

Supplementary Table 1. Primers used for Real-time PCR

Gene	Primer sequence (5'to3')	Product size (bp)	Genbank
Reference gene			
GAPDH	F: ATGGTGAAGGTCGGAGTGAA R: CCGTGGGTGGAATCATACTG	155	NM_001206359.1
Antioxidant status			
HO1	F: AGGCTGAGAATGCCGAGTTC R: TGTGGTACAAGGACGCCATC	90	NM_001004027.1
NQO1	F: CCAGCAGCCCCGGCCAATCTG R: AGGTCCGACACGGCGACCTC	160	NM_001159613.1
SOD1	F: TCCATGTCCATCAGTTTGGGA R: AGTCACATTGCCCAGGTCTC	131	NM_001190422.1
CAT	F: ACGCCTGTGTGAGAACATTG R: GTCCAGAAGAGCCTGAATGC	124	NM_214301.2
SOD2	F: TGGAGGCCACATCAATCATA R: TTTCGAAGGAACCAAAGTCG	113	NM_214127.2
GPX4	F: CACCCTCTGTGGAAGTGGAT R: TCACCACACAGCCGTTCTTA	112	NM_214407.1
GPX1	F: AAATGCTCACCCGCTCTTC R: GTCATTGCGACACACTGGAG	118	NM_214201.1
SOD3	F: ACGCTGCTCTGTGCTTACCT R: CTGCCAGATCTCCGTCCTT	135	NM_001078688.1
GCLC	F: CTTGCCTCTTGCTGTGTGAT R: CCACTCATGTGCCTCGATGT	159	XM_001926378.4
MGST1	F: TTGGCGCGCAATCTACCACA R: TCCTCGGCTCCCTTCCCACTTA	239	NM_214300.1
UGT1A1	F: GATCCTTTCCTGCAACGCAT R: GGAAGGTCATGTGATCTGAG	313	XM_001927673
TXNRD1	F: CTTTACCTTATTGCCCGGGT R: GTTCACCGATTTTGTTGGCC	162	NM_214154.2
Cytokines			
TNF- $\alpha$	CATGAGCACTGAGAGCATGA CGATAACTTCGAAGTGCAGT	170	NM_214022.1
IL- $\alpha$	F: CTGAAGAAGAGACGGTTGAG R: GCACTGGTGGTT GATGAC	162	NM_214029
IL-1 $\beta$	F: GTTCTCTGAGAAATGGGAGC R: CTGGTCATCATCACAGAAGG	143	NM_214055.1
IL-2	F: TTGCACTCATGGCAAACGGT R: ATTCTGTAGCCTGCTTGGGC	177	NM_213861.1
IL-6	F: AGCAAGGAGGTAAGTGGCAGA R: GTGGTGGCTTTGTCTGGATT	257	NM_001252429.1
IL-8	F: ACTTCCAAACTGGCTGTTGC R: GGAATGCGTATTTATGCACTGG	120	NM_213867.1
Tight junction proteins			
ZO-1	F: AGCTGCCTCTCAACAGAAAG R: GTCTCTGGGCACTGTGTGAG	217	XM_005659811.1
Occludin	F: GAGTACATGGCTGCTGCTGA R: AACAAGGTGGCCTCTGTCTC	173	NM_001163647.2
Claudin 1	F: CTGAACACCACTTTGCAAGC	137	NM_001244539.1

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R: ATCCGCATCTTCTGCACCTC

Glucose transportein

SLC2A1	F: GCCTGAGACCAGTTGAAAGCAC R: CTGCTTAGGTAAAGTTACAGGAG	155	XM_021096908.1
SLC2A3	F: TGCACGGGCTTTGTGCCGATG R: AAGGAGGTGAAGATTAGGAA	132	XM_021092391.1

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GPx4, glutathione peroxidase 4; GPx1, glutathione peroxidase 1; CAT, catalase; SOD3, superoxide dismutase 3; SOD2, superoxide dismutase 2; SOD1, superoxide dismutase 1; NQO1, NAD(P)H quinone dehydrogenase 1; HO1, heme oxygenase 1; CYP1A1, cytochrome P450 family 1 subfamily A member 1; TXNRD1, thioredoxin reductase 1; GCLM, glutamate-cysteine ligase modifier; MGST1, microsomal glutathione S-transferase 1; UGT1A1, UDP glucuronosyl-transferase family 1 member A1; IL-1, interleukin 1; IL-6, interleukin 6; IL-8, interleukin 8; TNF- $\alpha$ , tumor necrosis factor  $\alpha$

**Supplementary Table 2.** 16s rDNA sequencing data analysis

<b>Item</b>	<b>PE Reads</b>	<b>Raw Tags</b>	<b>Clean Tags</b>	<b>Effective Tags</b>	<b>AvgLen (bp)</b>	<b>Q20 %</b>	<b>Q30 %</b>	<b>GC %</b>	<b>Effective (%)</b>
Con1	48,276	43,350	35,892	35,321	419	94.48	89.48	53.35	73.16
Con2	51,487	45,215	36,303	35,366	422	94.13	88.80	53.50	68.69
Con3	34,880	31,082	25,449	24,811	420	94.30	89.13	53.19	71.13
Con4	57,363	52,459	45,059	43,699	416	94.80	90.12	52.02	76.18
Con5	41,882	37,718	31,338	30,484	422	94.39	89.35	52.93	72.79
PQQ1	37,162	34,150	29,107	28,369	419	94.93	90.34	52.79	76.34
PQQ2	50,437	45,283	38,170	37,370	419	94.40	89.44	52.45	74.09
PQQ3	35,494	32,272	27,076	26,449	420	94.62	89.78	52.71	74.52
PQQ4	47,231	42,655	36,441	35,041	417	94.70	89.97	50.91	74.19
PQQ5	68,548	60,036	49,295	48,797	418	94.23	89.00	52.99	71.19

PE Reads is the number of double-ended reads obtained by sequencing; Raw Tags is the number of original sequences obtained by double-ended reads; Clean Tags is the number of optimized sequences obtained by filtering the original sequence; and Effective Tags is the number of valid sequences after filtering the chimeras by Clean Tags ;AvgLen (bp) is the average sequence length of the sample; Effective (%) is the percentage of Effective Tags to PE Reads; Q20%, the percentage of the sequence with the quality value equal or greater than 20; Q30%, the percentage of the sequence with the quality value equal or greater than 30; GC%, the percentage of GC base; Con, post-weaning piglets from control group; PQQ, post-weaning piglets from PQQ·Na<sub>2</sub> group

**Supplementary Table 3.** 16s rDNA sequencing data analysis

Item	Kindom	Phylum	Class	Order	Family	Genus	Species
Con1	26,905	26,905	26,904	26,904	26,855	25,802	23,515
Con2	27,859	27,859	27,853	27,853	27,842	25,308	22,471
Con3	18,591	18,591	18,573	18,571	18,565	17,646	16,366
Con4	37,126	37,126	37,126	37,110	37,059	35,899	27,202
Con5	25,800	25,800	25,800	25,796	25,782	24,851	17,429
PQQ1	23,568	23,568	23,558	23,558	23,448	22,464	18,848
PQQ2	29,681	29,681	29,679	29,679	29,641	28,326	25,806
PQQ3	20,460	20,460	20,455	20,455	20,445	19,402	17,553
PQQ4	30,923	30,923	30,923	30,923	30,899	28,726	26,897
PQQ5	40,072	40,072	40,071	40,071	40,071	37,059	32,699