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Table S1. The primer sequences of the target genes

Genes	Sequences
IL-6	Forward: AAGCCAGAGCTGTGCAGATGAGTA Reverse: TTCGTCAGCAGGCTGGCATTGT
RUNX2	Forward: TGCTTCATTCGCCTCACAA Reverse: CTTGCTGTCCTCCTGGAGAAA
β -catenin	Forward: TGGTGAAAATGCTTGGGTCG Reverse: TCTGAAGGCAGTCTGTGCGTAATAG
NF- κ B	Forward: CTGAGAACTGCTCGTGGTGT Reverse: GTTCCCATCAATACGCGTGC
HIF-2 α	Forward: GGCCAAACATGGAGGATATG Reverse: AGACCACCACGTCATTCTTCTC-
TAK1	Forward: CCATCCCAATGGCGTATCTTACA Reverse: TCATCCTGGTCCAATTCTGCAA
MMP13	Forward: AGTCCTTTTGGCCAGAACTCC Reverse: AAGATGAACATGAGGTCTCGGG
GAPDH	Forward: GAAGGTGAAGGTCCGAGTC Reverse: GAAGATGGTGATGGGATTTC

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5 **Table S2. Upregulated proteins in the BIIP group compared with the model group.**

BIIP & Model	Protein ID	Protein Name
1	A0A0G2JSK9	Betaine--homocysteine S-methyltransferase 1
2	A0A0G2JZK2	Uncharacterized protein
3	A0A0G2K5U5	Polymeric immunoglobulin receptor
4	A0A0G2K5W3	Ig-like domain-containing protein
5	A0A0G2K607	Leukocyte immunoglobulin-like receptor subfamily B member 3A
6	B0BN33	C-type lectin domain-containing protein
7	B2RZA9	Ube2l3 protein
8	D4AB01	Histidine triad nucleotide binding protein 2 (Predicted), isoform CRA_a
9	F1M0Q9	Peptidase M20 domain-containing 1
10	F1M3X5	Maestro heat-like repeat family member 6
11	M0R838	Ig-like domain-containing protein
12	M0RCN6	Similar to immunoglobulin kappa-chain VK-1
13	P07756	Carbamoyl-phosphate synthase [ammonia], mitochondrial
14	P61983	14-3-3 protein gamma
15	P63039	60 kDa heat shock protein, mit ochondrial
16	Q2HWF0	Formin-binding protein 1-like
17	Q4KLF8	Actin-related protein 2/3 complex subunit 5
18	Q5PQU8	Tissue factor pathway inhibitor

19	Q66H11	GTP-binding protein Ran
20	Q6P505	Proteasome subunit alpha type
21	Q6P743	Adenosylhomocysteinase
22	Q8K571	ADH-like protein
23	Q924C3	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1
24	Q924S5	Lon protease homolog, mitochondrial

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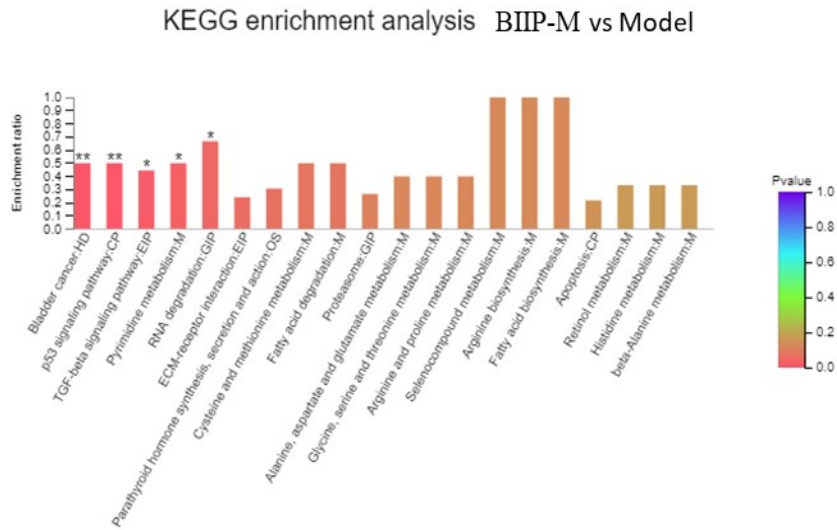
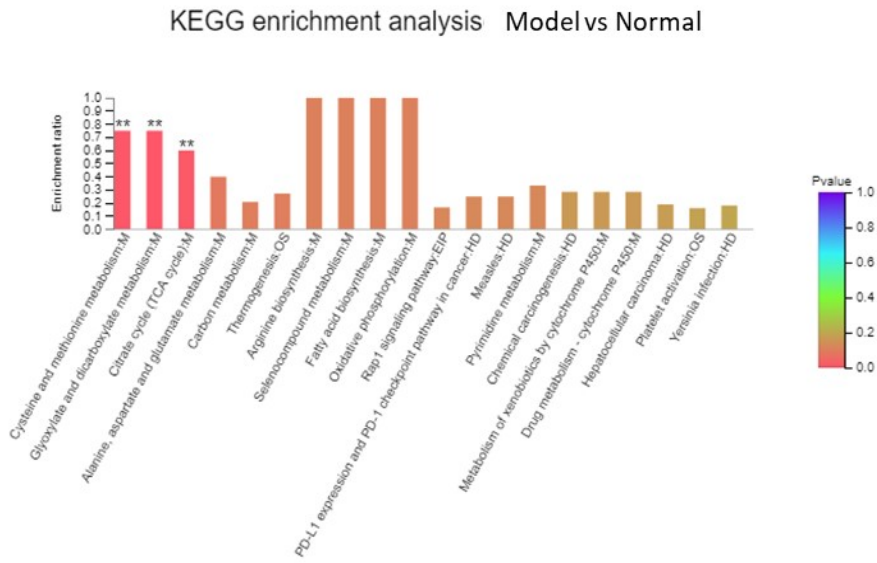
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8 **Table S3. Downregulated proteins in the BIIP group compared with the model group.**

BIIP& Model	Protein ID	Protein Name
1	A0A096MJM7	Neuralized E3 ubiquitin protein ligase 1
2	A0A0G2JVW1	Insulin-like growth factor-binding protein 5
3	A0A0G2K290	Ig-like domain-containing protein
4	A0A0G2K8E6	Vesicle-associated membrane protein-associated protein A
5	A0A0G2K8K3	Heparin cofactor 2
6	A0A0G2K905	Arp2/3 complex 34 kDa subunit
7	A0A0H2UHP7	Apolipoprotein A-V
8	A0S0A9	Brush border membrane zinc transporter ZIP10
9	B5DEZ8	Plexin domain containing 2 (Predicted)
10	D3ZD40	Papilin, proteoglycan-like sulfated glycoprotein
11	D3ZE87	G_PROTEIN_RECEP_F3_4 domain-containing protein
12	D3ZGF1	CD44 antigen
13	D3ZIE4	FYN-binding protein 1
14	D3ZPI8	Complement C8 gamma chain
15	F1LM84	Nidogen-1
16	F1LMS5	Thrombospondin-4
17	F1LS29	Calcium-activated neutral proteinase 1
18	F1LUM5	Tubulin alpha chain
19	G3V615	C3/C5 convertase

20	G3V6S0	Spectrin β chain
21	G3V6S3	Calumenin
22	G3V7Q6	Proteasome subunit β
23	G3V9R2	Complement factor H
24	M0R585	Ig-like domain-containing protein
25	M0R8B5	Ig-like domain-containing protein
26	M0R979	Thrombospondin 1
27	M0RBL2	Ig-like domain-containing protein
28	M0RCM6	Ig-like domain-containing protein
29	M0RD20	Calcium-activated neutral proteinase small subunit
30	M0RDF0	Ig-like domain-containing protein
31	M0RDL2	Ig-like domain-containing protein
32	O70513	Galectin-3-binding protein
33	O88656	Actin-related protein 2/3 complex subunit 1B
34	P00762	Anionic trypsin-1
35	P01681	Ig kappa chain V region S211
36	P01805	Ig heavy chain V region IR2
37	P01883	Ig delta chain C region
38	P02767	Transthyretin
39	P16296	Coagulation factor IX
40	P25113	Phosphoglycerate mutase 1

41	P28064	Proteasome subunit β type-8
42	P50123	Glutamyl aminopeptidase
43	P69897	Tubulin β -5 chain
44	Q3KR94	Vitronectin
45	Q4KM35	Proteasome subunit β type-10
46	Q4KM73	UMP-CMP kinase
47	Q5EBC0	Inter alpha-trypsin inhibitor, heavy chain 4
48	Q5M7T5	Antithrombin-III
49	Q5M7V3	LOC367586 protein
50	Q5RJR2	Twinfilin-1
51	Q62862	Dual specificity mitogen-activated protein kinase kinase 5
52	Q62975	Protein Z-dependent protease inhibitor
53	Q68FT8	RCG33981, isoform CRA_a
54	Q6IFV1	Keratin, type I cytoskeletal 14
55	Q6P3V8	RNA helicase
56	Q6PAH0	Apolipoprotein E
57	Q9JLJ3	4-trimethylaminobutyraldehyde dehydrogenase
58	Q6IRK9	Carboxypeptidase Q



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13 **Figure S1. KEGG functional enrichment analysis. ** represents $P < 0.01$, and * represents**

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$P < 0.05$.

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