

**Table S1.** Summary of Gene ontology (GO) enrichment terms related to the differentially expressed genes (DEGs)

Category	Term	Description	Count	P-Value	Genes
BP	GO:0051301	Cell division	12	1.13E-04	<i>FAM83D</i> , <i>CCNB1</i> , <i>CDK1</i> , <i>CCNB2</i> , <i>ZWINT</i> , <i>TPX2</i> , <i>BIRC5</i> , <i>AURKA</i> , <i>PTTG1</i> , <i>UBE2C</i> , <i>ASPM</i>
BP	GO:0007067	Mitotic nuclear division	8	0.003429	<i>FAM83D</i> , <i>CDK1</i> , <i>CCNB2</i> , <i>ZWINT</i> , <i>CENPW</i> , <i>PTTG1</i> , <i>ASPM</i>
BP	GO:0006954	Inflammatory response	11	0.00705	<i>CCL2</i> , <i>CCL20</i> , <i>CRHBP</i> , <i>KLKB1</i> , <i>CXCL2</i> , <i>TBXA2R</i> , <i>CCL19</i> , <i>CCL5</i> , <i>CXCL12</i> , <i>ECM1</i>
CC	GO:0070062	Extracellular exosome	86	2.82E-13	<i>STEAP4</i> , <i>NAMPT</i> , <i>S100A8</i> , <i>MASP2</i> , <i>SORL1</i> , <i>ANO1</i> , <i>CRP</i> , <i>SPINK1</i> , <i>CXCL12</i> , <i>BBOX1</i> , <i>PRKAR2B</i> , <i>TP53I3</i> , <i>GPC3</i> , <i>TKFC</i> , <i>LCAT</i> , <i>PGLYRP2</i> , <i>PROZ</i> , <i>SERPINA4</i> , <i>SHBG</i> , <i>F11</i> , <i>ALDH6A1</i> , <i>CDK1</i> , <i>CDHR2</i> , <i>FBP1</i> , <i>LIFR</i> , <i>IGFALS</i> , <i>F9</i> , <i>CFTR</i> , <i>SLC3A1</i> , <i>THY1</i> , <i>C8A</i> , <i>C8B</i> , <i>RND3</i> , <i>CTH</i> , <i>TACSTD2</i> , <i>SERPINF2</i> , <i>BHMT</i> , <i>HAO2</i> , <i>HSPB1</i> , <i>CA2</i> , <i>STMN1</i> , <i>AKR1D1</i> , <i>SLC27A2</i> , <i>C7</i> , <i>ACADSB</i> , <i>C9</i> , <i>ASS1</i> , <i>LUM</i> , <i>C6</i> , <i>PTH1R</i> , <i>JCHAIN</i> , <i>DPYS</i> , <i>KMO</i> , <i>SFN</i> , <i>ARG1</i> , <i>ANGPTL6</i> , <i>KLKB1</i> , <i>ENO3</i> , <i>HRG</i> , <i>SLC39A5</i> , <i>SPP2</i> , <i>SPP1</i> , <i>DPT</i> , <i>THBS4</i> , <i>GPD1</i> , <i>HOGA1</i> , <i>EPHX2</i> , <i>FTCD</i> , <i>ACMSD</i> , <i>CD5L</i> , <i>TKT</i> , <i>RACGAP1</i> , <i>ECM1</i> , <i>MAN1C1</i> , <i>PCK1</i> , <i>A1BG</i> , <i>LYVE1</i> , <i>AFM</i> , <i>GLYAT</i> , <i>HPX</i> , <i>FBLN5</i> ,

CC	GO:0072562	Blood microparticle	13	7.61E-09	<i>PONI, CP, HPGD, IGFBP3, FABP5</i>
CC	GO:0005615	Extracellular space	39	2.25E-06	<i>C9, JCHAIN, CD5L, C8A, A1BG, AFM, BCHE, HPX, SERPINF2, APOA5, PONI, HRG, CP</i>
CC	GO:0005739	Mitochondrion	29	0.002339	<i>XDH, MBL2, CCL2, S100A8, ADAMTS13, CRHBP, LUM, CRP, CXCL2, SORL1, CD109, SPINK1, CCL5, PTGIS, CCL20, BCHE, ANG, KLKB1, PROZ, SERPINA4, ENO3, NRG1, SPP1, THBS4, DPT, F11, IGF1, CCL19, F9, DBH, ECM1, BMPER, SERPINF2, TACSTD2, FBLN5, PONI, HSPB1, IGFBP3</i>
CC	GO:0005576	Extracellular region	18	0.009137	<i>ETNPPL, ACADSB, OGDHL, BBOX1, ACSL1, GSTZ1, SLC25A47, DMGDH, GPT2, FLVCR1, AADAT, ALDH6A1, GCDH, GPD1, CDK1, GABARAPL1, OTC, HOGA1, ACACB, ACADL, TAT, GLYAT, ANXA10, SDS, HAO2, AGXT2, SLC27A2, OAT, BCO2</i>
MF	GO:0020037	Heme binding	14	8.69E-07	<i>F11, C7, C6, PAMR1, CIR, COLEC11, PLG, LCN2, REG3A, CXCL14, PROZ, TEK, PONI, LECT2, DEFBI, TFPI2, GHR, SPP1</i>
					<i>CYP2C18, IDO2, CYP26A1, CYP2E1, CYP4V2, CYP4A11, TDO2, PTGIS,</i>

MF	GO:0008009	Chemokine activity	8	6.33E-06	<i>CYP39A1, HRG, CYP4F2, CYP8B1, HBB, CCL2, CXCL14, CCL20, CXCL2, CCL19, CCL5, CXCL12</i>
MF	GO:0016491	Oxidoreductase activity	12	1.11E-05	<i>XDH, HAO1, AKR1C3, AKR1B10, ADHIC, ADH6, HSD17B6, CP, MCM3, RDH16, AKR1D1</i>
MF	GO:0005506	Iron ion binding	13	2.99E-05	<i>XDH, CYP4A11, CYP39A1, PTGIS, CYP2C18, CYP26A1, CYP2E1, CYP4V2, CYP4F2, CYP8B1, HBB, BBOX1</i>
MF	GO:0030170	Pyridoxal phosphate binding	8	1.25E-04	<i>ETNPPL, AADAT, CTH, SDS, AGXT2, TAT, GPT2, OAT</i>
MF	GO:0042802	Identical protein binding	9	0.006021	<i>ETNPPL, UHRF1, ASS1, BCHE, FBP1, CIDEB, AGXT2, LECT2, OAT</i>

**Table S2.** Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of differentially expressed genes (DEGs).

Term	Description	Count	P-Value	Genes
bta01100	Metabolic pathways	65	2.46E-10	<i>ETNPPL, NAMPT, CNDP1, CYP2C18, OGDHL, ADHIC, TDO2, PTGIS, TKFC, GSTZ1, GPT2, HPD, AADAT, ALDH6A1, OTC, FBP1, CYP26A1, CYP2E1, ACADL, TAT, CTH, SDS, PANK1, SQLE, AKR1B10, BHMT, HAO2, OAT, AKR1D1, SLC27A5, XDH, ACADSB, HSD17B2, FOLH1B, ASS1, ADH6, DPYS, KMO, GLS2, ARG1, ACSL1, ADH4, ENO3, CDA, DMGDH, HSD17B6, GCDH, HOGA1, EPHX2, ACMSD, FTCD, IDO2, TKT, ACACB, DBH, CPS1,</i>

					<i>MANIC1, PCK1, GBA3, PHGDH, AGXT2, CYP4F2, CYP8B1, RDH16</i>
bta04610	Complement & coagulation cascades	14	1.64E-08		<i>F11, C7, MBL2, C9, MASP2, C6, F9, C1R, PLG, C8A, C8B, FGA, SERPINF2, KLKB1</i>
bta01230	Biosynthesis of amino acids	11	6.36E-06		<i>ARG1, CTH, ASS1, SDS, OTC, PHGDH, ENO3, TKT, CPS1, TAT, GPT2</i>
bta04976	Bile secretion	10	3.12E-05		<i>SLCO1B3, SULT2A1, SLC22A7, KCNN2, CFTR, CA2, SLC51A, SLC27A5, SLC10A1, SLC22A1</i>
bta01130	Biosynthesis of antibiotics	17	3.18E-05		<i>AADAT, GCDH, ASS1, OTC, OGDHL, FBP1, TKT, TAT, PCK1, ARG1, CTH, SDS, SQLE, HAO2, PHGDH, ENO3, OAT</i>
bta04115	p53 signaling pathway	10	4.44E-05		<i>STEAP3, CCNB1, CDK1, TP53I3, CDKN2A, CCNB2, IGF1, SFN, GADD45B, IGFBP3</i>
bta00220	Arginine biosynthesis	6	6.63E-05		<i>GLS2, ARG1, ASS1, OTC, CPS1, GPT2</i>
bta05020	Prion diseases	7	9.42E-05		<i>C8A, EGRI, C8B, C7, C9, C6, CCL5</i>
bta00380	Tryptophan metabolism	8	9.84E-05		<i>AADAT, GCDH, TDO2, OGDHL, IDO2, ACMSD, KMO, INMT</i>
bta01200	Carbon metabolism	11	2.68E-04		<i>ALDH6A1, TKFC, SDS, HAO2, OGDHL, PHGDH, FBP1, ENO3, TKT, CPS1, GPT2</i>
bta00350	Tyrosine metabolism	7	3.40E-04		<i>ADH4, ADH1C, ADH6, GSTZ1, DBH, TAT, HPD</i>
bta00260	Glycine, serine and threonine metabolism	7	3.91E-04		<i>CTH, SDS, BHMT, PHGDH, DMGDH, AGXT2, GNMT</i>
bta00071	Fatty acid degradation	7	3.91E-04		<i>GCDH, ACADSB, ACSLI, ADH4, ADH1C, ADH6, ACADL</i>
bta03320	PPAR signaling pathway	8	0.001359		<i>ACSL1, APOA5, CYP8B1, ACADL, SLC27A2, SLC27A5, FABP5, PCK1</i>
bta00250	Alanine, aspartate and	6	0.001545		<i>GLS2, ASS1, FOLH1B,</i>

---

	glutamate metabolism			<i>AGXT2, CPS1, GPT2</i>
bta00830	Retinol metabolism	7	0.002098	<i>CYP2C18, ADH4, ADH1C, ADH6, HSD17B6, CYP26A1, RDH16</i>
bta04110	Cell cycle	10	0.003013	<i>CCNB1, CDK1, CDKN2A, CCNB2, CDKN2C, SFN, PTTG1, MCM3, GADD45B</i>

---