TransnetYX®

Safeguarding Your Vital Colonies and Promoting Responsible and Reproducible Research

Getting your colonies off to the right start is critical! Furthermore promoting best practice, the 3Rs and adherence with the ARRIVE 2.0 guidelines. The miniMUGA panel consists of over 10,000 SNPs and includes diagnostic markers for over 241 classically inbred strains and sub-strains, we are committed to ensuring the Genetic Integrity of your lines.

Data provided by the miniMUGA panel includes:

- Genotyping Quality
- Chromosomal Sex
- Inbreeding Estimate
- Inbreeding and Genotyping Quality
- Constructs Detected
- Primary Background
- Secondary Background
- Background Ideogram
- Backgrounds Detected

miniMUGA - making it affordable and feasible for all researchers to perform this critical background check, all for just *$40!*

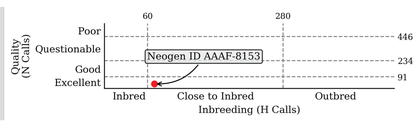
"to avoid problems related to an insufficiently defined genetic background, we advocate that for each study involving genetically modified mice, at least a detailed description of the origin and genetic background of both the WT control and the altered strain of mice is essential."
Geurts et al 2011, Insufficiently Defined Genetic Background Confounds Phenotypes in Transgenic Studies As Exemplified by Malaria Infection in Tlr9 Knockout Mice

Avoid the consequences of using contaminated lines:

- Animal waste
- Research cannot be reproduced
- Wasted time
- Increased costs with studies that have to be repeated
- Impact on personal and institutional reputation

A Recent Example from the University of Oxford

Inbreeding and Genotyping Quality (Plot)



As a result of our initial quality control check, sample quality is determined along with a visual guide to determine sample heterozygosity.

Constructs Detected

BlastR	bpA	Cas9	chlor	Cre	DTA	g_FP	hCMV_	hCMV_	hTK_p	iCre	IRES	Luc	r_FP	rtTA	SV40	tTA
-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-

The miniMUGA screens for the presence of 17 common genetic constructs, allowing many customers to detect them (expected/unexpected), particularly useful when importing, sharing, or freezing down lines.

Backgrounds Detected (Diagnostic Alleles)

Substrain	Homozygous	Heterozygous	Potential	% Observed
C57BL/6J	10	27	156	23.7%
B6N-Tyr<c-Brd>/BrdCrCrl	12	4	31	51.6%

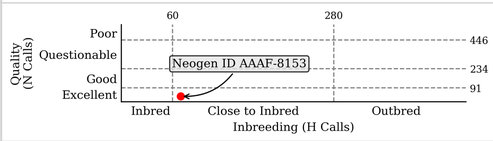
Diagnostic Alleles Observed

Strain Group	Homozygous	Heterozygous	Potential	% Observed
C57BL/6 (B6N-Tyr/BrdCrCrl, C57BL/6J, C57BL/6JEiJ, C57BL/6JOlaHsd, C57BL/6NCrl, C57BL/6NHsd, C57BL/6NJ, C57BL/6NRj, C57BL/6NTac)	3	3	21	28.6%

A concise break down of background(s) detected from a panel of 241 classically inbred strains and substrains, including details of primary and secondary backgrounds (where detected).

The above example was of a recently imported line to Oxford which the mouse passport suggested was a pure C57BL/6J. The miniMUGA identified that the mouse was actually on a mixed background, which would have led to wasted research and impacted animal welfare.

MiniMUGA Background Analysis v0009

Sample ID	M01920802
Neogen ID	AAAF-8153
Summary	The genotype of this sample is of **excellent** quality. It is **female** and **close to inbred**. However, the MiniMUGA report algorithm cannot explain this sample with current parameters. Either the sample includes a strain that is not present in the current MiniMUGA reference set, at least three genetic backgrounds are required to explain ≥99.8% of this sample, or the genotyping quality precludes a correct analysis of the sample background (particularly in samples from standard commercial inbred strains). Diagnostic SNPs indicate the presence of the background strain groups **C57BL/6** and the substrains **B6N-Tyr<c-Brd>/BrdCrCrl, C57BL/6J**. The sample contains the following genetic constructs: **"Greenish" Fluorescent Protein (EGFP, EYFP, ECFP)**
Genotyping Quality	**Excellent (29 N calls)** All reported results are dependent on genotyping quality.
Chromosomal Sex	XX
Inbreeding Estimate	Close to Inbred (71 H calls at autosomal, X, and PAR chromosome markers)
Inbreeding and Genotyping Quality (Plot)	
Constructs Detected	BlastR: - ; bpA: - ; Cas9: - ; chlor: - ; Cre: - ; DTA: - ; g_FP: + ; hCMV_a: - ; hCMV_b: - ; hTK_pr: - ; iCre: - ; IRES: - ; Luc: - ; r_FP: - ; rtTA: - ; SV40: - ; tTA: -
Primary Background (Autosomes, X Chromosome)	Not Applicable (Primary + Secondary Backgrounds < 99.8% or genotyping quality precludes correct background analysis)
Secondary Background (Autosomes, X Chromosome)	Not Applicable (Primary + Secondary Backgrounds < 99.8% or genotyping quality precludes correct background analysis)
Y Chromosome	Not Applicable
MT Chromosome	MT Haplogroup 1 - 100.0% Consistent Includes B6N-Tyr/BrdCrCrl and 158 other strains
Background Ideogram	Not Applicable
Backgrounds Detected (Diagnostic Alleles)	Diagnostic Alleles Observed Substrain: C57BL/6J — Homozygous 10, Heterozygous 27, Potential 156, % Observed 23.7% Substrain: B6N-Tyr<c-Brd>/BrdCrCrl — Homozygous 12, Heterozygous 4, Potential 31, % Observed 51.6% Diagnostic Alleles Observed Strain Group: C57BL/6 (B6N-Tyr/BrdCrCrl, C57BL/6J, C57BL/6JEiJ, C57BL/6JOlaHsd, C57BL/6NCrl, C57BL/6NHsd, C57BL/6NJ, C57BL/6NRj, C57BL/6NTac) — Homozygous 3, Heterozygous 3, Potential 21, % Observed 28.6%
Refined Analysis	Not Applicable
Refined Ideogram	Not Applicable

YX Genetic Monitoring