7 October 2025

GENETIC MONITORING INFORMATION

Strains

- **CBA/CaH** https://www.ozgene.com/cba-cah/
- **CBB6F1** https://www.ozgene.com/cbb6f1/

Strain background

- The **CBA/CaH** strain originates from the Animal Resources Centre (ARC) colony, supplied since 1997.
- Many ARC-maintained lines may have diverged into unique sub-strains over decades of breeding.
- The strain was transferred from the ARC to Ozgene ARC in 2023.
- All past and current shipments have been derived from this original ARC colony.
- This information also applies to the **CBB6F1 strain**, which is a CBA/CaH female × C57BL/6J male cross.

Genetic identification & testing

- MiniMUGA analysis identified the CBA/CaH strain as being **closest to CBA/CaHN-Btk^xid/J** (see following pages).
- Genotyping was performed to detect the mutation in the **Bruton's tyrosine kinase (Btk) gene**, responsible for the immunodeficient phenotype in CBA/CaHN-Btk^xid/J mice.
- Results show that the CBA/CaH colony **does not carry the c.C82T p.R28C mutation** associated with immunodeficiency.
- Therefore, the strain **cannot be classified as CBA/CaHN-Btk^xid/J**.
- The colony was also compared to **CBA/CaJ** and **CBA/J** reference strains, and results indicate that it is **not an exact match to either**.
- These findings suggest that the line represents a **distinct CBA/CaH sub-line**.

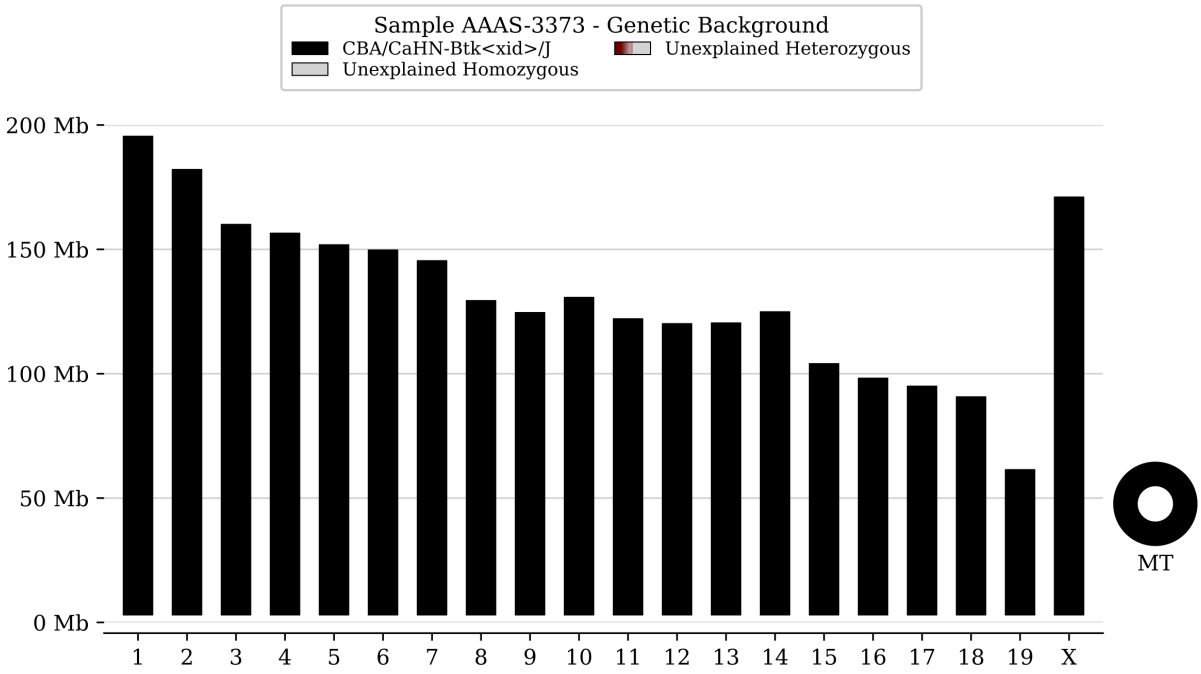
MiniMUGA Background Analysis v2.3.1

Sample ID	CBA/CaH_2
Neogen ID	AAAS-3373
Summary	The genotype of this sample is of **excellent** quality. It is **female** and **inbred**, and likely a **CBA/CaHN-Btk<xid>/J** mouse. No genetic constructs were detected in this sample.
Genotyping Quality	**Excellent (9 N calls)** All reported results are dependent on genotyping quality.
Chromosomal Sex	XX
Inbreeding Estimate	100.0% Inbred (Percentage of the genome (autosomal and X chromosomes) that is homozygous or hemizygous for primary, secondary, and unknown backgrounds. See Genome Analysis)

Constructs Detected

BlastR	bpA	Cas9	chlor	cHS4	Cre	DTA	Flp	g_FP	hCMV_a	hCMV_b	hTK_pr	iCre	IRES	Luc	r_FP	rtTA	SV40	tTA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Refined Ideogram



Genome Analysis

Background	Zygosity	Informative Markers	Informative Markers %	Genome %
CBA/CaHN-Btk<xid>/J	Homozygous	8844	100.0%	100.0%
Unexplained	Homozygous	1	0.0%	0.0%
	Total	8845	100.0%	100.0%

Y Chromosome	Not Applicable
MT Genome	MT Haplogroup 6 - 100.0% Consistent Includes CBA/CaHN-Btk/J and 167 other strains
Backgrounds Detected (Diagnostic Alleles)	No Backgrounds Detected via Diagnostic Alleles

MiniMUGA Background Analysis v2.3.1

	Chromosome	Start (Mb)	Stop (Mb)	Background	Zygosity
Diplotype Intervals	1	3000000	195471971	CBA/CaHN-Btk<xid>/J	Homozygous
	2	3000000	182113224	CBA/CaHN-Btk<xid>/J	Homozygous
	3	3000000	160039680	CBA/CaHN-Btk<xid>/J	Homozygous
	4	3000000	156508116	CBA/CaHN-Btk<xid>/J	Homozygous
	5	3000000	151834684	CBA/CaHN-Btk<xid>/J	Homozygous
	6	3000000	149736546	CBA/CaHN-Btk<xid>/J	Homozygous
	7	3000000	145441459	CBA/CaHN-Btk<xid>/J	Homozygous
	8	3000000	129401213	CBA/CaHN-Btk<xid>/J	Homozygous
	9	3000000	124595110	CBA/CaHN-Btk<xid>/J	Homozygous
	10	3000000	130694993	CBA/CaHN-Btk<xid>/J	Homozygous
	11	3000000	122082543	CBA/CaHN-Btk<xid>/J	Homozygous
	12	3000000	120129022	CBA/CaHN-Btk<xid>/J	Homozygous
	13	3000000	120421639	CBA/CaHN-Btk<xid>/J	Homozygous
	14	3000000	124902244	CBA/CaHN-Btk<xid>/J	Homozygous
	15	3000000	104043685	CBA/CaHN-Btk<xid>/J	Homozygous
	16	3000000	98207768	CBA/CaHN-Btk<xid>/J	Homozygous
	17	3000000	94987271	CBA/CaHN-Btk<xid>/J	Homozygous
	18	3000000	90702639	CBA/CaHN-Btk<xid>/J	Homozygous
	19	3000000	61431566	CBA/CaHN-Btk<xid>/J	Homozygous
	X	3000000	171031299	CBA/CaHN-Btk<xid>/J	Homozygous
	MT	0	0	CBA/CaHN-Btk<xid>/J	Hemizygous