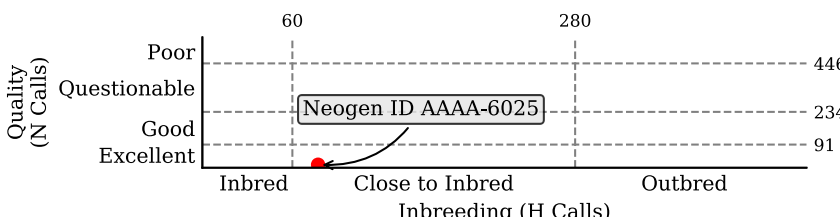
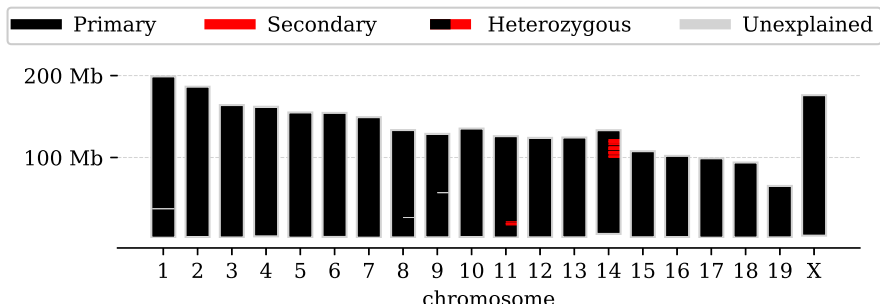


MiniMUGA Background Analysis v0008

Sample ID	Magnuson/B6.CG. Zfp329.1																																		
Neogen ID	AAAA-6025																																		
Summary	<p>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 (129P1/ReJ and/or 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).</p> <p>Diagnostic SNPs indicate the presence of the background strain groups C57BL/6 and the substrains C57BL/6J.</p> <p>No genetic constructs were detected in this sample.</p>																																		
Genotyping Quality	<p>Excellent (3 N calls)</p> <p>All reported results are dependent on genotyping quality.</p>																																		
Chromosomal Sex	XY																																		
Inbreeding Estimate	Close to Inbred (80 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>9268 (99.6%)</td><td>1 (0.0%)</td><td>32 (0.3%)</td><td>420</td></tr></table>	Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded	multiple C57BL/6 substrains	9721	9268 (99.6%)	1 (0.0%)	32 (0.3%)	420																						
Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded																														
multiple C57BL/6 substrains	9721	9268 (99.6%)	1 (0.0%)	32 (0.3%)	420																														
Secondary Background (Autosomes, X Chromosome)	<table><tr><td>Strain</td><td>Total</td><td>Explained</td><td>Unexplained</td><td>Excluded</td></tr><tr><td>129P1/ReJ and/or 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</td><td>33</td><td>29 (0.3%)</td><td>3 (0.0%)</td><td>1 (0.0%)</td></tr><tr><td></td><td>29 Clustered</td><td>29 Clustered</td><td>0 Clustered</td><td></td></tr></table>	Strain	Total	Explained	Unexplained	Excluded	129P1/ReJ and/or 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	33	29 (0.3%)	3 (0.0%)	1 (0.0%)		29 Clustered	29 Clustered	0 Clustered																				
Strain	Total	Explained	Unexplained	Excluded																															
129P1/ReJ and/or 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	33	29 (0.3%)	3 (0.0%)	1 (0.0%)																															
	29 Clustered	29 Clustered	0 Clustered																																
Background Ideogram																																			

Backgrounds Detected (Diagnostic Alleles)	Diagnostic Alleles Observed				
	Substrain	Homozygous	Heterozygous	Potential	% Observed
	C57BL/6J	106	37	156	91.7%
	Strain Group	Homozygous	Heterozygous	Potential	% Observed
	C57BL/6 (B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac, C57BL/6JEiJ, C57BL/6JOlaHsd)	2	4	21	28.6%

MiniMUGA Background Analysis v0008

Sample ID	Magnuson/B6.CG. Zfp329.2																																		
Neogen ID	AAAA-6026																																		
Summary	<p>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 (129P1/ReJ and/or 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).</p> <p>Diagnostic SNPs indicate the presence of the background strain groups C57BL/6 and the substrains C57BL/6J.</p> <p>No genetic constructs were detected in this sample.</p>																																		
Genotyping Quality	<p>Excellent (8 N calls)</p> <p>All reported results are dependent on genotyping quality.</p>																																		
Chromosomal Sex	XY																																		
Inbreeding Estimate	Close to Inbred (77 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																			
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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>9265 (99.7%)</td><td>1 (0.0%)</td><td>30 (0.3%)</td><td>425</td></tr></table>	Strain	Total	Consistent	Inconsistent	Heterozygous	Excluded	multiple C57BL/6 substrains	9721	9265 (99.7%)	1 (0.0%)	30 (0.3%)	425																						
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129P1/ReJ and/or 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	31 29 Clustered	29 (0.3%) 29 Clustered	1 (0.0%) 0 Clustered	1 (0.0%)																															
Background Ideogram																																			

Backgrounds Detected (Diagnostic Alleles)	Diagnostic Alleles Observed				
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