



Uncovering the Molecular Mechanisms of Bovine Tuberculosis Through Meta-Analysis of Differentially Expressed Genes

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Supplementary table 1. List of DEGs and their Fisher and Stouffer values including list of common DEGs

Upregulated gene	Fisher value	Downregulated gene	Fisher value
XM_005225965.5	0.000147834	NM_001046419.2	0.049481515
NM_001101179.2	0.043045398	XM_024984313.2	0.037445599
NM_001015570.3	4.15E-07	NM_001104611.2	0.048374604
XM_024997362.2	0.023416153	NM_001034532.2	0.020726373
NM_174027.2	3.35E-05	XM_003587406.5	0.023118377
NM_174035.4	9.28E-08	XM_005203578.5	0.046166262
XM_059886092.1	0.040089965	XM_010809076.3	0.045912963
XM_024977856.2	0.002850835	XM_005201681.5	0.037639012
NM_001034562.1	0.027283532	XM_005216236.2	0.021724109
XM_024979803.2	0.000161198	XM_059888749.1	0.031805922
NM_173959.4	0.030072857	NM_001244199.1	0.006470703
NM_001015639.1	0.004046981	NM_001167894.2	0.049190244
NM_001075733.1	0.010673851	XM_002693873.7	0.045014674
XR_009495704.1	0.033124707	NM_181014.2	0.038820315
NM_001034478.1	0.006638922	XM_024982697.2	0.04620775
NM_001046294.1	0.014027387	NM_001075552.1	0.019567417
NM_001046133.3	0.029510129	NM_173891.2	0.038264044
XR_009496776.1	0.048134235	NM_001192792.2	0.015135232
XM_003587769.6	0.008211431	XM_024999036.2	0.048000779
XM_005208875.4	0.036940154	XM_005221420.2	0.035692462
NM_001304338.1	5.98E-06	NM_001184724.1	0.027100355
XM_059877485.1	0.000222726	XM_002690940.7	0.042690423
XM_005227466.5	0.003617754	XM_024996654.2	0.041286253
XM_059882753.1	0.045433076	XM_005207061.5	0.031291095
XM_024991983.2	0.027952425	NM_001109795.2	0.047872789
XR_009491175.1	0.040622628	XM_059892748.1	0.045490122
NM_001105004.1	0.001284954	XM_010813128.4	0.025257624
XM_005223062.5	0.00209205	XM_059880872.1	0.049481251
XM_024996791.2	0.011136963	XM_059889955.1	0.020160179
XM_059891129.1	0.020355404	NM_001046097.1	0.03905645
NM_001205812.3	0.036288477	XM_002694517.7	0.030531635
XM_059887183.1	0.011727224	XM_059877947.1	0.032124827
XM_024979913.2	0.004713933	NM_001034394.2	0.047751643
NM_173900.2	9.55E-05	NM_001046529.2	0.04823306
XM_024981427.2	0.000309656	XM_010812654.4	0.025485
NM_174101.2	7.95E-05	XM_010802839.4	0.043213129

Supplementary table 2. List of enriched gene ontologies (Biological Process, Molecular Function and Cellular Component) and their fold enrichment and p-values

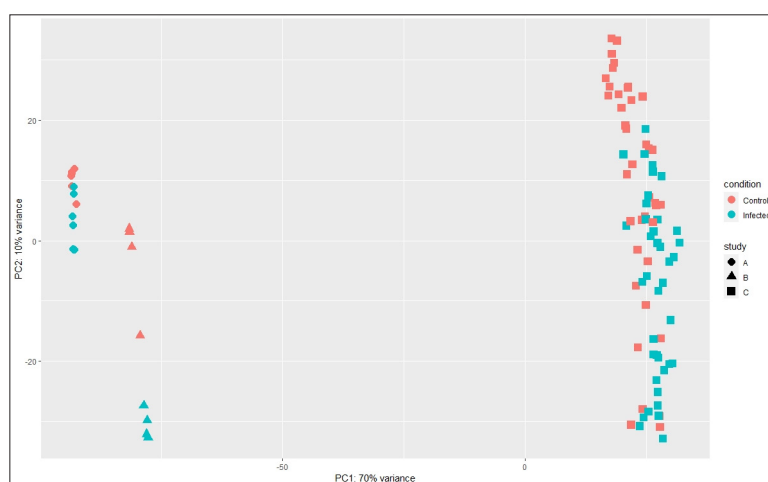
Analysis Type	PANTHER Overrepresentation Test (Released 20240807)						
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281/zenodo.12173881 Released 2024-06-17						
Analyzed List:	upreg_genes.txt (Bos taurus)						
Reference List:	Bos taurus (all genes in database)						
Test Type:	FISHER						
Correction:	FDR						
GO biological process complete	Bos taurus - REFLIST (23835)	upreg_genes.txt (4053)	upreg_genes.txt (expected)	upreg_genes.txt (over/under)	upreg_genes.txt (fold Enrichment)	upreg_genes.txt (raw P-value)	upreg_genes.txt (FDR)
regulation of dendritic cell antigen processing and presentation (GO:0002604)	5	5	0.85	+	5.88	1.42E-04	2.38E-03
beta-alanine biosynthetic process (GO:0019483)	3	3	0.51	+	5.88	4.91E-03	4.74E-02
glyceraldehyde-3-phosphate biosynthetic process (GO:0046166)	3	3	0.51	+	5.88	4.91E-03	4.73E-02
positive regulation of toll-like receptor 7 signaling pathway (GO:0034157)	3	3	0.51	+	5.88	4.91E-03	4.73E-02
regulation of toll-like receptor 7 signaling pathway (GO:0034155)	3	3	0.51	+	5.88	4.91E-03	4.73E-02
regulation of MyD88-dependent toll-like receptor signaling pathway (GO:0034124)	3	3	0.51	+	5.88	4.91E-03	4.72E-02
substrate-dependent cell migration, cell extension (GO:0006930)	3	3	0.51	+	5.88	4.91E-03	4.72E-02
peptide antigen assembly with MHC class I protein complex (GO:0002502)	3	3	0.51	+	5.88	4.91E-03	4.72E-02
regulation of T-helper 1 cell differentiation (GO:0045625)	3	3	0.51	+	5.88	4.91E-03	4.71E-02
growth hormone receptor signaling pathway via JAK-STAT (GO:0060397)	10	10	1.7	+	5.88	2.00E-08	6.95E-07
Fc receptor mediated stimulatory signaling pathway (GO:0002431)	3	3	0.51	+	5.88	4.91E-03	4.71E-02
heme B biosynthetic process (GO:0006785)	3	3	0.51	+	5.88	4.91E-03	4.70E-02
positive regulation of protein K63-linked ubiquitination (GO:1902523)	3	3	0.51	+	5.88	4.91E-03	4.70E-02
MHC class I protein complex assembly (GO:0002397)	3	3	0.51	+	5.88	4.91E-03	4.70E-02
cellular response to triacyl bacterial lipopeptide (GO:0071727)	3	3	0.51	+	5.88	4.91E-03	4.69E-02

Supplementary table 3. Topological analysis result for top 10% of genes based on degree obtained in PPI network.

Average Shortest Path Length	Betweenness Centrality	Closeness Centrality	Clustering Coefficient	Degree	Eccentricity	IsSingleNode	name	Neighborhood Connectivity	Number Of Directed Edges	Number Of Undirected Edges
2.07722998	0.029894786	0.481410344	0.093024387	812	4	FALSE	"9913. ENSBTAP000000037577"	82.00738916	0	812
2.093758906	0.024947555	0.477609909	0.125709417	764	4	FALSE	"9913. ENSBTAP000000022919"	83.85078534	0	764
2.132516386	0.033341074	0.468929574	0.06768476	712	4	FALSE	"9913. ENSBTAP000000026654"	65.3258427	0	712
2.214591052	0.016481515	0.451550637	0.139811577	704	4	FALSE	"9913. ENSBTAP000000035682"	86.92897727	0	704
2.292960958	0.010331423	0.436117325	0.145774805	600	4	FALSE	"9913. ENSBTAP000000019865"	77.39666667	0	600
2.287831291	0.008298116	0.437095167	0.163820907	504	4	FALSE	"9913. ENSBTAP000000028687"	86.05952381	0	504
2.198632089	0.009536236	0.454828257	0.139868603	482	4	FALSE	"9913. ENSBTAP000000017497"	84.21991791	0	482
2.36677116	0.005791522	0.422516556	0.191690099	466	4	FALSE	"9913. ENSBTAP000000053390"	90.41630901	0	466
2.420062696	0.0033877	0.413212435	0.20214568	462	5	FALSE	"9913. ENSBTAP000000008793"	83.63636364	0	462
2.306355087	0.007154072	0.433584579	0.151888751	440	4	FALSE	"9913. ENSBTAP000000019573"	88.95	0	440
2.250498718	0.008859667	0.444345954	0.135980897	438	4	FALSE	"9913. ENSBTAP000000011767"	87.7260274	0	438
2.281561698	0.006410032	0.438296278	0.162739678	428	4	FALSE	"9913. ENSBTAP000000010361"	93.20093458	0	428
2.354516956	0.004223082	0.424715565	0.210811052	424	5	FALSE	"9913. ENSBTAP0000000008190"	93.47169811	0	424
2.264747791	0.005304915	0.441550271	0.1741819	422	4	FALSE	"9913. ENSBTAP000000023277"	100.3270142	0	422
2.412083215	0.002888036	0.414579395	0.230151207	422	5	FALSE	"9913. ENSBTAP000000026275"	92.16113744	0	422
2.236819607	0.00952756	0.44706332	0.104236343	416	4	FALSE	"9913. ENSBTAP000000013623"	77.20192308	0	416
2.242519236	0.009024393	0.445927056	0.141629506	416	4	FALSE	"9913. ENSBTAP000000021838"	89.89423077	0	416

Supplementary table 4. Description of hub genes

Gene symbol	Ensemble Id	Gene name	score
PSMB3	ENSBTAP00000017816	Proteasome subunit beta type-6	5.18E+59
PSMD8	ENSBTAP00000042312	26S proteasome non-ATPase regulatory subunit 8	5.18E+59
PSMA5	ENSBTAP00000027507	Proteasome subunit alpha type-5;	5.18E+59
PSMA1	ENSBTAP00000008621	Proteasome subunit alpha type-1	5.18E+59
PSMB2	ENSBTAP00000058051	Proteasome subunit beta type-2	5.18E+59
PSMA4	ENSBTAP00000019203	Proteasome subunit alpha type-4	5.18E+59
PSMB10	ENSBTAP00000063146	Proteasome subunit beta type-10	5.18E+59
PSMA7	ENSBTAP00000006760	Proteasome subunit alpha type-7	5.18E+59
PSMD1	ENSBTAP00000006754	26S proteasome non-ATPase regulatory subunit 1	5.18E+59
PSMB4	ENSBTAP00000028364	Proteasome subunit beta type-4	5.18E+59



Supplementary fig. 1. PCA plot for the three studies: diamonds for study A (PRJNA194043), triangles for study B (PRJNA480009), and squares for study C (PRJNA264301). Pink dots represent controls, and blue dots represent infected samples.