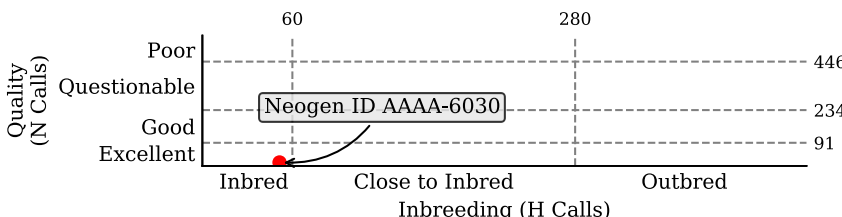
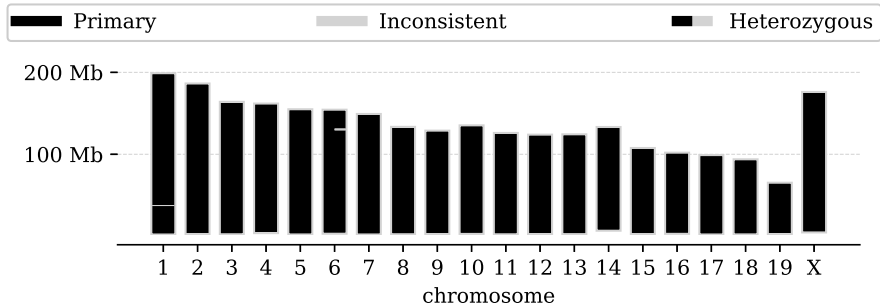


MiniMUGA Background Analysis v0008

Sample ID	Magnuson/B6.CG. ZFP92.1																																																	
Neogen ID	AAAA-6029																																																	
Summary	The genotype of this sample is of excellent quality. It is male and 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	Inbred (42 H calls at autosomal, X, and PAR chromosome markers)																																																	
Inbreeding and Genotyping Quality (Plot)	<p>The plot shows the relationship between Inbreeding (H Calls) on the x-axis and Quality (N Calls) on the y-axis. The y-axis has four levels: Poor, Questionable, Good, and Excellent. The x-axis has three regions: Inbred, Close to Inbred, and Outbred. A red dot representing Neogen ID AAAA-6029 is located at the 'Excellent' level, corresponding to 91 N calls. Dashed lines indicate thresholds at 60 and 280 H calls, with a total of 446 H calls shown on the right.</p>																																																	
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="2">Strain</td><td>Total</td><td colspan="2">Consistent</td><td colspan="2">Inconsistent</td><td colspan="2">Heterozygous</td><td colspan="2">Excluded</td></tr><tr><td colspan="2">multiple C57BL/6 substrains</td><td>9721</td><td colspan="2">9300 (100.0%)</td><td colspan="2">1 (0.0%)</td><td colspan="2">0 (0.0%)</td><td colspan="2">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	<p>The ideogram shows the lengths of chromosomes 1 through 19 and X. The y-axis represents length in Mb, with markers at 100 Mb and 200 Mb. The legend indicates three categories: Primary (black), Inconsistent (light gray), and Heterozygous (dark gray). Chromosomes 1 through 19 and X are primarily black, indicating they are primary background.</p>																																																	
Backgrounds Detected (Diagnostic Alleles)	Diagnostic Alleles Observed																																																	
	Substrain				Homozygous		Heterozygous		Potential		% Observed																																							
	C57BL/6J				106		33		156		89.1%																																							
	Strain Group				Homozygous		Heterozygous		Potential		% Observed																																							
C57BL/6				3		1		21		19.0%																																								
(B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd)																																																		

MiniMUGA Background Analysis v0008

Sample ID	Magnuson/B6.CG. ZFP92.2																																		
Neogen ID	AAAA-6030																																		
Summary	The genotype of this sample is of excellent quality. It is male and 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 (5 N calls) All reported results are dependent on genotyping quality.																																		
Chromosomal Sex	XY																																		
Inbreeding Estimate	Inbred (50 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>9296 (100.0%)</td><td>1 (0.0%)</td><td>2 (0.0%)</td><td>422</td></tr></table>	Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded	multiple C57BL/6 substrains	9721	9296 (100.0%)	1 (0.0%)	2 (0.0%)	422																						
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Secondary Background (Autosomes, X Chromosome)	Not Applicable																																		
Background Ideogram																																			
Backgrounds Detected (Diagnostic Alleles)	<table><tr><td rowspan="2">Substrain</td><td colspan="4">Diagnostic Alleles Observed</td></tr><tr><td>Homozygous</td><td>Heterozygous</td><td>Potential</td><td>% Observed</td></tr><tr><td>C57BL/6J</td><td>99</td><td>39</td><td>156</td><td>88.5%</td></tr><tr><td>Strain Group</td><td>Homozygous</td><td>Heterozygous</td><td>Potential</td><td>% Observed</td></tr><tr><td>C57BL/6 (B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd)</td><td>3</td><td>1</td><td>21</td><td>19.0%</td></tr></table>	Substrain	Diagnostic Alleles Observed				Homozygous	Heterozygous	Potential	% Observed	C57BL/6J	99	39	156	88.5%	Strain Group	Homozygous	Heterozygous	Potential	% Observed	C57BL/6 (B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd)	3	1	21	19.0%										
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