

Sanger Mouse Portal “How to” Guide

How to view a summary of all phenotyping data

1. From the Sanger Mouse Portal home page (<http://www.sanger.ac.uk/mouseportal/>), under **Phenotyping Overview**, click on “[Download](#) a heat map of phenotyping results by assay”:

The screenshot shows the Sanger Mouse Portal website. At the top left is the Wellcome Trust Sanger Institute logo. To the right is the text 'A- A A+'. Below the logo is a navigation bar with 'HOME', 'BROWSE', 'HELP', and 'ABOUT'. A search bar is located below the navigation bar with the text 'Enter gene/product identifiers or phenotyping test names (e.g. Mysz1, EPD0019_1_A05 or Dexa) or any other search term described in the help section.' Below the search bar is the 'About This Portal' section, followed by the 'Phenotyping Summary' section which contains a table with three rows: 'Comprehensive Phenotyping Substantively Complete' (564), 'Infection Challenge (Salmonella and Citrobacter)' (495), and 'LacZ Expression (Adult and E14.5)' (339). Below this is the 'Other Data Summary' section with a table showing the number of unique genes for various product types. To the right of the 'Phenotyping Summary' section is the 'Phenotyping Overview' section, which is highlighted with a red box. It contains a link to 'Download a heat map of phenotyping results by assay' and a description of the spreadsheet. Below this is a note about accessing data via the MGP Phenotyping BioMart and a 'NEW' section about disease predictions. At the bottom of the 'Phenotyping Overview' section is a mailing list sign-up link.

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.

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



- This opens an excel spreadsheet containing a colour coded heat map style summary of all phenotyping data. Details of each mutant mouse line are listed in columns A-C, one row representing one unique mutant mouse line:
 - Colony Prefix (column A): Unique identifier for the mutant mouse line
 - Allele Name (column B): Full allele name carried by the mutant mouse line
 - Strain (column C): Genetic background upon which the mutant mouse line was phenotyped

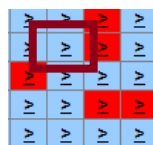
Colony Prefix	Allele Name	Strain	Viability at weaning	Recessive Lethal Study	Fertility	Embryo LacZ Expression	Adult LacZ Expression	General Observations	Weight Curves	Open Field	Modified SHIRPA	Grip Strength	Hot Plate	Dysmorphology	Rotarod	Non-Invasive Blood Pressure	Prepulse Inhibition	Indirect Calorimetry	Glucose Tolerance (ip)	Auditory Brainstem Response	Body Composition (DEXA)	X-ray Imaging	Stress Induced Hyperthermia	Eye Morphology	Plasma Chemistry	Plasma Immunoglobulins	Haematology (CBC)	Peripheral Blood Lymphocytes	Micronuclei	Tissue Biobank	Heart Weight	Heart Histology	Tail Epidermis Wholemount	Skin Histopathology	Brain Histopathology	Eye Histopathology	MicroCT & Quantitative Faxitron	Salmonella Challenge	Citrobacter Challenge	
MBAU	Sparc<tm1a(EUCOMM)	C57BL/6	IV	IV	IV	IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	
MBAX	Spnb2<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBBC	Mapk1<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBBM	Sympk<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBBQ	Ninl<tm1a(EUCOMM)Wt	C57BL/6	IV	IV	IV	IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBBS	Prmt1<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBBV	Lmnb1<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBBZ	Smc3<tm1a(EUCOMM)	C57BL/6	IV	IV	IV	IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCB	Ldha<tm1a(EUCOMM)W	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCD	Sms<tm1a(EUCOMM)W	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCH	Ncaph2<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCK	Atp5a1<tm1a(EUCOMM)	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCL	Pfkf1<tm1a(EUCOMM)Wt	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCQ	Kdm4b<tm1a(EUCOMM)	C57BL/6	IV	IV	IV	IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCS	Myh9<tm1a(EUCOMM)W	C57BL/6	IV	IV		IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV
MBCU	Prmt3<tm1a(EUCOMM)	C57BL/6	IV	IV	IV	IV	IV		IV	IV	IV	IV	IV	IV	IV			IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV

- The remaining columns represent each of the phenotyping tests performed by the Sanger Mouse Genetics Project

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4. The legend explaining the colour code used to summarise the outcome of each mutant mouse line/phenotypic test combination can be found to the right of the spreadsheet and is copied below:

LEGEND	
	Test complete and data/resources are available
	Test is complete and the data are considered interesting
	Preliminary indication of an interesting phenotype
	Test is complete but the data are not considered interesting
	Test not performed or applicable e.g. no lacZ reporter therefore no expression
	Test abandoned
	Test pending
	Link to a phenotyping test report page



5. Clicking on any \geq symbol opens the web page on the Sanger Mouse Portal describing the standard protocol and parameters collected for that mutant mouse line/phenotypic test combination.

Glucose Tolerance (ip) Data for Sptbn1 (MBAX)

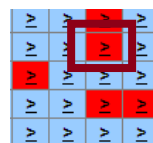
Standard Protocol

ipGTT (week 13) [Mice were fed on High Fat Diet (21.4% crude fat content, Western RD, 829100, Special Diets Services) from 4 weeks of age]: Mice are fasted overnight (maximum of 16 hours) before the glucose tolerance test. A fasting blood sample is taken before a bolus of glucose is administered by intra-peritoneal injection. Blood samples are tested for glucose concentration (Accu-Check Aviva, Roche) at 15, 30, 60 and 120 minutes following the glucose administration, and data presented as plasma glucose concentration.

view legend

Parameter	Female Het	Male Het	population parameter	Graph	MP Annotation
ip-GTT					
Fasted Plasma Glucose					

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6. Where the test is complete and the data are considered interesting (red cells), the \geq link opens the web page on the Sanger Mouse Portal describing the standard protocol, listing the parameters collected and the Mammalian Phenotype (MP) annotations assigned to describe each observed phenotype, and providing a link to view the graph for each parameter considered significant.



A- A A+

Mouse Resources Portal

HOME BROWSE HELP ABOUT

Body Composition (DEXA) Data for Sms (MBCD)

Standard Protocol - significant parameters

DEXA (week 14) [Mice were fed on High Fat Diet (21.4% crude fat content, Western RD, 829100, Special Diets Services) from 4 weeks of age]: Mice are anaesthetised and imaged on a dual energy X-ray absorptiometry machine (Lunar PIXImus II). This generates an image of the entire mouse and provides bone mineral and body composition data.

view legend


Legend - hover over each heading to get a more complete description

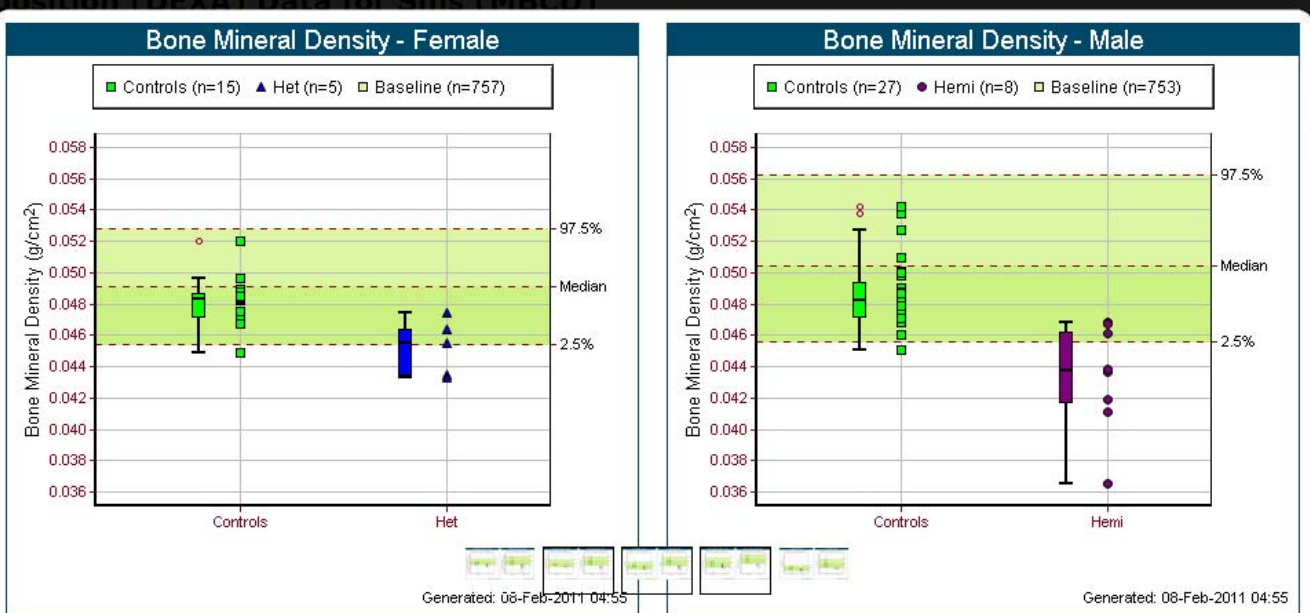
- Test complete and data/resources are available
- Test is complete and the data are considered interesting
- Preliminary indication of an interesting phenotype
- Test is complete but the data are not considered interesting
- Test not performed or applicable
- Test pending
- Test abandoned

Parameter	Female Het	Male Hemi	population parameter	Graph	MP Annotation
Bone Mineral Density				view graph	MP:0000063 - decreased bone mineral density
Bone Mineral Content				view graph	MP:0010124 - decreased bone mineral content
Body Weight				view graph	MP:0001262 - decreased body weight
Nose to Tailbase Length				view graph	MP:0001258 - decreased body length
Lean Mass				view graph	MP:0003961 - decreased lean body mass
Fat Mass					
Fat Percentage Estimate					



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- Click on the  view graph icon to open a window that allows you to scroll through graphs of data from both sexes for each significant parameter.



Bone Mineral Density - Female

■ Controls (n=15) ▲ Het (n=5) □ Baseline (n=757)



Bone Mineral Density - Male

■ Controls (n=27) ● Hemi (n=8) □ Baseline (n=753)

Protocol	Parameter	Female Het	Male Hemi	population parameter	MP Annotation
Standard Protocol	Bone Mineral Density	■	■		MP:0000063 - decreased bone mineral density

view data download data

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8. The raw data from mutant mice (Subjects), wildtype mice run on the same week as the mutants (Controls) and, where appropriate, all age, sex, genetic background and pipeline matched wildtype mice (Baseline) are viewable by clicking the  view data icon.
9. The raw data from mutant mice (Subjects), wildtype mice run on the same week as the mutants (Controls) and, where appropriate, all age, sex, genetic background and pipeline matched wildtype mice (Baseline) can be downloaded as an XML document by clicking the  download data icon.