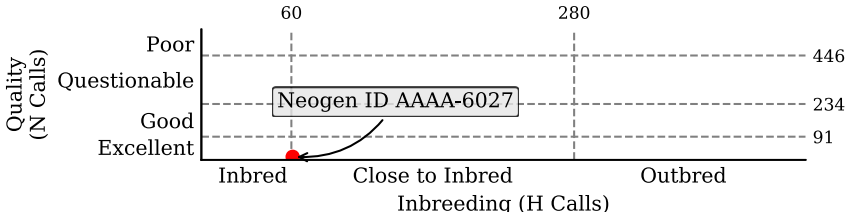
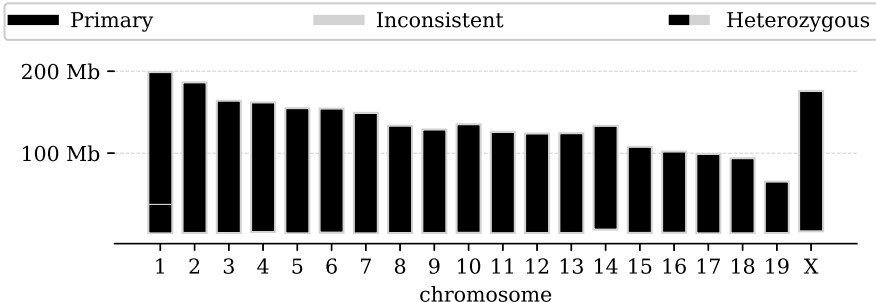
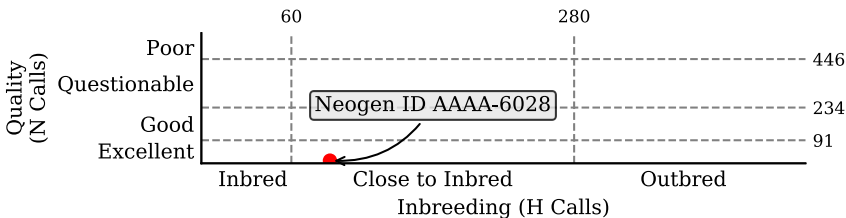


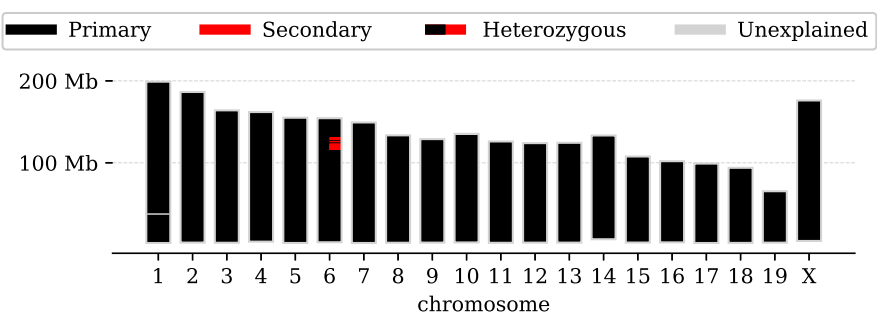
MiniMUGA Background Analysis v0008

Sample ID	Magnuson/B6.CG. Zfhx4.1																																																	
Neogen ID	AAAA-6027																																																	
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.																																																	
	Diagnostic SNPs indicate the presence of the background strain groups C57BL/6 and the substrains C57BL/6J.																																																	
	No genetic constructs were detected in this sample.																																																	
Genotyping Quality	Excellent (3 N calls) All reported results are dependent on genotyping quality.																																																	
Chromosomal Sex	XY																																																	
Inbreeding Estimate	Close to Inbred (61 H calls at autosomal, X, and PAR chromosome markers)																																																	
Inbreeding and Genotyping Quality (Plot)																																																		
Constructs Detected	<table><tr><td>BlastR</td><td>bpA</td><td>Cas9</td><td>chlor</td><td>Cre</td><td>DTA</td><td>g_FP</td><td>hCMV_a</td><td>hCMV_b</td><td>hTK_pr</td><td>iCre</td><td>IRES</td><td>Luc</td><td>r_FP</td><td>rtTA</td><td>SV40</td><td>tTA</td></tr><tr><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td></tr></table>																BlastR	bpA	Cas9	chlor	Cre	DTA	g_FP	hCMV_a	hCMV_b	hTK_pr	iCre	IRES	Luc	r_FP	rtTA	SV40	tTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
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)	<table><tr><td>Strain</td><td>Total</td><td>Consistent</td><td>Inconsistent</td><td>Heterozygous</td><td>Excluded</td></tr><tr><td>multiple C57BL/6 substrains</td><td>9721</td><td>9300 (100.0%)</td><td>1 (0.0%)</td><td>0 (0.0%)</td><td>420</td></tr></table>																Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded	multiple C57BL/6 substrains	9721	9300 (100.0%)	1 (0.0%)	0 (0.0%)	420																						
Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded																																													
multiple C57BL/6 substrains	9721	9300 (100.0%)	1 (0.0%)	0 (0.0%)	420																																													
Secondary Background (Autosomes, X Chromosome)	Not Applicable																																																	
Background Ideogram																																																		
Backgrounds Detected (Diagnostic Alleles)	Diagnostic Alleles Observed																																																	
	Substrain					Homozygous					Heterozygous					Potential	% Observed																																	
	C57BL/6J					88					48					156	87.2%																																	
	Strain Group					Homozygous					Heterozygous					Potential	% Observed																																	
	C57BL/6					4					2					21	28.6%																																	
(B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd, C57BL/6NCrI, C57BL/6NHsd, C57BL/6NJ, C57BL/6NRj, C57BL/6NTac)																																																		

MiniMUGA Background Analysis v0008

Sample ID	Magnuson/B6.CG. Zfhx4.2																																																																																																																																																																						
Neogen ID	AAAA-6028																																																																																																																																																																						
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 (129P2/OlaHsd and/or 129P3/J and/or 129S1/SvImJ and/or 129S2/SvHsd and/or 129S2/SvPasOrlRj and/or 129S4/SvJaeJ and/or 129S6/SvEvTac and/or 129T2/SvEmsJ and/or 129X1/SvJ).																																																																																																																																																																						
	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, "Greenish" Fluorescent Protein (EGFP, EYFP, ECFP), hCMV enhancer version a, hCMV enhancer version b																																																																																																																																																																						
The sample may contain the following genetic constructs: Cas9																																																																																																																																																																							
Genotyping Quality	Excellent (2 N calls) All reported results are dependent on genotyping quality.																																																																																																																																																																						
Chromosomal Sex	XY																																																																																																																																																																						
Inbreeding Estimate	Close to Inbred (90 H calls at autosomal, X, and PAR chromosome markers)																																																																																																																																																																						
Inbreeding and Genotyping Quality (Plot)																																																																																																																																																																							
Constructs Detected	<table><tr><td>BlastR</td><td>bpA</td><td>Cas9</td><td>chlor</td><td>Cre</td><td>DTA</td><td>g_FP</td><td>hCMV_a</td><td>hCMV_b</td><td>hTK_pr</td><td>iCre</td><td>IRES</td><td>Luc</td><td>r_FP</td><td>rtTA</td><td>SV40</td><td>tTA</td></tr><tr><td>-</td><td>+</td><td>?</td><td>-</td><td>-</td><td>-</td><td>+</td><td>+</td><td>+</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td></tr></table>																	BlastR	bpA	Cas9	chlor	Cre	DTA	g_FP	hCMV_a	hCMV_b	hTK_pr	iCre	IRES	Luc	r_FP	rtTA	SV40	tTA	-	+	?	-	-	-	+	+	+	-	-	-	-	-	-	-	-																																																																																																																				
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)	<table><tr><td colspan="6">Strain</td><td>Total</td><td colspan="3">Consistent</td><td colspan="3">Inconsistent</td><td colspan="2">Heterozygous</td><td>Excluded</td></tr><tr><td colspan="6">multiple C57BL/6 substrains</td><td>9721</td><td colspan="3">9277 (99.7%)</td><td colspan="3">1 (0.0%)</td><td colspan="2">24 (0.3%)</td><td>419</td></tr></table>																	Strain						Total	Consistent			Inconsistent			Heterozygous		Excluded	multiple C57BL/6 substrains						9721	9277 (99.7%)			1 (0.0%)			24 (0.3%)		419																																																																																																																						
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multiple C57BL/6 substrains						9721	9277 (99.7%)			1 (0.0%)			24 (0.3%)		419																																																																																																																																																								
Secondary Background (Autosomes, X Chromosome)	<table><tr><td colspan="6">Strain</td><td>Total</td><td colspan="3">Explained</td><td colspan="3">Unexplained</td><td colspan="2">Excluded</td></tr><tr><td colspan="6">129P2/OlaHsd and/or</td><td>25</td><td colspan="3">24 (0.3%)</td><td colspan="3">1 (0.0%)</td><td colspan="2">0 (0.0%)</td></tr><tr><td colspan="6">129P3/J and/or</td><td>24 Clustered</td><td colspan="3">24 Clustered</td><td colspan="3">0 Clustered</td><td colspan="2"></td></tr><tr><td colspan="6">129S1/SvImJ and/or</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr><tr><td colspan="6">129S2/SvHsd and/or</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr><tr><td colspan="6">129S2/SvPasOrlRj and/or</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr><tr><td colspan="6">129S4/SvJaeJ and/or</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr><tr><td colspan="6">129S6/SvEvTac and/or</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr><tr><td colspan="6">129T2/SvEmsJ and/or</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr><tr><td colspan="6">129X1/SvJ</td><td></td><td colspan="3"></td><td colspan="3"></td><td colspan="2"></td></tr></table>																	Strain						Total	Explained			Unexplained			Excluded		129P2/OlaHsd and/or						25	24 (0.3%)			1 (0.0%)			0 (0.0%)		129P3/J and/or						24 Clustered	24 Clustered			0 Clustered					129S1/SvImJ and/or															129S2/SvHsd and/or															129S2/SvPasOrlRj and/or															129S4/SvJaeJ and/or															129S6/SvEvTac and/or															129T2/SvEmsJ and/or															129X1/SvJ														
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Background Ideogram



Backgrounds Detected
(Diagnostic Alleles)

		Diagnostic Alleles Observed			
Substrain		Homozygous	Heterozygous	Potential	% Observed
C57BL/6J		90	53	156	91.7%
Strain Group		Homozygous	Heterozygous	Potential	% Observed
C57BL/6		3	0	21	14.3%
(B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd)					