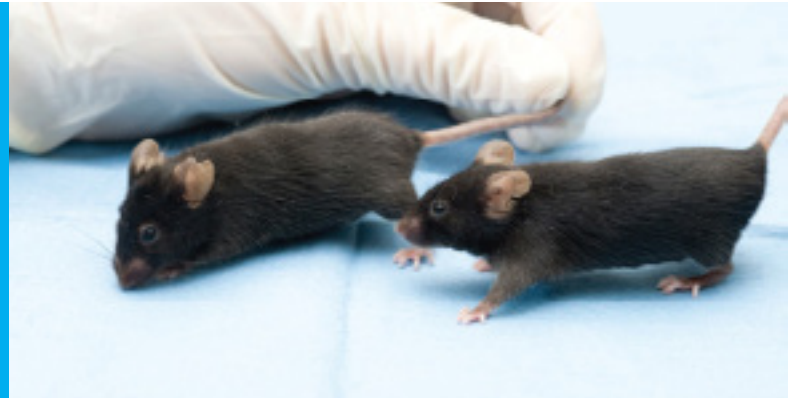


MOUSE LINKAGE MARKER SET

The mouse linkage marker set panel contains over 550 SNPs with an average distance of 3-5cM across the mouse genome and provides approximately 300 informative markers between common mouse crosses.



The Mouse Linkage Market Set (MLMS) SNP panel is run using our NATA-accredited SNP genotyping service. The SNPs have been carefully selected to maximise the polymorphism between common inbred strains.

Applications

- Speed congenics
- Preferential animal selection for breeding
- Validation of in-house mouse strains, ensuring consistency with established reference strains
- Combine with our fine mapping service to map mouse genome targeted regions

Key Benefits

This panel can preferentially select animals carrying the locus of interest for further breeding by identifying the highest percentage of recipient versus donor strain DNA. This accelerates the speed of congenic strain production. Utilising traditional, random backcrossing methods, it would take 10 generations (upwards of 2.5 years) to produce a comparable congenic strain.

Common Strains Covered

Visit our website to learn more about common strains covered by the MLMS panel and how many informative SNPs between common mouse strains.

Speed Congenics Overview

A congenic strain is identical to a reference strain at all genetic loci except one. The differing locus is usually the transgene or knockout region of interest. Congenic strains are widely used in biomedical research because they reduce genetic variability and provide insight into the contribution of genetic background to phenotype.

Service Access

Submission format

- Minimum submission of 10 samples
- Samples to be arrayed in 96 v well plates

DNA requirement

- 100ul concentration 10ng/ul
- A260/A280 between 1.6-2.0
- Our DNA extraction service is available

Data Analysis

Results are reported as an Excel spreadsheet of genotypes. Also included is a percentage similarity to the backcross strain.



Our funding partners

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