

MiniMUGA Background Analysis v0008

Sample ID	GPG_C3-Tag-T1-Luc_F																																		
Neogen ID	MM0924																																		
Summary	The genotype of this sample is of <b>excellent</b> quality. It is <b>female</b> and <b>inbred</b> , and likely a mix of <b>multiple FVB/N substrains</b> .																																		
	Diagnostic SNPs indicate the presence of the background substrains <b>FVB/NJ</b> .																																		
	The sample contains the following genetic constructs: <b>Luciferase, SV40 large T antigen</b>																																		
Genotyping Quality	<b>Excellent (22 N calls)</b> All reported results are dependent on genotyping quality.																																		
Chromosomal Sex	XX																																		
Inbreeding Estimate	<b>Inbred (16 H calls at autosomal, X, and PAR chromosome markers)</b>																																		
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: Excellent (91), Good (234), Questionable (446), and Poor. The x-axis has three regions: Inbred, Close to Inbred, and Outbred. A red dot representing Neogen ID MM0924 is located in the Inbred region at the Excellent level (91 N calls).</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	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	+	-
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Primary Background (Autosomes, X Chromosome)	<table><tr><th>Strain</th><th>Total</th><th>Consistent</th><th>Inconsistent</th><th>Heterozygous</th><th>Excluded</th></tr><tr><td>multiple FVB/N substrains</td><td>9721</td><td>9425 (100.0%)</td><td>0 (0.0%)</td><td>4 (0.0%)</td><td>292</td></tr></table>	Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded	multiple FVB/N substrains	9721	9425 (100.0%)	0 (0.0%)	4 (0.0%)	292																						
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Secondary Background (Autosomes, X Chromosome)	Not Applicable																																		
Background Ideogram	<p>The ideogram shows the distribution of genetic markers across chromosomes 1 to 19 and the X chromosome. The y-axis represents the number of markers, ranging from 0 to 200 Mb. The legend indicates three categories: Primary (black), Inconsistent (light gray), and Heterozygous (dark gray). The Primary category is the most prominent across all chromosomes.</p>																																		
Backgrounds Detected (Diagnostic Alleles)	<table><tr><th colspan="5">Diagnostic Alleles Observed</th></tr><tr><th>Substrain</th><th>Homozygous</th><th>Heterozygous</th><th>Potential</th><th>% Observed</th></tr><tr><td>FVB/NJ</td><td>67</td><td>8</td><td>79</td><td>94.9%</td></tr></table>	Diagnostic Alleles Observed					Substrain	Homozygous	Heterozygous	Potential	% Observed	FVB/NJ	67	8	79	94.9%																			
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