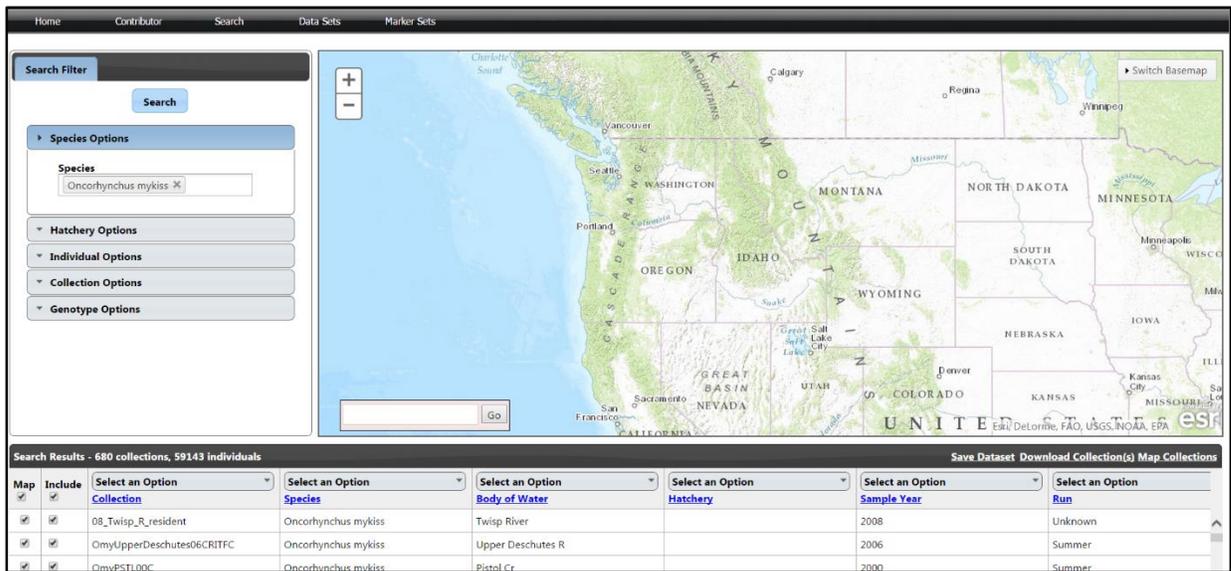


Figure 40 - Search Results by Species.

Under “Hatchery options”, several sub-options are available: Hatchery States, Hatchery, Funding Source and Organization. Selecting the “Hatchery States” sub-option will show you all States that currently have hatcheries represented in the database. After selecting a State and pressing “Search”, all hatchery collections present in the database from that State are shown in the Search Results table (Figure 41).

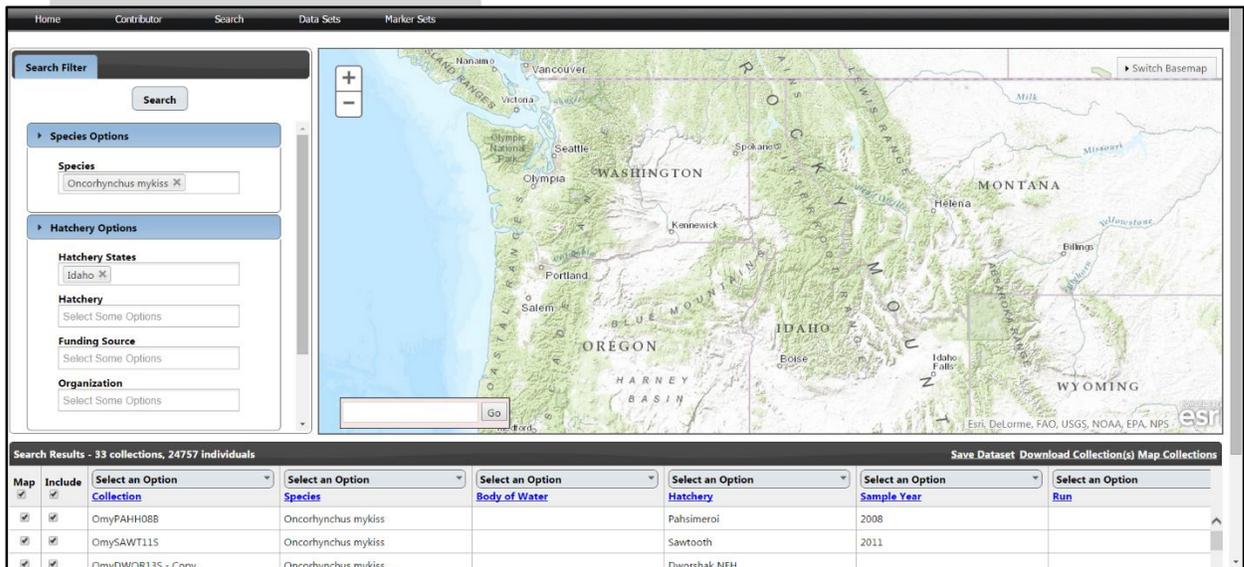


Figure 41. Search Results by hatchery collections.

Under “Individual options”, two sub-options are available:

Sex and Origin. In addition to these sub-options, several check boxes are also included: Has PIT Tag, Has CWT Tag, Has Jaw Tag and Has Floy Tag.

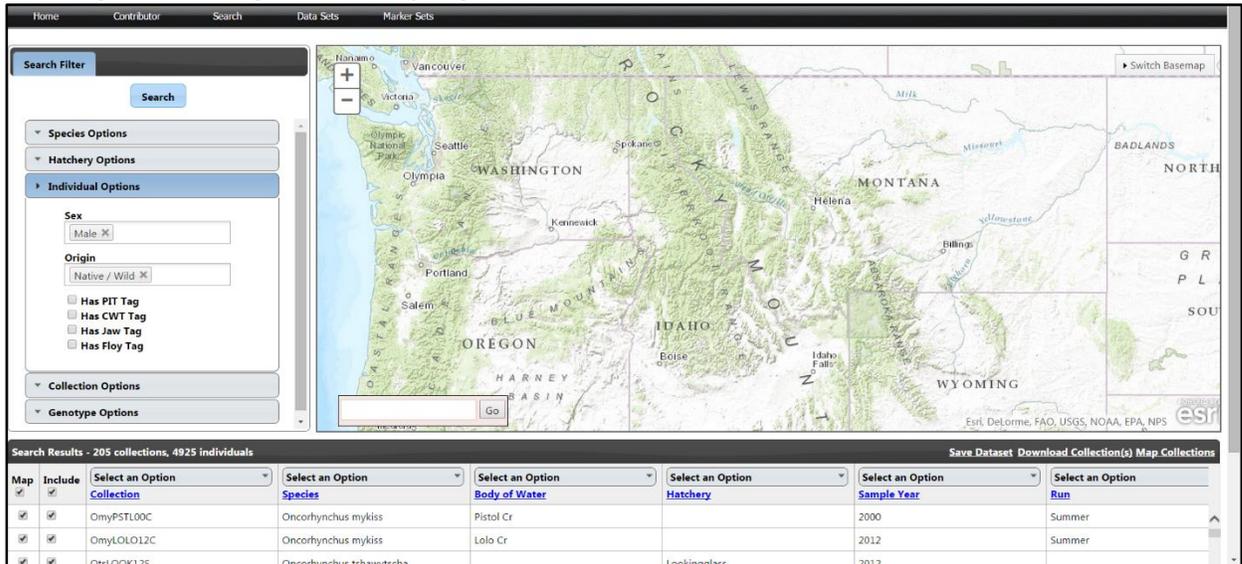


Figure 42 - Search Results by Individual.

Under “Collection Options”, the following sub-options are available: Sample Year range search, HUC4, BPA Projects, and Life Stage.

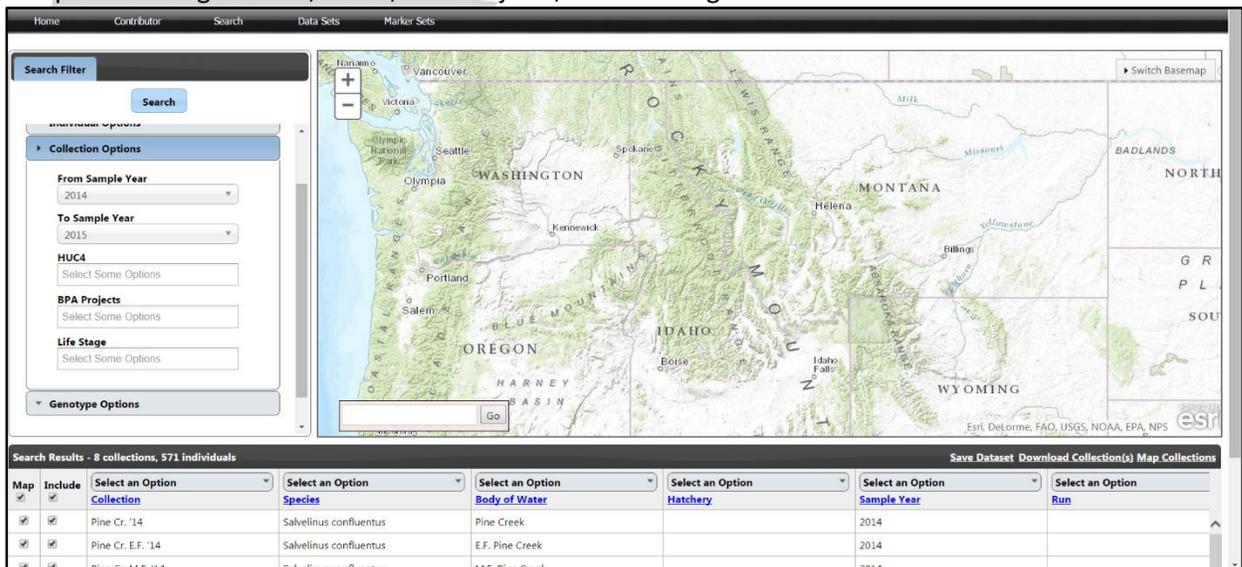


Figure 43 - Search Results by Collection.

Under “Genotype Options”, the following sub-options are available: Marker and Marker Set

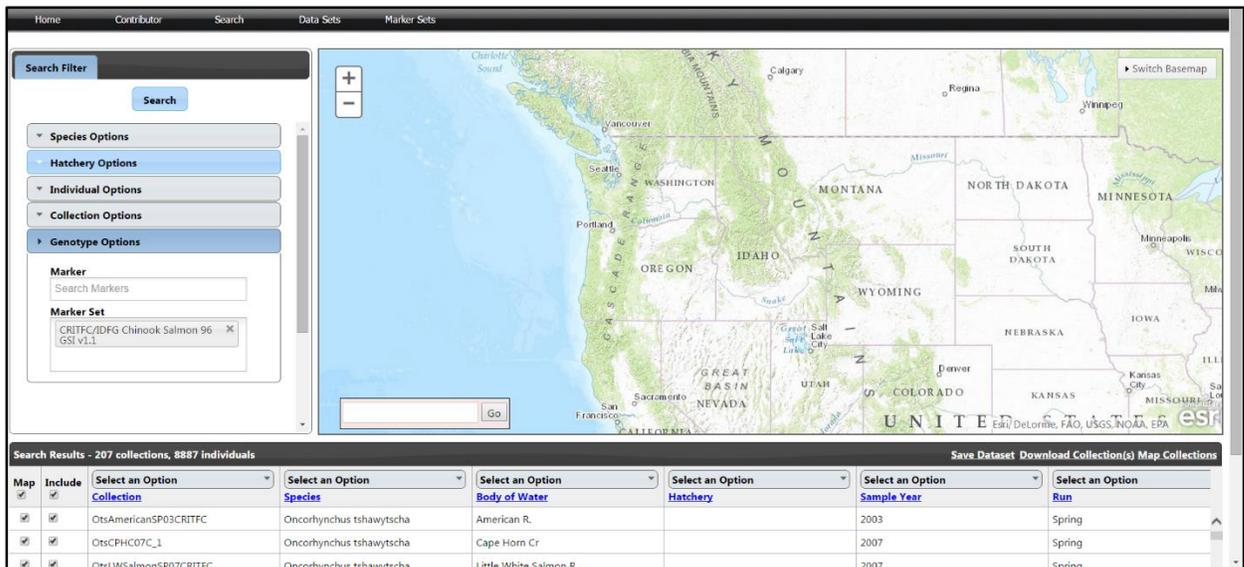


Figure 44 - Search Results by Genotype.

Search results may be plotted on the map at any time by clicking on the “Map Collections” link in the top right corner of the Search Results Table. Only rows that have the “Map” checkbox checked will be mapped. Individual rows can be included or excluded by toggling the “Map” checkbox for the selected row(s), or all rows can be included or excluded by checking the checkbox in the header row just under “Map”. The “Switch Basemap” dropdown can be used to select from different basemap options: Imagery With Labels, Streets, Topographic, National Geographic, HUC, and Open Street Map.

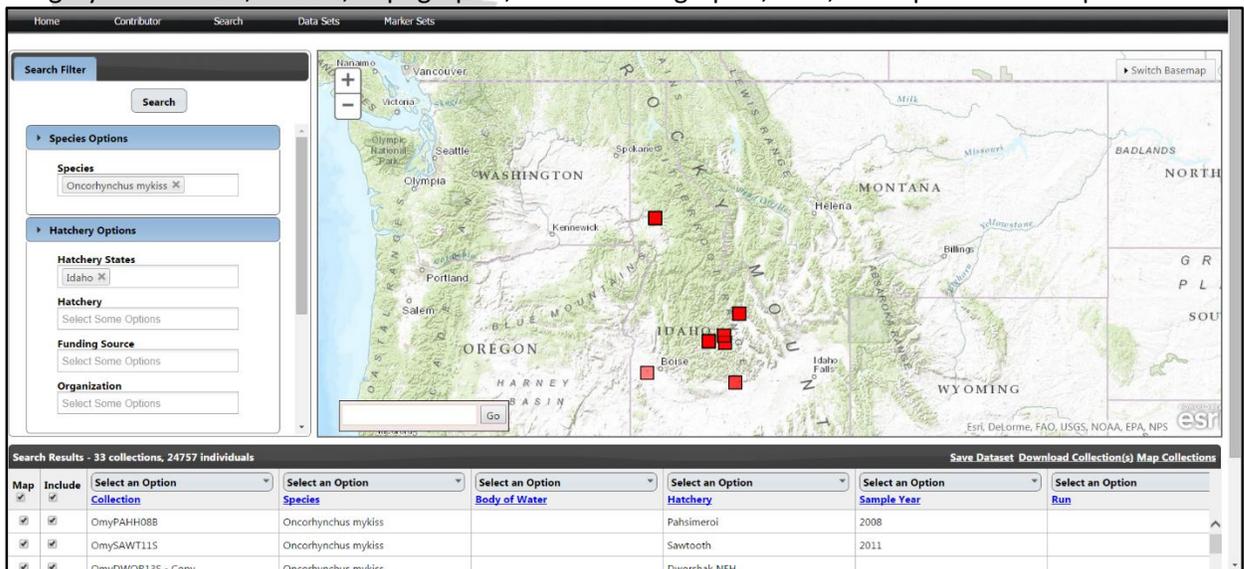


Figure 45 - Mapped Search Results.

Clicking a collection box (red square) will bring up a bubble that provides information about that collection: Name, sample size (N), sample year, species, region, subregion, basin, subbasin, and body of

water. The “Zoom to” link in the bottom left corner of the bubble can be used to zoom in on the selected collection.

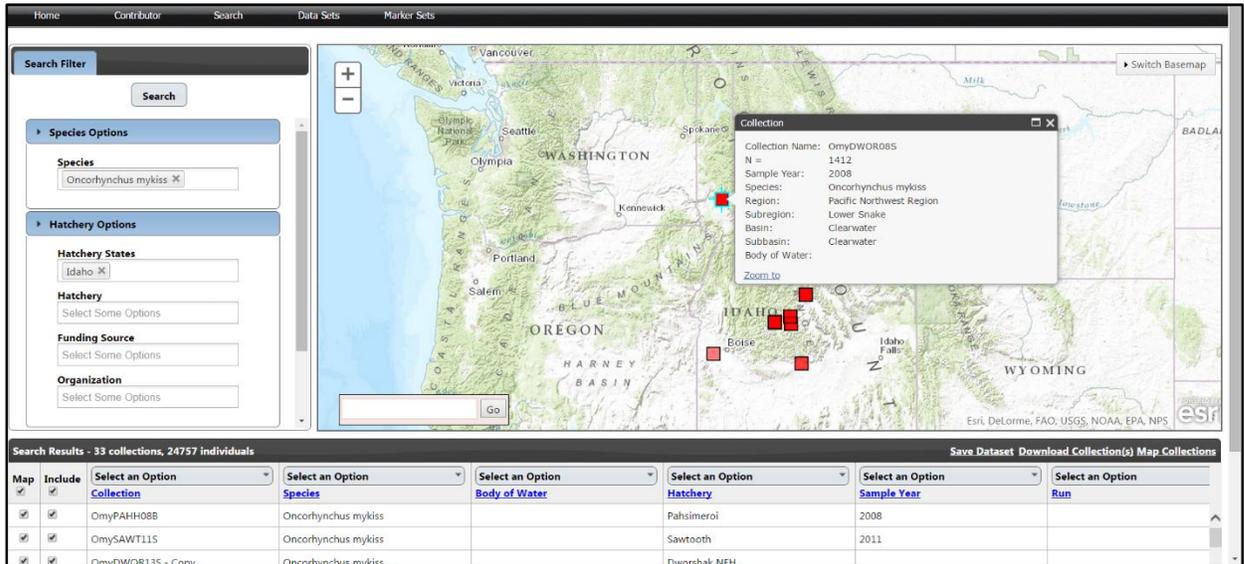


Figure 46 - Mapped Search Results with Bubble.

The result table from a search can be sorted or filtered by any of the columns. To sort on a column click on the “Select an Option” dropdown and then click away from the dropdown without making a selection. This will sort the result table in ascending order by the values in that column. To filter a result table by column click on the “Select an Option” dropdown on any column and choose from the available options. The options will consist of the ability to check or uncheck all values found in the column, or the ability to check individual values. To apply the filter click away from the dropdown.

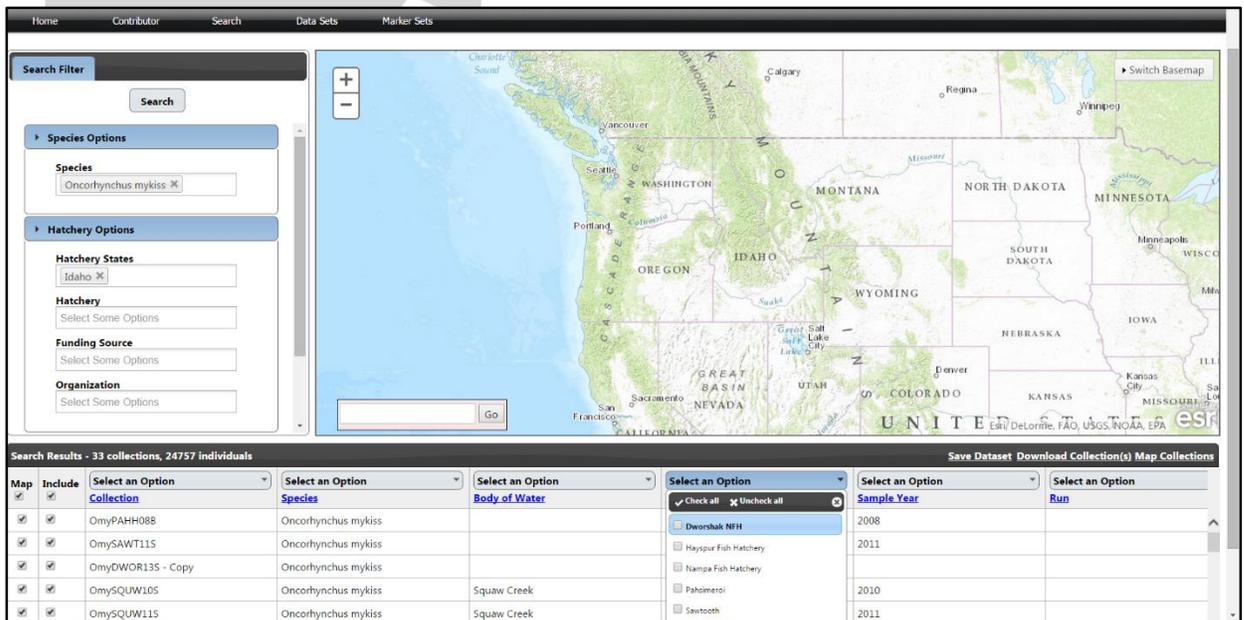


Figure 47 - Select an Option Dropdown

Search results can also be downloaded by clicking the “Download Collection(s)” link in the top right corner of the Search Results table (just to the left of the “Map Collections” link). Only rows that have the “Include” checkbox checked will be included in the download. Individual rows can be included or excluded by toggling the “Include” checkbox for that row, or all rows can be included or excluded by toggling the checkbox in the header row just below “Include”. Currently, collections and datasets in FishGen can be downloaded in GenePop format or FishGen format.

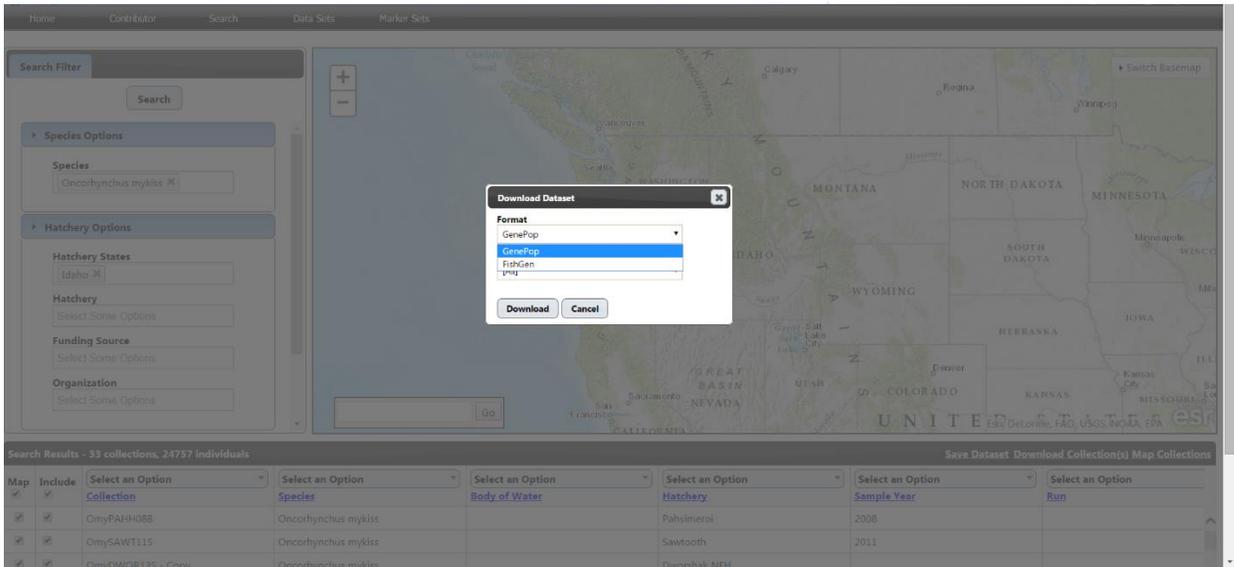


Figure 48 - Download Search Results

Additionally, an appropriate marker set must be selected in order to download search results.

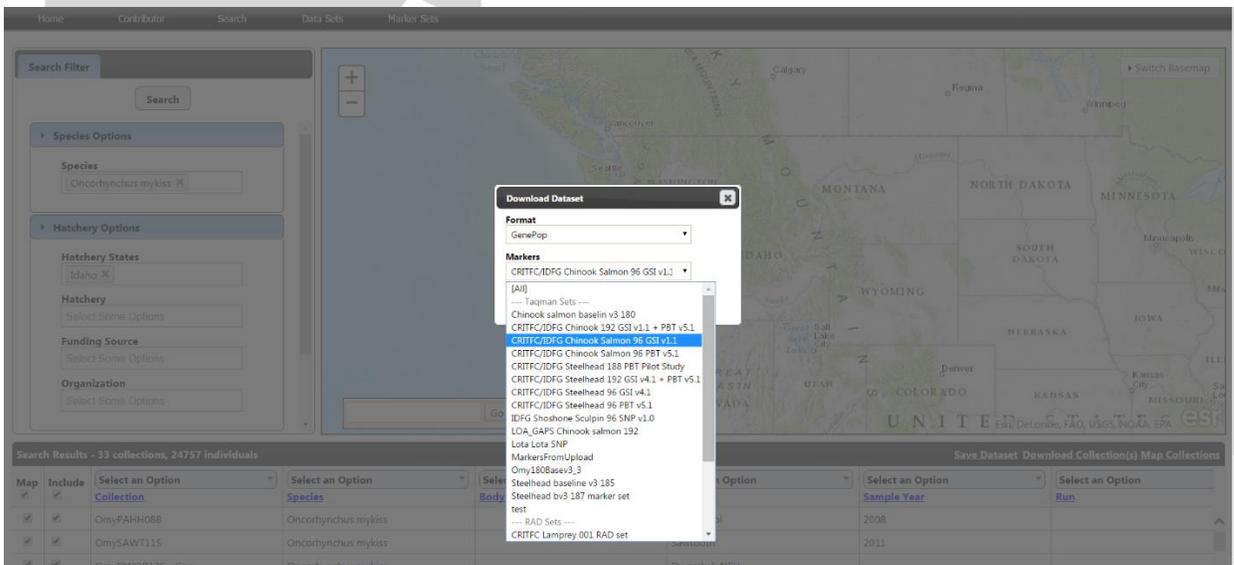


Figure 49 - Download Search Results Marker Selection

Appendix A. Collection Fields

	Body of Water	Hatchery	Country	State/Province	HUC 2 (Subregion)	HUC 4 (River Basin)	HUC 6 (Subbasin)	HUC 8 (Watershed)	HUC Number
Required?	YES (if hatchery is not selected)	YES (if Body of Water not selected)	YES-Auto	YES-Auto	YES-Auto	YES-Auto	YES-Auto	YES-Auto	YES-Auto
Description/ Definition	The river, stream, creek, lake, pond, ditch, etc. that your sample came from. FishGen will automatically calculate HUC8 designations, so additional details regarding drainage, basin, etc. are not needed.	The hatchery your sample came from. FishGen will automatically calculate HUC8 designations, so additional details regarding drainage, basin, etc. are not needed.	These fields are all auto-generated from user provided latitude/longitude coordinates.						
Example	Seven Suckers Ditch	Dworshak National Fish Hatchery	Canada	Oregon	Pacific Northwest Region	Middle Columbia	Deschutes	Upper Deschutes	17070301
Valid Entry	Alphanumeric, 30 character limit	See Hatchery Tab	AUTO	AUTO	AUTO	AUTO	AUTO	AUTO	AUTO

	BPA Project Number	Collection Species	Collection Comments	Collection Run	Collection Origin	Collection Life Stage	Collection Method
Required?	NO	YES	NO	NO	NO	NO	NO
Description/ Definition	If genetic data uploaded to FishGen was generated as part of a Bonneville Power Administration Project, you can provide your project number for reporting requirements.	Genus species Must be written out completely and spelled correctly. The term "Mixed" can be used for hybridization studies that involve sampling multiple species. However, Mixed is not intended to be used outside of hybridization studies (e.g. you wouldn't include a sample of steelhead and Chinook salmon under the same collection)	Field or lab comments that apply to the entire collection.	Runs have been identified on the basis of when adult salmon enter freshwater to begin their spawning migration.	Whether the collection consists of wild, hatchery or a mixture of wild and hatchery fish.	Life Stage of the collection. For collections that include fish of multiple life stages, please use "Mix".	How samples were collected. Names must match exactly from the list above. (e.g. Electroshocking will not work for Electrofishing). A collection method not listed (e.g. noodling), can be requested from the curator.
Example	2010-026-00	Oncorhynchus tshawytscha	Samples were collected on private property (Eagle Island State Park)	Summer	W	Adult	Electrofishing
Valid Entry	See www.fishgen.net/webpages/legalvalues.aspx	See Species appendix or www.fishgen.net/webpages/legalvalues.aspx	Alphanumeric	0 = N/A, 1 = Spring, 2 = Summer, 3 = Fall, 4 = Winter, 5 = Unknown, 6 = Spring/Summer, R = Resident	H = Hatchery W = Wild Mix = Mixture of hatchery and wild U = Unknown	Adult, Carcass, Egg, Fry, Juvenile, Larvae, Mix, Parr, PreSmolt, Smolt, Unknown	Adult Release, Anadromus Returns, Angling, Bait Trap, Captive Brood, Carcass Survey, Creel, Egg-box, Electrofishing, Fish Ladder at Dam, Gill net, Hatchery Sample, Multiple, Other, Outmigrants, Redd Pump, Screw trap, Seine, Snorkel, Trawl, Unspecified, Weir

Appendix A. Collection Fields (continued).

	Sample Year	Collection Latitude	Collection Longitude	Collection Name
Required?	YES	YES	YES	YES
Description/ Definition	<p>The year in which samples were collected. Generally samples collected from different years should be separated into unique collections. For samples spanning across years, like samples taken at a weir or dam, the range can be input (e.g. 2010-2011)</p>	<p>Collection latitude and longitude are extremely important, since FishGen will calculate and auto-populate HUC information for your collection. Collection Latitude and Longitude must be the same for all individuals in the collection. In a situation where you have sampled multiple locations within a stream, individual lat/lon coordinates can be entered at the individual level</p>	<p>Collection Name from uploader. We suggest that these are descriptive. Ours include: Species: Omy Sample location: Oxbow (OXBO) Sample year: 08</p> <p>Remember that Collection Names are unique in the database. So they must be unique enough that they don't match another collection, but they need to stay under the 30 character limit.</p>	
Example	2013	43.67731	-116.40309	OmyOXBO08S
Valid Entry	YYYY	These must be input as decimal degrees	These must be input as decimal degrees	Alphanumeric, 30 character limit

Appendix B. Individual Fields.

	Ad Clip	Brood Year	Brood Year Determination Method	Cross Data	CWT Number	Date Spawned	Disposition 1	Disposition Year 1
Required?	NO	NO	NO	NO	NO	NO	NO	NO
Description/ Definition	Whether the adipose fin was clipped or not. A clipped adipose fin is an indication that it is a hatchery fish.	A brood year is the year of spawning of the parental generation, e.g., an juvenile produced from parents spawned in 2013 is a brood year 2013 (BY13) fish	How was brood year determined, a physical tag, PBT assignment? Or was it estimated via length?	This is for broodstock sampled at a hatchery. Documents which fish it was spawned with.	Binary or alpha-numeric code that identifies a specific stock or release group	Sometimes the date that a fish is spawned differs from the date it was trapped/sampled.	The history of a fish following genetic sampling. Useful for PBT tracking, spawning programs, and for situations where fish are released following sampling.	Year in which the event occurred.
Example	Y	2013	PBT assignment	OmyOXBO08S	10110	7/19/2013	Spawned	2013
Valid Entry	N = No P = Partial U = Unknown Y = Yes	yyyy	Alphanumeric, 300 character limit	semi-colon separated alphanumeric	Alphanumeric, 30 character limit	mm/dd/yyyy	ARtoCB, Carcass, CBtoAR, Culled, CulledBKD, CulledHybrid, CulledIHN, CulledSurplus, EggsCulled, Immature, Killed, Maturing, Mort, NonProductiveSpawner, NotInMatrix, NotSpawned, OffSeasonMaturity, Poned, Precocial, Released, RelAboveWeir, RelBelowWeir, RelAnotherLoc, ReUsed, Spawned, Unknown	yyyy

Appendix B. Individual Fields (continued).

	Disposition 2	Disposition Year 2	Field ID 1	Field ID 2	Floy Tag Number	Sex (Genetic)	Sex (Phenotypic)	Hatchery Database ID
Required?	NO	NO	NO	NO	NO	NO	YES	NO
Description/ Definition	A secondary disposition for individuals. Important in cases where a fish is used for hatchery spawning, and then released back in the wild to spawn naturally. In this case Disposition1 would be ‘Spawned’ and Disposition2 would be ‘ReleasedAboveWeir’ or something similar.	Year in which the event occurred.			Binary or alpha-numeric code that identifies a specific stock or release group	Determined from running a genetic sex marker	What sex was the fish?	Unique number from the LSRCF FINS hatchery database
Example	Spawned	2013	F_001	F_001	FT12345	F	F	FINS_DWOR_13_0001
Valid Entry	ARtoCB, Carcass, CBtoAR, Culled, CulledBKD, CulledHybrid, CulledIHN, CulledSurplus, EggsCulled, Immature, Killed, Maturing, Mort, NonProductiveSpawner, NotInMatrix, NotSpawned, OffSeasonMaturity, Poned, Precocial, Released, RelAboveWeir, RelBelowWeir, RelAnotherLoc, ReUsed, Spawned, Unknown	YYYY	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	F = Female M = Male U = Unknown	F = Female M = Male U = Unknown	Alphanumeric, 30 character limit

Appendix B. Individual Fields (continued).

	Individual Comments	Individual Latitude	Individual Longitude	Latitude/Longitude Notes	Individual Name	Jaw Tag Number	LAB ID 1	LAB ID 1	Length FORK (mm)	Length MEHP (mm)
Required?	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Description/ Definition	Individual comments related to the fish or the genetic sample taken from the fish	In a situation where you have sampled multiple locations within a stream, lat/lon coordinates can be entered at the individual level.		Notes about lat/lon coordinates	Specific name lab uses to identify sample, must be unique for all individuals within a collection	Binary or alpha-numeric code that identifies a specific stock or release group	LAB specific ID number	LAB specific ID number	Fork length is the length from the most anterior part of a fish to the tip of the median caudal fin rays.	Mid-eye to end of hypural plate
Example	Fungused fin	43.67731	- 116.40309	Estimated at mouth	OmyOXBO08S_001	JT101	101035	Plate-0304B	510	475
Valid Entry	Alphanumeric, 300 character limit	These must be input as decimal degrees	These must be input as decimal degrees	Alphanumeric, 300 character limit	Alphanumeric, 300 character limit	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	Numeric (must be in millimeters)	Numeric (must be in millimeters)

Appendix B. Individual Fields (continued).

	Length POH (mm)	Length TOTAL (mm)	Life Stage	Life Stage Determination Method	Lineage	Offspring Reared Hatchery	Offspring Release Strategy	Opercle Punch
Required?	NO	NO	NO	NO	NO	NO	NO	NO
Description / Definition	Post-orbital hypural length	Total length is the measurement of the entire length of a fish's body, from the most anterior part of the fish to the tip of the longest caudal fin rays	A series of stages a fish follows as it develops from an egg to an adult	How was the life stage determined? A tag or physical attribute or measurement?	Lineage names and descriptions are not consistently used among biologists, managers or geneticists and they are not defined strictly by geography or run-timing. However, several are commonly used to describe salmon and steelhead populations throughout the PNW.	Used to designate where an adult's offspring will be raised.	Used to designate the release strategy of an adult's offspring	Does the fish have an opercle (gill cover) punch? This usually indicates that this fish is of hatchery origin
Example	350	575	Adult	Smolts were defined as fish with a silver coloration and a fork length >110 mm	Chinook - Lower Columbia	Magic Valley Fish Hatchery	Presmolt	Y
Valid Entry	Numeric (must be in millimeters)	Numeric (must be in millimeters)	Adult, Carcass, Egg, Fry, Juvenile, Larvae, Mix, Parr, PreSmolt, Smolt, Unknown	Alphanumeric, 300 character limit	Alphanumeric, 30 character limit. Suggested names are: Chinook - Lower Columbia, Chinook – Ocean, Chinook – Stream, Steelhead – Interior, Steelhead – Coastal, Mixed, Unknown	See Hatchery appendix or www.fishgen.net/webpages/legalvalues.aspx	Alphanumeric, 30 character limit	LOP = L Op Punch, LOP;ROP, L and R Op Punch, N = No ROP = R Op Punch, ROP;LOP L and R Op Punch, U = Unknown Y = Yes

Appendix B. Individual Fields (continued).

	Origin	PIT Tag Number	Individual Run	Sample Date	Species (Phenotypic)	Species (Genetic)	Stock Strain	Ventricle Clip
Required?	NO	NO	NO	NO	YES	NO	NO	NO
Description/ Definition	Is the fish of hatchery or wild origin?	Binary or alphanumeric code that identifies a specific stock or release group	Runs have been identified on the basis of when adult salmon enter freshwater to begin their spawning migration.	What day was the fish sampled?	What species is the fish you sampled?	Expectation is that this would match phenotypic species, unless genetics indicated otherwise. For example, a rainbow trout was identified in the field, but was determined to be an F1 Hybrid.	In this database, stocks are common names ascribed to individual spawning populations.	Whether the ventral (right or left pelvic fin) has been clipped or not. A clipped fin is an indication that it is a hatchery fish.
Example	H	3D9.1C2D1238F4	Summer	7/19/2013	Oncorhynchus tshawytscha	Oncorhynchus tshawytscha	Skamania	N
Valid Entry	H = Hatchery W = Wild Mix = Mixture of hatchery and wild U = Unknown	Alphanumeric, 30 character limit	0=N/A, 1=Spring, 2=Summer, 3=Fall, 4=Winter, 5=Unknown, 6=Spring/Summer, R=Resident	mm/dd/yyyy	See Species appendix or www.fishgen.net/webpages/legalvalues.aspx	See Species appendix or www.fishgen.net/webpages/legalvalues.aspx	Alphanumeric, 300 character limit	LV = L Vent Clip, LV;RV = L and R Vent Clip, RV;LV = L and R Vent Clip, N = No, U = Unknown Y = Yes

Appendix C. Hatcheries

Abernathy Fish Technology Center (USFWS)	Chelan	Dexter Ponds
Alsea Hatchery	Chewuch Pond	Dryden Ponds
American River Trout Hatchery	Chief Joseph	Dworshak NFH
Bandon Hatchery	Chinook River / Sea Resources	Eagle Creek NFH
Beaver Creek	Chiwawa Pond	Eagle Fish Hatchery
Big Canyon Satellite (NPT)	Clackamas	East Fork Satellite
Big Canyon Satellite (ODFW)	Clark Flat Satellite	Eastbank
Big Creek	Cle Elum Hatchery	Easton Satellite
Big Qualicum Hatchery	Clearwater	Elk River Hatchery
Birkenhead River Hatchery	Cole M. Rivers Hatchery	Elochoman
Birnie Creek (FFA)	Coleman National Fish Hatchery	Elwha Channel
Bonapart Pond	Cottonwood Creek Pond	Ennis National Fish Hatchery
Bonifer Pond	Cowlitz Salmon Hatchery	Entiat NFH
Bonneville	Cowlitz Trout Hatchery	Fall River Hatchery
Burley Creek (Safety-Net)	Coyote Valley Fish Facility	Fallert Creek
Capt John Rapids Satellite	Crystal Lake Hatchery	Feather River Hatchery
Carlton Pond	Crystal Lake Trout Hatchery	Feather River Hatchery-Thermalito An
Carson NFH	Curl Lake Ponds	Fillmore Trout Hatchery
Cascade Hatchery	Darrah Springs Trout Hatchery	Forks Creek Hatchery
Catherine Creek Satellite	Dayton Ponds	Garrison National Fish Hatchery
Cedar Creek Hatchery	Deep River Net Pens	George Adams Hatchery
Cedar Flats Satellite	Deer Mountain Hatchery	Gnat Creek Hatchery

Appendix C. Hatcheries (continued).

Gobar Pond	Klaskanine Hatchery	Magic Valley
Grays River Hatchery	Klickitat Fish Hatchery	Makah National Fish Hatchery
Grovers Creek Salmon Hatchery	Kooskia NFH	Makah Tribal Hoko Hatchery
Hagerman ARI	Kootenay Fish Hatchery	Manchester Marine Laboratory
Hagerman NFH	Lake Wenatchee Net Pens	Marblemount Fish Hatchery
Hayspur Fish Hatchery	Leaburg Hatchery	Marion Drain Hatchery
Hidden Falls Hatchery	Leavenworth NFH	Marion Forks Hatchery
Hot Creek Trout Hatchery	Lewis River Hatchery	McCall Fish Hatchery
Humptulips Salmon Hatchery	Lilliwaup Creek Hatchery	McKenzie Fish Hatchery
Hupp Springs Rearing Ponds	Little Port Walter Field Station	McKernan Hatchery
Hurd Creek Hatchery	Little Sheep Satellite	Medvejie Salmon Hatchery
Imeques Satellite	Little White Salmon NFH	Merced River Fish Hatchery
Imnaha Satellite	Livingston Stone National Fish Hatchery	Merwin Fish Hatchery
Iron Gate Hatchery	Lookingglass	Methow Fish Hatchery
Irrigon Hatchery	Lostine Satellite	Minter Creek Hatchery
Issaquah Salmon Hatchery	Lower Crooked River Satellite	Minthorn Springs Satellite
Jack Creek Satellite	Lower Elwha Klallam Hatchery	Minto Fish Collection Facility
Kalama Falls Hatchery	Lukes Gulch Satellite	Moccasin Creek Trout Hatchery
Kendall Creek Hatchery	Lummi Bay Complex	Mojave River State Fish Hatchery
Kern River Trout Hatchery	Lyons Ferry Hatchery	Mokelumne River Hatchery
Kingfisher Flat Fish Facility (Big Creek Hatchery)	Macaulay Salmon Hatchery	Morse Creek Hatchery
Klamath Hatchery	Mad River Hatchery	Mount Shasta Trout Hatchery

Appendix C. Hatcheries (continued).

Mt. Currie Fish Hatchery	Priest Rapids Fish Hatchery	Sawtooth
Mt. Lassen Trout Farm	Prosser Fish Hatchery	Shepherd of the Hills Fish Hatchery
Nampa Fish Hatchery	Pullen Creek Hatchery	Sherars Falls Trap
Nehalem Hatchery	Puyallup Hatchery	Silverado Fisheries Base
Newsome Creek Satellite	Quilcene National Fish Hatchery	Similkameen Acclimation Pond
Nez Perce Tribal	Quinault National Fish Hatchery	Skamania Hatchery
Niagara Springs	Rapid River Fish Hatchery	Sol Duc Hatchery
Nimbus Fish Hatchery	Red River Satellite	Soos Creek Hatchery
Nisqually Clear Creek Hatchery	Ringold Springs Hatchery	South Fork Salmon Satellite
North Lapwai Valley Satellite	Riverside Pond	South Fork Walla Walla Hatchery
North Toutle Hatchery	Roaring River Hatchery	South Santiam Hatchery
Oak Springs	Robertson Creek Hatchery	Speelyai Fish Hatchery
Omak Hatchery	Rock Creek Hatchery	Spius Creek Hatchery
Oregon Hatchery Research Center	Round Butte	Spring Creek NFH
Oxbow (IDFG)	Rowdy Creek Fish Hatchery	Springfield Hatchery
Oxbow (ODFW)	SAFE Blind Slough Net Pens	St. Marys Pond
Pahsimeroi	SAFE Tongue Point Net Pens	Stillaguamish Tribal Hatchery
Parkdale Hatchery	SAFE Youngs Bay Net Pens	Sweetwater Springs
Pelton Ladder	Salmon River Hatchery	Thornhollow Satellite
Pendleton Satellite	Samish Fish Hatchery	Three Mile Dam
Pittsburg Landing Satellite	San Joaquin Fish Hatchery (SCRF)	Tonasket Pond
Powell Satellite	Sandy River Hatchery	Trask River Hatchery

Appendix C. Hatcheries (continued).

Trinity River Hatchery	Upper Crooked River Satellite	Wells Fish Hatchery
Trojan Pond	Upper Grand Ronde Satellite	White River Hatchery
Tucannon	Voights Creek Hatchery	Whitman Lake Hatchery
Tumwater Falls	Wallace River	Willamette Hatchery
Turtle Rock Hatchery	Wallowa Fish Hatchery	Willard NFH
Twisp Rearing Pond	Warm Springs Hatchery	Winthrop NFH
Umatilla Fish Hatchery	Warm Springs NFH	Wizard Falls Hatchery
University of Washington	Washougal Fish Hatchery	Yoosa-Camp Creek Satellite

Appendix D. Valid Species List

Scientific Name	Common Name	Scientific Name	Common Name
<i>Acipenser transmontanus</i>	White Sturgeon	<i>Cottus leiopomus</i>	Wood River Sculpin
<i>Acrocheilus alutaceus</i>	Chiselmouth	<i>Cottus rhotheus</i>	Torrent Sculpin
<i>Alosa sapidissima</i>	American Shad	<i>Couesius plumbeus</i>	Lake Chub
<i>Ameiurus melas</i>	Black Bullhead	<i>Ctenopharyngodon idella</i>	Grass Carp
<i>Ameiurus nebulosus</i>	Brown Bullhead	<i>Cyprinus carpio</i>	Common Carp
<i>Carassius auratus</i>	Goldfish	<i>Esox lucius</i>	Northern Pike
<i>Catostomus ardens</i>	Utah Sucker	<i>Esox masquinongy x lucius</i>	Tiger Musky
<i>Catostomus</i>	Longnose Sucker	<i>Gambusia affinis</i>	Western Mosquitofish
<i>Catostomus columbianus</i>	Bridgelip Sucker	<i>Gila atraria</i>	Utah Chub
<i>Catostomus discobolus</i>	Bluehead Sucker	<i>Gila bicolor</i>	Tui Chub
<i>Catostomus macrocheilus</i>	Largescale Sucker	<i>Gila copei</i>	Leatherside Chub
<i>Catostomus platyrhynchus</i>	Mountain Sucker	<i>Ictalurus furcatus</i>	Blue Catfish
<i>Cichlasoma nigrofasciatum</i>	Convict Cichlid	<i>Ictalurus punctatus</i>	Channel Catfish
<i>Coregonus clupeaformis</i>	Lake Whitefish	<i>Lampetra tridentata</i>	Pacific Lamprey
<i>Cottus bairdi</i>	Mottled Sculpin	<i>Lepomis cyanellus</i>	Green Sunfish
<i>Cottus beldingi</i>	Piute Sculpin	<i>Lepomis gibbosus</i>	Pumpkinseed
<i>Cottus cognatus</i>	Slimy Sculpin	<i>Lepomis gulosus</i>	Warmouth
<i>Cottus confusus</i>	Shorthead Sculpin	<i>Lepomis macrochirus</i>	Bluegill
<i>Cottus extensus</i>	Bear Lake Sculpin	<i>Lota</i>	Burbot
<i>Cottus greenei</i>	Shoshone Sculpin	<i>Micropterus dolomieu</i>	Smallmouth Bass

Appendix D. Valid Species List (continued).

Scientific Name	Common Name	Scientific Name	Common Name
<i>Micropterus salmoides</i>	Largemouth Bass	<i>Pimephales promelas</i>	Fathead Minnow
<i>Misgurnus anguillicaudatus</i>	Oriental Weatherfish	<i>Poecilia mexicana</i>	Shortfin Molly
<i>Mylocheilus caurinus</i>	Peamouth	<i>Poecilia reticulata</i>	Guppy
<i>Notropis hudsonius</i>	Spottail Shiner	<i>Pomoxis annularis</i>	White Crappie
<i>Noturus gyrinus</i>	Tadpole Madtom	<i>Pomoxis nigromaculatus</i>	Black Crappie
<i>Oncorhynchus clarkii</i>	Cutthroat Trout	<i>Prosopium abyscicola</i>	Bear Lake Whitefish
<i>Oncorhynchus clarkii bouvieri</i>	Yellowstone Cutthroat Trout	<i>Prosopium coulteri</i>	Pygmy Whitefish
<i>Oncorhynchus clarkii henshawi</i>	Lahontan Cutthroat Trout	<i>Prosopium gemmifer</i>	Bonneville Cisco
<i>Oncorhynchus clarkii lewisi</i>	Westslope Cutthroat Trout	<i>Prosopium spilonotus</i>	Bonneville Whitefish
<i>Oncorhynchus clarkii utah</i>	Bonneville Cutthroat Trout	<i>Prosopium williamsoni</i>	Mountain Whitefish
<i>Oncorhynchus kisutch</i>	Coho Salmon	<i>Ptychocheilus oregonensis</i>	Northern Pikeminnow
<i>Oncorhynchus mykiss</i>	Rainbow Trout/steelhead	<i>Pylodictis olivaris</i>	Flathead Catfish
<i>Oncorhynchus mykiss aguabonita</i>	Golden Trout	<i>Rhinichthys cataractae</i>	Longnose Dace
<i>Oncorhynchus mykiss gairdneri</i>	Inland Columbia Basin Redband Trout	<i>Rhinichthys falcatus</i>	Leopard Dace
<i>Oncorhynchus mykiss x clarkii</i>	Rainbow X Cutthroat Trout	<i>Rhinichthys osculus</i>	Speckled Dace
<i>Oncorhynchus nerka</i>	Sockeye Salmon or kokanee	<i>Richardsonius balteatus</i>	Redside Shiner
<i>Oncorhynchus tshawytscha</i>	Chinook Salmon	<i>Salmo salar</i>	Atlantic Salmon
<i>Osmerus mordax</i>	Rainbow Smelt	<i>Salmo trutta</i>	Brown Trout
<i>Perca flavescens</i>	Yellow Perch	<i>Salvelinus alpinus</i>	Arctic Char
<i>Percopsis transmontana</i>	Sand Roller	<i>Salvelinus alpinus oquassa</i>	Blue Backed Trout

Appendix D. Valid Species List (continued).

Scientific Name	Common Name	Scientific Name	Common Name
Salvelinus confluentus	Bull Trout	F1 Hybrid	First Generation Hybrid
Salvelinus confluentus x fontinalis	Bull trout X brook trout	F2 Hybrid	Second Generation Hybrid
Salvelinus fontinalis	Brook Trout	O. mykissBC	Backcross hybrid
Salvelinus namaycush	Lake Trout	O. clarkiiBC	Backcross hybrid
Salvelinus namaycush x fontinalis	Splake	S. confluentusBC	Backcross hybrid
Stizostedion vitreum	Walleye	S. fontinalisBC	Backcross hybrid
Thymallus arcticus	Arctic Grayling	Hyb	Hybrid
Tilapia aurea	Blue Tilapia		
Tilapia mossambica	Mozambique Tilapia		
Tinca	Tench		
Xiphophorus helleri	Green Swordtail		