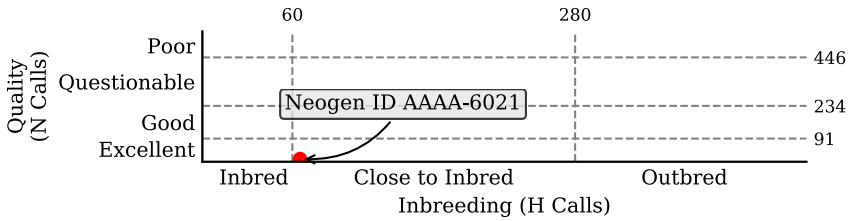
MiniMUGA Background Analysis v0008

Sample ID	Shiota/GCGRSR CR.58
Neogen ID	AAAA-6021
Summary	The genotype of this sample is of excellent quality. It is male and close to inbred, and likely a mix of multiple C57BL/6 substrains and 129S6/SvEvTac. Diagnostic SNPs indicate the presence of the background strain groups C57BL/6 and the substrains C57BL/6J. The sample contains the following genetic constructs: Bovine growth hormone poly A signal sequence, Cre recombinase, hCMV enhancer version a, hCMV enhancer version b, "Reddish" fluorescent protein (tdTomato, mCherry)
Genotyping Quality	Excellent (2 N calls) All reported results are dependent on genotyping quality.
Chromosomal Sex	XY
Inbreeding Estimate	Close to Inbred (66 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
-	+	-	-	+	-	-	+	+	-	-	-	-	+	-	-	-

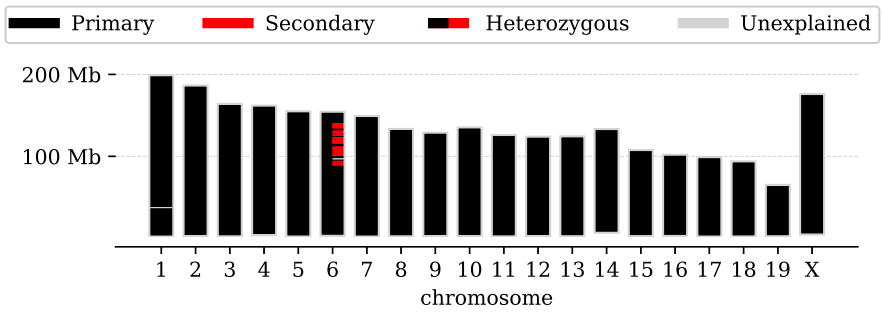
Primary Background (Autosomes, X Chromosome)

Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded
multiple C57BL/6 substrains	9721	9245 (99.4%)	1 (0.0%)	56 (0.6%)	419

Secondary Background (Autosomes, X Chromosome)

Strain	Total	Explained	Unexplained	Excluded
129S6/SvEvTac	57 55 Clustered	55 (0.6%) 55 Clustered	2 (0.0%) 0 Clustered	0 (0.0%)

Background Ideogram



Backgrounds Detected (Diagnostic Alleles)

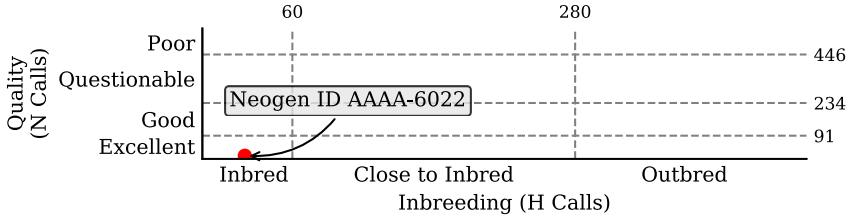
	Diagnostic Alleles Observed			
Substrain	Homozygous	Heterozygous	Potential	% Observed
C57BL/6J	144	7	156	96.8%
Strain Group	**Homozygous**	**Heterozygous**	**Potential**	**% Observed**
C57BL/6 (B6N-Tyr/BrdCrCrl, C57BL/6J, C57BL/6JBomTac,	5	1	21	28.6%

C57BL/6JEiJ, C57BL/6JOlaHsd)

MiniMUGA Background Analysis v0008

Sample ID	Shiota/GCGRSR CR.59
Neogen ID	AAAA-6022
Summary	The genotype of this sample is of excellent quality. It is male and inbred, and likely a mix of multiple C57BL/6 substrains and 129S6/SvEvTac. Diagnostic SNPs indicate the presence of the background strain groups C57BL/6 and the substrains C57BL/6J. The sample contains the following genetic constructs: Cre recombinase
Genotyping Quality	Excellent (3 N calls) All reported results are dependent on genotyping quality.
Chromosomal Sex	XY
Inbreeding Estimate	Inbred (23 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
-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-

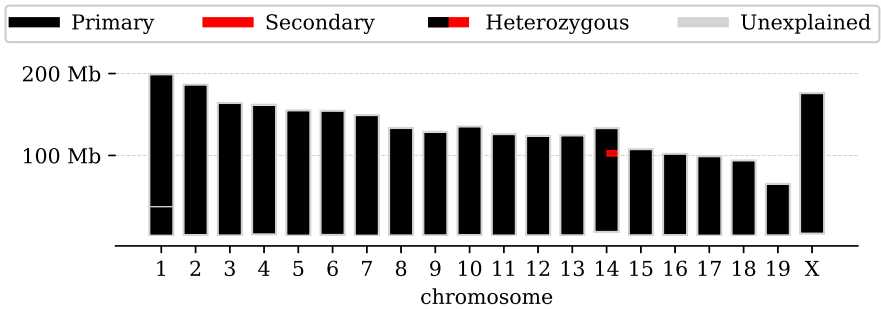
Primary Background (Autosomes, X Chromosome)

Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded
multiple C57BL/6 substrains	9721	9289 (99.9%)	1 (0.0%)	11 (0.1%)	420

Secondary Background (Autosomes, X Chromosome)

Strain	Total	Explained	Unexplained	Excluded
129S6/SvEvTac	12 11 Clustered	11 (0.1%) 11 Clustered	1 (0.0%) 0 Clustered	0 (0.0%)

Background Ideogram



Backgrounds Detected (Diagnostic Alleles)

Substrain	Diagnostic Alleles Observed			
	Homozygous	Heterozygous	Potential	% Observed
C57BL/6J	142	10	156	97.4%
Strain Group	**Homozygous**	**Heterozygous**	**Potential**	**% Observed**
C57BL/6 (B6N-Tyr/BrdCrCrl, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd)	6	0	21	28.6%