

§ User Reported Values

EXF2618

Sample Label	NE01234567	Laboratory	GenomNZ
Sex §	Female	Call Rate	99.79%
DOB §	Mar 30, 2026	GC Score	0.852
Species	Ovine	Inbreeding (F_ROH)	0.136 · max 35 Mb · median 7 Mb
Breed §	Australian White	Inbreeding (F_HOM)	0.095 (Method: HWE)
Submitted By	Example Producer	Analysis Run	#8213 · Oct 3, 2026
Requesting Farm	@EXF · Example Farm		

Parentage Verification

Sire · Verified

Claimed	EXF2209 · Accession ID: 789-321 840000123456789						
Accession ID	Tag Number	OH (thr)	Loci (nom)	LLR	Best fit	φ	Heaton OH
789-321	EXF2209	9 (≤40)	68178 (75205)	703.72	PO vs FS	0.339	0/163

Dam · No claim

Claimed	none recorded
---------	---------------

Sex Verification

This panel distinguishes males from females by heterozygosity on the X chromosome: a male carries one X and reads homozygous across it, a female carries two.

Verdict DNA agrees with claim (Female)

Chromosomal Female, LLR 1563.12

chrX het	34.2%	exp M ≤5% · F ~33.5%	n=1476	fits F
chrX tracts	18 of 19 windows at female het · best 48.6%			
chrY coverage	0.0%	exp M >0 · F 0	n=1	not informative
Autosomal het	31.0%	exp ~35%	n=73317	not elevated

SNP genotyping has a small error rate, where a true homozygote (e.g., AA) may be measured as heterozygous (AB), or rarely as the opposite homozygote (BB). True parent-offspring pairs must share at least one allele at every locus (Mendelian inheritance), but due to possible genotyping errors, a small number of opposing homozygotes (OH) is permitted.

Accession IDs: Composite key of the Animal ID and Sample ID, separated by a hyphen. When a sample is Redacted, the Accession ID is hashed to provide an anonymous but stable reference.

Chain of Custody. Allele does not hold sample chain of custody until the sample arrives for processing. To aid in forensic review, any change to tag numbers, any hand edit of a recorded sire or dam, and any change to which sample an animal's results were produced from, is logged on the Parentage Verification report under the Forensics section for both the subject animal and its Sire/Dam, as soon as results are received from the lab.

OH (thr) / Loci (nom): Opposing homozygotes vs effectively-independent loci after LD pruning, with the adaptive non-parentage threshold and the nominal (raw) loci count. An OH occurs when parent and offspring have no shared allele at a locus (e.g., parent AA, offspring BB). Low OH = strong match; counts above the adaptive threshold indicate non-parentage. The nominal count is the raw both-called loci before the scoring basis is formed, shown for context. Probe QC and LD pruning remove probes that are not suitable for parent verification. The log-likelihood methods assume per-locus independence, so this step is mandatory for their correctness.

Status: Verified = Meets the OH threshold, the likelihood favors parent-offspring, and the claimed parent outscores every other candidate by more than 1000:1. Qualified = Meets the OH threshold and the likelihood favors parent-offspring, but other valid candidates compete within 1000:1, and on review one of them was confirmed as the parent, with or without a prior claim; every candidate is listed. Also printed when a person otherwise intervened: a reviewer resolved the result, staff let a recorded claim stand over a DNA finding, or the sample was detached and later re-attached. The reasons are listed under the row. Inconclusive = Review needed: more than one candidate fits within 1000:1, a candidate exceeds the OH threshold but otherwise appears to be the parent (the likelihood strongly favors parent-offspring), or birth dates cannot establish which animal is the parent. Excluded = Fails the criteria for parentage, or another animal outscores the claimed parent by more than 1000:1. Wrong sex = Genetically parent-offspring, but the claimed parent's recorded sex does not fit the slot. No claim = No expected parent was provided. NOT TESTABLE — NO DNA = The claimed parent does not have a genotype on file.

LLR: Log-likelihood ratio — $\log(P(\text{best relationship}) / P(\text{second best}))$. 1.0 is 10:1 odds and 3.0 is 1000:1; both are conventional minima for a call, not a ceiling. The ratio sums across the effective set, so its size tracks the Loci column above: on the tens of thousands of loci used here, parent-offspring calls typically land in the hundreds. A small LLR means the two most likely relationships for this pair (for example parent-offspring and full sibling) fit the data almost equally well, so the relationship itself is uncertain, not that the match is weak.

Relationship codes: The best-fitting relationship for the pair; where two are shown ("PO vs 3QS") the second is the runner-up the LLR is measured against. Grouped by the kinship each expects, since codes within a group are not separable by ϕ alone — SELF 0.5 (same animal); PO 0.25 (parent-offspring), FS 0.25 (full sibling); 3QS 0.1875 (three-quarter sibling: half-sibs whose parents are themselves sibs); HS 0.125 (half sibling), GP 0.125 (grandparent), AV 0.125 (avuncular, i.e. aunt or uncle), DFC 0.125 (double first cousin); GGP, GAV, HAV and 1C 0.0625 (great-grandparent, great-avuncular, half-avuncular, first cousin); GGGP, 1C1R and H1C 0.03125 (great-great-grandparent, first cousin once removed, half first cousin); 2C 0.0156 (second cousin); U 0 (unrelated).

ϕ : PC-Relate kinship coefficient — supplemental evidence axis alongside OH and LLR. Expected: parent-offspring (PO) and full siblings (FS) 0.25, half-siblings (HS) and grandparent (GP) 0.125, unrelated ≈ 0 . ϕ is adjusted for ancestry against the reference panel. It measures recent family relationship rather than shared population history, and that adjustment has a limit: when a pair's breeds are poorly represented, or during crossbreeding, ϕ reads below expectation. It is not in and of itself an exclusionary filter.

F_ROH: Inbreeding from long runs of homozygosity: the fraction of the autosomal genome in runs of at least 1 Mb, read off this animal's own genotype with no population allele frequencies. Max and median are the longest and the median run; long runs point to recent inbreeding. Reads low when autozygous stretches are shorter than the 1 Mb the caller can see.

F_HOM: Inbreeding as excess homozygosity: how much more homozygous this animal is than a reference population's allele frequencies predict, here Hardy-Weinberg expectation against the pooled cohort (the method printed beside it). Reads high for a breed that reference describes poorly, so where it sits well above F_ROH the gap is about the reference population rather than this animal.

Method. Parentage scoring uses two axes. Opposing homozygotes (OH) are the screen: no claim that fails the adaptive threshold can be set as Verified. The 17-relationship LLR confirms parent-offspring (PO) and separates it from close kin that OH cannot rule out. ϕ is printed for information only and never decides a verdict. Allele frequencies are individual-specific, fitted against the reference panel's population structure. QC ruleset version 5.

Heaton OH: The 163-SNP sheep parentage set is provided for information only; it does not feed the analysis in this report. The method would predict OH to be <0.3 for a true parent, effectively zero.

References: Kinship and per-individual allele frequencies: Conomos et al. 2016 (PC-Relate) on Conomos et al. 2015 (PC-AiR). Relationship likelihood: Huisman 2017 (Sequoia). Per-locus likelihoods from IBD coefficients under Hardy-Weinberg: Thompson 1986; Lange 1997. False opposing-homozygote rate: Gordon et al. 1999. Parentage marker set: Heaton et al. 2014, PLoS ONE 9:e94851.

The raw genotypes behind this report were produced by GenomNZ. Allele independently performs sex / parent verification and translates A/B allele calls into genotype interpretations, none of which is reviewed or endorsed by GenomNZ.

Disclaimer. Allele has taken reasonable care in that work but does not warrant this report free of error or omission, and accepts no responsibility for any decision made in reliance on it unless separately agreed in writing. Laboratory results describe only the material actually received and tested. Neither party has verified the identity, parentage, breed or history of any animal as supplied by the submitter, and neither is responsible for the accuracy of that information. A result is a genotype and its published association — not a diagnosis, not a guarantee of how an animal will perform, and not a certification by any government agency. To the fullest extent permitted by law, Allele and the laboratory each exclude all liability arising out of this report, whether in contract, tort (including negligence), equity, statute or otherwise.