Extracting Mouse Genetic Project ontology calls

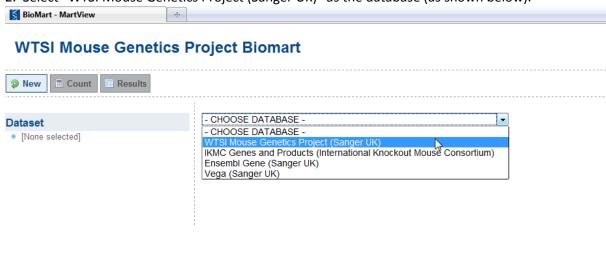
Introduction:

Raw and summary phenotyping data is available through a publicly available BioMart¹ interface. This can be accessed at the following web address http://www.sanger.ac.uk/htgt/biomart. Mouse Genetics Project data which has passed all necessary internal quality control checks is automatically published to this BioMart within 24 hours. Below are two step-wise examples of how to extract the summary data using the standard BioMart user interface. The first looks at how to extract data for a knockout line. The second demonstrates how to search for all knockout lines associated with a mammalian phenotype ontology term within the Mouse Genetics Project. Further information on using a BioMart can be found at: http://bowtie-bio.sourceforge.net/recount/biomaRt.pdf.

How to extract ontology calls for a knockout line?

The following example demonstrates the extraction of Mammalian Phenotype Ontology (MP) calls associated with the Mysm1 knockout line.

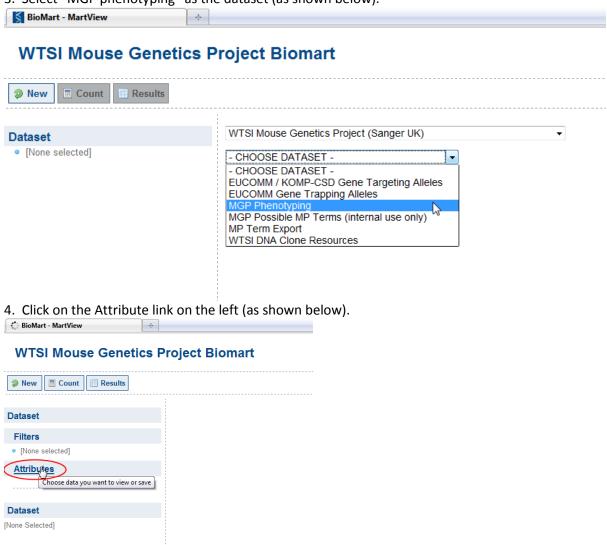
- 1. Open the BioMart by following the link: http://www.sanger.ac.uk/htgt/biomart.
- 2. Select "WTSI Mouse Genetics Project (Sanger UK)" as the database (as shown below).







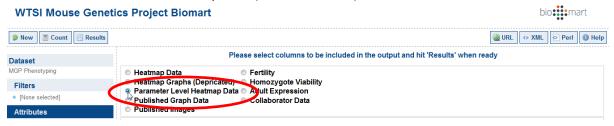
3. Select "MGP phenotyping" as the dataset (as shown below).



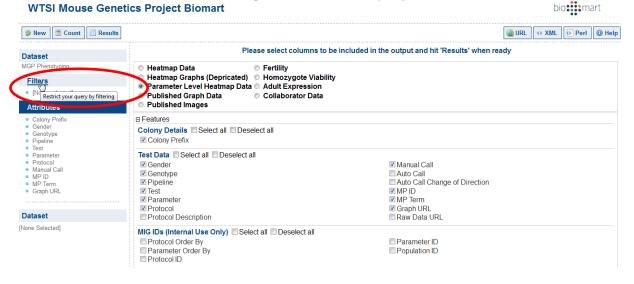




5. Select Parameter Level Heatmap Data (as shown below).



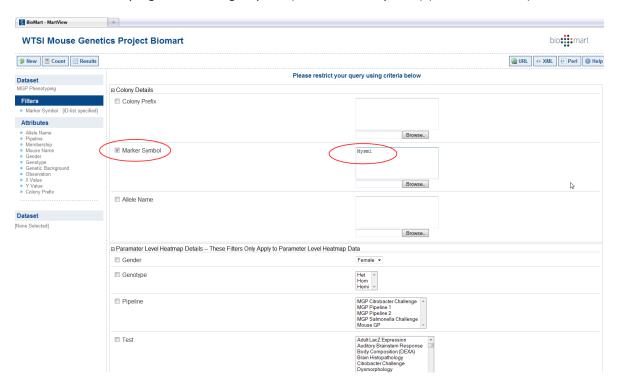
6. Now click on Filters to access a dialog box to restrict the query (as shown below). WTSI Mouse Genetics Project Biomart







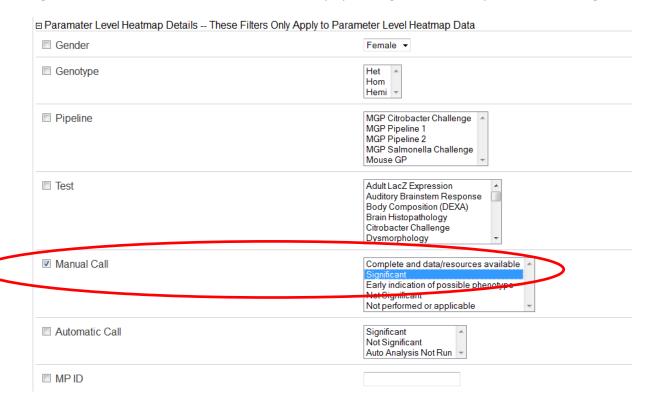
7. Filter the data by a gene name e.g. Mysm1 (a.k.a. Marker symbol) (as shown below).







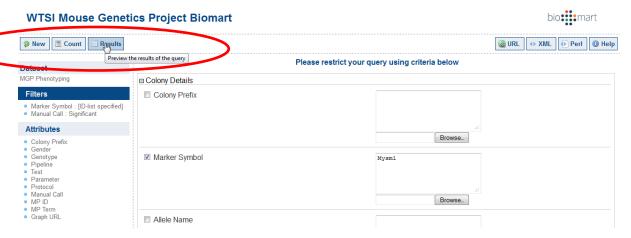
8. To isolate the significant phenotype traits, select Manual Call as a filter and Significant as the setting. Alternatively both the Significant and Not Significant filters could be selected simultaneously by holding the control key down and clicking on the terms.



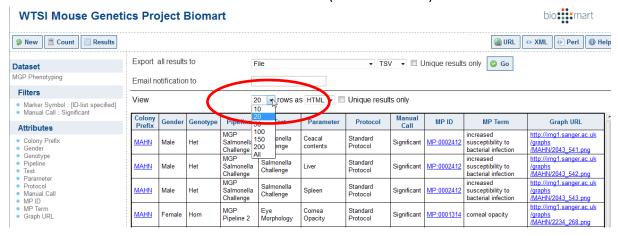




9. Click on the Results button (as shown below) to filter as specified.



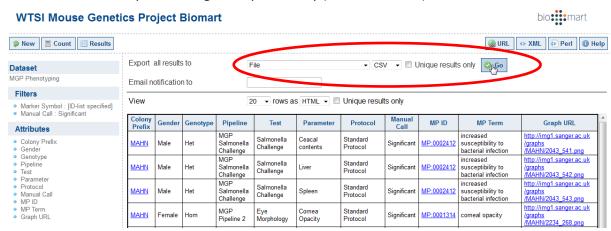
10. Edit the number of rows shown to view the data (as shown below).







11. Results can be exported using the export facility (as shown below).



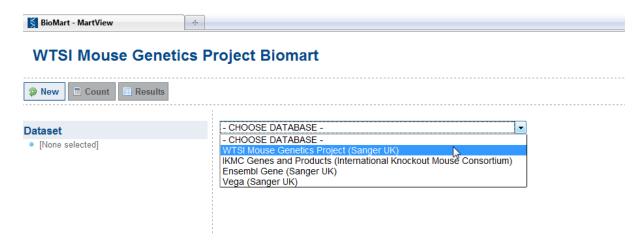




How to extract colonies with hits for a mammalian ontology term?

The following example, demonstrates the extraction of colonies associated with Mammalian Phenotype ontology terms within the Mouse Genetics Project.

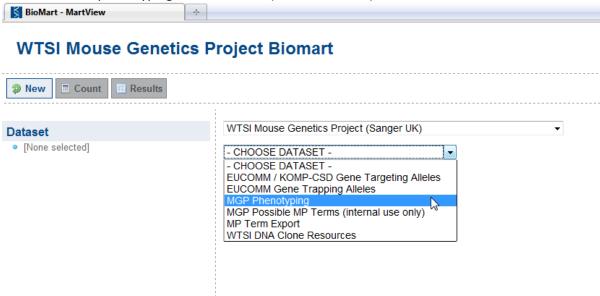
- 1. Open the BioMart by following the link: http://www.sanger.ac.uk/htgt/biomart.
- 2. Select "WTSI Mouse Genetics Project (Sanger UK)" as the database (as shown below).



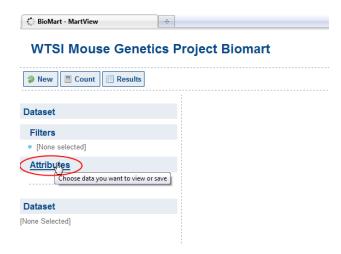




3. Select "MGP phenotyping" as the dataset (as shown below).



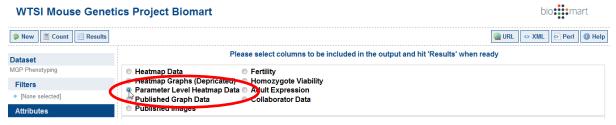
4. Click on the Attribute link on the left (as shown below).



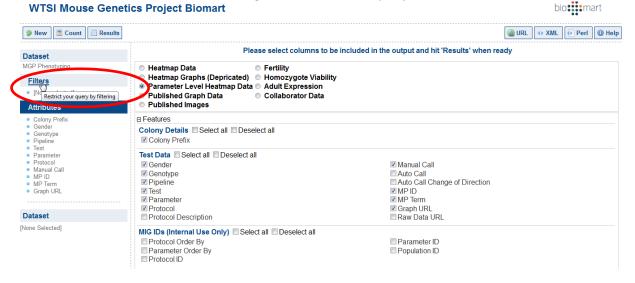




5. Select Parameter Level Heatmap Data (as shown below).



6. Now click on Filters to access a dialog box to restrict the query (as shown below). WTSI Mouse Genetics Project Biomart







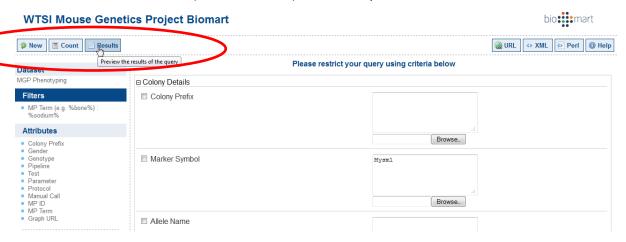
7. We can filter the data to see which colonies are associated with which mammalian phenotype terms. Exact MP terms can be searched using the filter MP ID (see http://www.informatics.jax.org/searches/MP_form.shtml for a browser showing possible terms and MP ID's). Alternatively the filter MP Term can be used with % as wildcard symbols e.g. %sodium% (as shown below).

□ Test	Adult LacZ Expression Auditory Brainstem Response Body Composition (DEXA) Brain Histopathology Citrobacter Challenge Dysmorphology
■ Manual Call	Complete and data/resources available Significant Early indication of possible phenotype Not Significant Not performed or applicable
☐ Automatic Call	Significant Not Significant Auto Analysis Not Run
■ MP ID	
☑ MP Term (e.g. %bone%)	%sodium%

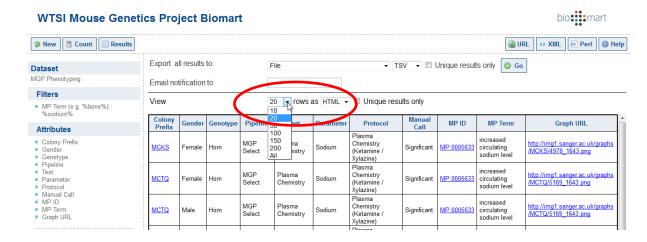




8. Click on the Results button (as shown below) to filter as specified.



9. Edit the number of rows shown to view the data (as shown below).







10. Results can be exported using the export facility (as shown below).

