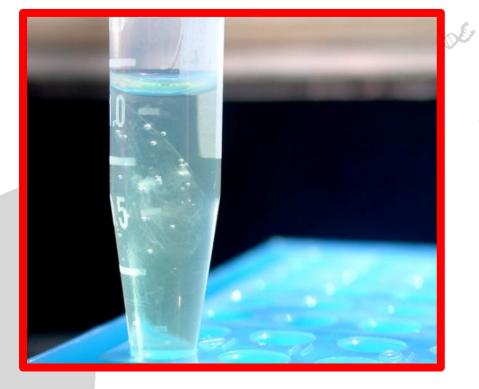
FishGen

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 <u>Learn</u> <u>about collaborating labs</u>. 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.



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.

		TP-	to
Welcome, Guest.			Home Log In Register User Manual Contact
			FishGen
Home Search Data Sets			
Request Account			
* denotes a required field			
*Email Address:	*Organization:		
*Password:	Other Organization:		
*Re-enter Password:	Street Address 1:		
Password Hint:	Street Address 2:		
*First Name:	City:		
*Last Name:	State: •		
Phone:	Zip Code:		
Send Request			

5

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 <u>Creating Marker Synonyms</u>.



Figure 3 - Selecting Upload Markers.

Home C	Contributor	Search Data Sets	Marker Sets		
Select your marker	s file	Choose File No file chosen			
Open					×
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Organize • New	folder			===	
Favorites	^ N	ame	Date modified	Туре	Size
Desktop	-	3 column format ots and omy usats 07jul	7/16/2015 8:33 AM	Text Document	3 KI
) Downloads		7 column format ots snps 19nov13	7/16/2015 8:42 AM	Text Document	21 KI
S Recent Places		Markers - GTSeq - OmyGTseq_v2-INFO	10/24/2014 2:14 PM	Text Document	36 KI
	=	Markers - Microsatellite All	7/21/2014 9:21 AM	Text Document	3 KI
🥞 Libraries		Markers - RAD - Lampray RAD Markers Fi	7/21/2014 9:21 AM	Text Document	337 KI
Documents		Markers - SNP definitions for O.Mykiss (R	10/14/2014 2:37 PM	Text Document	41 KI
al Git		Markers - SNP definitions for O.Mykiss (R	10/14/2014 2:37 PM	Text Document	41 KI
🕹 Music		Markers - SNP definitions for O.Mykiss (R	7/21/2014 9:21 AM	Text Document	21 Ki
lictures		Markers - SNP Taqman - OtsPBT96SNPs	7/16/2015 11:02 A	Text Document	11 KI
Judeos 🦉		Markers - SNP-GTSeq definitions for O.M	10/22/2014 10:30	Text Document	23 KI
💐 Computer					
as OSDisk (C:)	-				
File	e name:		•	- All Files	-
				Open	Cancel

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 colum	n format ots and omy usats 07jul15 -	Notepad	X
File Edit	Format View Help		
MarkerNa			
	GATCTGGGCCTAAGGGAAAC	ACTAGCGGTTGGAGAACCC	
	ACATCGCACACCATAAGCAT	GTTTCTTCGACTGTTTCCTCTGTGTTGAG	
	GTCGTCACTGGCATCAGCTA	GAGTGGAGATGCAGCCAAAG	
		GATGAATCGAGAGAATAGGGACTGAAT	
	AGGATGGCAGAGCACCACT	CACCCATAATCACATATTCAGA	
	CCAGCACTCTCACTATTT	CCAGAGTAGTCATCTCTG	
	TGTGCTATAGGGTGAATGTGC	AACACAGGCATCCCCACTAA	
	GACAGGTTGTGTCGAATGGA	GGTGGGATTCAGTGTGTAAAC	=
	GAGACTGACACGGGTATTGA	GTTATGTTGTCATGCCTAGGG	_
	GATTCCATAACCTCGCCTTC	GTCCTTGTGCTGCCTGCT	
	AACTTGCTATGTGAATGTGC	GACAAAAGTGACTGGTTGGT	
Omy27	TTTATGTCATGTCAGCCAGTG	TTTATGGCTGGCAACTAATGT	
	TGTGAGACTGTCAGATTTTGC	CGGAGTCCGTATCCTTCCC	
Omy7	TTAAGTTTTGCCTAGATAAGGG	CAAGGAATGGCACAGCTTG	
	CGTTCTCTACTGAGTCAT	GGGTCTTTAAGGCTTCACTGCA	
	AATGTTGAGAGCTATTTCAATCC		
	ATCTTTATGGTGGCAAGTCC	ATCTGGTACTTCCCTGATGC	
	TACCCTGCAAGACAGTGAGA	GCTGTTTAGGAAGGAGGGTT	
	TGCAGAGCCATACTAAACCA	GTTTAAGAATTGAGAGATGCAGGG	
	CCTCCATTTCAATCTCATCC	ACAGAGAACAGTGAGGGAGC	
	ATGACCAAGGAGCTTCTGC	TATCCAGGTACTCCACTGGC	
	GTGACCCAGACTCAGAGGAC	CACAACCCATCACATGAAAC	
	TCATTAATCTAGGCTTGTCAGC	GTTTTGCAGGTAAGACAAGGTATCC	
	CGCTATACATTTTCCATTTTCC	GTTTTTTTAAGTGGGAGAACTTGC	
	TCATACCCCATGCCTCTTCTGTT		
Oneu10.2			
	GTTTGGATGACTCAGATGGGACT		
Oneu14	AGAAACATGAGAACAGTCTAGGT	CCTTATGAGTTTGGTCTCCATGT	-
•			▶
		AND TRANSPORT MANAGEMENT OF A DECIDE OF THE CONTRACT OF THE CONTRACT.	

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.

First row is Header Marker Tune	Marker synonyms	
Select Delimiter Tab * Microsatellite	California Column Mapping Use Saved Column Mapping:	
SNP Acipenser trans	[Select Mapping]	
1	2	3
<ignore field=""></ignore>	<ignore field=""></ignore>	<ignore field=""></ignore>
arkerName	ForwardPrimerSequence	ReversePrimerSequence
jo1a	GATCTGGGCCTAAGGGAAAC	ACTAGCGGTTGGAGAACCC
	ACATCGCACACCATAAGCAT	GTTTCTTCGACTGTTTCCTCTGTGTTGAG
102		GAGTGGAGATGCAGCCAAAG
	GTCGTCACTGGCATCAGCTA	
go4	GTCGTCACTGGCATCAGCTA AGGCCCCAAAGTCTGTAGTGAAGG	GATGAATCGAGAGAATAGGGACTGAAT
go2 go4 ke4 ki1		

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								
Upload Cancel 3 column format ots and omy usats 07jul1	txt							
Data Formatting Marker Configuration	Additional Upload Options							
First row is Header	onyms Save Marker Set							
Select Delimiter Marker Type Tab * Microsatellite	Save Column Mapping							
	Use Saved Column Mapping: [Select Mapping]							
	Construction (1)							
Toggle fieldset View								
1	2	3						
Marker Name	Forward Primer •	Reverse Primer •						
Marker Name	Forward Primer	<ignore field=""> Forward Primer</ignore>						
Ots1	AGATAGGTGTACATCCATA	Lab Synonym Marker Name						
Ots2	AGTAATCGTATGCCGGTAT	Reverse Primer						
Ots3	AGATAGGTGTACATCCATA	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 subtypes 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 <u>compliment</u> 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 ٠
- FAM Probe •

 FAM Allele 		The second se	Q
Forward Primer			9
Reverse Primer			
VIC Probe		TD .	
		The	E de
FAM Probe		- CL	BOD B
Markers - SNP Taqman - OtsPl	BT96SNPs - Notepad	100	
File Edit Format View Help			
Assay VicAllele	FamAllele Fwd Primer	Rev Primer VIC probe	FAM probe
Ots_100884-287 T	C CGGAAGACCAGATTCTCCA		ATAGAACTACAATTCACATATAT
Ots 101554-407 C		TAGTGGTGGTG ACACGCCAGTCCACAAGT	
Ots_101704-143 T	G ACTTCTTGAGCCAATCGGA		
Ots_102414-395 A	G GCCTACTGATAAATGTATG	ACAGTAATGGA CAATAACAAACAAGCTAGGAAG	CAAAAGTGT CACATAGTGTAGCTT
Ots_102801-308 C	A TGGGACAGAGGTGGGAATT	GA CCCAAAGATGCTTAACTGAAGATGTG	AGGGACAGTTTCGCAGACG
Ots_103122-180 T	C CAAACGCGCACTCACACA	TCACAATGGTACGATTTTACGACTCAA	CATCAACACAATCTGC
Ots_104415-88 C	T CCTGAGCATCCCAGTTGAA		
Ots_105105-613 C	G AGTACAAGTGCAGAGAATG		ICTTTTAACTTTAAGCT CCGAGCT
Ots_105132-200 G	T CGATGTACTGAGGGCAGTG		
Ots_105385-421 A			TGGGTATATCG CTCCTGC
Ots_105407-117 T		ATTGAAGATAA CTGTGAGCTGCTGCAAACC	CAGGTTAGGAATGGTTG
Ots_108820-336 G	A TGAAATAAATTGTTCTGTT		
Ots_109525-816 C	T GCCAGATAGTAGCGTACAT		CATGAGGCGTTCGGC ATGAGGC
Ots_110064-383 C	T AACAAAGAATGTTAAACAC		
Ots_110201-363 A Ots 110495-380 G	T GTTTGGCTATTGAAATTAT		
0ts_110493-380 G	C GCCTAGGTATGTACGAAAC A GAGTGGTCAAGGTTTCAGT		
Ots 110689-218 T	A GAGTGGTCAAGGTTTCAGT G GTATAAACTAGAGTCCAGT		
Ots 112301-43 T	C GCATGGCTGCCCTAGAACA		CGTCGCATTCAGC CGTCGCG
0ts_112419-131 A	C GCATGGCTGCCCTAGAACA T GTGGGTAATCGATGCCAAA		
Ots 112820-284 C	T CATAGATGTTTATATGAAA		
Ots 112876-371 C	A GCCTACAGCAAATTCAGCT		
Ots_113242-216 C		GACT GACATCTTCAACAAGTGTTCATTCACC	ATTACCAACGGAGAACC
Ots 115987-325 T	G GGAGGTGTAGTGAAATGGG		
Ots_117432-409 A	G TCATCAAAACATGCCTCTT		
Ots_118205-61 T	C CCATACAGCCAGTCCAGGT		GCCCCTACACCTC TAGCCCC
Ots_118938-325 C	T ATTTTCAAACAGGCATTTA	TCATTGGTGAA GGTCTGTCCCTCATTCTTTGC/	
Ots_123921-111 A	G TCGCTAGGCAGAAATATAG	GGTTCT GAGCATGGCGCTTGCA	TGCTAAATGGCATATATTAT 🚽
•	Ш		

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

Upload Cancel Marker	s - SNP 1	aqman - OtsPBT96SNPs.txt				
Data Formatting First row is Header Select Delimiter	New	r Configuration narkers Marker synonyms or nr Type	Additional Upload Options			
Tab *		v sub-type Tagman ★	Use Save Column Mapping			
	SNP	RAD -GTSeq -Taqman	[Select Mapping]			
Toggle fieldset View		2	3	4	5	6
	•	<ignore field=""></ignore>	<ignore field=""></ignore>	<ignore field=""></ignore>	<ignore field=""></ignore>	<ignore field=""></ignore>
<ignore field=""></ignore>		10-10-1-1	FamAllele	Fwd Primer	Rev Primer	VIC probe
		VicAllele			CGACCAAGTAGCGGCACTT	ATAGAACTACAATTCACATAT
ssay		T	С	CGGAAGACCAGATTCTCCAAGAGTA	CGACCAAGTAGCGGLACTT	
ssay ts_100884-287		T C	C G	CGGAAGACCAGATTCTCCAAGAGTA TGAAAGATATCAATTGTAGTAGTGGTGGTG	ACACGCCAGTCCACAAGT	ATGGAGGATTGTGGTTGT
ssay bts_100884-287 bts_101554-407		T				
553y 715_100884-287 715_101554-407 715_101704-143		T	G	TGAAAGATATCAATTGTAGTAGTGGTGGTG	ACACGCCAGTCCACAAGT	ATGGAGGATTGTGGTTGT CTTAGACGTCAGAGGTC
1553y 115_100884-287 115_101554-407 115_101704-143 115_102414-305		т С Т	G G	TGAAAGATATCAATTGTAGTAGTGGTGGTG ACTTCTTGAGCCAATCGGATGATG	ACACGCCAGTCCACAAGT CCAGAGATAAACTAGTGGAGGAGAATCA	ATGGAGGATTGTGGTTGT
<pre><lp><lp></lp></lp></pre> Assay Dis_100884-287 Dis_101554-407 Dis_101554-407 Dis_10154-403 Dis_102414-306 Dis_102410-308 Dis_102401-308 Dis_1023122-180		T C T A	G G G	TGAAAGATATCAATTGTAGTAGTGGTGGTG ACTTCTTGAGCCAATCGGATGATG GCCTACTGATAAATGTATGACAGTAATGGA	ACACGCCAGTCCACAAGT CCAGAGATAAACTAGTGGAGGAGATCA CAATAACAAACAAGCTAGGAACAAAAGTGT	ATGGAGGATTGTGGTTGT CTTAGACGTCAGAGGTC CACATAGTGTAGCTTTACTA

Figure 9 - Selecting Marker Type Taqman SNP.

Upload markers								
Upload Cancel Ma	rkers - SNP Taqman - OtsPBT96SNPs.txt							
Data Formatting	Marker Configuration	1	Additional Upload Options					
First row is Header	New markers Marker synonyms		Save Marker Set					
Select Delimiter	Marker Type							
Tab *	SNP *		Save Column Mapping					
100	Marker Sub-type		2					
	SNP-Tagman *		Use Saved Column Mapping:					
	· · · · · · · · · · · · · · · · · · ·		[Select Mapping]	Ŧ				
	Select Species							
	Acipenser transmontanus *							
	A							
Toggle fieldset View	Oncorhynchus clarkii lewisi 🔹							
loggie fieldset view	Oncorhynchus clarkii utah							
1	Oncorhynchus kisutch		3	4		6		6
Ignore Field>	Oncorhynchus mykiss		<ignore field=""></ignore>	<ignore field=""></ignore>		<ignore field=""></ignore>		<ignore field=""></ignore>
	Oncorhynchus mykiss aguabonita	1	1 - 5					
Assay	Oncorhynchus mykiss gairdneri	_	FamAllele	Fwd Primer		Rev Primer		VIC probe
Ots_100884-287	Oncorhynchus mykiss x clarkii		С	CGGAAGACCAGATTCTCC		CGACCAAGTAGCGGCACTT		ATAGAACTACAATTCACATATA
Ots_101554-407	Oncorhynchus nerka		G	TGAAAGATATCAATTGTAG		ACACGCCAGTCCACAAGT		ATGGAGGATTGTGGTTGT
Ots_101704-143	Oncorhynchus tshawytscha		G	ACTTCTTGAGCCAATCGG		CCAGAGATAAACTAGTGGAGGAGA		CTTAGACGTCAGAGGTC
Ots_102414-395	Osmerus mordax .		G	GCCTACTGATAAATGTATC		CAATAACAAACAAGCTAGGAACAA		CACATAGTGTAGCTTTACTAC
Ots_102801-308			Α	TGGGACAGAGGTGGGAA		CCCAAAGATGCTTAACTGAAGATG		AGGGACAGTTTCGCAGACG
Ots_103122-180	Т		С	CAAACGCGCACTCACACA		TCACAATGGTACGATTTTACGACTC		CATCAACACAATCTGC
Ots_104415-88	C		T	CCTGAGCATCCCAGTTGA	ACT	TGTTTTCAATACACTGCAATTTAGT	TTTGGT	TCCTGAAAAACGACATCC

Figure 10 - Selecting Species Taqman SNP.

Upload Cancel Marker Data Formatting First row is Header Select Delimiter Tab	Mark New Mark SNP Mark	Taqman - OtsPBT96SNPs.txt er Configuration markers Marker synonyms er Type = Sub-type -Tagman * t Species	Additional Upload Options Save Marker Set Save Column Mapping Use Saved Column Mapping: [Select Mapping]	•		
Toggle fieldset View	Onc	2 VIC Allele	3 FAM Allele	4 Forward Primer	5 Reverse Primer	6 «Ignore Field»
					Ignore Field>	L
Assay		VicAllele	FamAllele	Fwd Primer	FAM Allele	VIC probe
Dts_100884-287		T	С	CGGAAGACCAGATTCTCCAAGAGTA	FAM Probe Forward Primer	ATAGAACTACAATTCACATAT
ts_101554-407		C	G	TGAAAGATATCAATTGTAGTAGTGGTGGTG	Lab Synonym	ATGGAGGATTGTGGTTGT
ts_101704-143		T	G	ACTTCTTGAGCCAATCGGATGATG	Marker Name Reverse Primer	CTTAGACGTCAGAGGTC
ts_102414-395		A C	G	GCCTACTGATAAATGTATGACAGTAATGGA	- VIC Allele	3T CACATAGTGTAGCTTTACTA
ts_102801-308		T T	A C	TGGGACAGAGGTGGGAATTGA	VIC Probe	AGGGACAGTTTCGCAGACO
ts_103122-180 ts_104415-88		C	C T	CCTGAGCATCCCAGTTGAACT	TCACAATGGTACGATTTTACGACTCAA TGTTTTCAATACACTGCAATTTAGTTTTGG	
	tin	g Column Header	s Taqman SNP.	A COLOR	FT	300
ploading RA equired Fields		NP markers				*

Uploading RAD SNP markers

- 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

Markers - RAD - Lampray RAD Markers Fina	II - Notepad	
File Edit Format View Help		
Locus Allele 1 5 3 Allele	2 5-3 Restriction Enzyme recognition site SNP Allele 1	SNP All A
Etr_SbfI_CRITFC_001_29_0001	CCTGCAGGATGGTGAAGGTGAGCACGTGTCCGCCCGGCGTGCGCAGCTGCATGCTGGCGAGGTCGCG	CCTGCAC =
Etr_SbfI_CRITFC_001_29_0002	CCTGCAGGGCAAAGTGGGGGCGACAACATCTTTCGTTTTGTAAATGTACACATTCATT	CCTGCAG
Etr_SbfI_CRITFC_001_40_0003	CCTGCAGGCGCTTGCTCGCTATGCGACGTTTTTGTCGCCATTTCGCCGGACGGCCACGGTTTGAGAT	CCTGCAG
Etr_SbfI_CRITFC_001_40_0004	CCTGCAGGCTCTTGCCTCGTGCCTAGAATGTGACGGACATTGGGATAACCGGCGTCTCAGAAATGAA	CCTGCAG
Etr_SbfI_CRITFC_001_40_0005	CCTGCAGGGTGCCCAGGTGAAACAAAAACTAAACGACAGTATATTTTTATTTA	CCTGCAG
Etr_SbfI_CRITFC_001_64_0006	CCTGCAGGAGCTCGTGCGCCTTGCTCCAGCTGCCGCCTCAAGGCCTCGGCCTCCTGCACGAACAAACA	CCTGCAG
Etr_SbfI_CRITFC_001_65_0007	CCTGCAGGGTGAACCCGCGCCCGCACACGCCGCACTTGTGTTCCTTGATGCCCTGCGGGGAGAGCCG	CCTGCAG
Etr_SbfI_CRITFC_001_38_0008	CCTGCAGGGGCCTCGACTCTTTGGATGACGTGTCCACTGCCCTGCCTG	CCTGCAG
Etr_SbfI_CRITFC_001_48_0009	CCTGCAGGAGGTCCGAGGGCGAAACGTCGCACGGGCGTCGTGTCCAACGGCACACGATGCAACGCGA	CCTGCAG
Etr_SbfI_CRITFC_001_30_0010	CCTGCAGGTCCGGACGATTTGCTCCAGCACCCCGCGGCCACGATGCTCATGCTCCGTGCCGTCACGC	CCTGCAG
Etr_SbfI_CRITFC_001_17_0011	CCTGCAGGAGCAGCTGTGGGATCTGGCGCAGGGGAGGGG	CCTGCAG
Etr_SbfI_CRITFC_001_40_0012	CCTGCAGGATAAGTTGAAGCGCAAAGGCACGCTCACATTCTTCTAGCCATTGCATGGGGCATGGGTG	CCTGCAG
Etr_SbfI_CRITFC_001_40_0013	CCTGCAGGAGGTCGTTGGTTCTATGCCGATCCTGACGCCGACTGCTGTATATTTTGACTTTGCGGTG	CCTGCAG
Etr_SbfI_CRITFC_001_40_0014	CCTGCAGGAGTACAATTTTCGAAAGCGGGAGAGCTGCTCAAGTCGGCGGTGATAATGAGCCTAATAA	CCTGCAG
Etr_SbfI_CRITFC_001_53_0015	CCTGCAGGGCGAGTGGACTAGGGTCAACGAGAAGAATCGGGAATAGGGGCATGGCCACGCACCGTAT	CCTGCAG
Etr_SbfI_CRITFC_001_20_0016	CCTGCAGGGCCCTGCAGCAACAGGTGACCGCTCACAATGGGCGCTCGCCCCCCCC	CCTGCAG
Etr_SbfI_CRITFC_001_34_0017	CCTGCAGGGTCGCGACATGGAACGACGCAAGGGCTCATGCAGTTGATGGAGTTGACGAGGTGGGGGG	CCTGCAG
Etr_SbfI_CRITFC_001_48_0018	CCTGCAGGGTCACCGATCCCCGCTTCCAGGCATCTCCCTGGGGGGCCCTGGCGGGACCACACGAGCGA	CCTGCAG
Etr_SbfI_CRITFC_001_38_0019	CCTGCAGGCACAACGTGGAAAGCGACGAGTGGCATTGGTGAAACTTATGCAATCGAGGCCTTGGCGA	CCTGCAC
Etr_SbfI_CRITFC_001_49_0020	CCTGCAGGGCGGCCTCCTGGAGGCGACCAGCAGTCGCGGGAGGGCGGCCGCCTCCCTGCCCGATCTC	CCTGCAG
Etr_SbfI_CRITFC_001_40_0021	CCTGCAGGCGCACCTCACCTACTACTGCGCCGGGCGCAACAAGACGGGAGGAGGCAGAGCGGCCTCC	CCTGCAG
Etr_SbfI_CRITFC_001_40_0022	CCTGCAGGCGCTGGAGCCGCCCCTCCAAGTCCCGCTTGGCCCTCAGCAGATCCTGAACCTCCTTCTC	CCTGCAC
Etr_SbfI_CRITFC_001_40_0023	CCTGCAGGCCGGCCCTCGACGTCCACAACCGCCCACCCGCCAGTCCCCATCTACTTGATCTGCTGAG	CCTGCAG
Etr_SbfI_CRITFC_001_31_0024	CCTGCAGGGTGATGCTCAACCCCGCACACCGCGTGACTCATTTGAGGCCGAGTGGACCTAGGGGATC	CCTGCAG
Etr_SbfI_CRITFC_001_40_0025	CCTGCAGGCTGGATTGTGTGAGGAGCTCACAAATGATAATTATTTTTTACCCTTCTATCTGGCAAC	CCTGCAC
Etr_SbfI_CRITFC_001_45_0026	CCTGCAGGCCGCCACCTGCTCCCGGCGTCGCGATGGCCTCTCCGCGCCGCCCCCCCTCTTCACG	CCTGCAG
Etr_SbfI_CRITFC_001_23_0027	CCTGCAGGTGGGCCCGTGCGCGGTGCTCTCCCGTGAAACGTGAAATCACGAATGATGTTTTCCCGA	CCTGCAG
Etr_SbfI_CRITFC_001_40_0028	CCTGCAGGCATTCACCACGTCCCATCTATGGGTCGGGCCTCAAGCGCATCACGGATGCATCTCCGTG	CCTGCAC 👻
-igure 12 - Example of a tab de	limited text file needed to upload RAD SNP marker information.	and the second s

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

Upload markers				
Upload Cancel Markers - RAD	- Lampray RAD Markers Final.txt			
	er Configuration Additional Upload Options markers Marker synonyms Additional Upload Options			
Tab *	Save countri mapping			
	er Sub-type Use Saved Column Mapping: Capture Column Colum	•		
	P-RAD P-GTSeq			
Toggle fieldset View	-Taqman			
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<ignore field=""></ignore>	<ignore field=""></ignore>	Ignore Field> •	<ignore field=""></ignore>	<ignore field=""></ignore>
Locus	Allele 1 5 3	Allele 2 5-3	Restriction Enzyme	recognition site
Etr_Sbfl_CRITFC_001_29_0001	CCTGCAGGATGGTGAAGGTGAGCACGTGTCCGCCCGGCGTGCGCAGCTGCATGCTG	CCTGCAGGATGGTGAAGGTGAAGGTGAGCACGTGGCCGCCCGGCGTGCGCAGCTGCATGCTGGCGAGGTCGCG	Sbfl	CCTGCAGG
Etr_Sbfl_CRITFC_001_29_0002	CCTGCAGGGCAAAGTGGGGGCGACAACATCTTTCGTTTTGTAAATGTACACATTCATT	ICATTTGTA CCT0CA000CCAAAGT000G0CGACAACACCTTTCGTTTTGTAAATGTACACATTCATTGCATTTGTA	Sbfl	CCTGCAGG
Etr_Sbfl_CRITFC_001_40_0003	CCTGCAGGCGCTTGCTCGCTATGCGACGTTTTGTCGCCATTTCGCCGGACGGCCAC	30TTTGAGAT CCT0CA00C0CTT0CTC0CTAT0C0ACGTTTTT0TC0CC0TTTC0CC0GAC00CCAC0GTTTGAGAT	Sbfl	CCTGCAGG
Etr_Sbfl_CRITFC_001_40_0004	CCTGCAGGCTCTTGCCTCGTGCCTAGAATGTGACGGACATTGGGATAACCGGCGTCTC	CAGAAATGAA CCTGCAGGCTCTTGCCTCGTGCCTAGAATGTGACGGACACTGGGATAACCGGCGTCTCAGAAATGAA	Sbfl	CCTGCAGG
Etr_Sbfl_CRITFC_001_40_0005	CCTGCAGGGTGCCCAGGTGAAACAAAAACTAAACGACAGTATATTTTTATTTA	TAAGAACC CCTGCAGGGTGCCCCAGGTGAAACAAAAACTAAACGACAGGATATTTTTTATTTA	Sbfl	CCTGCAGG
Etr_Sbfl_CRITFC_001_64_0006	CCTGCAGGAGCTCGTGCGCTTGCTCCAGCTGCCGCCTCAAGGCCTCGGCCTCCTGC	ACGAACAAACA CCTGCAGGAGCTCGTGCGCTTGCTCCAGCTGCCGCCTCAAGGCCTCGGCCTCCTGCACGAACACACA	Sbfl	CCTGCAGG
Etr_Sbfl_CRITFC_001_65_0007	CCTGCAGGGTGAACCCGCGCCCGCACACGCCGCACTTGTGTTCCTTGATGCCCTGC	366GAGAGCCG CCTGCAGGGTGAACCCGCGCCCGCACACGCCGCACTTGTGTTCCTTGATGCCCTGCGGGGGAGAGACG	Sbfl	CCTGCAGG
4				•

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Figure 13 - Selecting Marker Type RAD SNP.

Upload Cancel Marke	rs - RAD - Lampray RAD Markers Final:	bit					
Data Formatting First row is Header Select Delimiter Tab *	Marker Configuration New markers Marker syno Marker Type SNP Marker Sub-type SNP-RAD Select Species Acigeneer transmontanus	•	Additional Upload Options Save Marker Set Save Column Mapping Use Saved Column Mapping: (Select Mapping) *	-			
Toggle fieldset View	I Ictalurus furcatus Ictalurus punctatus	٩					
1	Lampetra tridentata		2	3	4		5
<ignore field=""></ignore>	Lepomis cyanellus Lepomis gibbosus			Ignore Field> •	<ignore field=""></ignore>	<ignore field=""></ignore>	
Locus	Lepomis gulosus			Allele 2 5-3	Restriction Enzyme	recognition site	
tr_Sbfl_CRITFC_001_29_0001	Lepomis macrochirus	TGTO	CGCCCGGCGTGCGCAGCTGCATGCTGGCGAGGTCGCG	CCTGCAGGATGGTGAAGGTGAGCACGTGGCCGCCCGGCGTGCGCAGCTGCATGCTGGCGAGGTCGCG	Sbfl	CCTGCAGG	
tr_Sbfl_CRITFC_001_29_0002	Lota lota	ACAT	CTTTCGTTTTGTAAATGTACACATTCATTGCATTTGTA	CCTGCAGGGCAAAGTGGGGGGGGGGACAACACCTTTCGTTTTGTAAATGTACACATTCATT	Sbfl	CCTGCAGG	
tr_Sbfl_CRITFC_001_40_0003	Micropterus dolomieu	CGT	TTTGTCGCCATTTCGCCGGACGGCCACGGTTTGAGAT	CCTGCAGGCGCTTGCTCGCTATGCGACGTTTTGTCGCCGTTTCGCCGGACGGCCACGGTTTGAGAT	Sbfl	CCTGCAGG	
tr_Sbfl_CRITFC_001_40_0004	Micropterus admoider	* AATO	TGACGGACATTGGGATAACCGGCGTCTCAGAAATGAA	CCTGCAGGCTCTTGCCTCGTGCCTAGAATGTGACGGACACTGGGATAACCGGCGTCTCAGAAATGAA	Sbfl	CCTGCAGG	
Etr_Sbfl_CRITFC_001_40_0005		ANACANAAC	TAAACGACAGTATATTTTTTTTTTTTTTTCCAGGTAAGAACC	CCTGCAGGGTGCCCAGGTGAAACAAAAACTAAACGACAGGATATTTTTTATTTA	Sbfl	CCTGCAGG	
Etr_Sbfl_CRITFC_001_64_0006	CCTGCAGGAGCTCGTGCGC	TTGCTCCAGC	TGCCGCCTCAAGGCCTCGGCCTCCTGCACGAACAAACA	CCTGCAGGAGCTCGTGCGCTTGCTCCAGCTGCCGCCTCAAGGCCTCGGCCTCCTGCACGAACACACA	Sbfl	CCTGCAGG	
Etr_Sbfl_CRITFC_001_65_0007	CCTGCAGGGTGAACCCGCG	CCCGCACAC	CCGCACTTGTGTTCCTTGATGCCCTGCGGGGGAGAGCCG	CCTGCAGGGTGAACCCGCGCCCGCACACGCCGCACTTGTGTTCCTTGATGCCCTGCGGGGGAGAGACG	Sbfl	CCTGCAGG	
igure 14 - S	electing Spe	cies f	RAD SNP	and U	C#		8

Figure 14 - Selecting Species RAD SNP

				J.	5			
Upload markers								
Upload Cancel Markers - RA	AD -	ampray RAD Markers Final.txt						
First row is Header Select Delimiter Tab	arke SNP arke SNP-	Configuration Ankers Marker synonyme Syno Syno Sub-type Sub-type Species sevent Column Mapping: Select Mapping: Select Mapping: *						
1	_	2	_	3	-	4		5
Marker Name		Sequence A 🔹		Sequence B		estriction Enzyme	<ignore< th=""><th>Field></th></ignore<>	Field>
Locus Etr_Sbfl_CRITFC_001_29_0001	_	Niele 1 5 3	_			Ignore Field> ab Synonym farker Name	recognit	
Etr_Sbfl_CRITFC_001_29_0001		CCTGCAGGGCAAAGTGGGGGGCGACAACATCTTTCGTTTTGTAAATGTACACATTCATT		CCT9CA000CAAAGT00000CGACAACACCCTTCGTTTTGTAAATGTACACATTCATTGCATTGTA	+ 1	ecognition Site	CCTGCA	
Etr_Sbfl_CRITFC_001_40_0003		CCTGCAGGCGCTTGCTCGCTATGCGACGTTTTTGTCGCCATTTCGCCGGACGGCCACGGTTTGAGAT		CCTGCAGGCGCTTGCTCGCTATGCGACGTTTTGTCGCCGTTTCGCCGGACGGCCACGGTTTGAGAT	1	equence A	CCTGCA	
Etr_Sbfl_CRITFC_001_40_0004	+	CCTGCAGGCTCTTGCCTCGTGCCTAGAATGTGACGGACATTGGGATAACCGGCGTCTCAGAAATGAA		CCTGCAGGCTCTTGCCTCGTGCCTAGAATGTGACGGACACTGGGATAACCGGCGTCTCAGAAATGAA		equence B np Allele A	CCTGCA	
Etr_Sbfl_CRITFC_001_40_0005	T	CCTGCAGGGTGCCCAGGTGAAACAAAAACTAAACGACAGTATATTTTTTATTTA	1	CCTGCAGGGTGCCCAGGTGAAACAAAAACTAAACGACAGGATATTTTTTATTTA	1	np Allele B	CCTGCA	GG
Etr_Sbfl_CRITFC_001_64_0006		CCTGCAGGAGCTCGTGCGCTTGCTCCAGCTGCCGCCTCAAGGCCTCGGCCTCCTGCACGAACAAACA	(A)	CCTGCAGGAGCTCGTGCGCTTGCTCCAGCTGCCGCCTCAAGGCCTCGGCCTCCTGCACGAACACACA	5	np Position	CCTGCA	4GG
Etr_Sbfl_CRITFC_001_65_0007		CCTGCAGGGTGAACCCGCGCCGCACACGCCGCACTTGTGTTCCTTGATGCCCTGCGGGGAGAGCCG	G	CCTGCAGGGTGAACCCGCGCCGCACACGCCGCACTTGTGTTCCTTGATGCCCTGCGGGGAGAGAGA	SI	a	CCTGCA	GG
								,

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

Markers - SNP-GTSeq definition	13 101 0.14	ykiss (Italiibu		
Assay: VIC Allele	FAM A		Fwd Primer Rev Primer VIC probe FAM probe	
M09AAC.055-GTSeq	C	Т		CCACGCTGTCC
M09AAD.076-GTSeq	Т	C G	ACTGTTACCACTCTCATCAACCTA GGGTCCAGGAGGTTTTTAAACAACATA	CACCAAC
M09AAE.082-GTSeq	T	G		TGTTTTACAAA
M09AAJ.163-GTSeq	C T G T	Α	TCCCATGGCCCTTACTCTATCAAA TTGAGGTGTATGTTGAAAAGTAAACTTA	
Ocl_gshpx-357-GTSeq		G	GAGATCCTGAGGTCCCTGAAGTATA AAGTGGAAATTTGGGCTCAAAGCA	ATCCTTC
OMGH1PROM1-SNP1-GTSeq	A	Т	TCAAACTGCATTTGATGGAAACAAACATA AGGACAATTCTAAGTGACCTCAAACTGA	
OMS00002-GTSeq A	C		ITTGATTTGTATCTGCTTCTTA CCAACATGCCTCACACAAAAA TGTTTTGCAGCG	
OMS00003-GTSeq T	Сестесеееееесессес		ACTGATGAGGATGAGATCA GTAATAAAGCCCTTTTGTGAGGAAAAACTAATA	CTTTACT
OMS00006-GTSeq T	C		TAGGACATAGTTTGAGCTAA TGTGGTGTCATGTTTGCCCTACA CACTTACAAATAG	
OMS00008-GTSeq A	T		TAAGGAGGATTTTTAAATATGTGAGATAGAAA GGATACAGCGTTTTGGAATGAAACTA	CTTCAAA
OMS00013-GTSeq A	G			TTTTCCCTTGC
OMS00014-GTSeq T	C		ACACAAGGGCTTCATTCTGA GATGTCTCTGGGTGGTTGTCAA TGATTTGATGAA	
OMS00015-GTSeq A	T			TCACACTTTTA
OMS00017-GTSeq A	G		GGAGAACAAAGTTCATCATAAATATTTTCCTTTA GGAGAACAAAGGGAAAGAGA	
OMS00018-GTSeq T	G			ACATAATTAAT
OMS00024-GTSeq T	G			ACCCAAATTTT
OMS00030-GTSeq T	G		IGACTACAGAGCTATACAACA GATCTGATCGGTCGGGAGAGAA ATGAGGGTCCCT/	
OMS00039-GTSeq A	G			GACACGTACGC
OMS00048-GTSeq T	C		AGCTGGAGAACAACGTA TGCAGTTGACAGAGGCTTTCTTTA CAGCTAAACTCA	
OMS00052-GTSeq T	G		ITTTCATCCCAATCATTCACA GGCATCAGGCTCTTCTTCCTA CTTCCTTTGAG/	
OMS00053-GTSeq T	C		AGGTCAAGGTGATCA GGATGTCTGGTGTGGCTGTAAAA TGTGTGATTGATACATATAA	
OMS00056-GTSeq T	C		AGTAAACTGAAAATTCCAATGTATGAA CCCCAACCATGCTTGTTATTGAACA	TAGCTTC
OMS00057-GTSeq T	G		AGGGAGCATGAGACAGAA GTTGGGCTCCGGTACGATA CTCCACAGAACCTTGA	CTCCACA
OMS00058-GTSeq A	G		ATTTGGAGCCACTGCA GCTAGGAGACAGAGGGTGAAAGA CAACACTTTGTACCCCTCA	CACTTTG
OMS00061-GTSeq T	C		GAGGCTGACCTGTTGA GCTGATGGCACCTGACAGTTAATTA CATTGCCATTTAG	
OMS00062-GTSeq T	С		GGAAGGCTACTGTACA TGAACAGAGATCTGGAGAGTTGGATA TTGACCAGCAGA	
OMS00064-GTSeq T	G		TATGTAGTTCGATGGAACAGTA TTTACAACAATCTTCTTTTAATAAAAATATAGCCAC	
OMS00068-GTSeq A	G	GCACT/	AACTGGACAACATTTTTAAGAATGAA GGCAGTTGAGCATTTTGGGATATTA AATA	
•		III		▶
			text file needed to upload GTSeq SNP marker information.	8

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

Upload markers								
Upload Cancel Markers	- SNP-GT	TSeq definitions for O.Mykiss (Rainbow Trout	- Steelhead).txt					
□ Data Formatting Marker Configuration ☑ First row is Header New markers Marker synonyms □ Calca Delivation Marker Type		Additional Upload Options						
Select Delimiter Tab *	SNP	*	Save Column Mapping					
	Marker SNP-T	Q,	Use Saved Column Mapping: [Select Mapping]	•				
Toggle fieldset View	SNP-1	laqman						
1		2	3	4	5	6	7	
<ignore field=""></ignore>	٠	<1gnore Field>	<ignore field=""></ignore>	<ignore field=""></ignore>	Ignore Field>	<ignore field=""></ignore>	<ignore field=""></ignore>	
Assay:		VIC Allele	FAM Allele	Fwd Primer	Rev Primer	VIC probe	FAM probe	
M09AAC.055-GTSeq		С	т	GTCTCCGACGTGTGGCTA	TGGAACGAACCTGAGAACATAAGGA	ACCTCCACGCTGTCCA	ACCTCCACACTGTCCA	
M09AAD.076-GTSeq		т	C	ACTGTTACCACTCTCATCAACCTA	GGGTCCAGGAGGTTTTTAAACAACATA	CACCAACCACTGGTGAAA	CCAACCGCTGGTGAAA	
M09AAE.082-GTSeq		т	G	CTATGTGCAGTGCCCTTCTCAA	GGCTTACAAGTATGCATGACTAGCTA	AGGTTGTTTTACAAATTTAAA	AGGTTGTTTTACACATTTAAA	
M09AAJ.163-GTSeq		G	A	TCCCATGGCCCTTACTCTATCAAA	TTGAGGTGTATGTTGAAAAGTAAACTTA	AACAAAGTGAAAGTGTCCTTAA	CAAAGTGAAAGTGTCTTTAA	
Ocl_gshpx-357-GTSeq		т	G	GAGATCCTGAGGTCCCTGAAGTATA	AAGTGGAAATTTGGGCTCAAAGCA	ATCCTTCCAGGAAATGA	TCCTTCCCGGAAATGA	
OMGH1PROM1-SNP1-GTSeq		A	т	TCAAACTGCATTTGATGGAAACAAACATA	AGGACAATTCTAAGTGACCTCAAACTGA	TAGTGTTCACTGACTTCAA	TAGTGTACACTGACTTCAA	
OMS00002-GTSeq		A	C	TTTGATTTGATTTGTATCTGCTTCTTA	CCAACATGCCTCACACAAAAA	TGTTTTGCAGCGCTCA	TGTTTGGCAGCGCTA	
4							÷	

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Figure 17 - Selecting Marker Type GTSeq SNP.

Uplead Cancel Mark	Marker Sub-type SNP-GTSeq Select Species Acipenser transmontanus		Additional Upload Options Save Marker Set Save Column Mapping Use Saved Column Mapping:							
Toggle fieldset View	Uncornynchus clarkii benshawi Oncorhynchus clarkii henshawi Oncorhynchus clarkii lewisi	-	3		4	5	6		7	
<ignore field=""></ignore>	Oncorhynchus clarkii utah Oncorhynchus kisutch	•	<ignore field=""></ignore>	•	<ignore field=""></ignore>	<lanore field=""></lanore>	Ignore Field>	•	<ignore field=""></ignore>	
	Oncorhynchus mykiss		F 4 4 4 1 - 1 -			Para Parlament	180 miles			
Assay: M09AAC.055-GTSeg	Oncorhynchus mykiss aguabonita		FAM Allele		Fwd Primer GTCTCCGACGTGTGGCTA	Rev Primer TGGAACGAACCTGAGAACATAAGGA	VIC probe ACCTCCACGCTGTCCA		FAM probe ACCTCCACACTGTCCA	
109AAD.076-GTSeq	Oncorhynchus mykiss gairdneri		C		ACTGTTACCACTCTCTCATCAACCTA	GGGTCCAGGAGGTTTTTAAACAACATA	CACCAACCACTGGTGAAA		CCAACCGCTGGTGAAA	
	Oncorhynchus mykiss x clarkii									
109AAE.082-GTSeq			0		CTATGTGCAGTGCCCTTCTCAA	GGCTTACAAGTATGCATGACTAGCTA	AGGTTGTTTTACAAATTTAAA		AGGTTGTTTTACACATTTAAA	
	Oncorhynchus nerka	*	A		TCCCATGGCCCTTACTCTATCAAA	TTGAGGTGTATGTTGAAAAGTAAACTTA	AACAAAGTGAAAGTGTCCTTAA		CAAAGTGAAAGTGTCTTTAA	
cl_gshpx-357-GTSeq	т		G		GAGATCCTGAGGTCCCTGAAGTATA	AAGTGGAAATTTGGGCTCAAAGCA	ATCCTTCCAGGAAATGA		TCCTTCCCGGAAATGA	
cl_gshpx-357-GTSeq MGH1PROM1-SNP1-GTSeq	T A		т		TCAAACTGCATTTGATGGAAACAAACATA	AGGACAATTCTAAGTGACCTCAAACTGA	TAGTGTTCACTGACTTCAA		TAGTGTACACTGACTTCAA	
409AAJ.163-GTSeq Xcl_gshpx-357-GTSeq XMGH1PROM1-SNP1-GTSeq XMS00002-GTSeq	T A A									
kd_gihpx-357-GTSeq MGH1PROM1-SNP1-GTSeq MS00002-GTSeq		es G	T C		TCAAACTGCATTTGATGGAAACAAACATA	AGGACAATTCTAAGTGACCTCAAACTGA	TAGTGTTCACTGACTTCAA	>	TAGTGTACACTGACTTCAA	

Toggle fieldset View						
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		FAM probe
109AAC.055-GTSeq	С	т	GTCTCCGACGTGTGGCTA	TGGAACGAACCTGAGAACATAAGGA	FAM Probe	ACCTCCACACTGTCCA
109AAD.076-GTSeq	т	С	ACTGTTACCACTCTCTCATCAACCTA	GGGTCCAGGAGGTTTTTAAACAACATA		CCAACCGCTGGTGAAA
109AAE.082-GTSeq	т	G	CTATGTGCAGTGCCCTTCTCAA	GGCTTACAAGTATGCATGACTAGCTA	Marker Name	AGGTTGTTTTACACATTTAAA
109AAJ.163-GTSeq	Seq G A		TCCCATGGCCCTTACTCTATCAAA	TTGAGGTGTATGTTGAAAAGTAAACTTA	Reverse Primer	CAAAGTGAAAGTGTCTTTAA
icl_gshpx-357-GTSeq	т	G	GAGATCCTGAGGTCCCTGAAGTATA	AAGTGGAAATTTGGGCTCAAAGCA	VIC Probe	TCCTTCCCGGAAATGA
MGH1PROM1-SNP1-GTSeq	A	т	TCAAACTGCATTTGATGGAAACAAACATA	AGGACAATTCTAAGTGACCTCAAACTGA	TAGTGTTCACTGACTTCAA	TAGTGTACACTGACTTCAA
DMS00002-GTSeq	A	С	TITGATTIGATTIGTATCTGCTTCTTA	CCAACATGCCTCACACAAAAA	TGTTTTGCAGCGCTCA	TGTTTGGCAGCGCTA

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

Markers - SNP definitions for O.Mykiss (Rainbow Trout - Steelhead) - Synonyms - Notepad File Edit Format View Help Assay: Synonym VIC Allele M09AAC.055 M09AAC.055 Fwd Syn Rev Primer FAM Allele Fwd Primer Rev Syn VIC probe M09AAC.055-Syn M09AAD.076-Syn M09AAE.082-Syn GTCTCCGACGTGTGGCT GTCTCCGACGTGTGGCTT TGGAACGAACCTGAC CT ACTGTTACCACTCTCTCATCAACCTT CTATGTGCAGTGCCCTTCTCAT GGCTTACAAGTATGC ACTGTTACCACTCTCTCATCAACCT M09AAD.076 M09AAE.082 T T C Ğ CTATGTGCAGTGCCCTTCTCA M09AAJ.163-Syn Ocl_gshpx-357-Sy OMGH1PROM1-SNP1 TCCCATGGCCCTTACTCTATCAA TCCCATGGCCCTTACTCTATCAAT G GAGATCCTGAGGTCCCTGAAGTAT GAGATCCTG M09AAJ.163 Ġ A T TCTATCAAT TTGAGGT GAGATCCTGAGGTCCCTGAAGTA Ocl_gshpx-357 OMGH1PROM1-SNP1 -Svn TCAAACTGCATTTGATGGAAACAAACAT TCAAACTGCATTTGATGGAAACA -Syn A C G C T TTTGATTTGATTTGTATCTGCTTCTTT OMS00002 0MS00002-Syn A TTTGATTTGATTTGTATCTGCTTCTT OMS00003 0MS00003-Syn GTGCCACTGATGAGGATGAGATC GTGCCACTGATGAGGATGAGATCT **GTAATAA** TCCACGTAGGACATAGTTTGAGCTAT OMS00006-Syn OMS00008-Syn OMS00006 т TCCACGTAGGACATAGTTTGAGCTA CCCTTTAAGGAGGAGTTTTTAAATATGTGAGATAGAA OMS00008 CCCTTTAAGGAGGATTTTAAATA Α Ġ C T CCTTIGGTGGTTAT GCCTTTGTTCTCCTTGGTGGTTAT A CTTACACACAAGGGCTTCATTCTG CTTACACACAAGGGCTTCATTCTG TCAGACCCTATTTTTGGCACAAGT TCAGACCCTATTTTTGGCACAAGT OMS00013 0MS00013-Syn A T A AGAAAAG OMS00014-Syn OMS00014 OMS00014 Syn OMS00015-Syn OMS00017-Syn OMS00018-Syn OMS00015 OMS00017 ATTAAGTTCATACAAAAGTTCATCATAAATATTTTCCTTT ATTAAGTTCATACAA GTCATAAATCAACAC A T T T 999999999999 OMS00018 AGAGTACATGTGTGGCTGCAAT AGAGTACATGTGTGGCTGCAA OMS00024 0MS00024-Syn CACATACAACCATCACCCTTCCTAA CACATACAACCATCACCCTTCCTAAT 0MS00030-Syn OMS00030 0MS00039-Syn OMS00039 CCATCTA A T T GGAAGAGCTGGAGAACAACGTT TGCAGTTGACAGAGG AC TGCGTTTTTCATCCCAATCATTCACT OMS00048-Syn OMS00052-Syn GGAAGAGCTGGAGAACAACGT G TGCGTTTTTCATCCCAATCATTCAC OMS00048 OMS00052 GGAGCCAGGTCAAGGTGATCT GGATGTCTGGTGTGG ATGTATGA TCAGGAAGTAAACTGAAAATTCC OMS00053 0MS00053-Syn GGAGCCAGGTCAAGGTGATC GGATGTCTGGTGTGC T T T OMS00056-Syn OMS00057-Syn TCAGGAAGTAAACTGAAAATTCCAATGTATGA OMS00056 GAGAAAGGGAGCATGAGACAGA GAGAAAGGGAGCATGAGACAGAT GTTGGGCTCCGGTAC OMS00057 Ğ C C OMS00058 0MS00058-Syn A T GTGACATTTGGAGCCACTGC GTGACATTTGGAGCCACTGCT GCTAGGAGACAGAG OMS00061 OMS00061-Syn AAGTGGAGGCTGACCTGTTG AAGTGGAGGCTGACCTGTTGT GCTGATGGCACCTGA OMS00062 0MS00062-Syn Ť ACCCTGGGAAGGCTACTGTAC ACCCTGGGAAGGCTACTGTACT TGAACAGAGATCTGG OMS00064 0MS00064-Syn т G G GTGGATATGTAGTTCGATGGAACAGT GTGGATATGTAGTTCGATGGAACAGTT GCACTAACTGGACAACATTTTTAAGAATGA GCACTAACTGGACAACATTTTTAAGAATGAT OMS00068 0MS00068-Syn Α

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.

Upload markers							
Upload Cancel Mar	kers - SNP	lefinitions for O.Mykiss (Rainbow Trou	t - St	eelhead) - Synonyms.txt			
Data Formatting	New	rr Configuration markers Marker synonyms		Additional Upload Options			
Select Delimiter	CNID			Save Column Mapping			
	Marker Sub-type SNP-Taqman			Use Saved Column Mapping: [Select Mapping]			
		Species orhynchus mykiss *		(bence mapping)			
Toggle fieldset View							
1		2		3		5	
Marker Name							6
		Lab Synonym	-	<ignore field=""></ignore>	<ignore field=""></ignore>	<ignore field=""></ignore>	6 <ignore field=""></ignore>
Assay:		Lab Synonym <ignore field=""> FAM Allele</ignore>	-	<ignore field=""></ignore>	<ignore field=""></ignore>	<ignore field=""> •</ignore>	
Assay: M09AAC 055		Ignore Field>FAM AlleleFAM Probe					<ignore field=""></ignore>
		Ignore Field> FAM Allele FAM Probe Forward Primer		VIC Allele		Fwd Primer	Ignore Field> Fwd Syn
M09AAC.055		Ignore Field>FAM AlleleFAM Probe	-	VIC Allele C	FAM Allele T	Fwd Primer GTCTCCGACGTGTGGCT	lgnore Field> Fwd Syn GTCTCCGACGTGTGGCTT
M09AAC.055 M09AAD.076		<grance field=""> FAM Allele FAM Probe Forward Primer Lab Synonym Marker Name Reverse Primer</grance>		VIC Allele C T	FAM Allele T C	Fwd Primer GTCTCCGACGTGTGGCT ACTGTTACCACTCTCTCATCAACCT	<pre>«Ignore Field> Fwd Syn GTCTCCGACGTGTGGCTT ACTGTTACCACTCTCTCATCAACCTT</pre>
M09AAC.055 M09AAD.076 M09AAE.082		djgnore Field> FAM Allele FAM Probe Forward Primer Lab Synanym Marker Name Reverse Primer VKC Allele		VIC Allele C T T	FAM Allele T C G	Fwd Primer GTCTCCGACGTGGGCT ACTGTTACCACTCTCCATCAACCT CTATGTGCAGTGCCCTTCTCA	<pre></pre>
M09AAC.055 M09AAD.076 M09AAE.082 M09AAJ.183		<grance field=""> FAM Allele FAM Probe Forward Primer Lab Synonym Marker Name Reverse Primer</grance>		VIC Allele C T T G	FAM Allele T C G A	Fwd Primer GTCTCCGACGTGTGGCT ACTGTTACCACTCTCTCATCAACCT CTATGTGCAGTGCCCTTCCA TCCCATGGCCCTTACTCTATCAA	dgnore Field> Feed Syn GTOTCCGACGTGTGGGCTT ACTGTTACCACTOTCTATCAACCTT CTATGTGCAGTGCCCTTGTAT TCCCATGGCCCTTACTCTAT TCCCATGGCCCTTACTCTATCAAT

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.

Home	Contributor	Search	Data Sets	Marker Sets
om Marker Se	t			
ustom Marker S	et			Upload Marker Set
Name	test mrc 29jul14	Ļ		Choose File No file chosen
Marker Type	Microsatellite		•	
Select Markers		go2 × Oke4 × ki23 × Omm10		

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.).



Uploading genetic data

hinook salmon baselin v3 180 RITEC/IDEG Chinook 192 GSI v

CRITFC/IDFG Chinook Salmon 90 PDI CRITFC/IDFG Steelhead 188 PBT Pilot CRITFC/IDFG Steelhead 192 GSI v4.1 -CRITFC/IDFG Steelhead 96 GSI v4.1 CRITFC/IDFG Steelhead 96 PBT v5.1 IDFG Shoshone Sculpin 96 SNP v1.0 LOA_GAPS Chinook salmon 192 Lota Lota SNP MarkersFromUpload

MarkersFromUpload Omy180Basev3_3 Steelhead baseline v3 18

ook 192 GSLv1.1 + PBT v5.1

+ PBT v5.1

Figure 24 - Export Custom Marker Set

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 <u>Appendix A</u> and <u>Appendix B</u> 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 <u>Appendix D Valid Species List</u> 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.

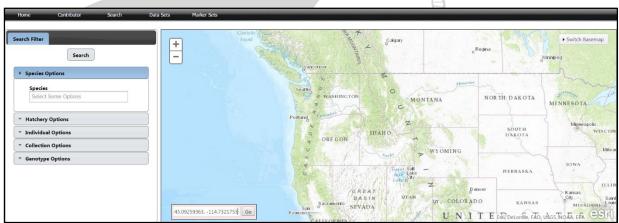


Figure 26. Verifying latitude/longitude coordinates.

00

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).

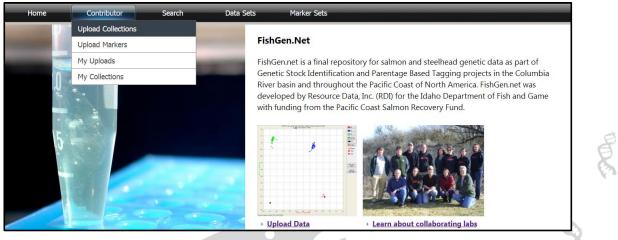


Figure 27. Upload collections from the Contributor dropdown.

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.



Home	Contribut	or Search	Data Sets	Marker Sets	
Upload Collectio	ons				
Select your upl		Standard	•		
Select your coll	lections file	Choose File No	file chosen		
💿 Open					X
	Collections			- - - + - - + - - + - + - - + - + - + - + - + - + - + - + - + - + - + + + + + + + + + +	Search Collections
Organize 🕶	New folder				≣ - □ 0
🚖 Favorites	^	Name	~		Date modified
E Desktop		Collection - GTSeg - 1 (Column - O.Mykiss Co	llection subset valid	10/22/2014 12:05
🐌 Downloads	5	Collection - MS - 2 Colu	-		7/21/2014 9:21 AM
🐉 Recent Plac	ces	Collection - MS - 2 Colu	umns - O.Nerka (Socke	eye) Trawls	7/21/2014 9:21 AM
	=	Collection - RAD - 2 Co	lumn - Matt's Ltr RAD	16jan14	7/21/2014 9:21 AM
🧮 Libraries		Collection - SNP - 1 Col	lumn - O.Mykiss Colle	ction subset valid - Copy (2)	10/24/2014 3:04 PM
Documents	5	Collection - SNP - 1 Col	lumn - O.Mykiss Colle	ction subset valid - Copy	8/31/2014 2:48 PM
al Git		Collection - SNP - 1 Col	lumn - O.Mykiss Colle	ction subset valid - Synonyms	- Copy 10/17/2014 3:15 PM
🕹 Music		Collection - SNP - 1 Col	lumn - O.Mykiss Colle	ction subset valid - Synonyms	10/17/2014 3:15 PM
Sector Pictures		Collection - SNP - 1 Col	lumn - O.Mykiss Colle	ction subset valid	8/29/2014 4:56 PM
JUI Videos		Collection - SNP - 2 Col	lumns - O.Mykiss Omy	DWOR13S	7/21/2014 9:21 AM
ik Computer			111		
🛤 OSDisk (C:)	+ 1				4
	File name:	Collection - SNP - 2 Colum	ns - O.Mykiss OmyDW	/OR13S 🔻 All F	iles 🔹
				С	open 🔻 Cancel

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).

Home Contributor	Search	Data Sets Marke	r Sets			
Upload Collections						
Upload Cancel Collection - St	NP - 2 Column	ıs - O.Mykiss OmyDWOR13S.	bit			
Data Formatting		-Allele Suffix Configuration		Additional Upload Options		
Select Delimiter	*	Allele 1 Suffix Pattern		Data is Private		
Column Number Where Genetic Data Begins Allele 2 Suffix Pattern				Save Data Set		
		Preview Marker Name		Save Column Mapping		
 Genetic data is in 2 columns SNP/RAD genetic data is numeric 	6			Use Saved Column Mapping:		
	-			[Select Mapping]	Ŧ	
Toggle fieldset View						
1		2	3	4	5	6
Ignore Field>	<ignore fi<="" th=""><th>eld> •</th><th><ignore field=""></ignore></th><th>Ignore Field> •</th><th><ignore field=""></ignore></th><th><ignore field=""></ignore></th></ignore>	eld> •	<ignore field=""></ignore>	Ignore Field> •	<ignore field=""></ignore>	<ignore field=""></ignore>
Pedigree	Individual N	lame	Hatchery	Gender	Species	Latitude
OmyDWOR13S	OmyDWOR	13S_0001	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR13S	OmyDWOR	13S_0002	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR13S	OmyDWOR	13S_0003	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR13S	OmyDWOR	13S_0004	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR13S	OmyDWOR	13S_0005	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR13S	OmyDWOR	13S_0006	Dworshak NFH	M	Oncorhynchus mykiss	46.50225
OmyDWOR13S	OmyDWOR	13S_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 <u>Creating Saved Datasets</u> 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 exisiting 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.

Home	Contribute	or Search	Data Sets	Marker Sets					
Upload Collectio	ns								
Select your upload type Merge Select your collections file Choose File No file chosen									
© Open									
	Collections			✓ 4 Sec	arch Collections 🔎				
Organize 🔻 N	lew folder				≣ - □ 0				
☆ Favorites	-	Name	~		Date modified				
📃 Desktop		Collection - GTSeg - 1 C	Column - O.Mvkiss Co	llection subset valid	10/22/2014 12:05				
🐌 Downloads		Collection - MS - 2 Colu			7/21/2014 9:21 AM				
🐉 Recent Place	s	Collection - MS - 2 Colu	umns - O.Nerka (Socke	eye) Trawls	7/21/2014 9:21 AM				
	=	Collection - RAD - 2 Co	lumn - Matt's Ltr RAD) 16jan14	7/21/2014 9:21 AM				
🧊 Libraries		Collection - SNP - 1 Co	lumn - O.Mykiss Colle	ction subset valid - Copy (2)	10/24/2014 3:04 PM				
left Documents		Collection - SNP - 1 Co	lumn - O.Mykiss Colle	ction subset valid - Copy	8/31/2014 2:48 PM				
al Git		Collection - SNP - 1 Co	lumn - O.Mykiss Colle	ction subset valid - Synonyms - Co	py 10/17/2014 3:15 PM				
🕹 Music		Collection - SNP - 1 Co	lumn - O.Mykiss Colle	ction subset valid - Synonyms	10/17/2014 3:15 PM				
rictures		Collection - SNP - 1 Co	lumn - O.Mykiss Colle	ction subset valid	8/29/2014 4:56 PM				
JUDE Videos		Collection - SNP - 2 Co	lumns - O.Mykiss Omy	DWOR13S	7/21/2014 9:21 AM				
🔍 Computer									
As OSDisk (C:)			111		. F				
	File name:	Collection - MS - 2 Column	s - O.Nerka (Sockeve)	Trawls Merge data 👻 All Files					
				Open					

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

Home Contribute	or S	Search Data Sets Marke	Sets			
Jpload Collections						
Upload Cancel Co	ollection - MS	- 2 Columns - O.Nerka (Sockeye) Trawls M	ferge data.txt			
Data Formatting		Allele Suffix Configuration		Additional Upload Options		
Select Delimiter		Allele 1 Suffix Pattern		Data is Private		
Column Number Where G	enetic Data B	Begins Allele 2 Suffix Pattern		Save Data Set		
		Preview Marker Name		Save Column Mapping		
 Genetic data is in 2 col SNP/RAD genetic data 		0		Use Saved Column Mapping: [Select Mapping]	*	
Toggle fieldset View						
1		2	3	4	5	6
<ignore field=""></ignore>	•	<ignore field=""></ignore>	<ignore field=""></ignore>	Ignore Field>	<ignore field=""></ignore>	<ignore field=""></ignore>
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	188
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).

No ob

TAN	ş			
Home	Contributor	Search	Data Sets	Marker Set
			Create	
			Export / Edit	

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.

OnerkaTrawls SD e	kample - Notepad	
File Edit Format	View Help	
collection Name	Individual Name	
OneALTL12CTR	OneALTL12CTR_0001	
OneALTL12CTR	OneALTL12CTR_0002	
OneALTL12CTR	OneALTL12CTR_0003	
OnePETL12CTR	OnePETL12CTR_0001	
OnePETL12CTR	OnePETL12CTR_0002	
OnePETL12CTR	OnePETL12CTR_0003	
OneRFLL12CTR	OneRFLL12CTR_0001	
OneRFLL12CTR	OneRFLL12CTR_0002	
OneRFLL12CTR	OneRFLL12CTR_0003	
OneRFLL12CTR	OneRFLL12CTR_0004	
OnePETL12CTR	OnePETL12CTR_0003	
OneRFLL12CTR	OneRFLL12CTR_0001	
OneRFLL12CTR	OneRFLL12CTR_0002	
OneRFLL12CTR	OneRFLL12CTR_0003	
OneRFLL12CTR	OneRFLL12CTR_0004	

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

TR_

					200	(
ľ	OnerkaTrawls Gro	up - Notepad		3	-	
	File Edit Format					
	Collection Nam OneALTL12CTR	e Individual Name Rep OneALTL12CTR_0001	Matt's Group 1	^		
	OneALTL12CTR OneALTL12CTR	OneALTL12CTR_0002 OneALTL12CTR_0003	Matt's Group 1 Matt's Group 1		25	
	OnePETL12CTR OnePETL12CTR	ONEPETL12CTR_0001 ONEPETL12CTR_0002	Matt's Group 1 Matt's Group 1			
	OnePETL12CTR	OnePETL12CTR_0003	Matt's Group 1		1 8	
	OneRFLL12CTR OneRFLL12CTR	OneRFLL12CTR_0001 OneRFLL12CTR_0002	Matt's Group 2 Matt's Group 2			
1	OneRFLL12CTR OneRFLL12CTR	OneRFLL12CTR_0003 OneRFLL12CTR_0004	Matt's Group 2 Matt's Group 2			
				Ŧ		

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.

Home	Contributor S	Search Data	Sets Marke	Sets			
Create Data Set	t						
Data set Name	OmyDWOR13S						
Data set is private							
manner bet	MarkersFromUpload	•					
Data set Notes	[All] Taqman Sets Chinook salmon baselin v. CRITFC/IDFG Chinook Salı CRITFC/IDFG Chinook Salı CRITFC/IDFG Steelhead 18 CRITFC/IDFG Steelhead 19	GSI v1.1 + PBT v5.1 non 96 GSI v1.1 non 96 PBT v5.1 88 PBT Pilot Study 92 GSI v4.1 + PBT v5.1					
Collection Name	CRITFC/IDFG Steelhead 96 CRITFC/IDFG Steelhead 96				Individual Name		
OmyDWOR13S	IDFG Shoshone Sculpin 96				OmyDWOR13S_0001		
	LOA_GAPS Chinook salmo						
	MarkersFromUpload						
	Omy180Basev3_3						
	Steelhead baseline v3 185 Steelhead bv3 187 marker						
	Steelhead bv3 187 marker test	set					
	RAD Sets						
	CRITFC Lamprey 001 RAD	set	*				

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:

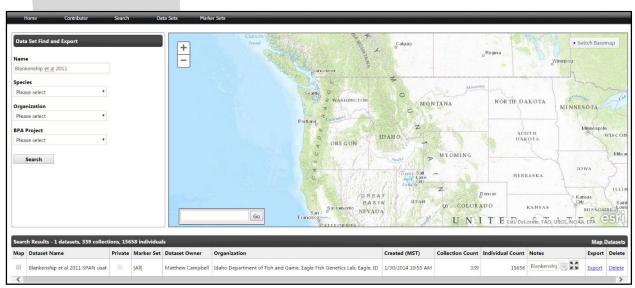


Figure 37. Data Set Find and Export page.

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.

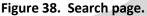
FishGen format details:

- 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.





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



Figure 39. Filtering by species.

• • • •	Hatcher Individu Collecti			Charlotte Security Sound Pontued	Contention Contention	Z WYOMING	Switch Basemap Winnpeg DAKOTA Minneapolis SOUTH DAKOTA Minneapolis VUS UEBRASKA IOWA IOWA IOWA
earch	n Results	- 680 collections, 59143 individuals		Go Francisco	BASIN Sactomento NEVADA	Save Datase	KANSAS Netorine, FÃO, USOS NOÃA, EPA
ap	Include	Select an Option	* Select an Option	* Select an Option	* Select an Option	* Select an Option	* Select an Option
-	•	Collection	Species	Body of Water	Hatchery	Sample Year	Run
8		08_Twisp_R_resident	Oncorhynchus mykiss	Twisp River		2008	Unknown
0	2	OmyUpperDeschutes06CRITFC	Oncorhynchus mykiss	Upper Deschutes R		2006	Summer
· .							

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" suboption 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).

P	lome	Contributor Search	Data Sets Marker Sets				
	Hatcher Hatch	Search Options si orkynchus mykliss X y Options ery States o X		anamo Vancouver vog nicional according Opmore Dama Seattle Dympia Oympia	Sprawer Sprawer GTON	n Mill n Monta Seguritaria	Missourh
	Fundin Selec Organ	ery t Some Options ng Source t Some Options ization t Some Options		Salem A BLUE OREGON A Go Toric	Boise	Lidabo Fais Z ^o Fris Del orme	
Searc	h Results	- 33 collections, 24757 individuals				Save Dataset Dov	vnload Collection(s) Map Collections
Иар	Include	Select an Option	Select an Option	Select an Option	Select an Option	Select an Option	Select an Option
2		Collection	Species	Body of Water	Hatchery	Sample Year	Run
1		OmyPAHH08B	Oncorhynchus mykiss		Pahsimeroi	2008	^
		OmySAWT11S	Oncorhynchus mykiss		Sawtooth	2011	
	28	OmyDWOR135 - Copy	Oncorhynchus mykiss		Dworshak NFH		

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.

* Co	dividual Options Sex Male X Inde X In	Clymp	Kennewick	To Alton A	idato Pario Z WYOMI	151 1/ 00
earch Re:	sults - 205 collections, 4925 indiv	iduals	And the second second second	12		eLorme, FAO, USGS, NOAA, EPA, NPS
ap Incl	lude Select an Option	* Select an Option	* Select an Option	* Select an Option	* Select an Option	* Select an Option
		Species	Body of Water	Hatchery	Sample Year 2000	Run Summer
	A CONTRACTOR OF A CONTRACTOR OFTA CONTRACTOR O	Oncorbynchus mykiss	Pistol Cr			
	OmyPSTL00C OmyLOLO12C	Oncorhynchus mykiss Oncorhynchus mykiss	Pistol Cr Lolo Cr		2012	Summer

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

	ome Irch Filter		arch Data Sets Marker Sets		p · ·		Switch Baseman
		Search an options	+ Sp Victoria	seattle	P 2 F 2 F 2 F 2 F 2 F 2 F 2 F 2 F 2 F 2 F	Milk Missourt	some :
	2014	nple Year	- Clymr	WASHINGTON	A STREET	MONTANA Helena	with
	HUC4 Selec BPA P		e P Saler	ortland	A A A A A A A A A A A A A A A A A A A	Billings	G R P L SOU
	Life St			OREGON	Boise n/ h	Idaho Fallo Z	1. Ja
		e Options - 8 collections, 571 individua		GoBASIN	all and	H Esri, Del	Lorme, FAO, USGS, NOAA, EPA, NPS
	Include	Select an Option	* Select an Option	* Select an Option	* Select an Option	Select an Option	Select an Option
2		Collection	Species	Body of Water	Hatchery	Sample Year	Run
		Pine Cr. '14	Salvelinus confluentus	Pine Creek		2014	~
	2	Pine Cr. E.F. '14	Salvelinus confluentus	E.F. Pine Creek		2014	
		Pine Cr. M.F. '14	Salvelinus confluentus	M.F. Pine Creek		2014	

Figure 43 - Search Results by Collection.

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

 Spe Hat Ind Col Ger Ma Se 	Search Search scles Options tchery Options lividual Options lividual Options notype Options rker arch Markers rker set		Christie Sourd Seating Portland	ID AH O ORE GON	Z WYOMING	Switch Basem Winnpeg TH D AK OTA SOUTH DAKOTA Minnespols Winnespols Winnespols Winnespols OWA NEBRASKA
C	RITFC/IDFG Chinook Salmon 96 X SI v1.1		Go Francisco	GREAT	Z genver	KANSAS MISSOUR MISSOUR
G	RITEC/IDFG Chinook Salmon 96 X		Go Francisco	GREAT BASIN Sacromento NEVADA	COLORADO	KANSAS MISSOUR
G	SI V11 ults - 207 collections, \$887 individua ude Select an Option	* Select an Option	Go Frances	G R E A T Sacramento NEVADA ALLEONIDA Select an Option	AN Deriver COLOR ADO UNITE En Save Date	KANSAS Sal Detorme, FÃO, USGSTROA, EÓA Letorme, FÃO, USGSTROA, EÓA Set Download Collection(s) Map Collect Select an Option
rch Res	SI V11 sults - 207 collections, 8887 individua ude Select an Option <u>Collection</u>	Select an Option Species	Go Francisco Select an Option Body of Water	GREAT BASIN Sactomento NEVADA	AN Deriver (A) COLORADO UNITEE Save Data (Select an Option Sample Year	KANSAS MISSOUR MISS
orch Res	SI V11 ults - 207 collections, \$887 individua ude Select an Option	* Select an Option	Go Frances	G R E A T Sacramento NEVADA ALLEONIDA Select an Option	AN Deriver COLOR ADO UNITE En Save Date	KANSAS Sal Detorme, FÃO, USGSTROA, EÓA Letorme, FÃO, USGSTROA, EÓA Set Download Collection(s) Map Collect Select an Option

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.

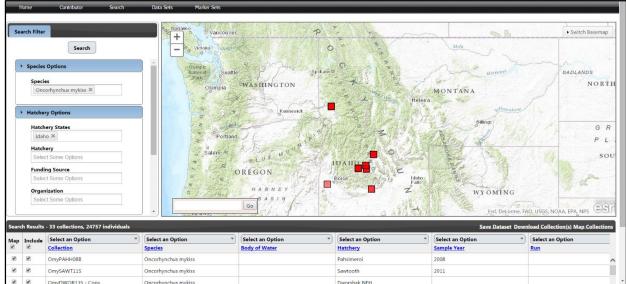


Figure 45 - Mapped Search Results.

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

Spy Hatc Hatc Ful Sr Orn	les Options scies incorrhynchus mykiss ≍ hery Options tchery States daho ≍ tchery sladect Some Options anding Source sladet Some Options ganization sladet Some Options		Oumpia Seattle Part Seattle Oympia WASHING Portland Salerm A DREGON HARN BAS	Kennevick	Oncortynchus mydas Pacific Northeer Region Lower Snake Cleanwater Cleanwater	BADL United States WY OMING etome, FAO, USGS, NOAA, EPA, NPS
Casarda Dama	lts - 33 collections, 24757 individu	ls			Save Data	aset Download Collection(s) Map Collection
earch Resu	Select an Option	Select an Option Species	* Select an Option	* Select an Option	* Select an Option	* Select an Option
ap Inclus			Body of Water	Hatchery Pahsimeroj	Sample Year 2008	Run
p Inclus	Collection				2000	
Inclus		Oncorhynchus mykiss Oncorhynchus mykiss		Sawtooth	2011	
Map Inclus	Collection					

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.

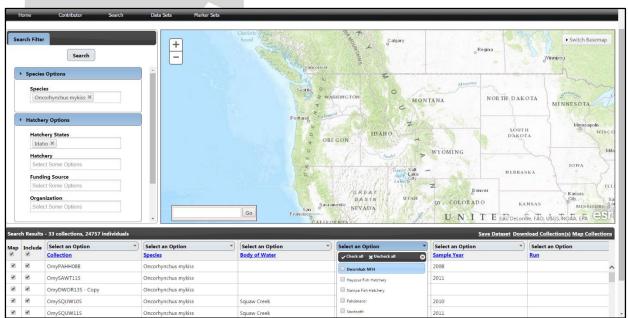


Figure 47 - Select an Option Dropdown

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.

Search Filter	Search	+			_o Regina	• Switch Basemap
Species Species Once			Download Dataset	MONT		
 Hatcher Hatch Hatch Idah Hatch 	ery States		Format GenePop GenePop FishGen Proj	· DAHO		
Selec Fundi Selec Organ	I Some Cotions ng Source I Some Cotions sization It Some Options		Download Cancel	GREAT BASIN UTAR NEVADA		
	Select an Option	Select an Option *	Select an Option	Select an Option *	Select an Option *	Select an Option Run
160						
82						
190						

Figure 48 - Download Search Results

Home	Contributor Search	h Data Sets Marker Sets		
Search Filter	Search	+	Challent Surger	• Switch Basemaj
> Species				
Speci	es sorhynchus mykiss 🕷		Download Dataset	
	ry Options		Format GenePop	
	nery States		Markers DARIO DARIO DARIO DARIO	
Hatch			[All]Tagman Sets Chinos kalmon baselin v3.180	
	ing Source		CRITC/DFG Chinook 192 CSI VL1 + PBT V5.1 CRITC/DFG Chinook Salmon 96 CSI VL1 CRITC/DFG Chinook Salmon 96 CSI VL1 CRITC/DFG Chinook Salmon 96 PST V5.1	
Orgai	nization ct Some Options		CRITC/DFG Steehed 188 PET PHOT Study CRITC/DFG Steehed 95 GSI 41 PET V5.1 CRITC/DFG Steehed 95 GSI 41 PET V5.1 CRITC/DFG Steehed 95 GSI 41 PET V5.1 CRITC/DFG Steehed 95 GSI 41 PET V5.1 DFG Steehed 95 GSI 41 PET V5.1 DFG Steehed 95 EV0 40 PET V5.1 D	
			Lota Lota SNP MarkersFromUpload Save Dataset Dow	
p Include	Select an Option	*) Select an Option Species	Omy 100 Beerly 3 Select an Option Sele	Select an Option
			test AD Sets	
1			CRITFC Lamprey 001 RAD set	
1				

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		
	YES (if hatchery	YES (if Body of Water not	YES-								
Required?	is not selected)	selected)	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								

Appendix A. Collection Fields (continued)

		Collection Species	Collection Comments	Collection Dun	Collection Origin	Collection	Collection Method
De sustan d'A	BPA Project Number	Collection Species		Collection Run	Ŭ,	Life Stage	
Required? Description/ Definition	NO 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.	YES 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)	NONOField 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.	NO Life Stage of the collection. For collections that include fish of multiple life stages, please use "Mix".	NO 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 <u>Species appendix</u> or <u>www.fishgen.net/webpages</u> <u>/legalvalues.aspx</u>	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	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)	important, since FishGe populate HUC informa Collection Latitude and Lo for all individuals in the where you have sampled stream, individual lat/lon	longitude are extremely in will calculate and auto- ation for your collection. ongitude must be the same collection. In a situation multiple locations within a coordinates can be entered ividual level	Collection Name from uploader. We suggest that these are descriptive. Ours include: Species: Omy Sample location: Oxbow (OXBO) Sample year: 08 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.
Example	2013	43.67731	-116.40309	OmyOXBO08S
Valid Entry	уууу	These must be input as decimal degrees	These must be input as decimal degrees	Alphanumeric, 30 character limit

	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	уууу	Alphanumeric, 300 character limit	semi-colon separated alphanumeric	Alphanumeric, 30 character limit	mm/dd/yyyy	ARtoCB, Carcass, CBtoAR, Culled, CulledBKD, CulledHybrid, CulledHN, CulledSurplus, EggsCulled, Immature, Killed, Maturing, Mort, NonProductiveSpawner, NotInMatrix, NotSpawned, OffSeasonMaturity, Ponded, Precocial, Released, RelAboveWeir, RelBelowWeir, RelAnotherLoc, ReUsed, Spawned, Unknown	уууу

Appendix B. Individual Fields.

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.		And and a second se	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 LSRCP 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, Ponded, Precocial, Released, RelAboveWeir, RelBelowWeir, RelBelowWeir, RelAnotherLoc, ReUsed, Spawned, Unknown	уууу	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	you have multiple within a str coordinat	tion where e sampled locations eam, lat/lon tes can be d at the ual 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 <u>Hatchery appendix</u> or <u>www.fishgen.net/webpages/</u> <u>legalvalues.aspx</u>	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
Descriptio n/ Definition	Is the fish of hatchery or wild origin?	Binary or alpha- numeric 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	н	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/Summ er, R=Resident	mm/dd/yyyy	See <u>Species</u> appendix or www.fishgen.net/ webpages/legalval ues.aspx	See <u>Species appendix</u> or www.fishgen.net/webpag <u>es/legalvalues.aspx</u>	Alphanumeric, 300 character limit	LV = L Vent Clip, LV;RV = L and R Vent Clip, RV = 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
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Appendix D. Valid Species List

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

Appendix D. Valid Species List (continued).

Scientific Name	Common Name	Scientific Name	Common Name
Micropterus salmoides	Largemouth Bass	Pimephales promelas	Fathead Minnow
Misgurnus anguillicaudatus	Oriental Weatherfish	Poecilia mexicana	Shortfin Molly
Mylocheilus caurinus	Peamouth	Poecilia reticulata	Guppy
Notropis hudsonius	Spottail Shiner	Pomoxis annularis	White Crappie
Noturus gyrinus	Tadpole Madtom	Pomoxis nigromaculatus	Black Crappie
Oncorhynchus clarkii	Cutthroat Trout	Prosopium abyssicola	Bear Lake Whitefish
Oncorhynchus clarkii bouvieri	Yellowstone Cutthroat Trout	Prosopium coulteri	Pygmy Whitefish
Oncorhynchus clarkii henshawi	Lahontan Cutthroat Trout	Prosopium gemmifer	Bonneville Cisco
Oncorhynchus clarkii lewisi	Westslope Cutthroat Trout	Prosopium spilonotus	Bonneville Whitefish
Oncorhynchus clarkii utah	Bonneville Cutthroat Trout	Prosopium williamsoni	Mountain Whitefish
Oncorhynchus kisutch	Coho Salmon	Ptychocheilus oregonensis	Northern Pikeminnow
Oncorhynchus mykiss	Rainbow Trout/steelhead	Pylodictis olivaris	Flathead Catfish
Oncorhynchus mykiss aguabonita	Golden Trout	Rhinichthys cataractae	Longnose Dace
Oncorhynchus mykiss gairdneri	Inland Columbia Basin Redband Trout	Rhinichthys falcatus	Leopard Dace
Oncorhynchus mykiss x clarkii	Rainbow X Cutthroat Trout	Rhinichthys osculus	Speckled Dace
Oncorhynchus nerka	Sockeye Salmon or kokanee	Richardsonius balteatus	Redside Shiner
Oncorhynchus tshawytscha	Chinook Salmon	Salmo salar	Atlantic Salmon
Osmerus mordax	Rainbow Smelt	Salmo trutta	Brown Trout
Perca flavescens	Yellow Perch	Salvelinus alpinus	Arctic Char
Percopsis transmontana	Sand Roller	Salvelinus alpinus oquassa	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	and U	8
Tilapia mossambica	Mozambique Tilapia	S North State	а.
Tinca	Tench		
Xiphophorus helleri	Green Swordtail		