

## CORRECTION

## Correction: Transcriptomics analysis of the bovine endometrium during the perioestrus period

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After the publication of this article [1], concerns were raised about identical tables across distinct time points and contradictory statements. Here, the authors have provided additional information to clarify these issues:

In the Results section of this paper, [Tables 1](#) and [2](#) contain duplicate data as that of Table 4 by error. Tables 1–5 –5 are intended as summaries of the data presented in S3 Table, which are correct. Please see the corrected [Tables 1](#) and [2](#) here.

The authors have provided the following corrections

In the Discussion section, the fourth paragraph under the subheading “Tissue remodelling and innervation in the proliferative phase” is incorrect. This paragraph should be disregarded.

In the Discussion section, the statement comprising the fourth and fifth sentences in the seventh paragraph under the subheading “Tissue remodelling and innervation in the proliferative phase” is incorrect. These sentences should be disregarded. The corrected paragraph is:

“For both time points before oestrus, transforming growth factor beta 1 (TGF- $\beta$ 1), the cytokine tumour necrosis factor (TNF), and HDAC (group of histone deacetylases) were among the top ranked upstream regulators (Table 7). TGF- $\beta$ 1 is required for the development of smooth muscle in the female reproductive tract [93], as well as being present in seminal fluid and altering the endometrium and oviduct to promote embryonic development and implantation [94]. In humans, expression of TNF has also been shown to rise in the mid- to late-proliferative phases [95], while in bovine endometrial cells, TNF-induced production of chemokines [96], directs the migration of leukocytes to inflammation sites [97]. These observations suggest that endometrial immunity is upregulated at this timepoint, actively preparing for sperm deposition and pathogen entry. The top interaction networks for CIDR+12 h and CIDR+24 h are centred on the transcription factor NF $\kappa$ B complex (Figs 4 and 5) although these are different networks. For the CIDR+12 h top network, involved in Endocrine system disorders, Hereditary disorders and Organismal injury and abnormalities, NF- $\kappa$ B is linked to various hub genes, such as *SUSD4*, which negatively regulates complement activation, and *ALDH1B1*, which links to various aldehyde dehydrogenases. The top network for CIDR+24 h is Neurological disease, Nervous System Development and



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**Table 1. Top DEGs in bovine endometrium at 12h post-CIDR removal versus oestrus, ranked by ascending B-H FDR.**

Entrez ID	Gene Name	Gene Symbol	Log <sub>2</sub> fold-change	P-Value	B-H FDR
<b>Upregulated</b>					
617325	kinase suppressor of ras 2	KSR2	4.71	$1.13 \times 10^{-13}$	$4.80 \times 10^{-10}$
282248	hypocretin (orexin) receptor 1	HCRTR1	3.23	$2.00 \times 10^{-12}$	$2.60 \times 10^{-09}$
509642	tubulointerstitial nephritis antigen-like 1	TINAGL1	2.14	$4.63 \times 10^{-09}$	$2.53 \times 10^{-06}$
522479	ovalbumin	LOC522479	4.54	$6.04 \times 10^{-09}$	$3.19 \times 10^{-06}$
282361	solute carrier family 5 (sodium/glucose cotransporter), member 1	SLC5A1	5.91	$8.10 \times 10^{-09}$	$4.15 \times 10^{-06}$
615277	acyl-coenzyme A thioesterase THEM4	LOC615277	6.26	$9.06 \times 10^{-09}$	$4.38 \times 10^{-06}$
104974435	uncharacterized LOC104974435	LOC104974435	6.38	$1.16 \times 10^{-08}$	$5.02 \times 10^{-06}$
786974	beta-hexosaminidase subunit beta	LOC786974	2.79	$1.94 \times 10^{-08}$	$7.82 \times 10^{-06}$
613555	disrupted in schizophrenia 1	DISC1	2.00	$3.05 \times 10^{-08}$	$1.17 \times 10^{-05}$
101905783	uncharacterized LOC101905783	LOC101905783	4.34	$5.19 \times 10^{-08}$	$1.76 \times 10^{-05}$
<b>Downregulated</b>					
509600	glycoprotein (transmembrane) nmb	GPNMB	-3.92	$4.61 \times 10^{-17}$	$7.81 \times 10^{-13}$
280852	midkine (neurite growth-promoting factor 2)	MDK	-2.13	$3.97 \times 10^{-16}$	$3.36 \times 10^{-12}$
353114	neuronatin	NNAT	-3.22	$1.10 \times 10^{-13}$	$4.80 \times 10^{-10}$
519120	pyridine nucleotide-disulphide oxidoreductase domain 2	PYROXD2	-2.2	$2.98 \times 10^{-13}$	$1.01 \times 10^{-09}$
531699	aldehyde oxidase 2	AOX2	-5.85	$3.90 \times 10^{-13}$	$1.10 \times 10^{-09}$
513038	cathepsin K	CTSK	-2.81	$7.59 \times 10^{-13}$	$1.61 \times 10^{-09}$
616777	family with sequence similarity 180, member A	FAM180A	-3.87	$6.75 \times 10^{-13}$	$1.61 \times 10^{-09}$
511839	ATPase, H <sup>+</sup> transporting, lysosomal 38kDa, V0 subunit d2	ATP6V0D2	-5.69	$8.94 \times 10^{-13}$	$1.68 \times 10^{-09}$
789851	histamine receptor H3	HRH3	-6.41	$1.21 \times 10^{-12}$	$2.04 \times 10^{-09}$
100140069	WD repeat domain 86	WDR86	-3.11	$1.68 \times 10^{-12}$	$2.54 \times 10^{-09}$

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**Table 2. Top DEGs in bovine endometrium at 24h post-CIDR removal versus oestrus, ranked by ascending B-H FDR.**

Entrez ID	Gene Name	Gene Symbol	Log <sub>2</sub> fold-change	P-Value	B-H FDR
<b>Upregulated</b>					
617325	kinase suppressor of ras 2	KSR2	3.42	$7.62 \times 10^{-09}$	$1.07 \times 10^{-05}$
615152	chromosome 14 open reading frame, human C8orf34	C14H8orf34	3.0	$8.62 \times 10^{-07}$	$4.42 \times 10^{-04}$
101906467	uncharacterized LOC101906467	LOC101906467	3.22	$1.29 \times 10^{-06}$	$6.22 \times 10^{-04}$
506696	paraspeckle component 1	PSPC1	0.95	$1.46 \times 10^{-06}$	$6.84 \times 10^{-04}$
280894	placental growth factor	PGF	1.81	$1.63 \times 10^{-06}$	$7.28 \times 10^{-04}$
530102	collagen, type VI, alpha 6	COL6A6	7.16	$2.08 \times 10^{-06}$	$9.03 \times 10^{-04}$
282361	solute carrier family 5 (sodium/glucose cotransporter), member 1	SLC5A1	4.48	$2.85 \times 10^{-06}$	$1.15 \times 10^{-03}$
616625	aquaporin 12B	AQP12B	5.12	$6.13 \times 10^{-06}$	$2.21 \times 10^{-03}$
286767	parathyroid hormone-like hormone	PTHLH	1.96	$8.81 \times 10^{-06}$	$2.98 \times 10^{-03}$
530709	Usher syndrome 1C (autosomal recessive, severe)	USH1C	2.96	$9.39 \times 10^{-06}$	$3.07 \times 10^{-03}$
<b>Downregulated</b>					
353114	neuronatin	NNAT	-3.19	$1.92 \times 10^{-13}$	$3.25 \times 10^{-09}$
509600	glycoprotein (transmembrane) nmb	GPNMB	-3.28	$7.72 \times 10^{-13}$	$6.53 \times 10^{-09}$
789851	histamine receptor H3	HRH3	-6.35	$1.84 \times 10^{-12}$	$1.04 \times 10^{-08}$
616010	anthrax toxin receptor 1	ANTXR1	-2.15	$3.25 \times 10^{-12}$	$1.37 \times 10^{-08}$
519120	pyridine nucleotide-disulphide oxidoreductase domain 2	PYROXD2	-1.95	$9.78 \times 10^{-11}$	$3.31 \times 10^{-07}$
281487	premelanosome protein	PMEL	-3.34	$2.09 \times 10^{-10}$	$5.88 \times 10^{-07}$
522392	matrix-remodelling associated 8	MXRA8	-2.12	$9.91 \times 10^{-10}$	$2.39 \times 10^{-06}$
508098	uncharacterized LOC508098	LOC508098	-7.26	$1.98 \times 10^{-09}$	$4.19 \times 10^{-06}$
338446	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	PPARGC1A	-2.73	$2.80 \times 10^{-09}$	$5.26 \times 10^{-06}$
616660	tetraspanin 11	TSPAN11	-1.79	$3.15 \times 10^{-09}$	$5.33 \times 10^{-06}$

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Function and Behavior, with links to voltage-dependent Na<sup>+</sup> channels and SYN genes, encoding synapsins that are associated with the trafficking of synaptic vesicles."

## Reference

1. Alfattah MA, Correia CN, Browne JA, McGettigan PA, Pluta K, Carrington SD, et al. Transcriptomics analysis of the bovine endometrium during the perioestrus period. PLoS One. 2024;19(3):e0301005. <https://doi.org/10.1371/journal.pone.0301005> PMID: 38547106