

## Final Report Import Format Layout

SNP Data can be supplied for loading into the Breed Society's ILR2 database via files generated directly from the Illumina sequencer machines using GenomeStudio software as a so-called 'Final Report' file format.

These Final Report files are supplied as a single zip file containing at least 5 files. It may optionally contain ABRI's prescribed '775' format result file. The name of the file within the .zip file can start with anything but must end as ...**AnimalDetails.csv**, ... **DNAReport.csv**, ... **Sample\_Map.txt**, ...**SNP\_MAP.txt** as well as the ...**FinalReport.txt**. The '...FinalReport.txt' file contains the actual genomic results and the other files contain supporting data.


There is only one field in the FinalReport.txt file called 'Sample Id' that identifies the sample. By cross referencing the Sample Id with other fields in the supporting files we are able to attempt to identify the animal the result belongs to. The Sample Id can be anything: an animal ident, an overseas animal ident, a dna case id, a TSU number, etc. If the ILR2 import process cannot identify the correct animal on the breed society database then the results cannot be loaded.

The FinalReport.txt and the SNP\_MAP.txt files are compulsory for loading genomic results via the Final Report file format. However, the more files that accompany the FinalReport.txt file the more likely the system will be able to correctly identify the animal on the breed society database.

We assume that these files are all generated in the same order. We also note the following relational links between the files: 'Sample\_Id' in the FinalReport = 'ID' in the Sample\_Map, 'Index' in Sample\_Map = 'Row' in the DNAReport and 'DNA\_Id' in the DNAReport = 'Barcode' or 'Barcode2' on AnimalDetails.






The filename of the .zip file **MUST** adhere to our filename conventions as:  
**<SOC\_CODE>\_<DNA\_LAB\_ID>\_775\_<BATCH\_NO>\_yyyymmdd\_hhmm.ZIP**

For Example:








 AUXX\_AUGNSK\_775\_multibatch\_20180308\_1604.zip

By loading this zip file into the ILR2 775 Import facility, ILR2 will unzip the file, recognise that it contains Final Report files, locate the data it needs from these files, and then process it like a normal 775 formatted result file.

Example of Final Report files contained within the '775' zip file:

 20180308\_CHAR\_multibatch\_BOVG50V01\_Sample\_Map.txt  
 20180308\_CHAR\_multibatch\_BOVG50V01\_AnimalDetails.csv  
 AUCH\_AUGNSK\_775v3\_multibatch\_20180326\_014650\_SNP\_MAP.txt  
 20180308\_CHAR\_multibatch\_BOVG50V01\_FinalReport.txt  
 20180308\_CHAR\_multibatch\_BOVG50V01\_DNAReport.csv

Some laboratories may supply Final Report files and 775 files together in the zip file. In this instance the 775 '..SNP\_DATA.txt' and '...SNP\_MAP.txt' files will be used for the data import.

 20180308\_CHAR\_multibatch\_BOVG50V01\_AnimalDetails.csv  
 20180308\_CHAR\_multibatch\_BOVG50V01\_DNAReport.csv  
 20180308\_CHAR\_multibatch\_BOVG50V01\_FinalReport.txt  
 20180308\_CHAR\_multibatch\_BOVG50V01\_Sample\_Map.txt  
 AUCH\_AUGNSK\_775v3\_multibatch\_20180326\_014650\_ANIM\_DATA...  
 AUCH\_AUGNSK\_775v3\_multibatch\_20180326\_014650\_SNP\_DATA.txt  
 AUCH\_AUGNSK\_775v3\_multibatch\_20180326\_014650\_SNP\_MAP.txt

**AnimalDetails.csv** (comma separated csv file). This file is optional (but very beneficial).

This is an important file that allows us to determine the animal the result belongs to. Its a cross reference from the data in the FinalReport to an actual animal data via the ‘Sample Id’ in the FinalReport file. This ‘Sample Id’ MUST reference one of the two animal identifying fields (Animal Id or Registration Number) or one of the two barcode fields (Barcode or Barcode2) in the AnimalDetails file. This file is currently being generated by Neogen Australasia, but may not be available from other laboratories.

If this file is not supplied then the breed society may have to add alternate identifiers on their database to cross reference the FinalReport Sample Id to the appropriate animal. (Refer to the FinalReport file section for more details).  
NOTE: A Call Rate of blank will be interpreted as a ‘No Result’ if there are no accompanying SNP’s.

Field Name	Field Value	Optional or Required	Example
Order	Order number allocated by the society or the laboratory. Often Order & Batch ID are the same value.	Optional	123456
Batch ID	A batch number allocated by the society or the laboratory. Often Order & Batch ID are the same value.	Optional. Beneficial If the society has allocated via ILR2	1901001
Barcode	Either the DNA Case Id or the TSU #	Required	654321
Call Rate	Proportion of the NUM-SNPS to TOTAL-SNPS (eg.09982). The quality of the result. For an ‘No Results’ please leave this field blank.	Required if known otherwise 0.0 if unknown otherwise ‘blank’ for <b>No Result</b>	0.9982
File ID	Name of the results file.	Optional	20180308_CHAR_multibatch_BOVG50V01
Animal ID	The animal ident exactly as recorded on the society database, or the Animal Identifier as provided in the request.	Required	XXXY9999
Registration Number	The animal ident exactly as recorded on the society database ie the society allocated Identifier for a recorded animal.	Optional. Required if known	XXXY9999
Ear Notch	Notch details as provided in the request	Optional	
Barcode 2	The DNA Case ID if the TSU# is in Barcode otherwise DNA Case ID.	Required if Barcode set to TSU#	654321
Sample Type	Described the sample type	Optional	Hair, Semen, TSU
Date of Birth	dd/mm/yyyy	Optional	15/04/2019
Breed	Breed Description	Optional	CHAROLIAS
Sex		Optional	M or F
Organization	Full name of the society the animal or request belongs to	Optional	CHAROLAIS SOCIETY OF AUSTRALIA LTD
Member Code	The Membership ident allocated to the member by the society.	Optional	XXX

**Data Example – Animal Details.csv**

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	Order	Batch ID	Barcode	Call Rate	File ID	Animal ID	Registration Number	Ear Notch	Barcode 2	Sample Type	Date of Birth	Breed	Sex	Organization	Member Code	
2	354248	354248	672326	0.9982	20180308_CHAR_multibatch_BOVG50V01	DAS N13E	DAS N13E		672326	Hair		CHAROLAIS	M	CHAROLAIS SOCIETY OF AUSTRALIA LTD	DAS	
3	354248	354248	672327	0.9982	20180308_CHAR_multibatch_BOVG50V01	DAS N15E	DAS N15E		672327	Hair		CHAROLAIS	M	CHAROLAIS SOCIETY OF AUSTRALIA LTD	DAS	
4	354248	354248	672328	0.9982	20180308_CHAR_multibatch_BOVG50V01	DAS N2E	DAS N2E		672328	Hair		CHAROLAIS	M	CHAROLAIS SOCIETY OF AUSTRALIA LTD	DAS	
5	354248	354248	672329	0.9984	20180308_CHAR_multibatch_BOVG50V01	DAS N12E	DAS N12E		672329	Hair		CHAROLAIS	M	CHAROLAIS SOCIETY OF AUSTRALIA LTD	DAS	
6	354249	1802007	672330	0.9983	20180308_CHAR_multibatch_BOVG50V01	DOULTON LARRIKIN (DSM L4E) (P)	DSM L4E		672330	Hair	02/10/2015	CHAROLAIS	M	CHAROLAIS SOCIETY OF AUSTRALIA LTD	DSM	

**DNAReport.csv** (comma separated csv file). This file is optional (but beneficial).

The main field of interest in this file is the DNA\_ID as it helps to identify the animal by cross referencing to a DNA Case Id on the society database.

The first two rows are a chip and a test description

Eg. Row 1 column A

DNA Report on Q:\Illumina Project Data 2018\Beef\_GAA\_BOVG50V01\_20180308\  
Beef\_GAA\_BOVG50V01\_20180308\Beef\_GAA\_BOVG50V01\_20180308\_DNAReport.csv

Eg. Row 2 columns B to L

# LOCI = 46242 # DNAs = 12 ProjectName = Beef\_GAA\_BOVG50V01\_20180308\_DNAReport GenCall Version = 7.0.0 Low GenCall Score Cutoff = 0.0500

The data starts in row 3

Field Name	Field Value	Optional or Required	Example
Row	Row number	Optional	26
DNA_ID	A unique identifier allocated to an animal and its sample material by the DNA lab	Required	672326
#NO_CALLS	A total count of the SNPs that did not generate a valid result	Optional	81
#Calls	A total count of the SNPS that did generate a valid result	Optional	46161
Call Rate	Proportion of the NUM-SNPS to TOTAL-SNPS (eg.09982). The quality of the result.	Optional	0.9982
A/A_Freq		Optional	0.29279
A/B_Freq		Optional	0.3871
B/B_Freq		Optional	0.3149
Minor_Freq		Optional	0.4915
50%_GC_Score		Optional	0.7762
10%_GC_Score		Optional	0.6017
0/1		Optional	1

### Data Example

Row	DNA_ID	#NO_CALLS	#Calls	Call_Rate	A/A_Freq	A/B_Freq	B/B_Freq	Minor_Freq	50%_GC_Score	10%_GC_Score	0/1
26	672326	81	46161	0.9982	0.29279	0.3871	0.3149	0.4915	0.7762	0.6017	1
27	672327	85	46157	0.9982	0.3122	0.3556	0.3323	0.4899	0.7762	0.6016	1
28	672328	85	46157	0.9982	0.3003	0.3833	0.3164	0.492	0.7763	0.6018	1
29	672329	74	46168	0.9984	0.2969	0.3882	0.3149	0.491	0.7761	0.6016	1
30	672330	79	46163	0.9983	0.2953	0.3867	0.3181	0.4886	0.7764	0.6033	1
31	672331	101	46141	0.9978	0.3406	0.3013	0.358	0.4913	0.7765	0.6014	1
32	672332	136	46106	0.9971	0.3005	0.3731	0.3265	0.487	0.775	0.592	1
33	672333	57	46185	0.9988	0.3083	0.3647	0.327	0.4906	0.7767	0.6027	1
34	672334	65	46177	0.9986	0.2948	0.3884	0.3168	0.489	0.7767	0.6038	1
35	672335	79	46163	0.9983	0.2973	0.3827	0.32	0.4886	0.7764	0.6018	1
36	672336	261	45981	0.9944	0.2907	0.3944	0.3149	0.4879	0.7713	0.5788	1
37	672337	103	46139	0.9978	0.2891	0.4017	0.3091	0.49	0.7767	0.6039	1

**Sample\_Map.txt** (tab delimited text file). This file is optional (but very beneficial).

This file is useful for cross referencing the 'Sample Id' in the FinalReport to the 'ID' field in this file. This reference may help us to identify the animal the result belongs to, especially if it is an animal identifier that exists on the breed society database. This file may be useful if the AnimalDetails.csv is not supplied. SentrinxPosition is also an important field to help in our quality control processes.

Field Name	Field Description	Optional or Required	Example
Index	Row number	Required	26
Name	Animal Identifier	Required	XXXY999
ID	This is the Sample Id supplied in the FinalReport. They should be the same value.	Required	654321
Gender		Optional	Male,Famale,UNKNOWN
Plate	The lab plate identifier	Optional	143971
Well	The well position on the plate	Optional	D10
Batch ID	Batch number allocated by society or lab	Optional	1802005
Parent 1	Parent Identifier	Optional	
Parent 2	Parent Identifier	Optional	
Replicate		Optional	
SentrinxPosition	Sentrinx position (sample,location,plate)	Required	202282380030_R12C02

## Data Example

Index	Name	ID	Gender	Plate	Well	batch	Parent1	Parent2	Replicate	SentrinxPosition
26	DAS N13E	672326	Unknown	143971	D10	354248				202282380030_R12C02
27	DAS N15E	672327	Unknown	143971	E10	354248				202282380030_R15C02
28	DAS N2E	672328	Unknown	143971	F10	354248				202282380030_R18C02
29	DAS N12E	672329	Unknown	143971	G10	354248				202282380030_R21C02
30	DSM L4E	672330	Unknown	143962	H12	1802007				202334030032_R24C04
31	BAU M4E	672331	Unknown	143997	F1	1802004				202282380039_R16C01
32	ANC L279F	672332	Unknown	143997	G1	1802004				202282380039_R19C01

**SNP\_Map.txt** (tab delimited text file). This file is Compulsory for all genotypes except parentage.

The SNP Map is important for our quality control processes. If it is not supplied, an error will occur, and the result data will not be loaded onto ILR2. The SNP Names listed in the SNP Map should correspond exactly to the SNP Names supplied within the FinalReport SNP results, including the 'No Calls'.

Field Name	Field Description	Optional or Required	Example
Index	Row sequence no	Required	26
Name	SNP Name	Required	ARS-BFGL-BAC-10919
Chromosome	Chromosome Number	Required	14
Position		Required	31267746
GenTrain Score		Optional	0.7455
SNP		Required	[A/G]
ILMN Strand	Top or Bottom	Optional	TOP or BOT
Customer Stand	Top or Bottom	Optional	TOP or BOT
NormID		Optional	100

### Example File

```

1 |Index|Name|Chromosome|Position|GenTrain Score|SNP|ILMN Strand|Customer Strand|NormID|CRUF
2 |1|ARS-BFGL-BAC-10919|14|31267746|0.7455|[A/G]|TOP|TOP|0|CRUF
3 |2|ARS-BFGL-BAC-10975|10|21225382|0.7042|[A/G]|TOP|TOP|0|CRUF
4 |3|ARS-BFGL-BAC-11000|10|79252023|0.8459|[T/G]|BOT|BOT|0|CRUF
5 |4|ARS-BFGL-BAC-11003|10|80410977|0.8801|[T/C]|BOT|BOT|0|CRUF
6 |5|ARS-BFGL-BAC-11025|10|84516867|0.8560|[T/G]|BOT|BOT|0|CRUF
7 |6|ARS-BFGL-BAC-11044|1|12805406|0.8861|[T/C]|BOT|BOT|0|CRUF
8 |7|ARS-BFGL-BAC-11193|1|29303546|0.8123|[T/C]|BOT|TOP|0|CRUF
9 |8|ARS-BFGL-BAC-11215|12|90704572|0.7441|[A/G]|TOP|TOP|0|CRUF
10|9|ARS-BFGL-BAC-11218|1|24549757|0.8716|[A/G]|TOP|TOP|0|CRUF
11|10|ARS-BFGL-BAC-11276|13|2153905|0.8155|[T/C]|BOT|TOP|0|CRUF
12|11|ARS-BFGL-BAC-11283|13|23196342|0.8106|[A/C]|TOP|TOP|0|CRUF
13|12|ARS-BFGL-BAC-11513|14|7428315|0.7885|[A/G]|TOP|TOP|0|CRUF
14|13|ARS-BFGL-BAC-11612|10|27228918|0.8355|[T/C]|BOT|BOT|0|CRUF
15|14|ARS-BFGL-BAC-11657|10|48926752|0.8042|[T/C]|BOT|TOP|0|CRUF
16|15|ARS-BFGL-BAC-11666|10|49656226|0.8151|[A/G]|TOP|TOP|0|CRUF
17|16|ARS-BFGL-BAC-11718|0|0|0.6882|[T/C]|BOT|BOT|0|CRUF
18|17|ARS-BFGL-BAC-11724|11|60498991|0.6985|[A/G]|TOP|BOT|0|CRUF
19|18|ARS-BFGL-BAC-11748|11|58442169|0.9014|[G/C]|BOT|TOP|100|CRUF
20|19|ARS-BFGL-BAC-11750|1|19778380|0.8753|[T/C]|BOT|TOP|0|CRUF
21|20|ARS-BFGL-BAC-11761|1|19709807|0.7892|[A/G]|TOP|TOP|0|CRUF

```

**FinalReport.txt** (tab delimited text file). This file is Compulsory as it contains the genomic results.

This data represents the SNPs tested on the animal and should maintain a one-to-one relationship with the accompanying SNP\_MAP file. THESE RESULTS SHOULD INCLUDE 'NO CALLS'.

- If no SNP results were obtained for the animal, then no Final Report result is generated. This can be handled a via two ways.
  - If you are generating a 'Final Report' result file for those animals that obtained a result, then this means a 'Final Report' file is going to be generated along with the accompanying 'Animal Details'. Therefore, those animals that will not appear in the 'Final Report' file can be included in the 'Animal Details' file, with a *'blank'* in the call rate. These records will flag the animal as having a 'NO RESULT'. Note we can only load the 'Animal Details' file if it is accompanied with the other files. Refer to the Animal Details file section for more details.
  - If no Final Report file is being generated at all, the only other way to indicate a 'No Result' is to supply a result record via the 781 format. Please discuss with ABRI if you require the 781 file formats layouts.
- If a particular SNP test did not give a result ie. a 'NO CALL', please include the SNP Name and leave other fields blank (or supply a dash ie. -).
- ILR2 will check the 'Content' field in the incoming FinalReport and expect it to match to an existing SNP Manifest name reference stored on the breed society database.
- Each and every SNP record in this file references the Sample Id. The Sample Id is typically an animal identifier (either an animal ident or an alternate ident for overseas SNP results) or a DNA\_Case\_Id. To link this Sample Id to an animal on the breed society database, the importing process must interrogate the animal identifiers and barcodes in the AnimalDetails.csv. If the AnimalDetails.csv is not supplied then this interrogation will happen between the Sample Id and the ID and Name in the Sample\_Map file and the DNA\_Id in the DNAreport file.

If the Sample Id corresponds to a valid 'Animal Ident' on the breed society database then a match can be made.

If the Sample Id is a 'DNA Case Id' that already exists on the breed society database then a match can be made.

If the Sample Id is an overseas animal ident then a match can only be made if that ident exists on the 'Alternate Idents' table on the breed society database.

If the Sample Id cannot be linked to an animal or a DNA request an error will occur, 'Sample Id XXXXXXX is not on the database'. If the society Registrars can determine the correct animal, they will have to add the Sample Id as either a DNA\_Case\_Id or a cross reference record, depending on the Sample Id.

There are two header sections and a column heading row included in the FinalReport file prior to the actual SNP result data:

- [Header] – occurs once at the start of the file. The label is of mixed case and wrapped in square brackets, no further space or data on the row after the closed square bracket.
- [Data] – occurs once at the start of the file after the [Header] section label. The label is of mixed case and wrapped in square brackets, no further space or data on the row after the closed square bracket.
- The data column headings appear directly after the [Data] section label and before the actual data.

**[Header]**

- Field names and field values are separated by a tab.

Field Name	Field Value	Optional or Required	Example
GSGT Version	Version number	Optional	2.0.3
Processing Date with Time Stamp	DD/MM/YYYY HH:MM AP	Date is required Time is optional	3/8/2018 3:26 PM
Content	SNP Manifest description (Note that this Manifest must already exist on the breed society database)	Required	GGP_Bovine_50K_b.b pm
Num SNPs	Number of SNPs in the [TEST-DATA] section for this animal	Required	47843
Total SNPs	Total number of SNPs on the SNP chip	Required	49463
Num Samples	Total number of samples in this result	Optional	12
Total Samples	Total number of samples in this result	Required	12

**[Data]**

- Field names and field values are separated by a tab

Order	Field Description	Optional or Required	Example
1	SNP Name	Required – uppercase	ABS-BFGL-BAC-10919
2	Sample Id	Required	672326
3	Allele1 - Forward	Optional	A
4	Allele2 - Forward	Optional	A
5	Allele1 - Top	Optional	A
6	Allele2 - Top	Optional	A
7	Allele1 - AB	Required must be an A or B or -	A
8	Allele2 - AB	Required must be an A or B or -	A
9	GC Score	Optional	0.7241
10	X	Optional	1.250
11	Y	Optional	0.051





# FINAL REPORT File Format – V1 For loading via ILR2 775 Import

Last Updated March 2019

## Example File

```

[Header] CRUF
GSGT Version -> 2.0.3 CRUF
Processing Date -> 3/8/2018 3:26 PM CRUF
Content -> GGP_Bovine_50K_B.bpm CRUF
Num SNPs -> 47843 CRUF
Total SNPs -> 49463 CRUF
Num Samples -> 12 CRUF
Total Samples -> 12 CRUF
[Data] CRUF
SNP Name Sample ID Allele1 - Forward Allele2 - Forward Allele1 - Top Allele2 - Top Allele1 - AB Allele2 - AB GC Score X Y CRUF
ARS-BFGL-BAC-10919 -> 672326 -> A -> A -> A -> A -> 0.7241 -> 1.250 -> 0.051 CRUF
ARS-BFGL-BAC-10975 -> 672326 -> A -> A -> A -> A -> 0.6473 -> 1.403 -> 0.057 CRUF
ARS-BFGL-BAC-11000 -> 672326 -> I -> G -> A -> C -> A -> B -> 0.8793 -> 0.302 -> 0.334 CRUF
ARS-BFGL-BAC-11003 -> 672326 -> I -> T -> A -> A -> A -> A -> 0.9175 -> 1.227 -> 0.010 CRUF
ARS-BFGL-BAC-11025 -> 672326 -> T -> G -> A -> C -> A -> B -> 0.8913 -> 0.545 -> 0.605 CRUF
ARS-BFGL-BAC-11044 -> 672326 -> T -> C -> A -> G -> A -> B -> 0.9234 -> 0.607 -> 0.614 CRUF
ARS-BFGL-BAC-11193 -> 672326 -> A -> G -> A -> G -> A -> B -> 0.8340 -> 0.237 -> 0.298 CRUF
ARS-BFGL-BAC-11215 -> 672326 -> G -> G -> G -> G -> B -> B -> 0.7216 -> 0.030 -> 0.787 CRUF
ARS-BFGL-BAC-11218 -> 672326 -> A -> G -> A -> G -> A -> B -> 0.9087 -> 0.644 -> 0.828 CRUF
ARS-BFGL-BAC-11276 -> 672326 -> A -> G -> A -> G -> A -> B -> 0.8386 -> 0.804 -> 0.647 CRUF

```

```

387 ARS-BFGL-NGS-101070 -> 672326 -> C -> C -> G -> G -> B -> B -> 0.7931 -> 0.041 -> 1.183 CRUF
388 ARS-BFGL-NGS-101084 -> 672326 -> - -> - -> - -> - -> - -> - -> 0.0000 -> 0.648 -> 0.538 CRUF
389 ARS-BFGL-NGS-101098 -> 672326 -> A -> G -> A -> G -> A -> B -> 0.8320 -> 0.267 -> 0.352 CRUF
390 ARS-BFGL-NGS-10111 -> 672326 -> T -> T -> A -> A -> A -> A -> 0.7451 -> 1.251 -> 0.066 CRUF
391 ARS-BFGL-NGS-101113 -> 672326 -> A -> A -> A -> A -> A -> A -> 0.7039 -> 1.880 -> 0.077 CRUF
392 ARS-BFGL-NGS-101114 -> 672326 -> A -> A -> A -> A -> A -> A -> 0.7030 -> 1.205 -> 0.040 CRUF
393 ARS-BFGL-NGS-101117 -> 672326 -> A -> A -> A -> A -> A -> A -> 0.7351 -> 1.196 -> 0.020 CRUF
394 ARS-BFGL-NGS-101135 -> 672326 -> - -> - -> - -> - -> - -> - -> 0.0000 -> 0.790 -> 0.739 CRUF
395 ARS-BFGL-NGS-101156 -> 672326 -> T -> C -> A -> G -> A -> B -> 0.7174 -> 1.220 -> 1.083 CRUF
396 ARS-BFGL-NGS-101195 -> 672326 -> T -> T -> A -> A -> A -> A -> 0.6825 -> 0.922 -> 0.017 CRUF

```

NO CALLS

```

95680 SMA_2 -> 672327 -> G -> G -> G -> G -> B -> B -> 0.3875 -> 0.110 -> 1.229 CRUF
95681 SMA_3 -> 672327 -> G -> G -> G -> G -> B -> B -> 0.7722 -> 0.114 -> 1.265 CRUF
95682 Thrombopathia_2 -> 672327 -> A -> A -> A -> A -> A -> A -> 0.7701 -> 1.063 -> 0.003 CRUF
95683 Thrombopathia_3 -> 672327 -> A -> A -> A -> A -> A -> A -> 0.8720 -> 0.902 -> 0.030 CRUF
95684 Tyrosinase-OA-F -> 672327 -> G -> G -> G -> G -> B -> B -> 0.9212 -> 0.006 -> 0.662 CRUF
95685 Tyrosinase-OA-R -> 672327 -> G -> G -> G -> G -> B -> B -> 0.4097 -> 0.018 -> 1.415 CRUF
95686 UMD3-39263696_1 -> 672327 -> C -> C -> C -> C -> A -> A -> 0.3893 -> 1.432 -> 0.002 CRUF
95687 UMD3-39263696_2 -> 672327 -> C -> C -> C -> C -> A -> A -> 0.9149 -> 0.944 -> 0.000 CRUF
95688 UMD3-39263696_3 -> 672327 -> C -> C -> C -> C -> A -> A -> 0.9315 -> 1.095 -> 0.000 CRUF
95689 UMD3-39339348_1 -> 672327 -> C -> C -> G -> G -> B -> B -> 0.7755 -> 0.056 -> 1.370 CRUF
95690 UMD3-39339348_2 -> 672327 -> C -> C -> G -> G -> B -> B -> 0.7784 -> 0.079 -> 1.449 CRUF
95691 UMD3-39339348_3 -> 672327 -> C -> C -> G -> G -> B -> B -> 0.7753 -> 0.095 -> 1.331 CRUF
95692 WVR_49878773 -> 672327 -> C -> C -> G -> G -> B -> B -> 0.9218 -> 0.021 -> 1.205 CRUF
95693 WVR_49878773_2 -> 672327 -> C -> C -> G -> G -> B -> B -> 0.8805 -> 0.030 -> 1.183 CRUF
95694 WVR_49878773_3 -> 672327 -> C -> C -> G -> G -> B -> B -> 0.9361 -> 0.037 -> 1.137 CRUF
95695 YellowFat-FA -> 672327 -> G -> G -> G -> G -> B -> B -> 0.7686 -> 0.019 -> 0.638 CRUF
95696 YellowFat-RA -> 672327 -> G -> G -> G -> G -> B -> B -> 0.8934 -> 0.047 -> 0.852 CRUF
95697 ARS-BFGL-BAC-10919 -> 672328 -> A -> A -> A -> A -> A -> A -> 0.7241 -> 1.248 -> 0.047 CRUF
95698 ARS-BFGL-BAC-10975 -> 672328 -> A -> A -> A -> A -> A -> A -> 0.6473 -> 1.370 -> 0.067 CRUF
95699 ARS-BFGL-BAC-11000 -> 672328 -> T -> G -> A -> C -> A -> B -> 0.8793 -> 0.303 -> 0.388 CRUF
95700 ARS-BFGL-BAC-11003 -> 672328 -> T -> T -> A -> A -> A -> A -> 0.9175 -> 1.204 -> 0.028 CRUF
95701 ARS-BFGL-BAC-11025 -> 672328 -> T -> G -> A -> C -> A -> B -> 0.8913 -> 0.586 -> 0.575 CRUF
95702 ARS-BFGL-BAC-11044 -> 672328 -> T -> T -> A -> A -> A -> A -> 0.9234 -> 1.079 -> 0.006 CRUF
95703 ARS-BFGL-BAC-11193 -> 672328 -> G -> G -> G -> G -> B -> B -> 0.8340 -> 0.049 -> 0.502 CRUF
95704 ARS-BFGL-BAC-11215 -> 672328 -> G -> G -> G -> G -> B -> B -> 0.7216 -> 0.040 -> 0.740 CRUF
95705 ARS-BFGL-BAC-11218 -> 672328 -> A -> A -> A -> A -> A -> A -> 0.9087 -> 1.119 -> 0.030 CRUF
95706 ARS-BFGL-BAC-11276 -> 672328 -> A -> G -> A -> G -> A -> B -> 0.8386 -> 0.804 -> 0.647 CRUF
95707 ARS-BFGL-BAC-11283 -> 672328 -> A -> A -> A -> A -> A -> A -> 0.8316 -> 1.522 -> 0.039 CRUF
95708 ARS-BFGL-BAC-11513 -> 672328 -> A -> G -> A -> G -> A -> B -> 0.7975 -> 1.142 -> 1.064 CRUF
95709 ARS-BFGL-BAC-11612 -> 672328 -> T -> C -> A -> G -> A -> B -> 0.8660 -> 0.620 -> 0.662 CRUF
95710 ARS-BFGL-BAC-11657 -> 672328 -> A -> A -> A -> A -> A -> A -> 0.8220 -> 1.374 -> 0.033 CRUF
95711 ARS-BFGL-BAC-11666 -> 672328 -> G -> G -> G -> G -> B -> B -> 0.8381 -> 0.045 -> 0.640 CRUF
95712 ARS-BFGL-BAC-11718 -> 672328 -> T -> C -> A -> G -> A -> B -> 0.6168 -> 0.400 -> 0.457 CRUF
95713 ARS-BFGL-BAC-11724 -> 672328 -> T -> C -> A -> G -> A -> B -> 0.5670 -> 0.283 -> 0.367 CRUF
95714 ARS-BFGL-BAC-11748 -> 672328 -> C -> G -> C -> G -> A -> B -> 0.9374 -> 0.450 -> 0.632 CRUF
95715 ARS-BFGL-BAC-11750 -> 672328 -> G -> G -> G -> G -> R -> R -> 0.9126 -> 0.032 -> 0.657 CRUF

```



## File Naming Convention

### ZIP File

The FinalReport file and the accompanying data files MUST be compressed into a single ZIP file for ease of data transfer and processing by the breed society Registrars. The file naming convention for the ZIP file is:

<SOC\_CODE>\_<DNA\_LAB\_ID>\_775\_<BATCH\_NO>\_yyyymmdd\_hhmm.ZIP

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\_hhmm is a date and time stamp (24 hr format).

For example the zip filename for batch 1811074, from Neogen Australasia, created at 13:12:01 on the 9<sup>th</sup> Nov 2018, for animals in the Australian Wagyu Association, is:

AUWY\_AUGNSK\_775\_1074\_20161109\_1312.ZIP

\* ( [http://breedplan.une.edu.au/booklets/Soc\\_codes\\_BP.pdf](http://breedplan.une.edu.au/booklets/Soc_codes_BP.pdf))

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

The .zip file should not contain other zip files.

**FinalReport File** must be suffixed with the words FinalReport (nb. no spaces between the words)

ie. ....\_FinalReport.txt

**AnimalDetails File** must be suffixed with the words AnimalDetails (nb. no spaces between the words)

ie. ....\_AnimalDetails.csv

**DNAReport File** must be suffixed with the words DNAReport (nb. no spaces between the words)

ie. ....\_DNAReport.txt

**Sample\_Map File** must be suffixed with the words Sample\_Map (nb. an underscore between the words)

ie. ....\_Sample\_Map.txt

**SNP\_Map File** must be suffixed with the words SNP\_Map (nb. an underscore between the words)

ie. ....\_SNP\_MAP.txt

## File Download Area

A single DNA data download area has been set up as a central repository and distribution point for all ABRI breed society clients.

ABRI will:

- Check the files and advise the DNA Lab if there are any problems with file names.
- Automatically transfer the files to the relevant Breed Society ILR2 server and database.
- Notify the Breed Society that the file has been sent from the DNA Lab and that the Import process has been initiated.
- Backup the files.

Each DNA Lab will have its own username and password. Contact ABRI for these details.

\* end \*