



Background Characterization

A key feature of a genetic model is a defined background. The purity of a strain or line should be determined before beginning experiments.

NOD/SCID Testing

Non-obese diabetes (NOD) is a polygenic recessive mutation with several loci contributing to this phenotype. Charles River, utilizing microsatellite analysis, is able to identify markers linked to these loci allowing for verification of the disease state. Severe combined immunodeficiency (SCID) is the result of a spontaneous autosomal recessive mutation. Charles River can confirm the presence or absence of this point mutation using PCR.

Colony Maintenance

Take advantage of Charles River's experienced, highly trained workforce for animal breeding, boarding, backcrossing, intercrossing and development of homozygous colonies.

Genotyping and Zygosity Testing

Determination of two-fold difference in copy number between hemi- or hetero- and homozygote status of knockout and transgenic rodents using quantitative PCR (Q-PCR) methods.

Phenotyping

Comprehensive full-life evaluation of clinical signs and attributes, growth and breeding performance, necropsy with organ weight, histopathology and clinical chemistry.

Expression Testing

Estimation of the level of expression from a transgene or knockout construct using reverse transcription quantitative PCR (RT-QPCR) methods to quantify the level of RNA production within an animal model.

MAX-BAX

Charles River speed congenic services uses microsatellite analysis to reduce the number of generations needed to move transgenes or knockout constructs onto different inbred backgrounds.