A UCI TMF TUTORIAL: FINDING TARGETING VECTORS AND DOWNLOADING SEQUENCE FOR A MUTANT ALLELE OF YOUR GENE OF INTEREST VIA THE INTERNATIONAL KNOCKOUT MOUSE CONSORTIUM (IKMC) MARTSEARCH WEB PAGE



Viewing IKMC Data in Ensembl

Most of the products/data found within this portal can also be viewed as DAS tracks in the Ensembl genome browser. Follow these links to have the tracks automatically activated for you:

CIKMC alleles in Ensembl Mouse CIKMC alleles on orthologous genes in Ensembl Human

Federated Searches

The links below take you to the standard MartView interface for several examples of federated queries:

- 1. Find all IKMC targeted ES cells for genes encoding transcription factors on Chromosome 1. (This query joins IKMC Projects/Alleles to Ensembl).
- 2. Find all IKMC mice available from the EMMA Repository with information on the vector used to make the mutation. (This query joins IKMC Targeting Repository to Mouse Production data).
- 3. Find all IKMC targeted ES cells for genes expressed in heart. (This query joins IKMC Projects/Alleles to EurExpress).

The Biomarts

This portal integrates information on IKMC mouse knockout resources with numerous other relevant datasets, including Ensembl, Europhenome, EurExpress and EMMA. For more information about this portal and the way in which it unites and searches the data, please see the about page.



Information for Developers

All the code and data that we produce is open-source and free to use. The following links will guide you to our source-code and documentation on how you can interact with the services we provide.

- · All the code used to create this portal
- The ruby API used to interact with the Biomarts
- · Using our search engine in your application

The results page



The Project Report page – more details of the mutant alleles



Currently, two types of targeted alleles are available. Both alleles are "mutant first"; i.e. the presence of the [splice acceptor – IRES- lacZ – poly A] cassette may result in a truncated, non-functional protein product. The locus can be reverted to a nearly wildtype sequence by expression of FIp recombinase, which will excise sequences between the Frt sites. In the case of the "conditional potential" allele, this will leave one or more exons of the gene flanked by two loxP sites ("floxed"). Expression of cre recombinase should cause deletion of the (in this example) two floxed exons. The location of the loxP sites is designed to generate a frame-shift mutation that should result in degradation of any remaining mRNA via nonsense-mediated decay (NMD) systems.



Details of the predicted mutant allele in GenBank format

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Next, import your saved ".txt" file into Lasergene suite's "EditSeq" application



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