# T3/Oat tutorials

**Tutorial 4:** Uploading marker information

https://triticeaetoolbox.org/oat/

# T3 marker records

- The marker name is the unique identifier for a marker record
- Marker information needs to be submitted before related genotype data can be uploaded to T3/Oat
- Marker annotations for new or existing markers are uploaded to T3/Oat using the same submission template

**Marker avgbs_122634.1.12**

| | |
|---|---|
| **Marker name** | avgbs_122634.1.12 |
| **Updated on** | 2016-02-18 06:17:31 |
| **A allele** | G |
| **B allele** | T |
| **Sequence** | TGCAGTTCTTA[G/T]GGGCTCATAATACGGAACACATGAAGTTGATTTGGAAAGGGTGGGCACCAGC |

**Marker Types**

| Marker Type Name | |
|---|---|
| GBS | View |

**Annotations**

| Dataset | Entry | Dataset Description |
|---|---|---|
| Haplotag Feb 2016 | avgbs_122634 | POGI 2015 passport file, Agri-Food Canada |

**Allele Information**

**Line Data:** Show alleles for all lines

**Map locations**

| Map | Chromosome | Start | End |
|---|---|---|---|
| 2016ExpandedConsensus_Mrg19 | Mrg19 | -14.1 | -14.1 |

**Selection List**

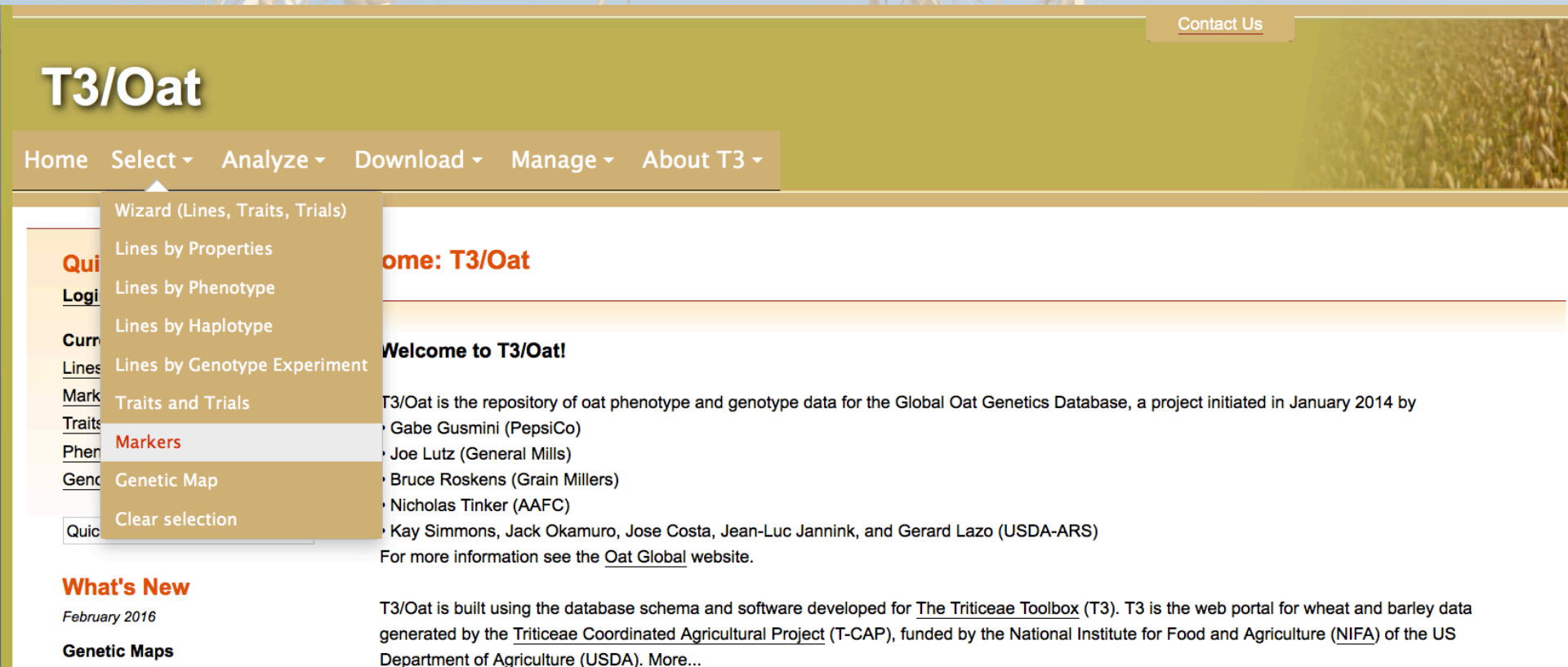
Add this marker

# Tutorial 4: Outline

1. Searching existing marker records in T3/Oat
2. Downloading the marker submission templates
3. Completing the marker submission templates
   1. Selecting a marker sequence template
   2. Completing the marker annotation template
   3. Completing a marker sequence template
4. Test loading the marker submission templates
5. Submitting the marker submission templates

# Section 1: Searching existing marker records in T3/Oat

- Navigate to the T3/Oat homepage at https://triticeaetoolbox.org/oat/
- Choose the Select menu> Markers



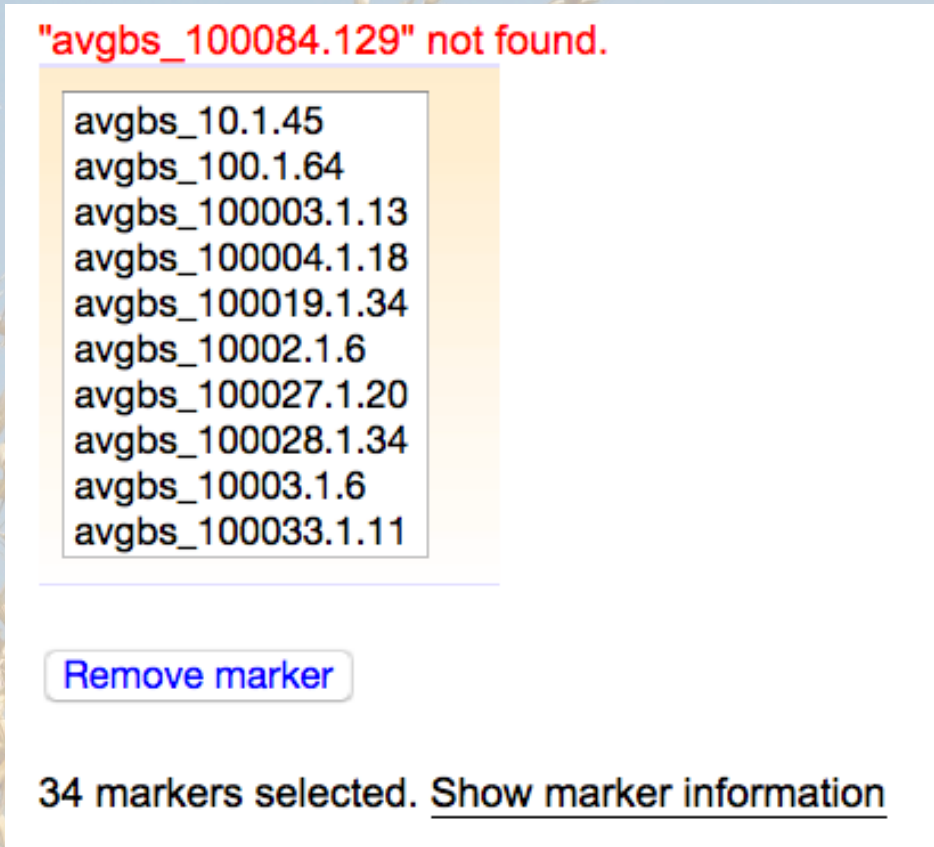
# Section 1: Searching existing marker records in T3/Oat

Existing marker records can be queried by:

- Exact marker name
  - Copy and paste (or type) a list of marker names into the window
  - Click "Select by name"
- Approximate marker name
  - Enter a single name or name fragment into the window
  - Wildcard values can be used as described
  - Click "Select by pattern matching"

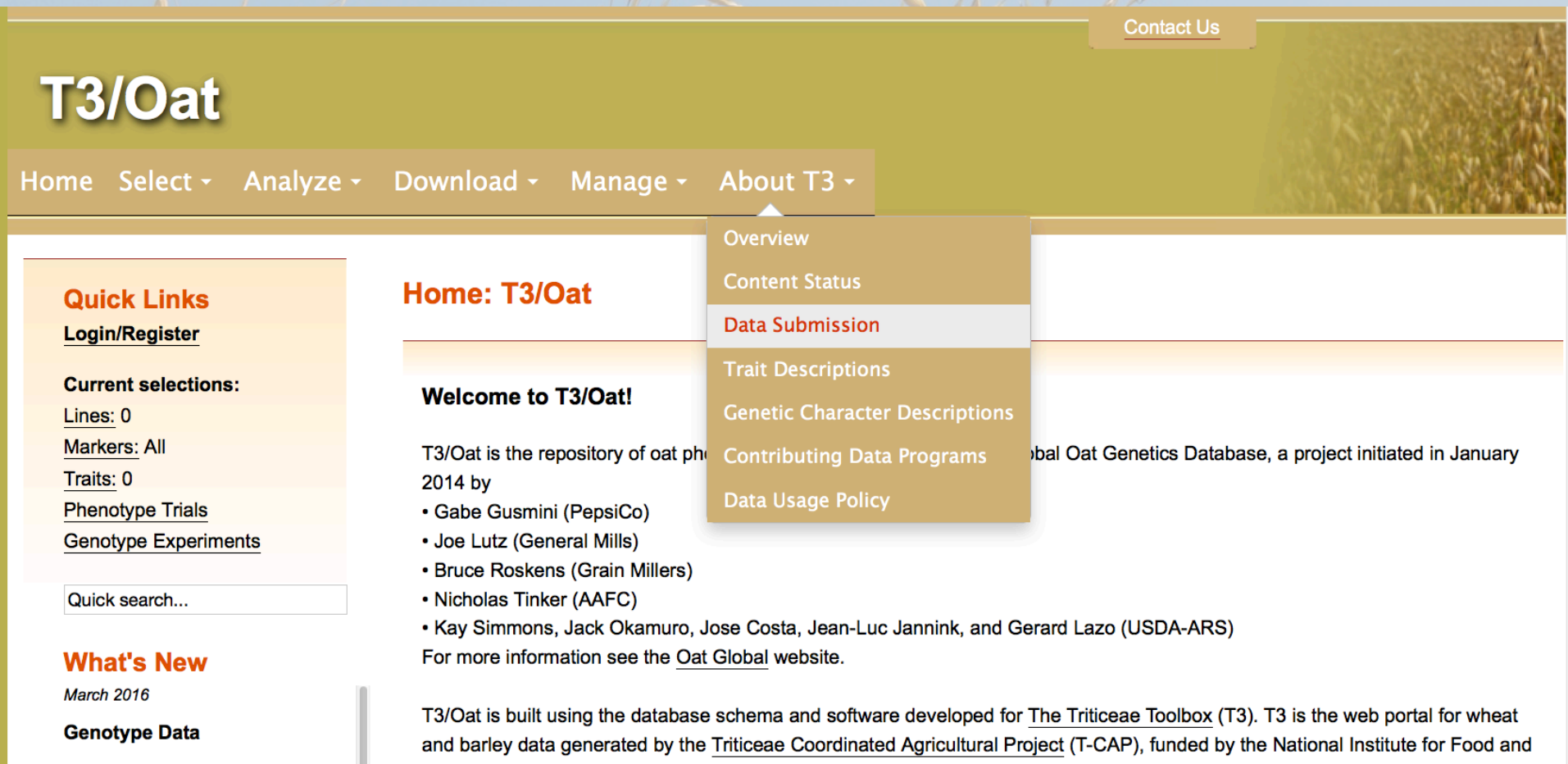
# Section 1: Searching existing marker records in T3/Oat

- Markers that are already stored in the database will appear in the results box
- Click "Show marker information" to view or download the existing information for these markers
- Markers that are not stored in T3/Oat should be added using one of the marker submission templates



# Section 2: Downloading a marker submission template

Choose the About T3 menu> Data Submission



# Section 2: Downloading a marker submission template

| | | | |
|---|---|---|---|
| **Markers** | Sequence Generic | 21Feb14 | Marker sequences and allele definitions |
| | Sequence Illumina OPA | 16Sep11 | Markers from Illumina Manifest, Golden Gate OPA format |
| | Sequence Illumina Infinium | 21Aug12 | Markers from Illumina Manifest, Infinium HD format |
| | Markers from DArT | 17Jun13 | Markers from Diversity Array Technologies |
| | Gene function | 26Oct11 | Sequence annotations and name synonyms |

AKA the marker annotation template

The "Markers" section of the "Data Submission" page contains two categories of data upload template:

1. Templates for uploading marker sequences
2. The template for uploading marker annotations

# Section 2: Downloading a marker submission template

- Each of the marker template links will take you to a webpage displaying the template in .txt or .csv format
- Right click the link and "Save Link As…" to download the file
- This tutorial will use Excel to display the templates


```
© Illumina, Inc. 2004
[Heading]
OPA,GS0007511-OPA
Test Version,1807914
Test Version Name,1807914
Test Name,WO#1807914_209tubes_BarleyOPA1
Bundle Index,1 of 1
SNP Position,1
Assay Format,Golden Gate
Date Manufactured,3/13/07
Loci Count,1536 of 1536
Comment,
Ilmn ID,Name,oligo1,oligo2,oligo3,IllumiCode name,Illumicode Seq,Ilmn Strand,SNP,CHR,Ploidy,
1375-2534-20070122_B_R_2133872,1375-2534,ACTTCGTCAGTAACGGACTCTACGAACGAAAAAAGCACAGGAG,GAGTCGAG
CTATATAAATCATCATCACTGCCAATCGAGCGCGATACATGTCTGCCTATAGTGAGTC,0003,CTGCCAATCGAGCGCGATACAT,BOT,[
vulgare,0,GGGAGCGAGTTCCGGTTCGCTGACCAGCCGGCTGCGGGCGCTGCCTCTGCCGCTGCGGCCGACCCTTTTGCATCCGCTGCCT
CCTGTGCTTTTTCGTTCGTAGATGTGGTGCTTTGGTATGTACACGGGAAAACTATGTTCTTAAGTTAATATACTGTGATGCACAGTTAATCG
5019-879-20070122_B_R_2133873,5019-879,ACTTCGTCAGTAACGGACGACAGAGACTCCTACTATGCGCCGT,GAGTCGAGG
GGACTCCATTGTTGCGTTGCGACTACCGATACGTGTCTGCCTATAGTGAGTC,0010,TGCGTTGCGACTACCGATACGT,BOT,[T/C],0
vulgare,0,TGATGAATTCTGTGGGAAGATTGTTGCTTCCACTACCAGCATTCCGTGTGACATTGTGCTACATGATAGCAAAGTGAGTGGT
GGCGCATAGTAGGAGTCTCTGTGGATGAGATGCTGGTGTTGACTGTTGCGGCTGCTGTCGGTGATGATGCTTTATCTGCCTGCACTGTTCAG
5764-430-20070122_B_F_2133874,5764-430,ACTTCGTCAGTAACGGACGTGGAAGTGAGTGAGATGCCTGGT,GAGTCGAGGT
ATTAGGCCGTACTCCGTATCGCACGCAAGACGTCTGCCTATAGTGAGTC,0021,TACTCCGTATCGCACGCAAGAC,BOT,[T/C],0,di
vulgare,0,ACCAACTATCGACGGTTCAGACATCATCAGAGCTATAGGACAGACAGATGATAGCGTCGCTTAACACAGGACAATGAGCCAG
CAGGCATCTCACTCACTTCCAGGCTGGGTACGAGTTGTCCCGCCTGTTGTTCCTGAAAGCGCAGCACCCAACAGAGTAGACGATGATGAGGA
5128-1831-20070122_T_R_2133875,5128-1831,ACTTCGTCAGTAACGGACCTCAACTCTCTCACTCCCAGCAAGA,GAGTCGA
ATGTAGACATCCTCGGGATGACGACCGAATACCGTTGGTCTGCCTATAGTGAGTC,0023,GGATGACGACCGAATACCGTTG,TOP,[A/G
vulgare,0,CTTCTGGGCCAAAGCAAAGATGACATCTCCAAGAGCAGAAAGAGATTTATTAATATGTTGTGCTTCCTTTAATCTATCTCCG
CAATCAGATGTAGACATCCTCGAGAAGTAGATCCATTCTTCACGTCCAGCCCTCTCACATGCACGGTTAAAATGCTGTGGGACCTACTACTC
3026-1011-20070122_B_F_2133876,3026-1011,ACTTCGTCAGTAACGGACAGAGGTGGATTATTGGATTGCCCT,GAGTCGAG
TGTACTATTTTGGTCCGTGTATCCGCGCAAGTTCTAGTCTGCCTATAGTGAGTC,0027,CCGTGTATCCGCGCAAGTTCTA,BOT,[T/C]
vulgare,0,CAATTAATTGATCAACATAACACAGCGTTGTTTCTTTTGACATTTCACAGTATTGTCTACAGCACTTTGGAAACAGTGGGTG
GGCAATCCAATAATCCACCTCTTCATGGGAAATTCRGTCCAAAGTTGAAAGAAAAGAGAGGCAAATCACACAATCCTTTCCAATTCCCTCGC
4407-1344-20070122_T_F_2133877,4407-1344,ACTTCGTCAGTAACGGACAGGGAATTTGTCCACCCGGTA,GAGTCGAGGTC
TGATAACTGGTCTGACGCGACGAAGTAGAGTCTGCCTATAGTGAGTC,0028,TGGTCTGACGCGACGAAGTAGA,TOP,[A/C],0,dipl
vulgare,0,AAGGGTTGCAGCAGTGGGACCAACAGATTGCTGGGCTGTGCCAAGCGTTGAACGACATCCTTGACAGCATGTCGAGCAAGGG
TTTCGATGGTACCTGTGATAACTTTGATCAACCTGCTGGATACACATTTTGTACAGATGTTTTGCCGTTGAAGGTGCAACGAGTACTTTCGG
6157-1233-20070122_T_R_2133878,6157-1233,ACTTCGTCAGTAACGGACGCAGTAGTTTCCATGCAAAGTGATGA,GAGTCG
TGTCACATAACGCTATCGTAGAGCGCGGACAATTCGGTCTGCCTATAGTGAGTC,0030,ATCGTAGAGCGCGGACAATTCG,TOP,[A/C]
vulgare,0,ACATGTATGCAGGTGCTAGCTCTTCACACCGCATCCAATTATTCAGTGATCATCTGTCTACATCTTTGGACAAGTAATCATT
ACGGCTGTCACATAACGCTGTGCTAGAGCTCATCATCATGAGCGACGGCCAAGTTCACCGGCGCGGCGACGTCGCSGCTGCTGTGSGCYTTG
9251-852-20070122_T_R_2133879,9251-852,ACTTCGTCAGTAACGGACCAACACACCTGAAGCACAGCACA,GAGTCGAGGTC
ATCTGCCTCTCGGTCGAACGATCAAACGGGTCTGCCTATAGTGAGTC,0031,TCTCGGTCGAACGATCAAACGG,TOP,[A/G],0,dipl
vulgare,0,TTTTTGTTCCTTCCAGCAACTACTTGACCACACTATAGTTCTCGAGTGACCAAACTGAATTGAGATGTTTGAAACAACAAAA
CAAGAGATCAGTCATCTGCCAATTCTCCGCCTTTTGGTTGCCGAAGAGGCTTGGTAGCATGTTGCTGGAGATCCAACAGCAGTATCATCACT
ABC11290-sfp44-06-20070122_B_R_2133880,ABC11290-
sfp44-06,ACTTCGTCAGTAACGGACGACTCTGCTAGTGGTTCCAGCATAACT,GAGTCGAGGTCATATCGTGACTCTGCTAGTGGTTCCA
ACGTATTCCGAGTCTGCCTATAGTGAGTC,0033,CGCAGTCAACGACGTATTCCGA,BOT,[T/C],0,diploid,hordeum
vulgare,0,YGAARCARAACTTACAATCATCACTCACAGAACCAGGTGTAAAGWCACTTGGCATCAGACCTCAGTAAGGCCAAAAAAATAT
TTATGCTGGAACCACTAGCAGAGTAAACAGAGTMCAAAGTAAGATCTGCTATAATTATTCTTCTAAGAAAATGCAGTCCAGARAATTTTGCT
5893-1285-20070122_B_F_2133881,5893-1285,ACTTCGTCAGTAACGGACGCGGGTCGGCCCAGCTTT,GAGTCGAGGTCATA
TTCTGGAATCGCACGCGAATGGTAGGTCTGCCTATAGTGAGTC,0036,TGGAATCGCACGCGAATGGTAG,BOT,[T/C],0,diploid,
vulgare,0,CACATACTCGGGCCTCTCTAGTCTGTCTGTCATGGAGATAACCTACCATCATAGCACCACATTACTAGGGTTAACAGTCAAT
AGCTGGGCCGACCCGCCGACCCAGGACTATGACCCACGGACCCAGGACTACTACTTCCATTGTCCCAGAGGTTTCTCCTTGTCCGCAGGAGA
```

# Section 3.1: Selecting a marker submission template

| Marker | T3 marker sequence template | | Marker annotation template required |
|---|---|---|---|
| AB base calls | Illumina Manifest | OPA Golden Gate format | ✔ |
| | | Infinium HD format | ✔ |
| ACTG base calls | Generic format | | ✖ |
| DArT markers (A allele= 1, B allele= 2) | DArT format | | ✔ |

- New marker records are created by uploading a completed marker annotation document
- The marker sequence template can then be used to add sequence information to existing marker records
- The “generic” marker sequence template can be used to create new marker records, and therefore does not require the use of a marker annotation template

# Section 3.2: Completing the marker annotation template

**The marker annotation template**

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | Name | Marker_type | Synonym | Synonym_type | Annotation | Annotation_type |
| 2 | 1_0001 | OPA SNP Name | 1005-549 | EST Name | POPA1_0001 | GrainGenes |
| 3 | 1_0001 | | | | 1005 | HarvEST_U32 |
| 4 | 1_0001 | | | | 264 | HarvEST_U35 |
| 5 | 1_0001 | | | | Contig1489_at | U32_Probe_Set |
| 6 | 1_0001 | | | | HT06A08u_s_at | U32_Probe_Set |
| 7 | 1_0001 | | | | LOC_Os05g07700 | U32_Rice_Locus |
| 8 | 1_0001 | | | | protein 60S ribosomal prot | U32_Rice_Description |
| 9 | 1_0001 | | | | Contig1489_at | U35_Probe_Set |
| 10 | 1_0001 | | | | HT06A08u_s_at | U35_Probe_Set |
| 11 | 1_0001 | | | | LOC_Os05g07700 | U35_Rice_Locus |
| 12 | 1_0001 | | | | protein 60S ribosomal prot | U35_Rice_Description |
| 13 | 2_0065 | OPA SNP Name | 1119-1157 | EST Name | POPA2_0065 | GrainGenes |
| 14 | 2_0065 | | | | 1119 | HarvEST_U32 |
| 15 | 2_0065 | | | | 14582 | HarvEST_U35 |
| 16 | 2_0065 | | | | Contig1668_at | U32_Probe_Set |
| 17 | 2_0065 | | | | Contig1671_at | U32_Probe_Set |
| 18 | 2_0065 | | | | Contig1671_s_at | U32_Probe_Set |
| 19 | 2_0065 | | | | LOC_Os03g18570 | U32_Rice_Locus |

**The marker annotation template:** notes section

| | |
|---|---|
| 51 | ---------- CUT ---------- |
| 52 | Fields and values are tab delimited. |
| 53 | |
| 54 | LEGEND: |
| 55 | Line 1 contains field designations |
| 56 | Line 2 starts the marker data |
| 57 | |
| 58 | FIELD DEFINITIONS: |
| 59 | Name - Official marker name |
| 60 | Marker_type - A marker type name |
| 61 | Synonym - Other known marker names |
| 62 | Synonym_type - type name of corresponding secondary name |
| 63 | Annotation - an annotation value |
| 64 | Annotation_type - type/source of the annotation information |
| 65 | |
| 66 | Current Synonym_type values: |
| 67 | EST Name - Original Lab EST Name |
| 68 | POPA Name - Name from POPA array |
| 69 | BOPA Combined Name - New name showing tracking between POPAs and BOPAs |
| 70 | BOPA Name - Original BOPA name |
| 71 | DArT Name - DArT marker |
| 72 | Historical Name - Historical SNP Name from Grain Genes |
| 73 | |
| 74 | Current Annotation_type values: |
| 75 | GrainGenes - Reference name to annotation record from GrainGenes |
| 76 | HarvEST_U32 - Unigene ID for HarvEST U32 assembly |
| 77 | HarvEST_U35 - Unigene ID for HarvEST U35 assembly |
| 78 | U32_Probe_Set - A reference to PLEXdb probe record |
| 79 | U32_Rice_Locus - A reference to Gramene record |
| 80 | U32_Rice_Description - Annotation description |
| 81 | U35_Probe_Set - A reference to PLEXdb probe record |
| 82 | U35_Rice_Locus - A reference to Gramene record |
| 83 | U35_Rice_Description - Annotation description |

The marker annotation template is used to create new marker records in T3/Oat, or to provide additional information about existing markers.

Marker name and marker type are the only required fields. Allowed marker types (as of March 2016):

- AFLP
- DArT Marker
- GBS
- Historical
- Infinium
- OPA SNP Name
- QTL
- RFLP
- SNP
- SSR

Please contact the curator if you require a new marker type to be added to T3/Oat

# Section 3.3: Completing a marker sequence template

Two of the four marker sequence templates are designed for Illumina data, either in Golden Gate OPA or Infinium HD formats.

**"Sequence Illumina OPA" submission template:** Markers from Illumina Manifest Golden Gate OPA format

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | © Illumina | Inc. 2004 | | | | | | | | | | | | | |
| 2 | [Heading] | | | | | | | | | | | | | | |
| 3 | OPA | GS0012040-OPA | | | | | | | | | | | | | |
| 4 | Test Version | 5231431 | | | | | | | | | | | | | |
| 5 | Test Version Name | 5231431 | | | | | | | | | | | | | |
| 6 | Test Name | 5231431 | | | | | | | | | | | | | |
| 7 | Bundle Index | 1 of 0 | | | | | | | | | | | | | |
| 8 | SNP Position | 1 | | | | | | | | | | | | | |
| 9 | Assay Format | Golden Gate | | | | | | | | | | | | | |
| 10 | Date Manufactured | 2/11/10 | | | | | | | | | | | | | |
| 11 | Loci Count | 1536 of 0 | | | | | | | | | | | | | |
| 12 | Comment | | | | | | | | | | | | | | |
| 13 | Ilmn ID | Name | oligo1 | oligo2 | oligo3 | IllumiCode name | Illumicode Seq | Ilmn Strand | SNP | CHR | Ploidy | Species | MapInfo | TopGenomic | CustomerStrand |
| 14 | GMI_ES15_c2714_291-0_T | GMI_ES15_c2714_ | ACTTCGTC | GAGTCGA | AGGCTGA | 3 | CTGCCAATCGAG | TOP | [A/G] | 0 | diploid | Other | 0 | AGACACTCA | TOP |

**"Sequence Illumina Infinium" submission template:** Markers from Illumina Manifest Infinium HD format

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Illumina | Inc. | | | | | | | | | | | | | | | |
| 2 | [Heading] | | | | | | | | | | | | | | | | |
| 3 | Descriptor File Name | Oat_GenMills_PrivCons_6k_11625575_A.csv | | | | | | | | | | | | | | | |
| 4 | Assay Format | Infinium HD Ultra | | | | | | | | | | | | | | | |
| 5 | Date Manufactured | 5/27/12 | | | | | | | | | | | | | | | |
| 6 | Loci Count | 4975 | | | | | | | | | | | | | | | |
| 7 | [Assay] | | | | | | | | | | | | | | | | |
| 8 | IlmnID | Name | IlmnStrand | SNP | AddressA_ID | AlleleA_ProbeSeq | AddressB_ID | AlleleB_ProbeSeq | GenomeBuild | Chr | MapInfo | Ploidy | Species | Source | Sou | Sourc | SourceSeq |
| 9 | BA_grs_c10318_236-( | BA_grs_c10318_236 | BOT | [T/C] | 25672485 | CTGTCGCCTTTATTT | | | 0 | 0 | 0 | diploid | other | Unknown | 0 | BOT | CATACTTATTAGGAGAA |
| 10 | BA_grs_c10611_259-( | BA_grs_c10611_259 | TOP | [A/G] | 54650429 | GTAGGTTCCTGGTG | | | 0 | 0 | 0 | diploid | other | Unknown | 0 | TOP | ATTCGCGGCGGCGGTG |
| 11 | BA_grs_c7937_259-0 | BA_grs_c7937_259 | BOT | [T/C] | 51648369 | GGTGGGAGTTGTTC | | | 0 | 0 | 0 | diploid | other | Unknown | 0 | TOP | NGNCAAGTTTACTCTAA |

# Section 3.3: Completing a marker sequence template

The remaining two marker sequence templates are designed for DArT data or to allow the submission of generic markers. The generic marker template should be used for GBS marker data.

**"Markers from DArT" submission template:** Markers from Diversity Array Technologies

| | A | B | C | D |
|---|---|---|---|---|
| 1 | Assay Format | DArT | | |
| 2 | marker_name | A_allele | B_allele | sequence |
| 3 | bPb-2121 | 1 | 0 | |
| 4 | bPb-7983 | 1 | 0 | |

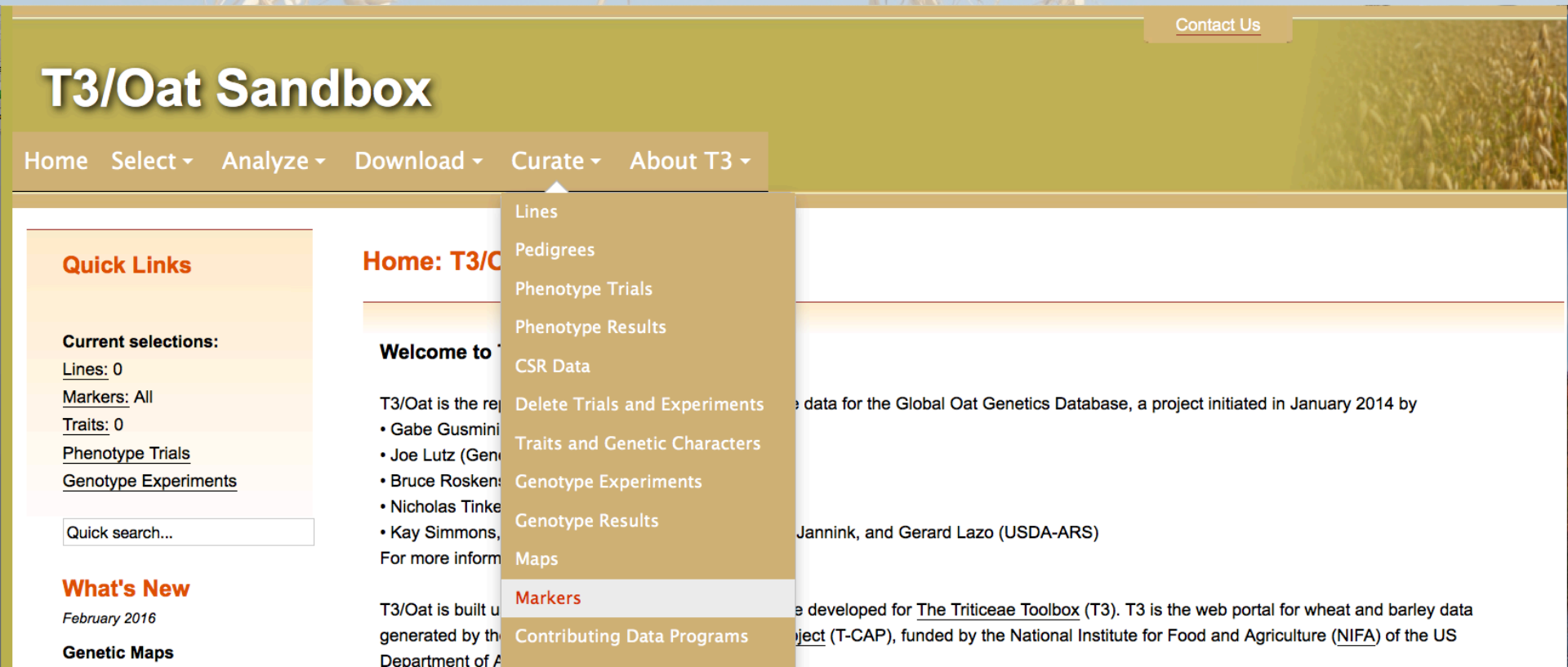
**"Sequence Generic" submission template:** Marker sequences and allele definitions

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | marker_name | marker_type | A_allele | B_allele | sequence |
| 2 | avgbs_593567 | GBS | A | C | TGCAG[A/C]AAAAAAACATTCTAAAGTCGCTTTGCAAATTTAATGGCATCTTTCTTACGCGAACGAA |
| 3 | avgbs_248631 | GBS | A | C | TGCAG[A/C]AAAAAATCTTGTCTCCGCGCGGCAGAGGCGACGACTTTTGCTGCTTTTTTTGCCACCC |
| 4 | avgbs_294546 | GBS | A | C | TGCAG[A/C]AAAAAATCTTGTCTCTGCGCGGCAGAGGCGACGACTTTTGCTGCTCTTTTTGCCACCC |
| 5 | avgbs_314609 | GBS | A | C | TGCAG[A/C]AAAAAATGGCCATGTGGTGGTCCTTTAGTCCCG |
| 6 | avgbs_311416 | GBS | A | C | TGCAG[A/C]AAAAAATGGCCATGTGGTGGTCCTTTAGTCCCGAGATCGGAAGAGCGGTTCAGCAGGA |
| 7 | avgbs_216199 | GBS | A | C | TGCAG[A/C]AAAAACAAAAATGCCGCCACTGTTCCATCAGCTACCAAAACAAACAAACATCAGATTA |
| 8 | avgbs_430130 | GBS | A | C | TGCAG[A/C]AAAAACGCCCATATGGTGGCCCTCTAGTCCCGAGATCGGAAGAGCGGTTCAGCAGGAA |
| 9 | avgbs_430179 | GBS | A | C | TGCAG[A/C]AAAAATCAATCTTTCTATGTTTCTTCGACTTGAGTGAAGGGATACGGGTAGGCTACAC |

Please enter "Unavailable" in the sequence field if the marker sequence is not known.

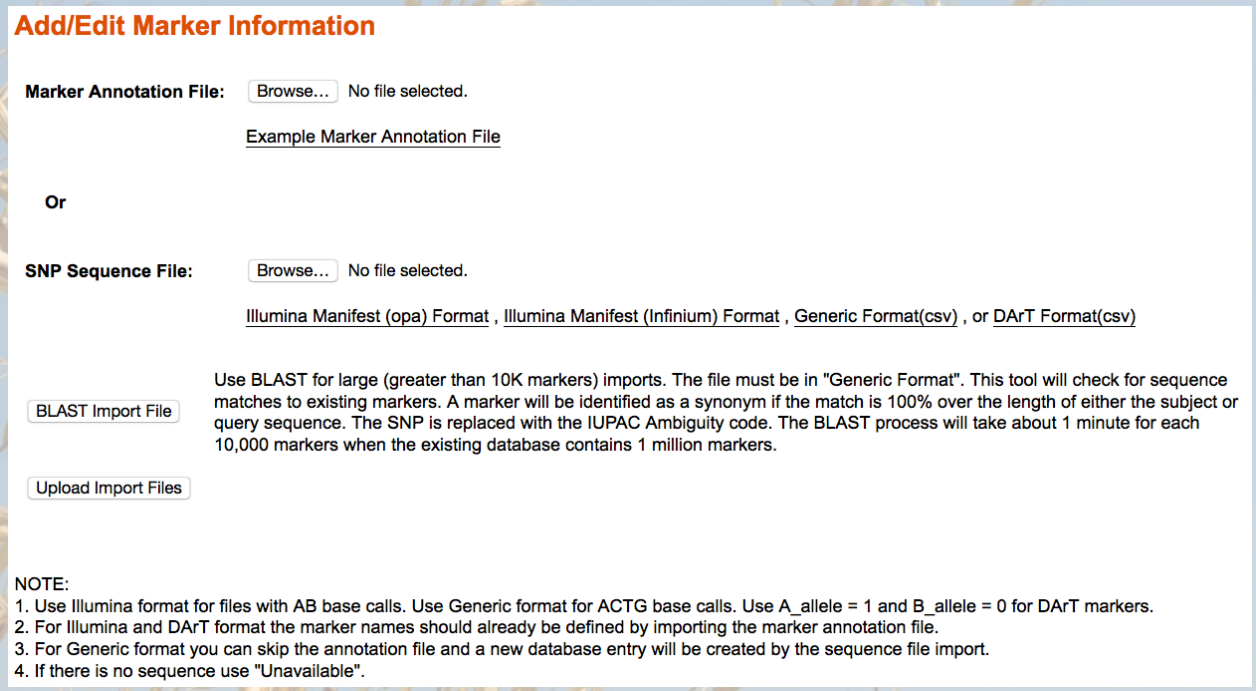
# Section 4: Test loading the marker submission templates

- Navigate to the Oat Sandbox at https://t3sandbox.org/t3/sandbox/oat/
- The curation menu will appear once you register and login
- Choose the Curate menu> Markers



# Section 4: Test loading the marker submission templates

The sandbox allows you to test load your template. The Oat Sandbox reverts to an exact copy of T3/Oat overnight.



**Add/Edit Marker Information**

**Marker Annotation File:** Browse... No file selected.

Example Marker Annotation File

**Or**

**SNP Sequence File:** Browse... No file selected.

Illumina Manifest (opa) Format , Illumina Manifest (Infinium) Format , Generic Format(csv) , or DArT Format(csv)

BLAST Import File

Use BLAST for large (greater than 10K markers) imports. The file must be in "Generic Format". This tool will check for sequence matches to existing markers. A marker will be identified as a synonym if the match is 100% over the length of either the subject or query sequence. The SNP is replaced with the IUPAC Ambiguity code. The BLAST process will take about 1 minute for each 10,000 markers when the existing database contains 1 million markers.

Upload Import Files

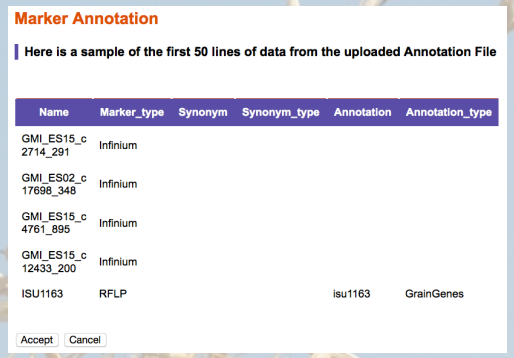
NOTE:
1. Use Illumina format for files with AB base calls. Use Generic format for ACTG base calls. Use A_allele = 1 and B_allele = 0 for DArT markers.
2. For Illumina and DArT format the marker names should already be defined by importing the marker annotation file.
3. For Generic format you can skip the annotation file and a new database entry will be created by the sequence file import.
4. If there is no sequence use "Unavailable".

Remember to load a marker annotation file before attempting to load Illumina or DArT marker sequences.

# Section 4: Test loading the marker submission templates

- T3 will highlight illegal entries in your upload file
- The data validation windows show how T3 has read the upload file. Please take the time to validate that your data appears there correctly.
- Don't forget to "Accept" the upload if the information is correct

**Marker annotation:** Data validation window



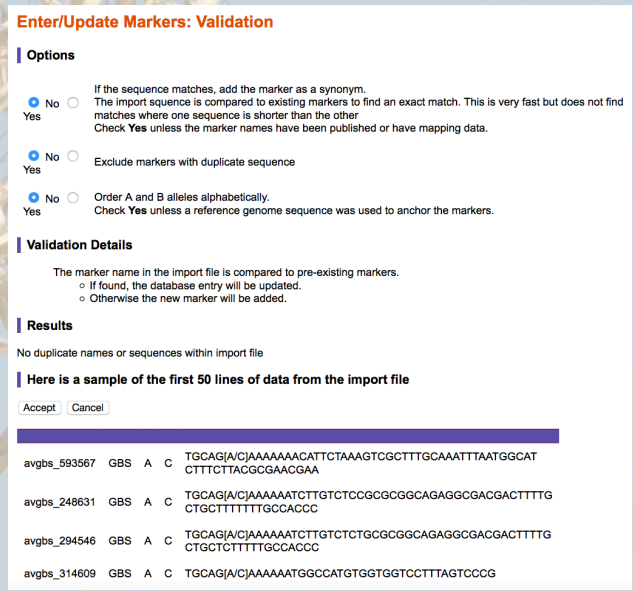
Marker Annotation

Here is a sample of the first 50 lines of data from the uploaded Annotation File

| Name | Marker_type | Synonym | Synonym_type | Annotation | Annotation_type |
|---|---|---|---|---|---|
| GMI_ES15_c 2714_291 | Infinium | | | | |
| GMI_ES02_c 17698_348 | Infinium | | | | |
| GMI_ES15_c 4761_895 | Infinium | | | | |
| GMI_ES15_c 12433_200 | Infinium | | | | |
| ISU1163 | RFLP | | | isu1163 | GrainGenes |

Accept Cancel

**Marker sequence:** Data validation window



Enter/Update Markers: Validation

Options

No / Yes — If the sequence matches, add the marker as a synonym. The import squence is compared to existing markers to find an exact match. This is very fast but does not find matches where one sequence is shorter than the other. Check **Yes** unless the marker names have been published or have mapping data.

No / Yes — Exclude markers with duplicate sequence

No / Yes — Order A and B alleles alphabetically. Check **Yes** unless a reference genome sequence was used to anchor the markers.

Validation Details

The marker name in the import file is compared to pre-existing markers.
- If found, the database entry will be updated.
- Otherwise the new marker will be added.

Results

No duplicate names or sequences within import file

Here is a sample of the first 50 lines of data from the import file

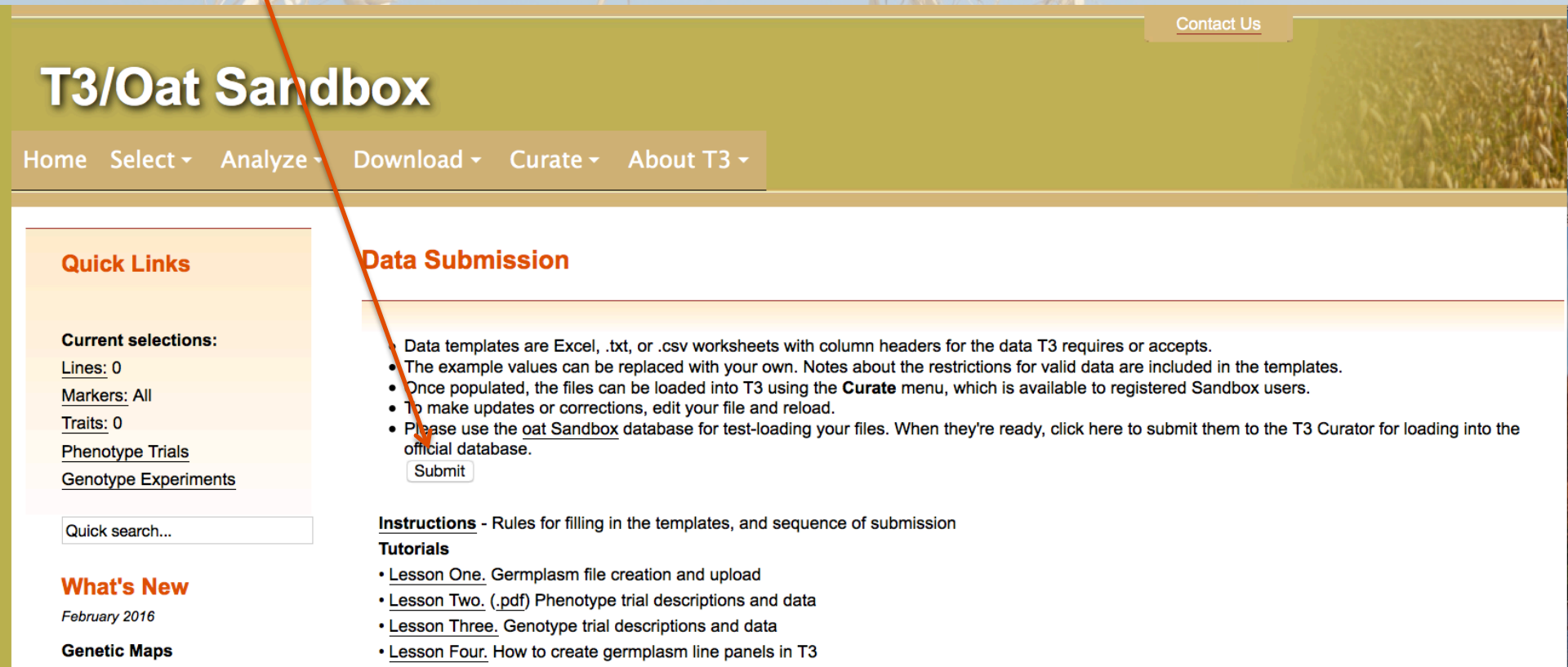
Accept Cancel

| | | | | |
|---|---|---|---|---|
| avgbs_593567 | GBS | A | C | TGCAG[A/C]AAAAAAACATTCTAAAGTCGCTTTGCAAATTTAATGGCAT CTTTCTTACGCGAACGAA |
| avgbs_248631 | GBS | A | C | TGCAG[A/C]AAAAAATCTTGTCTCCGCGCGGCAGAGGCGACGACTTTTG CTGCTTTTTTTGCCACCC |
| avgbs_294546 | GBS | A | C | TGCAG[A/C]AAAAAATCTTGTCTCTGCGCGGCAGAGGCGACGACTTTTG CTGCTCTTTTTGCCACCC |
| avgbs_314609 | GBS | A | C | TGCAG[A/C]AAAAAATGGCCATGTGGTGGTCCTTTAGTCCCG |

# Section 4.1: Submitting the template

Finally, submit the document to the curator for upload to T3/Oat

- Navigate to the Data Submission page
- Click the "Submit" button



# Section 4.1: Submitting the template

## Data Submission

Please submit a data file for the curator to load into the production database. File names should not contain spaces.

**Data Type**

- Germplasm lines
- **Phenotyping**
  - Experiment annotation
  - Results
- **Genotyping**
  - Experiment annotation
  - Results

**Comments**

This file loads successfully in the Sandbox. Yes No

This file contains phenotype data private to project members only.

**File:** Browse... No file selected.

Upload

You can submit files that do not successfully upload to the Oat Sandbox to receive help from the curator

# Contact Us

Please contact us if you need help using T3/Oat

Contact Us

T3/Oat

Home Select Analyze Download Manage About T3

## Quick Links

Login/Register

**Current selections:**

Lines: 0

Markers: All

Traits: 0

Phenotype Trials

Genotype Experiments

Quick search...

## What's New

*February 2016*

**Genetic Maps**

An expanded oat consensus map (50,668 markers) is now available in addition to the Framework Oat Consensus Map (7,202 markers) and the 12 component maps used

## Home: T3/Oat

**Welcome to T3/Oat!**

T3/Oat is the repository of oat phenotype and genotype data for the Global Oat Genetics Database, a project initiated in January 2014 by

- Gabe Gusmini (PepsiCo)
- Joe Lutz (General Mills)
- Bruce Roskens (Grain Millers)
- Nicholas Tinker (AAFC)
- Kay Simmons, Jack Okamuro, Jose Costa, Jean-Luc Jannink, and Gerard Lazo (USDA-ARS)

For more information see the Oat Global website.

T3/Oat is built using the database schema and software developed for The Triticeae Toolbox (T3). T3 is the web portal for wheat and barley data generated by the Triticeae Coordinated Agricultural Project (T-CAP), funded by the National Institute for Food and Agriculture (NIFA) of the US Department of Agriculture (USDA). More...

**Participants**: The templates and instructions for data submission are here. If your data are not totally public, please check the Data Usage Policy.

Data submission