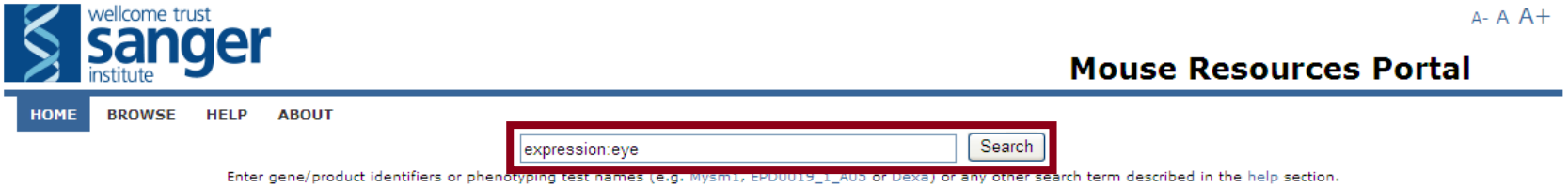
How to search and view *lacZ* reporter gene expression data

1. From the Sanger Mouse Portal home page (http://www.sanger.ac.uk/mouseportal/), enter your tissue or organ of interest prefixed with "expression:" (e.g. expression:eye) into the **Search** field and click search:



About This Portal

The Wellcome Trust Sanger Institute generates, characterises, and uses a variety of reagents for mouse genetics research. It also aims to facilitate the distribution of these resources to the external scientific community. Here, you will find unified access to the different resources available from the Institute or its collaborators. The resources include: 129S7 and C57BL6/J bacterial artificial chromosomes (BACs), MICER gene targeting vectors, knock-out first conditional-ready gene targeting vectors, embryonic stem (ES) cells with gene targeted mutations or with retroviral gene trap insertions, mutant mouse lines, and phenotypic data generated from the Institute's primary screen.

Phenotyping Summary

The table below displays the **number of alleles** that have completed different stages of the MGP Phenotyping pipeline (funded by WTSI & EUMODIC)

Comprehensive Phenotyping Substantively Complete	564
Infection Challenge (Salmonella and Citrobacter)	495
LacZ Expression (Adult and E14.5)	339

Other Data Summary

The table below displays the **number of unique genes** with each individual product type produced at the Wellcome Trust Sanger Institute.

Funding:	WTSI EUMODIC	KOMP EUCOMM	KOMP EUCOMM	WT	WT	WT
Products:	**Mice**	**Targeted ES Cells**	**Gene Targeting Vectors**	**MICER**	**C57Bl/6J BACs**	**129S7 BACs**
	904	13011	15105	6719	12037	11874

Phenotyping Overview

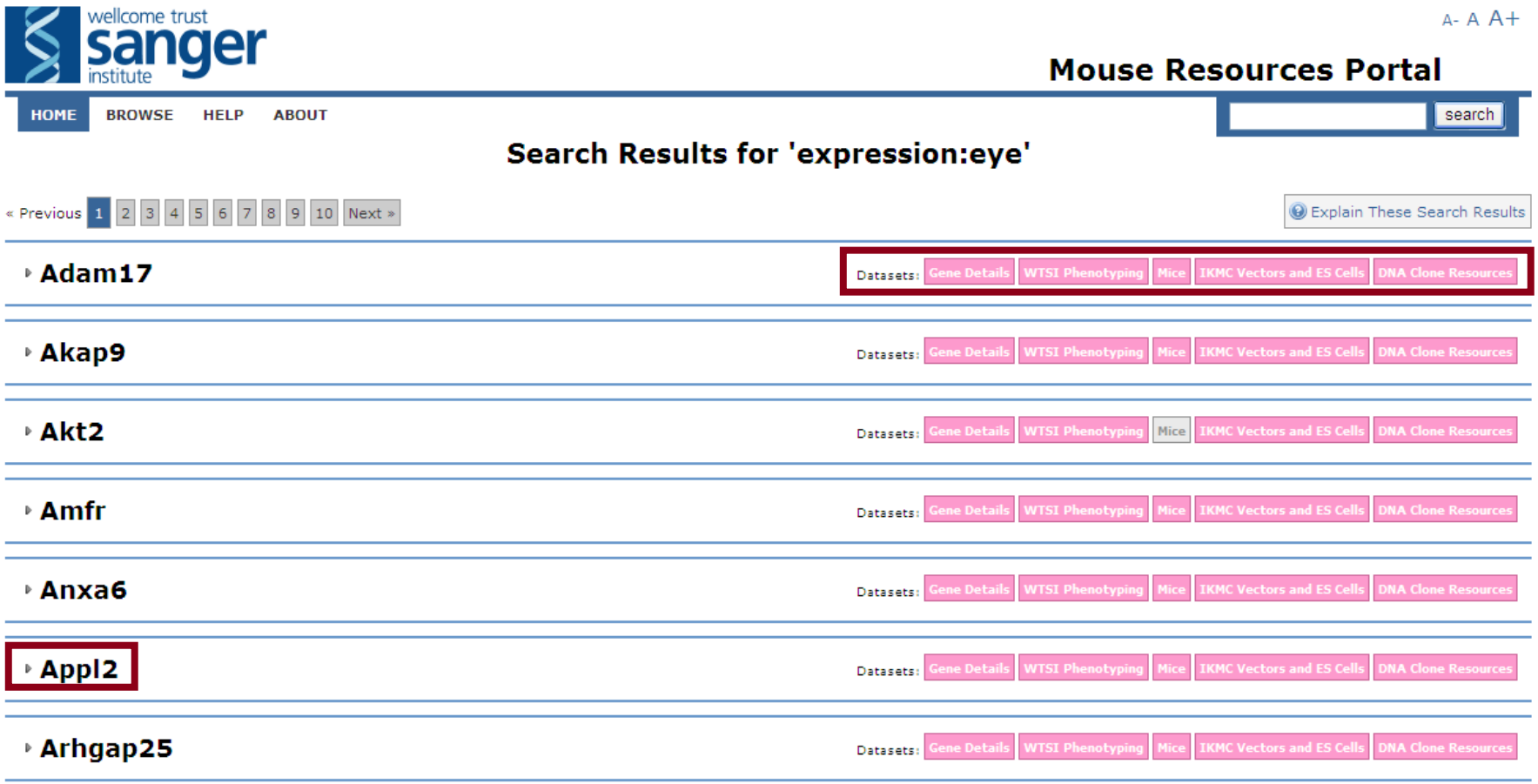
Download a heat map of phenotyping results by assay. This spreadsheet also links to the detailed phenotyping data on this portal.

You can also access (and search) the same data via the MGP Phenotyping BioMart.

NEW - Disease predictions based on semantic similarity between OMIM disorder clinical features and model organism phenotypes.

If you would like to be kept updated with information on our phenotyping data, please subscribe to our mailing list.

2. This returns a list of genes in which *lacZ* reporter gene expression has been detected in the eye of at least one animal.



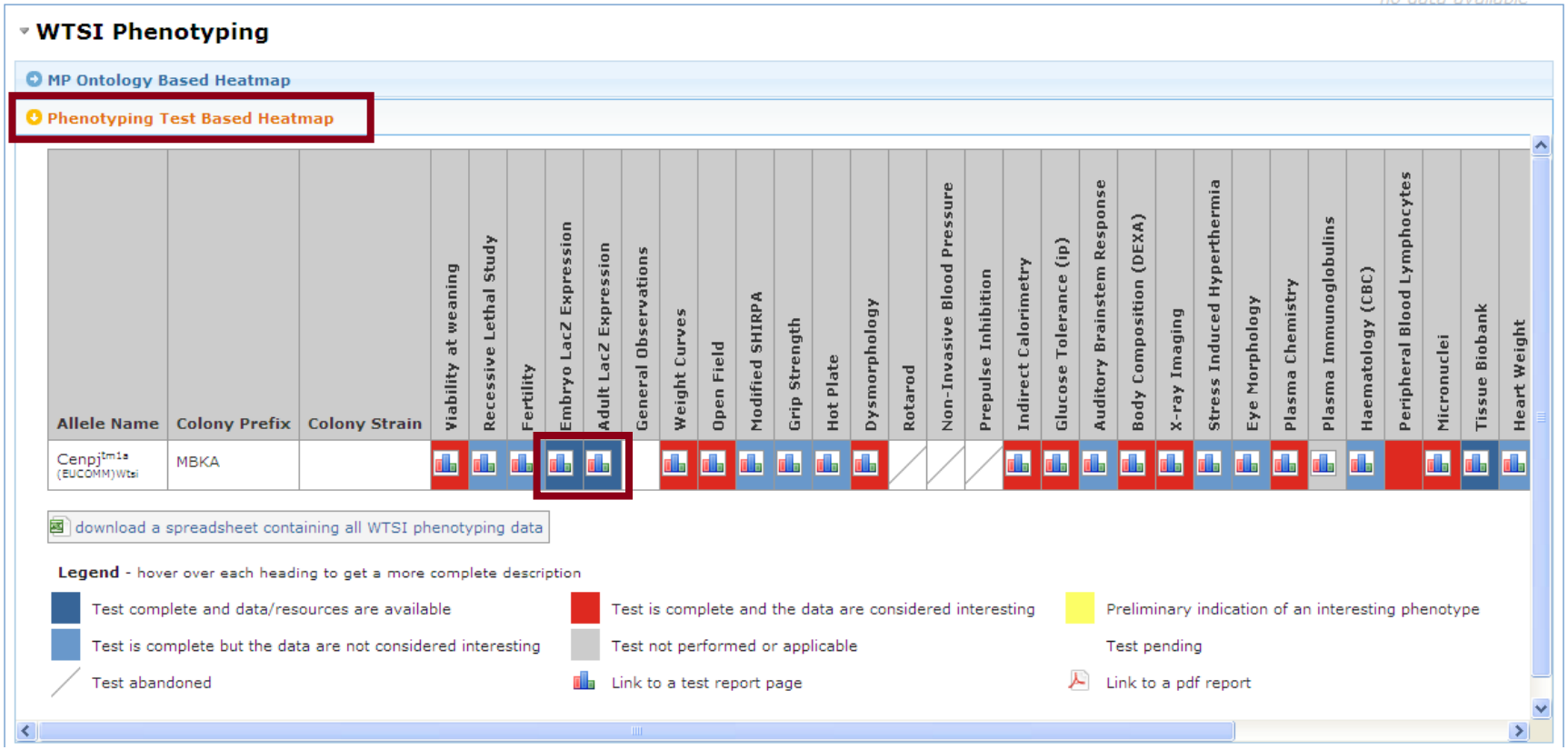
3. This list summarises the available data for each gene split into the following datasets that are populated (pink with white writing) when resources are available and grey when no information is available:

   i. Gene Details
   ii. WTSI Phenotyping
   iii. Mice
   iv. IKMC Vectors and ES Cells
   v. DNA Clone Resources

4. These data can be reviewed one gene at a time as follows. Click on the first gene of interest e.g. *Appl2*. This rolls down the gene specific information split into the above datasets.

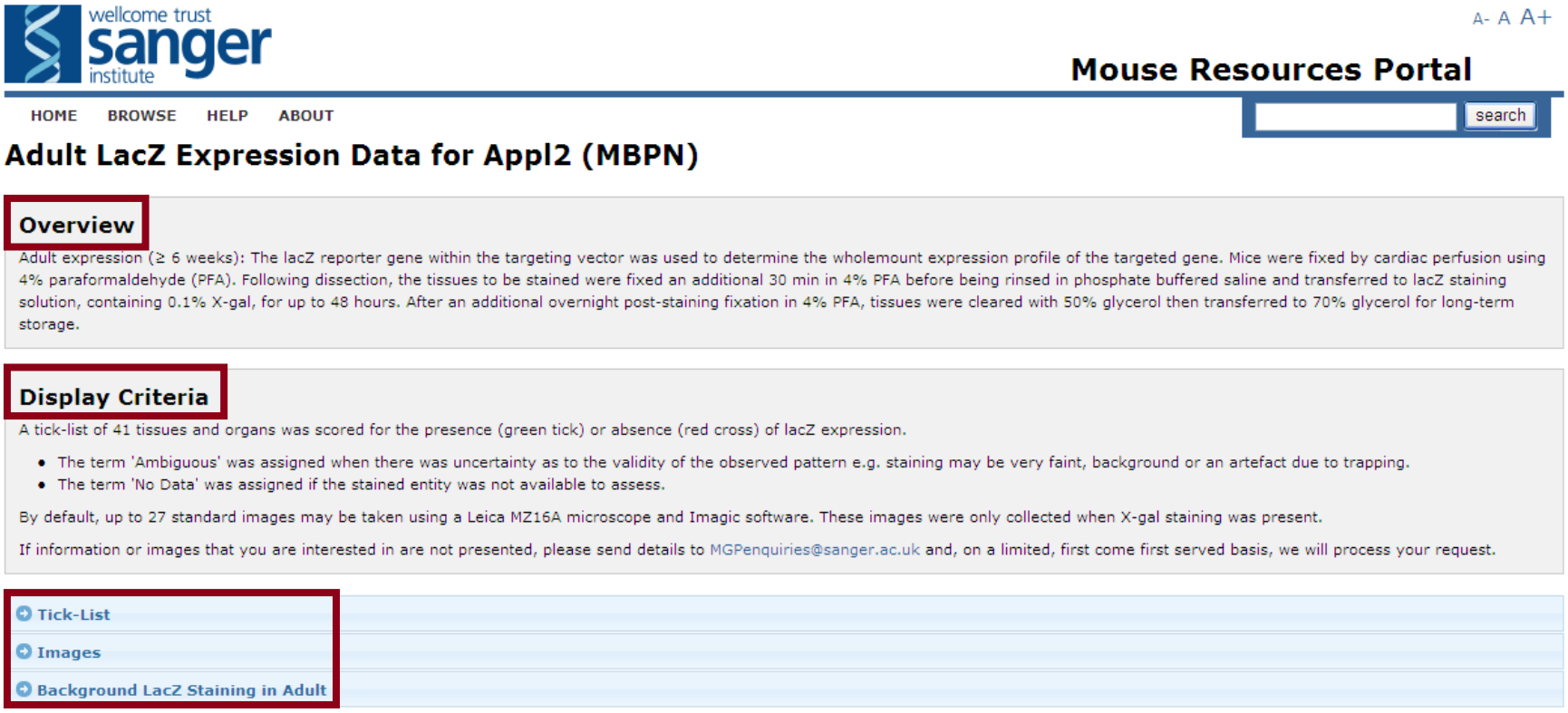
5. The WTSI Phenotyping panel presents the primary phenotyping data as a colour coded heat map style summary of all phenotyping data for that gene. Data are grouped for presentation in two ways:
   i. As a Mammalian Phenotype (MP) Ontology Based Heatmap
   ii. As a Phenotyping Test Based Heatmap

6. To view the *lacZ* expression analysis data, open the Phenotyping Test Based Heatmap by clicking the bar of the same name. Note this action causes the MP Ontology Based Heatmap to roll up.



7. Adult *lacZ* Expression and Embryo *lacZ* Expression (E14.5) data are available when the associated heatmap cells are dark blue  indicating that the test is complete and data/resources are available.

8. Clicking on the graph symbol in the Adult *lacZ* Expression cell opens the web page on the Sanger Mouse Portal presenting an overview of the standard protocol used and describing the display criteria applied. At the bottom of that page there are three roll down options
   i. Tick-List
   ii. Images
   iii. Background *LacZ* Staining in Adults



9. Open the Tick-List by clicking the bar of the same name. This presents a tabulated view of expression data from individual mice (one column per mouse) processed for that mutant line. Details of each mutant mouse are presented in rows 1-4:
   i. Colony Name (row 1): Full name of the mouse colony including the ID of the ES cell clone from which it was derived
   ii. Genotype (row 2): Genotype of the animal that was phenotyped
   iii. Gender (row 3): Sex of the animal that was phenotyped
   iv. Age In Weeks (row 4): Age of the animal at the time of analysis
10. The remaining rows summarise the result of the *lacZ* expression analysis for 41 tissues and organs assessed as part of the screen. Possible outcomes are *lacZ* present, absence, ambiguous or no data. Note you may need to scroll down to see all contents of the table.

Adult LacZ Expression Data for Appl2 (MBPN)

Overview

Adult expression (≥ 6 weeks): The lacZ reporter gene within the targeting vector was used to determine the wholemount expression profile of the targeted gene. Mice were fixed by cardiac perfusion using 4% paraformaldehyde (PFA). Following dissection, the tissues to be stained were fixed an additional 30 min in 4% PFA before being rinsed in phosphate buffered saline and transferred to lacZ staining solution, containing 0.1% X-gal, for up to 48 hours. After an additional overnight post-staining fixation in 4% PFA, tissues were cleared with 50% glycerol then transferred to 70% glycerol for long-term storage.

Display Criteria

A tick-list of 41 tissues and organs was scored for the presence (green tick) or absence (red cross) of lacZ expression.

- The term 'Ambiguous' was assigned when there was uncertainty as to the validity of the observed pattern e.g. staining may be very faint, background or an artefact due to trapping.
- The term 'No Data' was assigned if the stained entity was not available to assess.

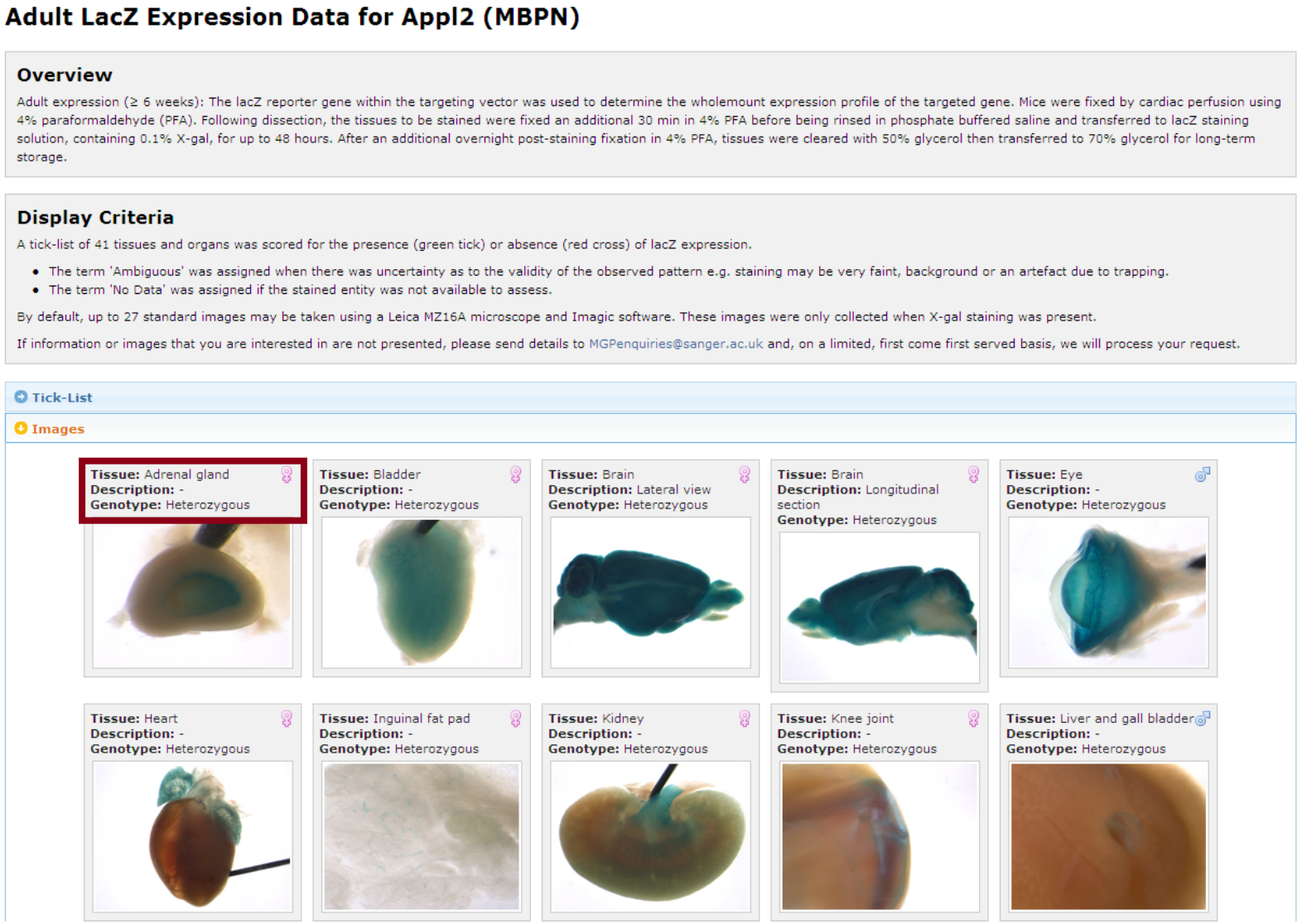
By default, up to 27 standard images may be taken using a Leica MZ16A microscope and Imagic software. These images were only collected when X-gal staining was present.

If information or images that you are interested in are not presented, please send details to MGPenquiries@sanger.ac.uk and, on a limited, first come first served basis, we will process your request.

Tick-List

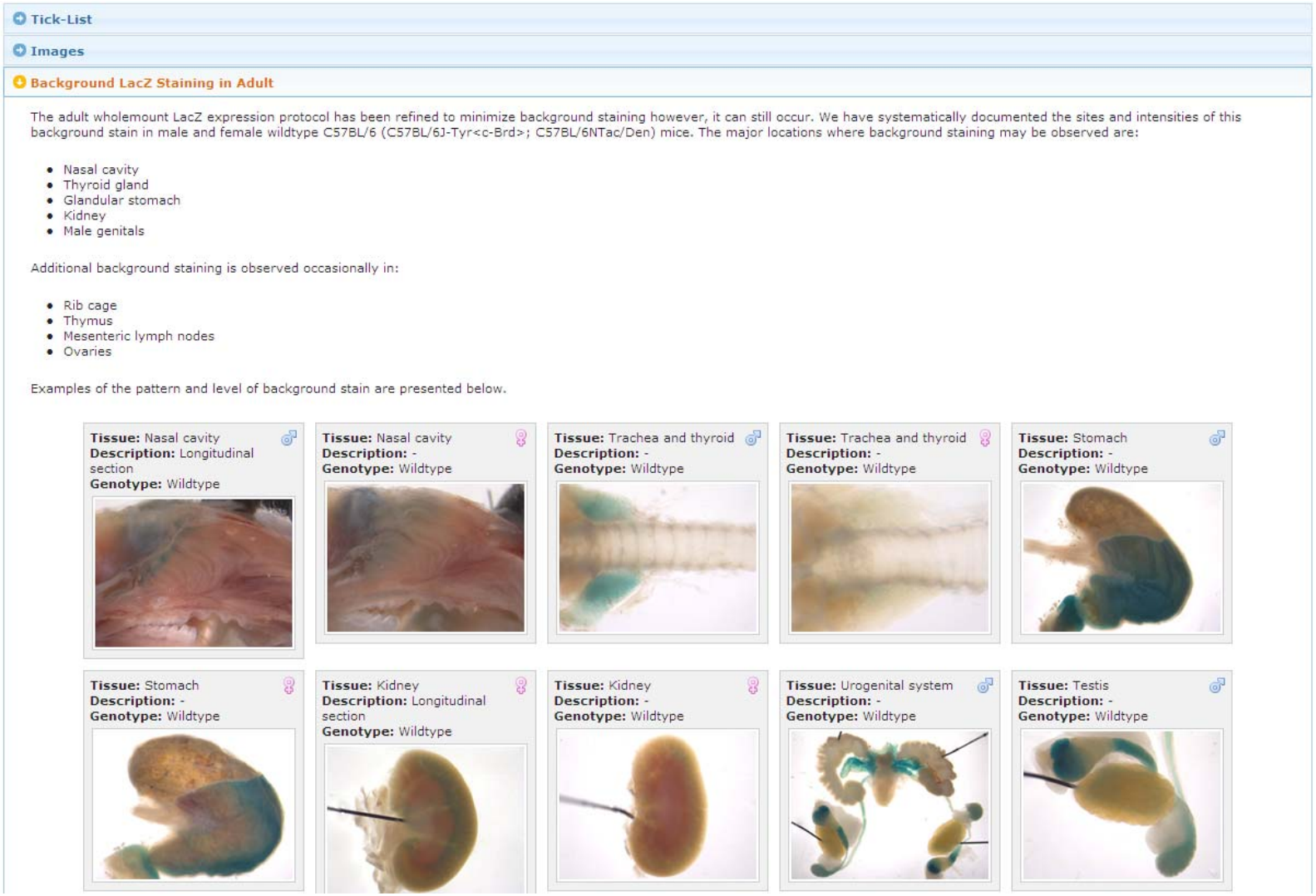
Colony Name	Appl2 Knockout First EPD0101_4_F09	Appl2 Knockout First EPD0101_4_F09	Appl2 Knockout First EPD0101_4_F09
Genotype	Appl2/+	Appl2/+	Appl2/+
Gender	Male	Male	Female
Age In Weeks	8.8	5.5	5.9
Adrenal Gland	✓	✓	✓
Bone	✓	✓	✓
Brain	✓	✓	✓
Brown Adipose Tissue	✗	✗	✗
Cartilage	✓	✓	✓
Colon	✗	✗	✗
Eye	*ambiguous*	✓	✓
Gall Bladder	✗	✓	✓
Heart	✓	✓	✓
Kidney	✓	✓	✓

11. Open the Images by clicking the bar of the same name. Note this action causes the Tick-List to roll up. Thumbnails of all available images are presented, annotated with the tissue, description, genotype and sex of the animal.



12. To view a larger version of any image, click the associated thumbnail image. This opens a window that allows you to scroll through all available *lacZ* expression images and provides additional annotation including the age of the mouse and the adult Mouse Anatomy (MA) term used to describe the observed expression pattern.

13. Open the Background *lacZ* Staining in Adults by clicking the bar of the same name. Note this action causes the Tick-list and Image panels to roll up. This page contains static content summarising the background *lacZ* staining that is routinely observed in wild type adult mice using this wholemount protocol. This information is important when interpreting expression profiles.



14. Limited Embryo expression (E14.5 wholemount) is available via the Embryo *lacZ* Expression cell on the Phenotyping Test Based Heatmap. Expression is simply recorded as *lacZ* present, absence, ambiguous or no data, with no further granularity. Clicking the Images bar opens all images collected. These can be viewed as described above (steps 11-12).