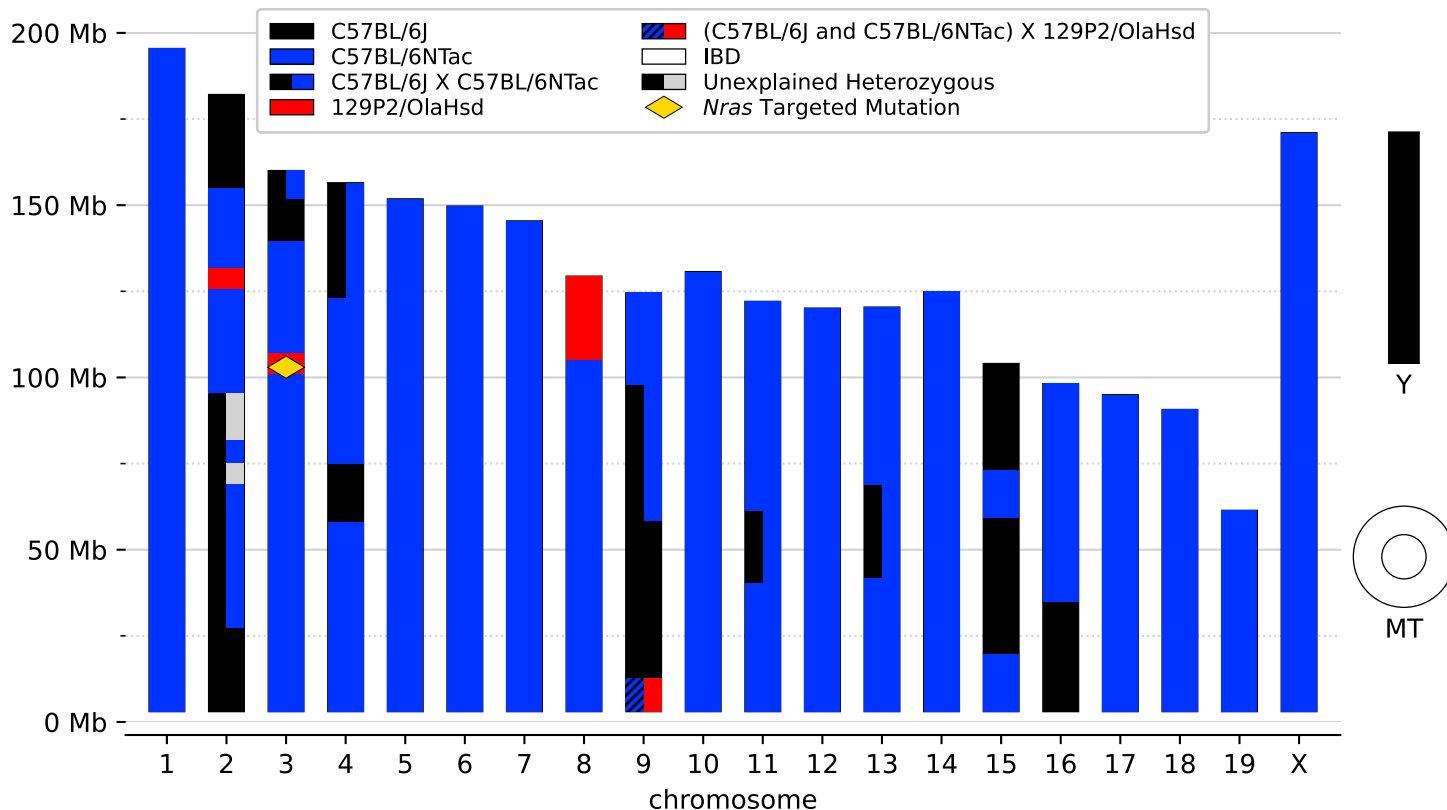


Summary: Incipient congenic strain carrying the tm1.1Nesh allele of the *Nras* gene and an inducible Cre transgene under the tyrosinase promoter on mixed C57BL/6 background. The allele of interest present on chromosome 3 is on the donor background (129P2/OlaHsd). The donor background is also present on chromosomes 2, 8, and 9. At least one additional unexplained genetic background was detected. 129P2/OlaHsd, C57BL/6J, and C57BL/6NTac were detected with diagnostic alleles. The genome of this strain is not fully replicable because up to 0.4% of the genome is segregating for the donor background, at least 6.9% of the genome is segregating for the substrains of the primary background, and at least 0.7% of the genome is segregating for the unexplained background. This GQC report is based on the MiniMUGA G3 2024 pipeline using 2 samples genotyped in 2019.



Genetic Background	Zygosity	Genome %	Estimated # Segregating SNPs
C57BL/6J and C57BL/6NTac	N/A	97.5%	N/A
C57BL/6J	Homozygous	8.9%	N/A
C57BL/6NTac	Homozygous	81.7%	N/A
C57BL/6J X C57BL/6NTac	Heterozygous	6.9%	700
129P2/OlaHsd	Homozygous	1.4%	N/A
(mixed C57BL/6) X 129P2/OlaHsd	Heterozygous	0.4%	4,600
Unexplained	Heterozygous	0.7%	N/A
<b>Total</b>		<b>100.0%</b>	<b>5,300</b>

Substrain Detected	# present in EU3955	# present in EU5983	Total SNPs Annotated
C57BL/6J	19	24	160
C57BL/6NTac	23	23	32
129P2/OlaHsd	1	1	27

Constructs Detected
Cre