

ILR2

Standard DNA Module

User Manual

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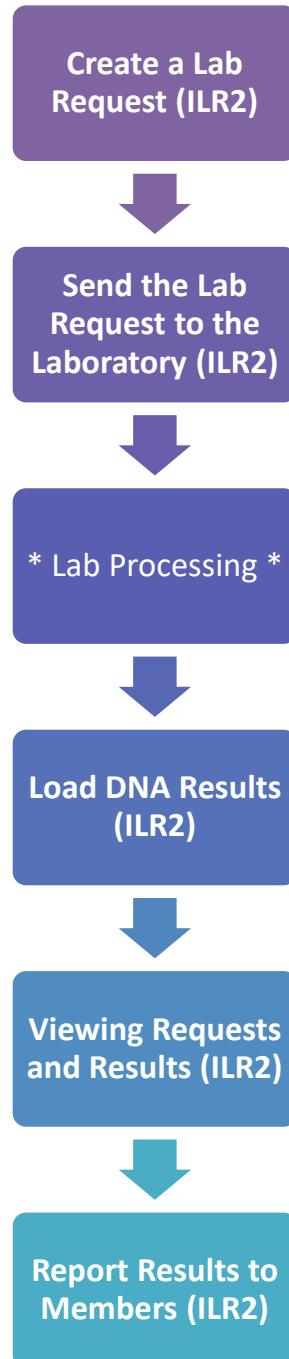
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1 Introduction

This document is a step-by-step guide to the standard job pipeline for handling DNA requests and data using the DNA Module in ILR2. It is intended as a basic instructional manual for use by beef breed society/association data processors. Some functions have been modified at the request of societies/associations, so some details may be different.

This document is structured to follow the basic DNA job pipeline, as depicted in the flow chart below.



2 Create a DNA Lab Request Worksheet

Create a lab request via the worksheet for a member and add animals and include the DNA test requests for those animals. It is best practice to use one worksheet per member. A lab batch number will be allocated on update. It is made up of the year, month, and a sequence up to 999. For example, the first lab request created in June 2021 will be assigned a number 2106001. You can edit this worksheet to add/delete or change rows as many times as necessary.

Alternatively, the Lab Request Worksheet can be built using a CSV file in the 780 Import Format.

2.1 Manually Create a Lab Request

1. ILR2 > DNA > Lab Request Worksheet

Column Name	Use as Default	Default Value
Sample Type	Yes	H-HAIR
Test 1	Yes	
Test 2	Yes	
Test 3	Yes	
Test 4	Yes	
Test 5	Yes	
Test 6	Yes	
Sire 1	Yes	
Dam 1	Yes	
Priority	Yes	

- Click the *Add* button on the top right of the screen. The *Defaults* tab will display.
- Enter in the *Processing ID*. This is an optional field but is usually the member requesting the DNA tests.
- Fill in your *Laboratory ID*. See Appendix to find a list of Laboratories known to ILR2.
- The *Batch Status* will default to *Ready* until you send it to the lab.
- The *Batch Type* is used to group all one type of requests into one batch. E.g. if a breeder sends in 20 PV requests (the animals have already been typed they just now need to be PV'd). You can enter them in all one batch and flag it as Parent Verifies Only. This will change the file name sent to the laboratory indicating its pvnly so the lab knows they need to action and not wait for samples to arrive.
- Set up any defaults for quicker entry.
- Click on the *Animal List* tab to start entering the animals.
- Click on the *Ident* column and enter the animal ident, use the *browse* option if needed.
- If the animal is located on the society database this will prefill its Name, DOB, Sex, Current Owner and any default values you have setup previously. It will also prefill the current sire and dam of that animal. If the current owner is not the person requesting the test, then override the current owner with the member actually requesting the tests as they are the ones who will be charged and receive the results report. If this member does not have a work order open it will prompt you to open one.

11. Tab across to fill in the *Sample Type* and then the *Tests*.
12. To move to the next row, use the arrow down key. If you get hung up on a field press *escape*.
13. Once all the animals, tests and sires/dams have been entered, click the *Update* button.
14. It will ask you whether you want to create another batch. If you say *No* it will allocate a *Lab Batch Number* and leave you on the animals list screen

2.1.1 Sample types

Indicator	Sample Type	Description
H	Hair	A new hair sample supplied with request. A new DNA case ID will be issued for this sample.
S	Semen	A new semen sample supplied with request. A new DNA case ID will be issued for this sample.
B	Bone	A new bone sample supplied with request. A new DNA case ID will be issued for this sample.
T	Tissue	A new tissue sample supplied with request. A new DNA case ID will be issued for this sample.
B	Blood	A new blood sample supplied with request. A new DNA case ID will be issued for this sample.
G	TSU	A new Tissue Sampling Unit sample supplied with request. A new DNA case ID will be issued for this sample.
D	Done	Indicates a test has already been done on this animal, so a sample already exists at the lab and that sample should be used for this new request. ILR2 will automatically look for the DNA case ID stored on file (linked to the laboratory you are creating new requests for). If it does not find one, then you will get an error to say you cannot use a DONE sample type.
U	Build	This indicates no sample exists and a profile for the animal must be built, i.e. 'constructed up', based on the animal's progeny/parents. In this instance the sample type is <i>Build</i> and the test type will be either a <i>MIP</i> or <i>SNP</i> as you want to build this type of profile. Since there is no option to enter the progeny required, this needs to be done in a special email to your laboratory contact. The batch number from your test request will indicate for which animal the profile is to be built. The result will be a DNA case ID from the lab which will indicate the constructed profile, unless your society loads MIP profiles.
P	Profile	This indicates the need to send a MIP profile created by a different laboratory to the laboratory this request is for. This was mainly used for MIPs if the society stored its MIPs on file. However, since SNP data has become more prominent, this sample type is becoming redundant, as we have no interface to send SNPs created by one laboratory to another laboratory. This now needs to be done via the labs themselves.

2.1.2 Important Notes on Test 1

If the animal is having a ‘profile’ test, for example a MIP (microsatellite) profile or a SNP (GGPHD,50K, SeekSire) profile, then this request should always be entered into the *Test 1* column. Then continue by entering PV and any genetic conditions in the next *Test* columns. This is required because validation checks use this *Test 1* value to determine if certain errors need to be generated.

If the animal is not having a MIP or SNP test then enter whatever test the animal is having starting at *Test 1*, then *Test 2* etc. Do NOT leave *TEST 1* blank!

Tab across the row and enter up to 9 tests. If the animal is having a SNP + PV then enter the SNP test in *Test 1* and the PV in *Test 2*. Even though the lab combines these tests from a costing point of view, they need to be requested separately. If no PV is being requested, then ensure to remove the *Sires* and *Dams* that may have pre-filled. Do this by tabbing across to the field and hit the space bar then tab off.

2.1.3 Adding More Sires/Dams

You can enter up to 4 sires and 4 dams per row. If more are needed then enter the animal ident again on the next line, enter PV into *Test 1* and continue entering more sires and dams. You do not need to re-enter any other genomic tests that you entered in the row above, as this row is just for adding in more sires and dams, so PV in *Test 1* is all that is required.

Some labs allow sending in a list of additional sires and dams to be tested for PV. Please note that this does not pass those idents through the ILR2 checks. You will need to talk to your lab about sending sire & dam lists if you wish to process lab requests this way.

2.1.4 Editing DNA Worksheets

You can come back to *Edit*, *Delete* or *Add* rows in the worksheet as required.

To find an existing worksheet, open the *Lab Batch Worksheet* screen and enter the year and month (format YYMM) and hit <Enter>. This will list all the batches in the year/month. Select the batch you want and it will open the *Animal List* tab.

The screenshot shows the ILR2 software interface for managing lab batches. On the left is a navigation tree with categories like Members, Accounts, Animals, Background Processing, Import Data, DNA, and Sales. A search criteria window is open at the top, with 'Batch Number' set to 'like' and '1707' entered. Red arrows point to the search bar and the results table below. The main area displays a 'Lab Request Worksheet' with a table showing 'Worksheets'. Below that is an 'Animal List' tab showing details for two animals: WEBPD010 (Ident. WEBB D010, Name WEBB D010, Date of Birth 20/04/2008, Sex M, S. # 7, Member ID WEB, Sample Type H-Hair, Test 1 MiP, Test 2 PV) and WEBPD011 (Ident. WEBPD011, Name WEBB D011, Date of Birth 22/04/2008, Sex F, S. # 6, Member ID WEB, Sample Type H-Hair, Test 1 GGPLD). A status table at the bottom shows 'Batch Number' 1707001 as 'Submitted' with 'Batch Key' 1, and 'Batch Number' 1707002 as 'Pending' with 'Batch Key' 2.

Ident.	Name	Date of Birth	Sex	S. #	Member ID	Sample Type	Test 1	Test 2
WEBPD010	WEBB D010	20/04/2008	M	7	WEB	H-Hair	MiP	PV
WEBPD011	WEBB D011	22/04/2008	F	6	WEB	H-Hair	GGPLD	

You can *Edit* a submitted batch but you will have to resend it to the Lab for them to update their records.

2.2 Creating Lab Requests using a CSV

Lab requests can be created via a csv import for animals that are recorded on your database.

Obtain the 780 Template .xlsx for your society. This will contain instructions of what to enter in each field. Once this Template has been supplied it is up to your society to maintain the Template as changes occur.

See Template for further instructions.

The main thing to remember is the ‘Profile’ tests column (Column F) is for the main test for profiling the animal. Then the other tests are entered in Test 1 through to Test 8. If an animal is to have both a SNP and a MIP (both profiling tests) then enter the SNP code into the Profiling test (column F) and the MIP code into Test 1 (column N).

1. ILR2 > Import Data Order
 - a. Click on the *Add* button
 - b. Choose *Local* as the File Location
 - c. Choose *780 – DNA Requests* as the Format
 - d. Select the Filename
 - e. Select the processing (billing) member for the Member ID
 - f. Verify and Post the data as per normal for an import
2. Once the 780 data is posted, go to DNA > DNA Lab Request Worksheet
 - a. Find the most recently created lab requests by typing YYMM in the *Search Criteria*
 - b. The batch with a ‘ready’ status is the most recent one

3 Sending Lab Requests to the Laboratory

Once your worksheet of requests is ready to send to the lab, run the batch job by filling in the lab batch number.

1. Submit New Job > DNA > Send DNA Requests to Lab & Bill Member
2. Enter the *Lab Batch No.*
3. Click *Update*, which:
 - a. Creates a CSV file of DNA requests in the selected lab request batch and automatically emails the file to the nominated DNA Lab.
 - b. Produces 3 reports:
 - i. A list of animals included and their requested tests.
 - ii. An acknowledgement letter emailed to the requesting member.
 - iii. A billing report detailing who and what was charged.
 - c. Opens a work order and the relevant charges applied. Turn *Off* the billing if you want to do the billing manually or are resending the requests.
 - d. Changes the Lab Batch status from *Ready* to *Submitted*.

3.1.1 Example of File Sent to the Laboratory

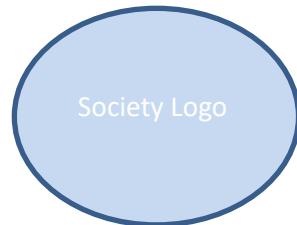
CASE-NUMBER	PRIORITY	SOCIETY	BATCH-NO	SAMPLE-NO	SAMPLE-TYPE	DNA-TESTS+GENE-TESTS-REQUESTED	RE-TEST-COI	HERD	IDENT	TAG	DOB	SEX	NAME	SIRE-NAME-1:SIRE-ID
	Normal	AUHF	1707032	1	Hair	GGPLD	HY+DL+IE+GGP_POLL	0	16627	DLRK22	25/06/2014	M	THE RANCH	
	Normal	AUHF	1707032	2	Hair	SEQ1		0	16627	IHSJ042	05/04/2013	F	INJEMIRA HA	
	Normal	AUHF	1707032	3	Hair	SEQ1		0	16627	IHSJ005	01/04/2012	F	INJEMIRA HA	

3.1.2 Example of Billing Report

DNA Lab Requests Charges - Report							
System ID: ir2_db2 Job: 515333 Report ID: LR_WS_SEND_REQUESTS_CHARGI				Selection: Filename: dna_requests_1707002.csv Page 1 Date 31/07/2017 Time 13:38:32			
Lab: The University of Queensland				Batch Number: 1707002			
Herd: WEB				Create On: 31/07/2017			
Animal	Sample	Urgent	Retest	DNA Tests Requested	Gene Tests Requested	Item Codes	Charge
WEBPD011	Hair	No	No	GGPLD		8037	\$ 64.90
WEBPD010	Hair	No	No	MIP+PV		8036	\$ 27.50
Total Number of Samples For : WEB 2				Total Charges For : WEB \$ 92.40			
Abbreviation and Description				Count			
MIP - DNA Profile (includes PV)				1			
PV - Parent Verify after DNA Profiling				1			
GGPLD - Genesek Low Density SNP (40K)				1			
Dispatched Filename: dna_requests_1707002.csv							Total Batch Charges: \$ 92.40

3.1.3 Example of Acknowledgement Letter

Society Name
 Society Mailing Address
 State Postcode
 T: 99 999 9999
 F: 99 999 9999
 E: xxxx@xxxx.xxx.xx
 W:www.xxxx.com.au



Member ID
 Member Name
 Member Address
 State Postcode

Date: July 31, 2017

Processor: Leonie Lane

RE: DNA SAMPLE ACKNOWLEDGEMENT

Dear Member

We acknowledge receipt of your sample/s to be forwarded to The University of Queensland for testing. Details of each request are listed below.

As soon as we have received a result, they are loaded onto our database and a copy of the results will be forwarded to you for your records. Please note that results take 4 to 5 weeks.

Animal Ident	Society Reference	Sample Type	Retest Count	DNA Tests Requested	Gene Tests Requested	Priority
WEBPD011	1707002-1	Hair	0	GGPLD		Normal
WEBPD010	1707002-2	Hair	0	MiP+PV		Normal

Total Samples Received : 2

Total charge is: \$92.40

Please Note: This acknowledgement is not a guarantee that a result will be successfully obtained from the supplied sample/s. Please ensure that you would be able to supply another sample if any of the supplied sample/s are not suitable for testing.

Kind Regards

The Member Service Officers

3.1.4 Example of Lab Report

DNA Lab Requests - Report												Page 1	Date 31/07/2017	Time 13:38:32	
Selection: Lab Batch No. is 1707002												Dispatched Filename: dna_requests_1707002.csv			
Lab: The University of Queensland															
Batch Number: 1707002 Create On: 31/07/2017															
Priority	Herd	Sample No.	Animal Rego No. (Case No.)	Date of Birth	Sex	Sire 1 Ident (Case No.)	Sire 2 Ident (Case No.)	Sire 3 Ident (Case No.)	Dam 1 Ident (Case No.)	Dam 2 Ident (Case No.)	Dam 3 Ident (Case No.)	Sample Type	Retest Count	Tests Requested	
Normal	WEB	1	WEBPD011	22/04/2008	F	-----	-----	-----	-----	-----	-----	Hair	0	GGPLD	
Normal	WEB	2	WEBPD010	20/04/2008	M	IMUPS151 (48431)	-----	-----	PED3X2408 (7363329)	-----	-----	Hair	0	MiP+PV	
Total Samples Sent : 2															
Test Request Summary															
Abbreviation and Description															
MiP - DNA Profile (includes PV) 1															
PV - Parent Verify after DNA Profiling 1															
GGPLD - Genesek Low Density SNP (40K) 1															

4 Loading DNA Results

Loading the DNA results is done via the Import File process. Results can also be added manually. All Parent Verifications and Recessive Genetic conditions are loaded via the import format 781. All SNP results are loaded via import format 775. All MVP results are loaded via import format 764.

4.1 Loading Results via 775, 781 and 764 Import Formats.

The lab can send back results via a **ShareFile** address which they will advise, or to the **ABRI FTP Repository Directory**. We are encouraging the latter.

4.1.1 ABRI FTP Repository

If the data is sent to the ABRI FTP repository, then provided the file has the correct name, we forward the file to your server for you. You will be sent a system notification including the file name to load. It will look like this:



1. ILR2 > Import Data Order
2. Select *Server* as your File Location.
3. Choose the correct Format from the drop down menu:
 - a. All PV and *Genetic Condition* results are loaded via the [ILR2 Imports format 781](#).
 - b. All SNP *genomic* data is loaded via the [ILR2 Imports format 775](#).
4. Click on the *Filename* field and select your DNA results file.
5. Enter the Lab ID
6. Process like any other import

4.1.2 ShareFile

If the SNP data is sent to you via the ShareFile, you will need to download and save the SNP file to a local drive somewhere, prior to starting the import. Genetic conditions, PV and other results usually come as a CSV attached to an email. These will also have to be saved locally.

File names are generally like:

```
<soc_code>_<lab_id>_<import_format>_<batch_no>_yyyyymmdd_hhmm_<data_type>_data.<ext>
E.g.    AUAA_AUNE_775_1708017_20170907_1107_SNP_DATA.zip
        AUCH_AUNE_781_1708017_20171017_1309_DNA_DATA.csv
        AUBB_AUZOET_764_1708017_20171017_1309_MVP_DATA.csv
```

NOTE: files with 775 in their name are loaded via the 775 import format and files with the 781 in their name are loaded via the 781 import format, if 'MVP's' are used by your society then they are loaded via import format 764.

7. ILR2 > Import Data Order

8. Select *Local* as your File Location.
9. Choose the correct Format from the drop down menu:
 - a. All PV and *Genetic Condition* results are loaded via the [ILR2 Imports format 781](#).
 - b. All SNP *genomic* data is loaded via the [ILR2 Imports format 775](#).
10. Click on the ellipses (...) to the right of *Filename* and navigate to your DNA results file.
11. Enter the Lab ID
12. Process like any other import

4.2 Loading a Result Manually

Sometimes you may get a paper report from a laboratory and wish to load the DNA result manually. This often happens if a result comes from an overseas laboratory or a laboratory is not set up to supply our standard data import file formats of 781(DNA results and PVs), 775 (SNPs) or 764(MVPs).

DNA Result records are entered firstly as a header *Test* record and then as *Result* records.

You can manually add in a result for SNP data as Test Record, however you cannot manually add in all the SNP results. Full SNP results can only be added via the 775 import format.

4.2.1 Entering the Test Record

1. ILR2 > DNA > DNA Test Results
1. Find the animal
2. Click the *Add* button
3. Enter as much detail as possible
 - a. Enter the Test Date
 - b. Enter the lab Id
 - c. Enter Sample and Batch No. if known
 - d. Enter the DNA Case Id
 - e. Select the Request Type from the drop down e.g. GGP50K or MIP
 - f. Set the Request Status to Completed
 - g. Add in any comments if needed
 - h. Tick the flags to indicate DNA Profile, SV, DV, or PV as appropriate
4. Click on the *Update* button, then the *Refresh* button.

MIP entry example:

The screenshot shows the 'DNA Test Results' dialog box. At the top, there is a tree view of the system navigation. The main area displays a table of 'DNA Test Results' with columns: Test Date, Member ID, Lab. ID, Lab. Sample Code, Lab. Batch No., DNA Case Id, and Comments. A new row is being added for 'JAMENCO 4 82'. The 'Details' panel on the right contains fields for Test Date (18/03/2019), Lab. ID (UNISTEL), Lab. Sample Code (dropdown), Lab. Batch No. (dropdown), DNA Case Id (dropdown, set to '12345'), Request Type (dropdown, set to 'MIP - MicroSatellite DNA Profile'), Request Status (dropdown, set to 'Completed'), and other optional fields like 'Profile on File?' and 'DNA Test Key'. The status bar at the bottom indicates 'Member ID: 316838' and 'Lab. Sample Code: MNR J.J.W. ALBERTS'.

After the clicking *Refresh*:

The screenshot shows the 'DNA Test Results' interface. At the top, there's a header with fields for Ident (AL820004), Date of Birth (12/11/1982), Sex (Male), and Current Owner (316838). Below the header is a table with columns: Lab. ID, Test Date, Member ID, Lab. Batch No., DNA Case Id., Request Type, Request Status, Comments, and PV. A single row is visible with values: UNISTEL, 18/03/2019, 316838, 1903001, 123456, MIP -, Completed, and No. To the right of the table is a vertical toolbar with buttons for Add, Edit, Delete, Cancel, Update, Refresh, Print, and About.

Ident	AL820004	JAMENCO 4 82	Sire Ident	NEL160079	SOMBRERO OTTOMAN 16 9 79			
Date of Birth	12/11/1982		Dam Ident	NEL450078	SOMBRERO JUAN'S WINNIE 45 78			
Sex	Male							
Current Owner	316838	MNR J.J.W. ALBERTS						

Tests | Results |

Lab. ID	Test Date	Member ID	Lab. Batch No.	DNA Case Id.	Request Type	Request Status	Comments	PV
UNISTEL	18/03/2019	316838	1903001	123456	MIP -	Completed		No

4.2.2 Entering the Result Record

Once you have created the Test Record you can now add the test results.

Note: This is not required for MIPs or SNPs. Since they are large, complicated results. Just the header is enough to indicate the test has been done. To load the full SNP results this can only be done via a 775 import.

1. Select the *Test Record* created in the previous step. (The black arrow to the left should be on the row you wish to select)
2. Click the *Results* tab. This will take you to the Results Screen
3. Click on the **Add** button
4. Enter in the result details
 - a. Entering a *Genetic Condition* Result:
 - i. Find the **Gene Ident** that describes the genetic condition.
 - ii. Select a **Gene Test Result** that describes the result values. If the result is a Carrier, Non Carrier, or Affected. Use this field, otherwise leave it blank and use the **Display Result** field.
 - iii. If you selected a Gene test Result the **Display Result** will pre-fill with default wording. You can override this with your own wording if you like.
 - iv. Set the **Publish Flag** to Yes or No. This may be used by the web extract to display the result on Internet Solutions.
 - b. Entering a *Parent Verification* Result:
 - i. **Gene Ident** enter/select PV.
 - ii. **Display Result** enter wording like "Sire ABC123 (sire dna_case_id) x Dam ERS432 (dam DNA case id) Qualified". The parent DNA case id in brackets is optional.
 - iii. **Sire Ident** enter the sire ident (you can also lookup the ident here).
 - iv. **Sire Result** select Qualified or Excluded.
 - v. **Dam Ident** enter the dam ident.
 - vi. **Dam Result** select Qualified or Excluded
 - vii. Set the **Publish Flag** to Yes or No. This may be used by the web extract to display the result on Internet Solutions.
 - c. Entering a List of *Parent Exclusion* Results: (example on next page)
 - i. the breeder may offer several parents for verification. If more than one Sire or Dam have been excluded you can enter them as a string in the **Display Result** field.
 - ii. **Gene Ident** enter/select PV.

- iii. In the **Display Result** field enter words 'Excluded Sires:' and then list all the sire idents separated by a comma. Ensure there is no space between the end of the ident and the comma. You can enter one space after the comma then the next ident e.g. Excluded Sires: AAA123, AAA124, AAA125 then update.
 - iv. Create a second result for the Dams in the same way e.g. Excluded Dams: BBB123, BBB124, BBB125.
 - v. Set the publish flag. Generally these results are not displayed publicly.
5. Click on the *Update* button, then the *Refresh* button.
- a. Any mistakes can be edited following the update.

SNP entries after refresh:

	Lab. Batch No.	DNA Case Id.	Request Type	Request Type Status
	1512112	470224	GGPLD	Completed
►	1512112	470224	GGPHD	Completed

Examples of Parent Verification Results:

Test Date	Request Status	Gene Ident	Display Result	Import ID	Last Updated	sire_key	dam_key
18/03/2019	3	PV	Excluded Dams:{BPTF04,}	190318-002	18/03/2019 3:25:06 PM		91016352
18/03/2019	3	PV	Excluded Sires:{PAR66A,RRR54C,CNZ2Z,}	190318-002	18/03/2019 3:25:06 PM		91016352
► 18/03/2019	3	PV	Dam: RLB 41R (827219) Qualifies	190318-002	18/03/2019 3:25:06 PM		91016352

Details

Gene Ident: PV - PARENT VERIFY - COMMERCIAL TEST

Allele 1:

Allele 2:

Gene Test Result:

Display Result: Dam: RLB 41R (827219) Qualifies

Publish: Yes - Publish

Test Rank %:

Sire Id: ... Sire Result:

Dam ID: RLB 41R ... Dam Result: Qualified

5 Viewing Requests and Results

Lab requests and corresponding results loaded can be viewed per animal. Also, a list of Lab Request Batches can be view per animal, and per member.

5.1 Animal Enquiry

There is a tab on the *Animal Enquiry* screen called *DNA Tests*. This lists all the requested tests for an animal and all the results loaded for that animal.

Ident	JAD Q13	>>	Sex	Male																																																		
Name	JAD QUICKSILVER Q13 (AI) (ET) (P) (White)																																																					
Date of Birth	4/09/2019	Status	Active																																																			
Internal ABRI Key	91026079	Held Reason																																																				
Sire Ident	MSM E11	MAINSTREAM ELDORADO E11 (ET) (P) (White)																																																				
Dam Ident	JAD N5	JAD 46Y AMY'S GIRL N5 (AI) (ET) (P) (Speckled)																																																				
Details Breeding Pedigree Progeny Raw EBVs EBVs Traits Alternate IDs Summary Images Audits Import Orders Inventory DNA Tests Errors																																																						
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5.2 Member Enquiry

On the *Member Enquiry* screen there is a tab called *DNA Lab Requests*.

Record Type	Member ID	Membership Status	Financial	Renew												
XXX	XXX	Membership Type	Full													
First Name	Surname	Last Membership Year / Status	2020 Financial													
XXX	XXX	Last Active Year / Date Paid	2020	01/08/2019												
Sort Name: (Surname, Initials)																
<input type="text" value="XXX"/> Internal ABRI Key <input type="text"/>																
General General 2 Tax & Security Work Orders Trans Summary Alternate IDs Trait Summary Jobs Data Imports Owned Animals Links Performance Images Audits Inventory DNA Lab Requests																
<table border="1"> <thead> <tr> <th>Lab Batch No.</th> <th>Sample Count</th> <th>Batch Status</th> </tr> </thead> <tbody> <tr> <td>2011018</td> <td>23</td> <td>Submitted</td> </tr> <tr> <td>2010052</td> <td>75</td> <td>Pending</td> </tr> <tr> <td>2010040</td> <td>5</td> <td>Pending</td> </tr> </tbody> </table>					Lab Batch No.	Sample Count	Batch Status	2011018	23	Submitted	2010052	75	Pending	2010040	5	Pending
Lab Batch No.	Sample Count	Batch Status														
2011018	23	Submitted														
2010052	75	Pending														
2010040	5	Pending														

5.3 DNA Test Results

ILR2 > DNA > DNA Test Results

This screen has two sections: the '**Tests**' tab where you select the tests and the '**Results**' tab that displays the results for the test selected. Select the test and click the Result tab to view the results.

You can also manually ADD/EDIT & DELETE (Deleting a DNA Result) results from this screen.

6 DNA Result Reporting

DNA Result reports are automatically generated after the 781 and the 775 import results are posted and the corresponding DNA Request batch is completed.

The DNA Result reports can also be run manually as required.

The Animal Genetic Results report is designed to report results back to the member.

The Lab Result reports are comprised of 4 reports generated after the 781 import results are posted and are designed for office use.

The DNA Request for Information report is generated after the 775 import results are posted.

There is also a SNP result export process that will extract the SNP data for an animal (or list of animals) and format the data as a Final Report zip file.

6.1 Reporting Post 781 Import Processing

6.1.1 Animal Genetic Results

The Animal Genetics Results report is automatically submitted once 781 Imports have been posted ONLY if the Lab Request batch is completed. As all the results for the entire Lab requests are retrieved and reported, this report will correspond to the DNA Requests Acknowledgement Letter that was previously emailed to the member.

This report is intended for external use and will automatically be emailed to the member who submitted the test request. It is also converted to a PDF and placed on the web in the member's Download Files area. A CSV of the results is also generated, but not dispatched. These dispatching criteria can be changed to suit the society's individual requirements.

This report can also be submitted manually any time. The run parameters can be by Animal Ident, Member Ident, import ID, lab request batch ID or a date range. If import ID or request batch ID are used then this will limit the results to the information in those processes. If Animal, member or date range is used then all results meeting the selection criteria will be reported.

DNA Results Report Example 1:

Animal Genetic Test Results Report							Page 1		
Selection: Animal Idents is WEBPD010							Date 31/07/2017		
							Time 16:15:54		
Animals Listed for Member: WEB									
Animal ID	DNA Case Id	Tattoo	Sex	Animal Name	Progeny Count	Test Date	Test Requested	Test Result	Status
WEBPD010	12345	D010	Male	WEBB D010 (P) (ET) (AI) (B)	0				
						31-07-2017	MIP	Profiled	Completed
						31-07-2017	PV	Sire: MLUPS151 (4843) Qualified x Dam: PED3X2408 (7363329) Qualified	Completed
Total Animals Listed for Member: WEB				1	Total Progeny: 0				

DNA Results Report Example 2:

User Leonie Lane

System ID ilr2_nzpbp
Job 524408
Report ID AN_GENETIC_TEST_RESULTS_RPT

Australian XXXX Association

Animal Genetic Test Results Report
Selection: Animal Idents is 18954016M382

Page 1
Date 15/05/2018
Time 16:49:13

Animals Listed for Member: XYZ SMITHYS STUD

Animal ID	DNA Case Id	Tattoo	Sex	Animal Name	Progeny Count	Test Date	Test Requested	Test Result	Status
XYZGY123	231344	M382	Male	WALTER M382	0				
						19-04-2018	I50K	Animal has a Genotype Profile	Completed
						12-05-2018	PV	No Result Obtained.	Completed
						11-05-2018	MVP	MVP_ADG:0.18, MVP_BW:4.41, MVP_CED:1.41, MVP_CEM:-0.52, MVP_CW:51.01, MVP_DC:-3.01, MVP_DMI:-0.14, MVP_EMA:3.03, MVP_GL:-3.27, MVP_IMF:1.77, MVP_MCW:88.71, MVP_MILK:12.56, MVP_NIF:0.38, MVP_NFP:0.14, MVP_RBY:-0.53, MVP_RIB:0.73, MVP_RMP:0.97, MVP_SC:1.5	Completed

Total Animals Listed for Member: 18954 1 Total Progeny: 0

Request Types:
AM - Arthrogryposis Multiplex, CA - Contractural Arachnodactyl, COAT - Coat Colour Analysis, DD - Developmental Duplications, HD - High Definition MVPs , HD50K - HD50K - Zoetis, MANOS - Mannosidosis, MIP - Microsatellite DNA Profile, NH - Neuropathic Hydrocephalus, OST - Osteopetrosis, PV - Parentage Verification, SireTrace - SireTrace - Zoetis

6.1.2 Lab Result Reports

This is automatically submitted and contains four Import and Action Reports and is generated with corresponding CSV's. The reports are automatically set to Dispatch Holding.

These are intended for internal use only. They list animals that may need some action taken, e.g. their parents updated or to update any pending animals, now the results are on file. A list of loaded results is also generated.

View Jobs | Submit New Job | Import Data Order |

Only Show My Jobs Automatically Refresh List

Display Jobs for Period (Max: 1000 Jobs)
 24 hours 2 days 7 days 30 days

Include Finished Jobs Show All Manifests

List | Details | **Results** | MyQ Jobs | MyQ Printing |

Reports

Target	Status	Pages	Stationery	Dispatch to
Held Animals Updated	Dispatch Holding	1	Plain White	Default Printer (26)
Held Animals Updated (CSV)	Completed		Plain White	
New Laboratory Animal Info	Dispatch Holding	1	Plain White	Default Printer (26)
New Laboratory Animal Info (CSV)	Completed		Plain White	
New Parentage Results	Dispatch Holding	1	Plain White	Default Printer (26)
New Parentage Results (CSV)	Completed		Plain White	
Laboratory DNA Test Results	Dispatch Holding	2	Plain White	Default Printer (26)
Laboratory DNA Test Results (CSV)	Completed		Plain White	

6.1.3 New Parentage Results *** EXTREMELY IMPORTANT REPORT ***

Animals will be listed in this report IF a PARENT DIFFERS from the parent recorded on file.

NOTE: You should investigate these animals and update the PARENTS manually.

The Parents are not updated automatically. This is because many things change when a parent is changed, blood%, breed% registration qualification, grade calculations, etc, so by updating these animals on the screen ensures they go through all the normal validations and calculations.

Example of New Parentage Report:

User	Bohr IL2 User	New Parentage Results				Australian XXX Association Limited
System ID	ilr2_db2	Selection: (Import 781) Import ID is 171019-011				Page 1
Job	524539					Date 21/05/2018
Report ID	LR_NEW_LAB_PARENT_INFO_RPT					Time 10:21:34
Animal Ident	Name	Reg. Sire ID	Reg. Dam ID	New Verified Sire ID	New Verified Dam ID	
?xxxxxxxxx xxxxxxxx	xxxxxxxxxxxxxxxx xxxxxxxxxxxxxxxx	xxxxxxx xxxxxxx	xxxxxxx	xxxxxxxxxx xxxxxxxxxx	xxxxxxxxxx xxxxxxxxxx	

Total Animals to update: 2

6.1.4 Laboratory DNA Test Results

Results listed for these animals have been loaded onto the Society database via the Import Id listed in the heading. It will only report the results from this Import; it will not list any other results this animal has. This report can be sent to breeders as an Interim Report.

Example of Imported Test Results Report:

User	Bohr IL2 User	Laboratory DNA Test Results				Australian Cow Association Limited
System ID	ilr2_db2	Selection: (Import 781) Import ID is 171019-011				Page 1
Job	525004					Date 12/08/2018
Report ID	LR_TEST_RESULTS_RPT					Time 16:40:18
Animal Ident	DNA Case ID	Test Type	Test Result	Paren Verification	Excluded Sires	Excluded Dams
Results Loaded into ILR2						
MMMBIG RANCH COWS	MMMXXX1111	(416146)	MIP	COMPLETE PV Sire: MMMGY123 (223344) x Dam: MMGY543 (554433) Qualifies	Excluded Sires: (sire1, sire2, sire3, sire4, sire5, sire6, sire7)	Excluded Dams: (dam1, dam2, dam3, dam4)

Total Animals for Herd: MMM 1

6.1.5 Held Animals Updated

Animals will be printed on this report because they are currently on HOLD and some new DNA PV results have been loaded AND the PVs are verified. This may be what the registration is waiting for. The society needs to investigate these animals and update them now they have their new DNA PV results loaded.

NOTE1: the parents of these animals will automatically be set based on the parent verification results in the 781 process. This is done for HELD animals only because they still have to be updated and be subjected to society validations prior to becoming a real registration.

Results listed above for an animal have now been loaded onto the Society Database.

NOTE2: These animals may also be listed on the **New Parentage Results report**.

Example of Held Animals Report:

User	Bohr ILR2 User <th data-cs="5" data-kind="parent">Held Animals Updated</th> <th data-kind="ghost"></th> <th data-kind="ghost"></th> <th data-kind="ghost"></th> <th data-kind="ghost"></th> <th>Australian Wagyu Association Limited</th>	Held Animals Updated					Australian Wagyu Association Limited
System ID	ILR2_db2	Selection: (Import 781) Import ID is 171019-011					Page 1
Job	524789						Date 29/08/2018
Report ID	LR_PV_MAINT_ANIMS_RPT						Time 17:08:40
Ident	Name	Changed Sire	Changed Dam	Changed DNA Case ID	Changed SNP Case ID	Changed PV	
?XXXXXXX	Black Bull the 2nd			MMMYG0004		Verified to Mating	
Remaining errors: *** Recorded Dam DOES NOT MATCH Verified Dam. Please Investigate and Update. Remaining warnings: Warning - NO PV DNA Results found for DNA Case ID: [7810]							
?XXXXXXX	Brown Cow the 3rd			MMMYG0015		Verified to Mating	
Remaining errors: *** Recorded Dam DOES NOT MATCH Verified Dam. Please Investigate and Update. Remaining warnings:							
Total Animals that might need Updating: 2							

6.1.6 New Laboratory Animal Info

Animals will be printed on this report because data from the laboratory (DOB, Sex or Animal Name) is different in some way from that with which the animal is recorded.

NOTE: If any one of the fields (DOB, Sex, or Animal Name) differs then it will report. You may use this report to update the Society records manually.

Example of New Info Report

User	Bohr ILR2 User	New Laboratory Animal Info					Australia Cow Association Limited
System ID	ILR2_db2	Selection: (Import 781) Import ID is 171019-011					Page 1
Job	525064						Date 12/08/2018
Report ID	LR_NEW_LAB_INFO_RPT						Time 16:40:18
Ident	Name	Date of Birth	Sex	LAB Name	LAB Date of Birth	LAB Sex	
?MMMGY002	Held Animal Y002	03/04/2016	F	PLNM0002	03/04/2016	F	
?MMMGY003	Held Animal Y003	31/08/2014	F	PLNK003	31/08/2014	F	
MMMGY005	Y0005	28/10/2014	F	ARWIK0034	01/04/2016	F	
MMMGY006	Y006	04/09/2016	F	PLNM003	04/09/2016	F	
Total Animals you might need to update: 4							

Animals will print on this report if data from the laboratory (DOB, sex or animal name) differs in some way (DOB, sex, or animal name) from what the animal is recorded with. Note: If any one of the fields is different it will report. If that data back from the laboratory is of relevance, you may use this list to update the society records manually.

6.2 Reporting Post 775 Import Processing

A Pending Progeny report based on DNA errors is automatically submitted once the 775 data is posted.

This is the standard Pending Progeny report created at registration time, but only for DNA validations. So if a calf is on HOLD because the sire/dam does not have DNA on file, then when the sires DNA result comes in, this report will list the pending progeny that can now be processed.

Example of the Pending Progeny RFI report:

User	Registrar	Pending Progeny / Calf Report	Cattle Society XXXXXX
System ID	ilr2_auhf	Selection: Import ID is 180612-005	Page 1
Job	238196		Date 12/06/2018
Report ID	AN_PROGENY_RFI_RPT		Time 12:30:25
Animal Ident			
Tested Parent: JHOL54 MINLACOWIE LABYRINTH L54 (P)			
?13623 ←	RO SENTHAL NATIONAL N048 (P)	Severe - Sire JHOL54 does not meet current DNA standards for calf born in 2017 . [7241]	
?13631 ←	ROSENTHAL NEVE N043 (P)	Severe - Sire JHOL54 does not meet current DNA standards for calf born in 2017 . [7241]	
?13633 ←	ROSENTHAL NIC N046 (P)	Severe - Sire JHOL54 does not meet current DNA standards for calf born in 2017 . [7241]	
?13638 ←	RO SENTHAL NOVALEIGH N045 (P)	Severe - Sire JHOL54 does not meet current DNA standards for calf born in 2017 . [7241]	
?13647 ←	RO SENTHAL LABYRINTH N042 (P)	Severe - Sire JHOL54 does not meet current DNA standards for calf born in 2017 . [7241]	
Tested Parent: DAYK168 DAYS EXECUTIVE K168 (P) (689199)			
?R5XN099 ←	TALBALBA EXECUTIVE N099 (P)	Severe - Sire DAYK168 does not meet current DNA standards for calf born in 2017 . [7241]	

Extract a SNP result as a Final Report format.

Many societies have the need to forward a set of SNP results to another society, country or lab.

The following will explain how to run a job to extract the SNP result of an animal into the final report .zip file ready for you to forward.

The result file is in the standard Final Report format for loading into ILR2 via the 775 format, with the required file name format: <society code>_ILR2_775_<chip/manifest/map key>_<date stamp>_<time stamp>.zip. This is useful if the recipient of the results is also an ILR2 client. If the recipient is an ILR2 client, the animal identifier in the results file must be on the society database as an ident or alternate ident.

The laboratory will be set to 'ILR2', since this is an extract of data from ILR2.

You will need to ensure you have FTP or equivalent protocol set up to point to the \$ILR2EXPORTS directory, for you to transfer the result file to your PC.

1. ILR2 > Submit New Job > DNA > SNP Final Report Extract
2. Click on the *Add* button
3. There are two starting points for this process:
 - a. Enter one or more animal idents into the parameters at the time of submitting the batch. Do this by entering a comma separated list of idents into the *Animal Ident* field.
 - b. Load a CSV file import format 5152 with a list of animal idents to be extracted (see Load an Excel CSV File). Do this by entering the import ID into the *Import ID* field.
4. If you want a list of specific results only then you can further filter the selection by ticking the Test Type, otherwise leave it unticked, and the system will select the largest of SNP result for each animal.
5. Click on the *Update* button.
6. When the job has completed:
 - a. ILR2 > View Jobs
 - b. Select the job
 - c. Click on the *Details* tab
7. Click the *View Run Messages* hyperlink to see a summary of what was extracted. The extracted data will be placed in the \$ILR2EXPORTS directory; this should already be setup in your ftp or file transfer protocol, if it's not then please contact support to get it set up.
8. The file name is listed on the *Job Comments* and in the *View Run Message* link, to help you identify which files to select via ftp.
9. Copy the zip file(s) to store wherever you want them.

Note: The data will be split on manifest or map grouping (chip key) which means all the same tests are grouped into a file. If you enter multiple idents, and one has a 50K on file and the other has a SeekSire on file then you will have two result files. If both animals had the same 50K test then both these results will be in the one zip file. The example below shows two result files one for chip_key 10003 and one for chip key 21.

[List](#) [Details](#) [Results](#) [MyQ.Jobs](#) [MyQ Printing](#)

AN SNP_FINAL_REPORT_EXTRACT - SNP Final Report Extract

Submission Details	Editable Fields
Job No. 1282710	<input type="checkbox"/> Hold Execution
Submitted By abri	<input checked="" type="checkbox"/> Hold Dispatching
Submit Date 13/12/2019 12:49:09 PM	<input type="checkbox"/> Delete/Deleted
Submit Member	Job Priority Normal
Charge Member	Queue NORMAL - Standard
	Start After 13/12/2019 12:48:41 PM
	Retain Results Until 15/03/2020
Job Details	Job Comments
Job Status Completed	\$ILR2EXPORTS/AUSM/AUSM_ILR2_775_10003_191213_1349.zip
Start Date 13/12/2019 12:49:15 PM	\$ILR2EXPORTS/AUSM/AUSM ILR2 775 21 191213 1349.zip
End Date 13/12/2019 12:49:49 PM	
Total Pages	
Run Time 35 seconds	
Estimated Run Time 26 seconds	
Processing Host kvmwinxpmyq3	
Submitting Host DESKTOP-74F66JD	
Email Notification	
Parent Job	
View Run Messages	
View All Reports Re-run this Job	

View Run Messages - 1282710, AN SNP_FINAL_REPORT_EXTRACT - SNP Final Report Extract, Cor

```
-- Date 2019-12-13 --
13:49:24 -
13:49:24 - Animal not found      0
13:49:24 - DNA test not found    0
13:49:24 - DNA Tests             7
13:49:24 - Map                  95686
13:49:24 - Sample                7
13:49:24 - DNA Report            7
13:49:24 - Animal Details        7
13:49:41 - Final Report          331344
13:49:44 - $ILR2EXPORTS/AUSM/AUSM_ILR2_775_10003_191213_1349.zip
13:49:44 - $ILR2EXPORTS/AUSM/AUSM_ILR2_775_21_191213_1349.zip
```

6.2.1 Load an Excel CSV File

1. Add your list of idents into column A of an Excel Spreadsheet.
2. Make sure there is NO header row.
3. Save the file as a comma delimited CSV.
4. Load this file into the ILR2 Imports using **import format 5152**.
5. Process this import as per normal, the animal idents will be verified and the system will ensure a SNP result can be extracted.
6. The system attempts to find the largest SNP result on file. The test type of the test found is populated into the import data. View the data after the first verify. If more than one test is available, the system will list these tests in the 'Available Test Results Field'. If you want to extract a different test, edit the data and change 'DNA Test Type' column to a test that is listed in the 'Available Test Result column, update and re-verify the import.

Import ID: 191210-012		Internal Key: 3632	If more than one SNP result is available then they will be listed in this column.		This is the result that will be extracted. To change it edit the data, enter a test code that is listed in the 'Available Test Results' column.						
List		Details	Bulk Data Correction								
Line #	Warnings	Errors	Messages	Status	Animal	Reg #	Available Test Results	DNA Test Type	DNA Test Key	Chip	Test Details
1	0	0	0	Verified OK	BXNPN067	BXNPN067	GGP50K	GGP50K	506091	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47021/10a)
2	0	0	0	Verified OK	BXNPN018	BXNPN018	GGP50K	GGP50K	506090	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47011/10a)
3	0	0	0	Verified OK	BXNPN008	BXNPN008	GGP50K	GGP50K	506089	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47018/10a)
4	0	0	0	Verified OK	BXNPN070	BXNPN070	GGP50K	GGP50K	506088	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47016/10a)
5	0	0	0	Verified OK	BXNPN035	BXNPN035	GGP50K	GGP50K	506087	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47040/10a)
6	0	0	0	Verified OK	BXNPP103	BXNPP103	GGP50K	GGP50K	506086	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47014/10a)
7	0	0	0	Verified OK	BXNPN084	BXNPN084	GGP50K	GGP50K	506085	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47010/10a)
8	0	0	0	Verified OK	BXNPL058	BXNPL058	GGP50K	GGP50K	506084	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47021/10a)
9	0	0	0	Verified OK	WPH1B195	WPH1B195	GGP50K	GGP50K	503019	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:47002/10a)
10	0	0	0	Verified OK	LGP0H043	LGP0H043	GGP50K	GGP50K	503018	10003	20190106 GGP_Bovine_50K_C.bpmGGP50K SNP(valid cnt:46982/10a)

7. Once the Import has been posted and at least one animal has validated, proceed to submitting the batch where you enter the Import Id as the batch parameter, instead of the individual animal idents.

7 Society Responsibilities

Test request codes are agreed upon between the society and the laboratory. ABRI must be informed of new codes or changes to these codes. This is because functions in ILR2 such as the ability to request tests, bill the member and load results all hinge on these codes being accurate in the system.

Please notify *ABRI Support* of the following to ensure your *DNA Module* functions correctly:

- If a new DNA test ‘Request Code’ needs to be added. Include a brief explanation of what the test is and the results you expect to receive from the lab.
- If a new *Item Code* is setup for DNA tests that needs to be programmed into the billing program.
- If a lab offers or changes their DNA test *bundling* makeup.
- If the lab you want to use does not exist in the *List of known Laboratories*.
- Maintain and distribute the 780 Import Template.

8 Appendix (Processing Hints)

8.1 Transferring of DNA Results to another animal

Sometimes you might be told by a breeder or laboratory the DNA result belongs to a different animal. One WOULD hope this is a very infrequent issue. There is an option to Transfer the Results.

1. ILR2 > DNA > DNA Test Results
2. Find the animal that has the result you want to transfer.
3. Highlight the result you want to transfer. The row should have a black arrow to the left.
- a. If you want to move more than one result, you must do them one at a time.
4. Click on the *Transfer* button at the bottom right of the Tests screen.

The screenshot shows the 'Tests' tab selected in the top navigation bar. A table displays DNA test results with columns: Lab. ID, Test Date, Member ID, Lab. Sample Code, Lab. Batch No., DNA Case Id., Request Type, Request Status, Transferred from, and DNA. A row for 'AUGSOL' is highlighted with a yellow background and a black arrow pointing to its left. A red arrow points from the 'Transfer' button at the bottom right of the main window area towards the bottom right of the screenshot.

Lab. ID	Test Date	Member ID	Lab. Sample Code	Lab. Batch No.	DNA Case Id.	Request Type	Request Status	Transferred from	DNA
AUGSOL	11/01/2017	QPD	Hair	1612045	12806545	SNP	Completed	134629751	

Details

Test Date: 11/01/2017
 Lab. ID: AUGSOL Lab. Sample Code: Hair
 Lab. Batch No.: 1612045

Profile on File ?
 Preferred Sample
 SV

SNP Count: 274
 DNA Test Key: 990145
 Create Date: 11/01/2017 10:25:16 AM

Transfer

5. Click on the Yes button to confirm that want to transfer the result.
6. An *Animal Search...* box will appear and you need to find the animal you want to transfer the results to.
7. Once you have found the animal, hit <ENTER> on your keyboard. The animal details will appear in the results grid, then double click the correct animal ident displaying in the results grid to select it.

The screenshot shows the 'Animal Search...' dialog box. The search criteria 'Animal ID like ?QPDL128' is entered. The results grid shows one row for 'BULLIAC L128' with 'Unregistered' status. A red arrow points to the 'Search' button at the bottom right of the dialog.

Animal ID	Name	Rego Status	Sex	Calving Year	Tattoo	Inventory Seaso	Date
1 ?QPDL128	BULLIAC L128	Unregistered			L128		

8. Click on the Yes button to confirm for a second time that want to transfer the result.
9. You will then be asked if you want to transfer the DNA/SNP case Numbers.
 - a. **CAUTION:** The system will do its best to determine if it is transferring a DNA related result or a SNP related result and will transfer the case id's where applicable.

Lab. ID	Test Date	Lab. Batch No.	DNA Case Id.	Request Type	Request Status	DNA Test Key	Last Updated
AUGNSK	14/03/2018	356989	664202	GGP50K	Completed	273013	12/04/2018 1:20:10 PM

Confirm

Do you also want to update SMOFP0208's DNA/SNP case IDs?

No Yes

Details

Test Date: 14/03/2018 Transfer

Lab. ID: AUGNSK GENESEEK AUSTRALASIA

Lab. Sample Code: Profile on File? SNP Count: 46153

- b. If you say Yes it will remove the Case ID on the FROM animals BUT it will only update the TO animal if the field on the TO animal is blank. If there is a value in the case id field it will NOT be overwritten.
10. The system **cannot** do both sides of the DNA case id updates if you are swapping results between animals.
 - a. E.g. Animal A has a case id of 111111 and animal B have a case id of 222222. You select animal A and transfer the result to animal B and say yes to update the case IDs. The result is moved, and the case ID of 111111 is deleted from animal A but it cannot update the DNA case ID on animal B as 222222 already resided in the case ID field. The new number 111111 does however reside with the result on the DNA Test Results screen.
You then move result 222222 from animal B to animal A, the result is transferred, 222222 is deleted from animal B and it is now updated to the case id field on animal A as animal A now has a blank field to update.
So you are now left with having everything correct on Animal A and a blank case ID on animal B. You will need to manually correct animal B's case id as you see fit.
 - b. This is only an issue when you are swapping results between two animals. If you just transfer a result to another animal, it will leave the FROM animal in the correct state, it will only update the DNA case ID field on the TO animals if the field is blank. Hence it will not overwrite this field.

8.2 Deleting a DNA Result

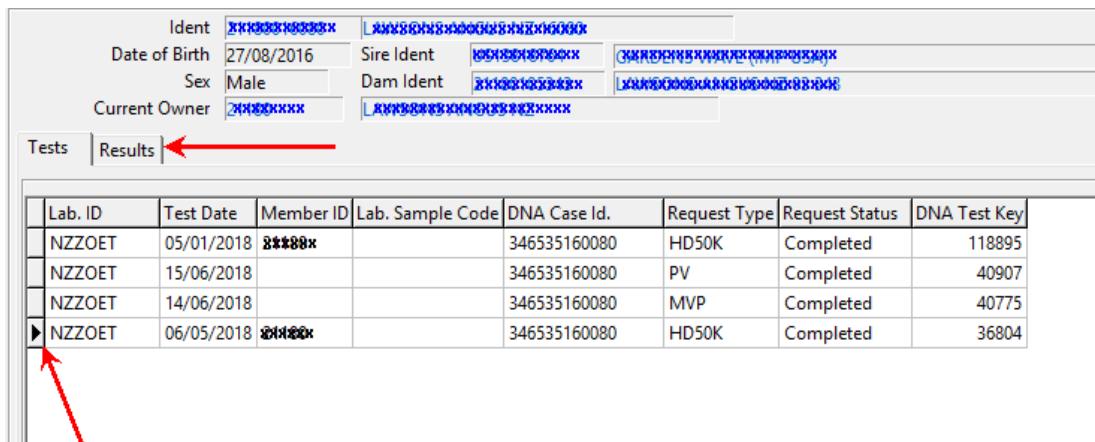
When a DNA result is loaded to ILR2, there are two layers to the information:

ILR2 > DNA > Genetic Test Results

1. The test type is loaded into the *Tests* tab.
2. The result is loaded to the *Results* tab that is related to the test type (select the test type in the *Tests* tab then click on the *Results* tab).

To delete a result you need to delete both layers of information. If it is an incorrect result then delete both the Result and the Test, so you can reload the correct result. Deletion must be done in the correct order; you need to delete all the results before you can delete the test.

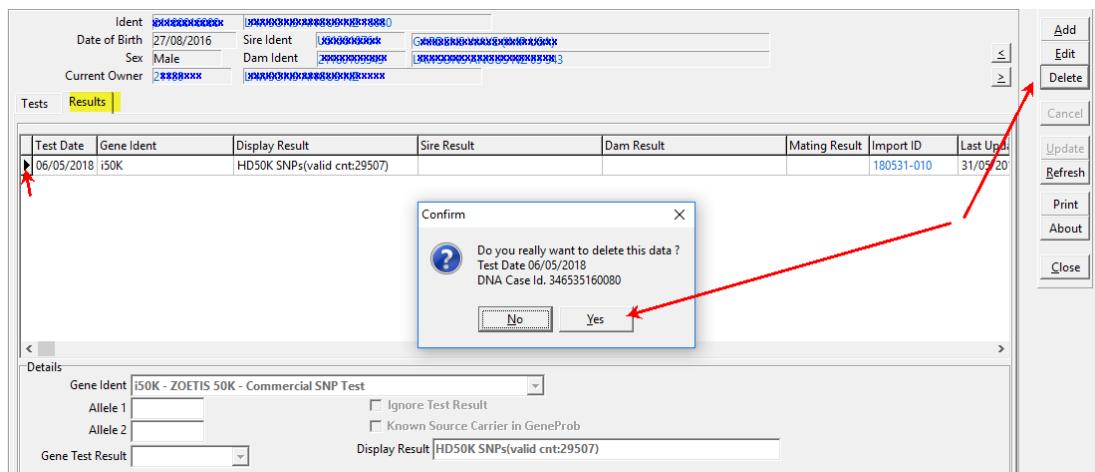
1. ILR2 > DNA > Genetic Test Results
2. Highlight the row of the Test you want to delete. Make sure there is a black arrow to the left of the row.
3. Click on the *Results* tab.



The screenshot shows the ILR2 DNA module interface. At the top, there are several input fields: Ident (xx1xxxxx1xxxxx), Date of Birth (27/08/2016), Sex (Male), Current Owner (2xxxxxxx). Below these are two tabs: 'Tests' and 'Results'. The 'Tests' tab is selected. A red arrow points from the text above to the 'Results' tab. The main area displays a table of test results:

Lab. ID	Test Date	Member ID	Lab. Sample Code	DNA Case Id.	Request Type	Request Status	DNA Test Key
NZZOET	05/01/2018	2*****		346535160080	HD50K	Completed	118895
NZZOET	15/06/2018			346535160080	PV	Completed	40907
NZZOET	14/06/2018			346535160080	MVP	Completed	40775
► NZZOET	06/05/2018	2*****		346535160080	HD50K	Completed	36804

4. Select the result you wish to remove.
5. Click on the *Delete* button.
6. Click on the *Yes* button to delete the result.
7. Continue doing this for all the results you wish to delete.



The screenshot shows the ILR2 DNA module interface with the 'Results' tab selected. At the top, there are several input fields: Ident (xx1xxxxx1xxxxx), Date of Birth (27/08/2016), Sex (Male), Current Owner (2xxxxxxx). On the right side, there is a toolbar with buttons: Add, Edit, Delete, Cancel, Update, Refresh, Print, About, Close. A red arrow points to the 'Delete' button. The main area displays a table of results:

Test Date	Gene Ident	Display Result	Sire Result	Dam Result	Mating Result	Import ID	Last Upd
06/05/2018	150K	HD50K SNPs(valid cnt:29507)				180531-010	31/05/20

A confirmation dialog box is displayed in the center: "Confirm" with the message "Do you really want to delete this data? Test Date 06/05/2018 DNA Case Id. 346535160080". It has 'No' and 'Yes' buttons. A red arrow points to the 'Yes' button. Below the table, there is a 'Details' section with fields: Gene Ident (150K - ZOETIS 50K - Commercial SNP Test), Allele 1, Allele 2, Gene Test Result (HD50K SNPs(valid cnt:29507)), and checkboxes for Ignore Test Result and Known Source Carrier in GeneProb.

8. Once the results have been deleted, return to the *Test* tab, highlight the test, and click the *Delete* button, answer *Yes* to the question to delete the test.

The screenshot shows the ILR2 Standard DNA Module interface. In the top right corner, there is a toolbar with several buttons: Add, Edit, Delete, Cancel, Update, Refresh, Print, About, and Close. The 'Delete' button is highlighted with a red arrow. Below the toolbar, a confirmation dialog box is displayed, asking 'Do you really want to delete this data?'. It lists the Test Date (06/05/2018), DNA Case Id (346535160080), and Lab ID (NZZOET). At the bottom of the dialog box, there are 'No' and 'Yes' buttons, with 'Yes' also highlighted by a red arrow. The main window shows a table of test results under the 'Tests' tab. One row in the table has a red arrow pointing to its first column. The table has columns: Lab. ID, Test Date, Member ID, Lab. Sample Code, DNA Case Id, Request Type, Request Status, and DNA Test Key. The data in the table includes:

Lab. ID	Test Date	Member ID	Lab. Sample Code	DNA Case Id	Request Type	Request Status	DNA Test Key
NZZOET	05/01/2018	21180		346535160080	HD50K	Completed	118895
NZZOET	15/06/2018			346535160080	PV	Completed	40907
NZZOET	14/06/2018			346535160080	MVP	Completed	40775
NZZOET	06/05/2018	21180		346535160080	HD50K	Completed	36804

Below the table, there is a 'Details' section with fields for Test Date (06/05/2018), Lab. ID (NZZOET), and Lab. Sample Code (ZOETIS NEW ZEALAND). There is also a checkbox for 'Profile on File?' which is unchecked. In the top right of the details section, there is a 'Transfer' button. At the bottom right of the main window, it says 'SNP Count 30507'.

9. Refresh the screen to see that the data has been removed.

8.3 Building a 781 Result File Manually

Sometimes a result may not be in an import format form. Therefore, you need to load the DNA result manually. It is best to enter the results in a 781 formatted CSV and load via the Imports screen using the 781 format. This ensures the results get loaded in a consistent manner.

If you have a template, then use that otherwise just follow the columns listed below.

- **Ensure the first row is a header row**, as the system will drop the first row on import.
- Enter one result per row, only enter the columns that are relevant to that result. Many columns may be blank, but the column must exist.
- Save the file as a .CSV using the **file naming conventions** below.

8.3.1 781 File Layout

Column	Data	Description
A	DNA Case ID	A unique identifier allocated to an animal and its sample material by DNA Lab.
B	Anim ident	The society allocated Animal-ID exactly as recorded on the society database.
C	Test type/ request type	A Code identifying the test, e.g. MIP or PV or POLL or COAT etc.
D	Test result	<p>Result of the test type.</p> <p>For Genetic Conditions the result is: N = non carrier; C = carrier; A = affected; NR = no result obtained; RECOLLECT.</p> <p>For PV, SEEKSIRE or MIP the result is: COMPLETE, FAILED, RECOLLECT, NO RESULT or NR. The PV details are then entered in the relevant parentage fields.</p> <p>For COAT the Result is a string of letters, both upper and lowercase e.g. ED/e.</p> <p>For HORN/POLL test result is a string of HP, PP or HH.</p> <p>MIP horn tests have a percentage e.g. HP 98% ..</p> <p>SNP horn tests have a small letter after the P e.g. HPc, PfPc.</p> <p>For TEND there is a number 1 to 10.</p>
E	sire_case_q	the dna_case_id of the qualifying sire.
F	sire_ident_q	the animal ident of the qualifying sire.
G	dam_case_q	the dna_case_id of the qualifying dam.
H	dam_ident_q	the animal ident of the qualifying dam.
I	mating_q	A single character of Q or E Or the word 'Qualified' or 'Excluded'. If only one parent is entered in the columns E or H then this column is left blank, as you do not have a mating result. Just a single

	qualifying parent.																	
J	sires_excluded A comma separated list of sire ident's that were tested and found to be excluded.																	
K	dams_excluded A comma separated list of dam ident's that were tested and found to be excluded.																	
L	birthdate <i>dd/mm/yyyy</i> The birth date of the animal identified in column B. This can be used to identify the correct animal if duplicate ident's are found.																	
M	sex as F/M/S This can be used to identify the correct animal if duplicate ident's are found.																	
N	anim_name As shown on the society database. This can be used to identify the correct animal if duplicate ident's are found.																	
O	member_ident The current owner of the animal.																	
P	barcode This is may be the TSU number or the animals NLIS number.																	
Q	comments Any laboratory special notes, e.g. further testing required.																	
R	lab_batch_number The ILR2 batch number as provided in the request.																	
S	lab_batch_sample The sample number within the batch as provided in the request. <i>no</i>																	
T	lab_batch_request_key request key as provided in the request																	
U	lab_id The ILR2 laboratory Identifier.																	

8.3.2 Example File Layout

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
1	dna_case_ic	anim_id	ident	test	type	test_result	sire_case	Q_sire	Q_dam	Q_dam	Q_mating	Q_sires_excluded	dams_excluded	birthdate	sex	anim_name	member_ident	barcode	comments	
2	111111	LBYM	PV	COMPLETE					JXYF44.PHAL19.HHDL18				15/09/2006	F	RAMBLE LANE LADY	LBY				
3	222222	LBYM	HY	C									15/09/2007	F	RAMBLE LANE LADY	LBY				
4	333333	LBYM	DL	N									15/09/2007	F	RAMBLE LANE LADY	LBY				
5	444444	LBYM	IE	NR									15/09/2007	F	RAMBLE LANE LADY	LBY				
6	555555	LBYM33	MIP	COMPLETE									22/04/2009	M	RAMBLE LANE BLUEY	LBY				
7	666666	LBYM33	PV	COMPLETE		553201.PHA198		727790.PHA17	Q	PHF20.PHF22			22/04/2009	M	RAMBLE LANE BLUEY	LBY				
8	777777	LBYM33	POLL	HPc									22/04/2009	M	RAMBLE LANE BLUEY	LBY				
9	888888	LBYM33	TEND				5						22/04/2009	M	RAMBLE LANE BLUEY	LBY				
0																				
1																				
2																				

8.3.3 File Naming Convention

<SOC_CODE>_<DNA_LAB_ID>_781_<BATCH_NO>_yyyymmdd_hhmm_DNA_DATA.CSV

Where: <SOC_CODE> is the ABRI assigned Society Code

<DNA_LAB_ID> is the DNA Lab Identifier #

<BATCH_NO> is the lab requests batch number. If no request has come from the society then enter 7 zeros.

<yyyymmdd> the date stamp

<hhmm> the time stamp (24 hr format).

8.3.4 *List of known Laboratories with ABRI*

(<http://breedplan.une.edu.au/booklets/DNA%20Genetic%20Labs%20Codes.pdf>)

Example: filename for batch 1903022 from Laboratory Unistel created at 13:12:01 on the 9th April 2018 for animals in the South African Brahman Association:

SABB_SAUNIS_781_1903022_20190409_1312_DNA_DATA.CSV

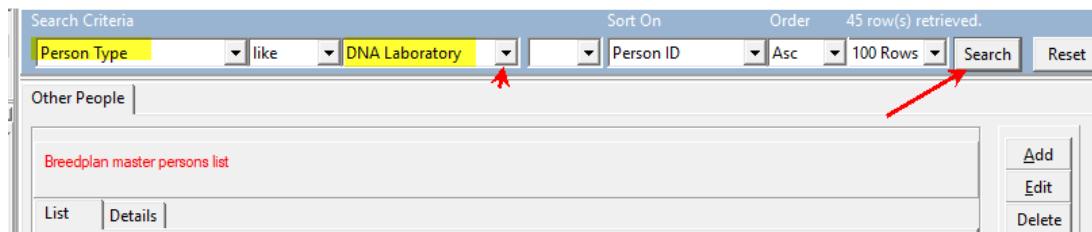
If there is no lab request for these results then the file name should be

SABB_SAUNIS_781_**0000000**_20190409_1312_DNA_DATA.CSV

Create your empty spread sheet and save as a CSV first. Enter the results throughout the days/weeks, as they come in then when you ready load into ILR2 via the imports using format 781. Quickly review a few results via animal enquiries to ensure they are displaying correctly in ILR2.

8.4 Finding a List of Known Laboratory Codes in ILR2

1. ILR2 > System Configuration > Other People
2. In the Other People screen select *Person Type* in the search Criteria then select *DNA Laboratory* from the drop down then click *Search*



3. A list of known Laboratory codes will appear in the left-hand side Grid of the screen

Internal Key	Person ID	Name	Person Type
-1 1	ROSS ANDERSON		Accredited Scanner
-10 10	PETER HARVEY		Accredited Scanner
-1001 1001	ROSS ANDERSON		Accredited Scanner
-1006 1006	JIM GREEN		Accredited Scanner
-1008 1008	GEOFF TWINE		Accredited Scanner
-1011 1011	DAVID REID		Accredited Scanner
-1012 1012	MATT WOLCOTT		Accredited Scanner
-1013 1013	BEN GLATZ		Accredited Scanner
-1017 1017	WAYNE MCLAREN		Accredited Scanner
-1018 1018	ROGER EVANS		Accredited Scanner
-1020 1020	ANDREW COULTHARD		Accredited Scanner
-1021 1021	PETER HALLSTROM		Accredited Scanner
-1023 1023	PAUL WILLIAMS		Accredited Scanner
-1024 1024	NICK CORBET (PIE)		Accredited Scanner
-1026 1026	MAX BOWMAN		Accredited Scanner
-1027 1027	MIKE STEPHENS		Accredited Scanner
-1028 1028	NATALIE LANE		Accredited Scanner
-1029 1029	DAVID COOPER		Accredited Scanner
-1030 1030	NATHAN COUPER		Accredited Scanner
-1031 1031	ADAM PORCH		Accredited Scanner

4. Scroll through this Grid to find and make a note of your laboratory code found in the Person ID Column.