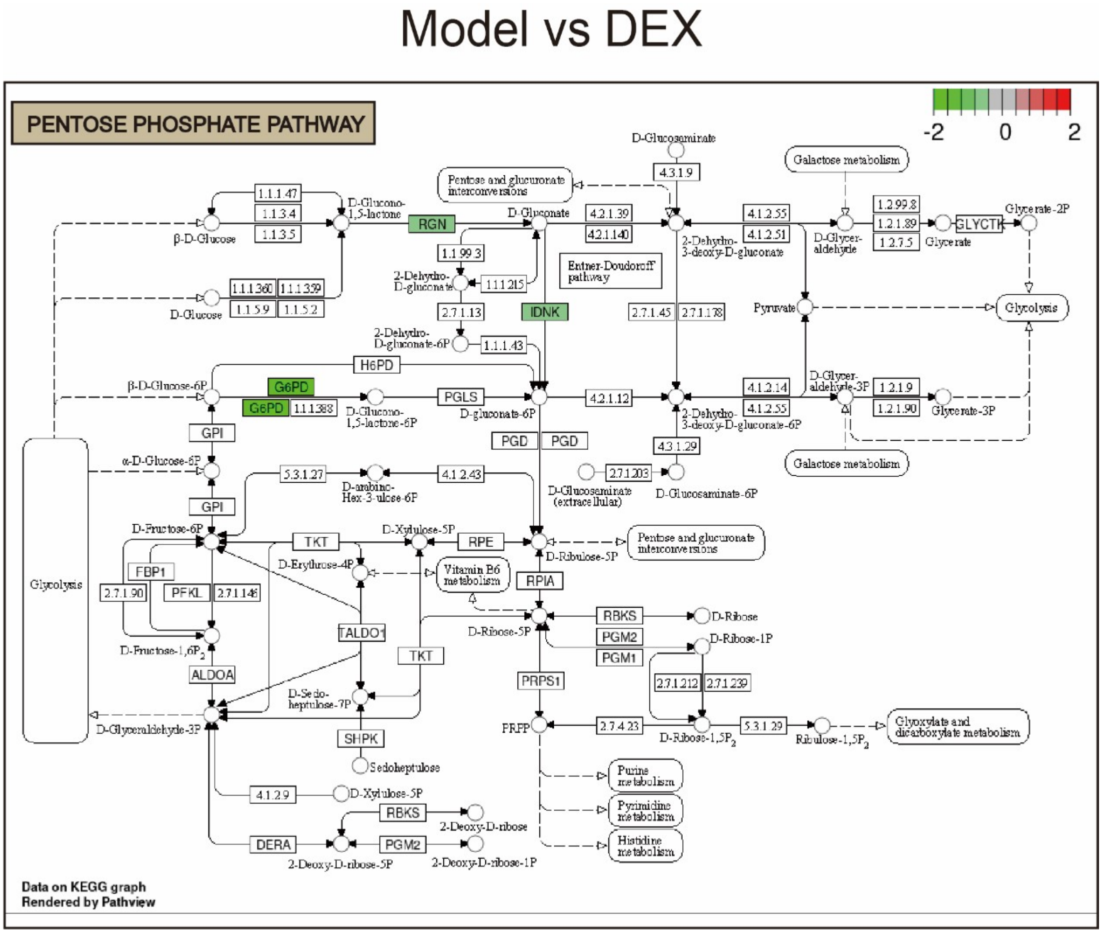
Electronic Supplementary Material (ESI) for Food & Function.

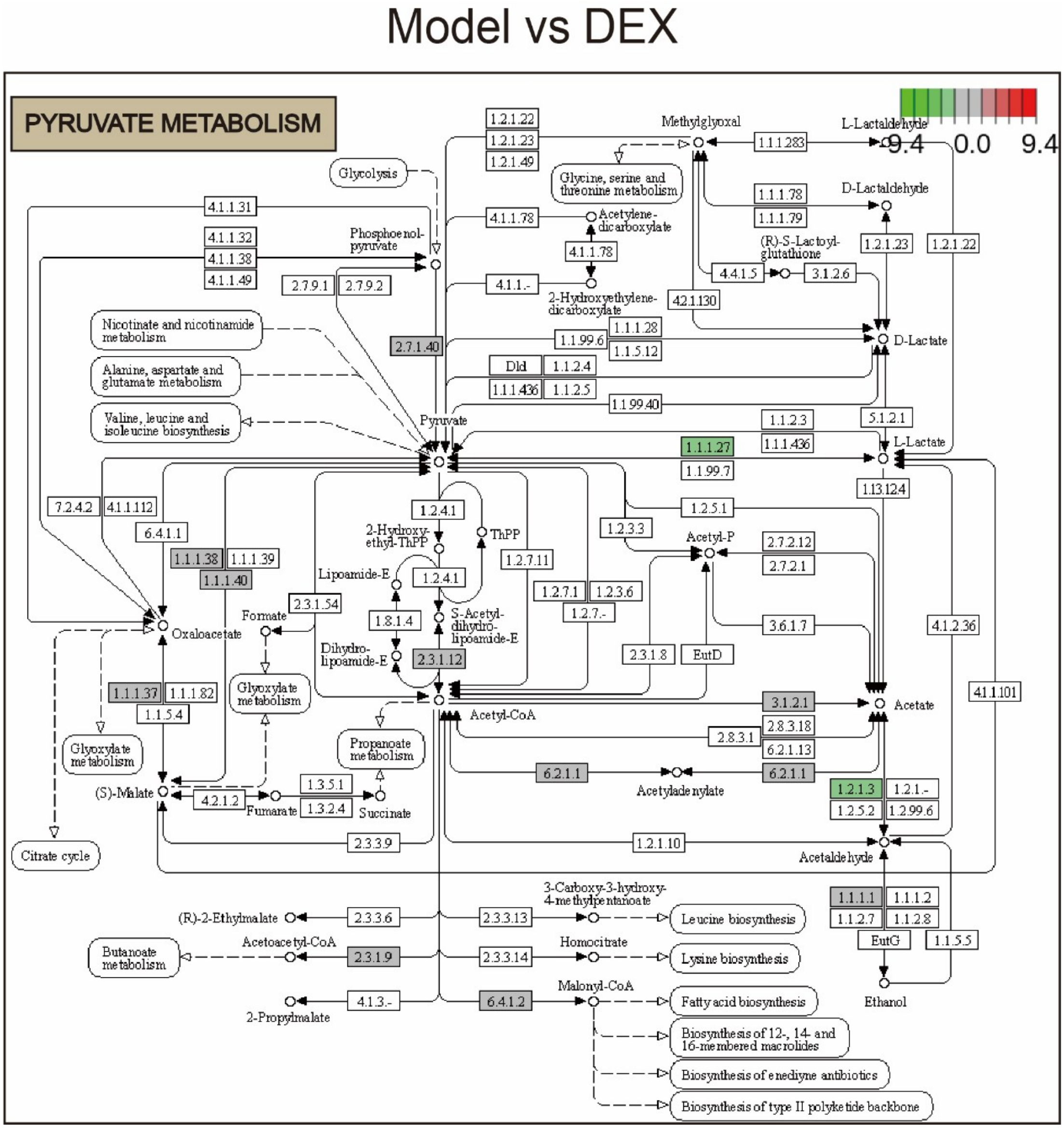
Supplementary Figure and Table

Supplementary Figure S1



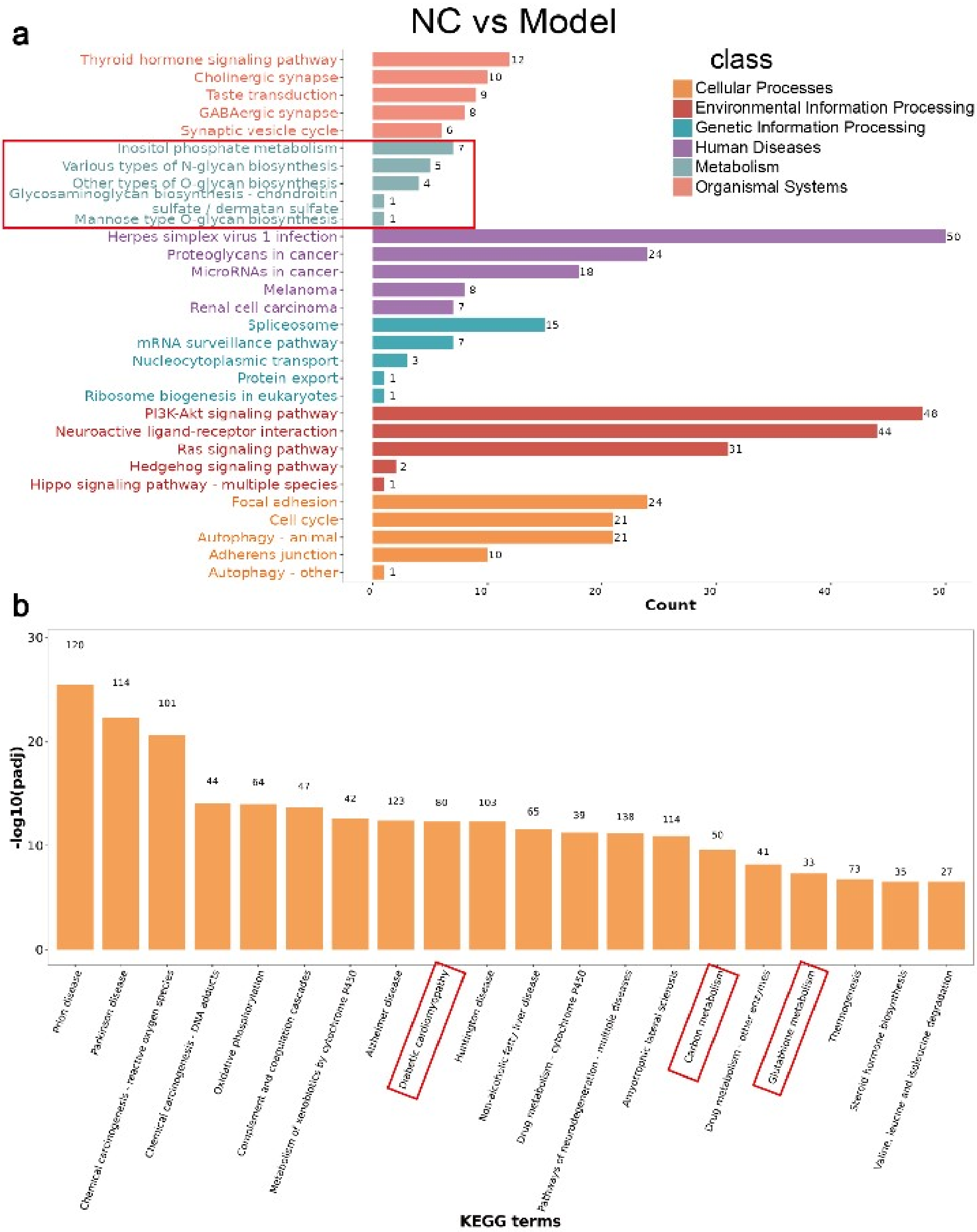
KEGG map show the genes involved in pyruvate metabolism (n=3, *P*＜0.05).

Supplementary Figure S2



KEGG map show the genes involved in pentose phosphate pathway. (n=3, $P < 0.05$)

Supplementary Figure S3



KEGG pathway enrichment analysis in Model group

KEGG pathway enrichment analysis of the top-ranked enriched pathways according to different functional categories (**a**) or the top 20 pathways (**b**) enriched in hepatic tissue of AA rats. (n=3, *P*＜0.05)

Supplementary Table1 Specific primers for quantitative real-time PCR analysis (qRT-PCR)

Gene	**Forward primer (5′ to 3′)**	**Reverse primer (5′ to 3′)**
Rat-*PCK1*	AACTGTTGGCTGGCTCTCACTG	CACGGTGTCTCTCTGCTCTTGG
Rat-*G6PD*	CGCAAACAGAGTGAGCCCTTC	GTGGCTGTTGAGGTGCTTGTAG
Rat-*β-actin*	TGTCACCAACTGGGACGATA	GGGGTGTTGAAGGTCTCAAA
Human-*TNF-α*	AGCACTGAAAGCATGATCCG	CCGATCACTCCAAAGTGCAG
Human-*IL-10*	CCTGCCTAACATGCTTCGAG	GGCAACCCAGGTAACCCTTA
Human-*PCK1*	CCAATGCCATCAAGACCATCCAG	TCATCAATGCCTTCCCAGTAAACG
Human-*G6PD*	CAGCCACATGAATGCCCTCCAC	CTTCTCCACGATGATGCGGTTCC
Human-*RARRES2*	ATGCGACGGCTGCTGATCC	GGCGGGTGCTTGTGAAATTCC
Human-*MMP25*	CGACCTGAGCCTCTGGGAAG	CTCGGTCTTGATGCTGTTCTTGG
Human-*FILIP1*	GGCACTGTCCTTCGCTCTCC	CCTGACACTGACTGGGTTCCTC
Human-*MATR3*	GTCCAAGTCATTCCAGCAGTCATC	TGGGTAGCAGCAGCAAGAAGG
Human-*β-actin*	CCTGGCACCCAGCACAAT	GGGCCGGACTCGTCATAC

Supplementary Table2 Statistical results of differentially expressed genes by RNA sequencing of RA-FLS

Comparision	**# up-regulated genes**	**# down-regulated genes**	**Total**
Control vs DEX	156	159	315
Control vs GCK	149	188	337

Notes: $^{\#}P<0.05$ *vs*. Control group （n=3）.

Supplementary Table 3 GR target genes co-regulated by GCK and DEX in RA-FLS

Comparision	# up-regulated genes	# down-regulated genes
Control vs DEX	FRRS1 C8orf44-SGK3 C18orf25 SNAP25 TSNAXIP1 **MATR3** SLC12A6 SH3TC1 FAM171B **FILIP1** TRPC3 TAPT1 MORC2	CBX4 SRCAP GLUL UBXN11 PDE4C FAM53B RHOF TSC22D3 **MMP25** ESR2 **RARRES2** SNURF
Control vs GCK	FRRS1 C8orf44-SGK3 C18orf25 SNAP25 TSNAXIP1 SLC12A6 **MATR3** GLUL SH3TC1 TSC22D3 FAM171B **FILIP1** TRPC3 TAPT1 MORC2	CBX4 SRCAP UBXN11 PDE4C FAM53B RHOF **MMP25** ESR2 **RARRES2** SNURF

Notes: differential genes co-regulated by DEX and GCK in the RNA-sequence of RA-FLS results from intersections taken with the target genes predicted by the chip-atlas database for NR3C1 (±1k from the transcription start site TSS). Genes in bold font are genes suggested by the pubmed database to be associated with arthritis development. $^{\#}P<0.05$ *vs*. Control group （n=3）.