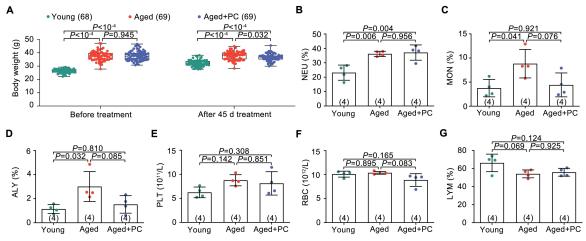
## Supplementary Information (SI) for Food & Function. This journal is © The Royal Society of Chemistry 2025



1YoungAged

3 Body weight mensurements were taken at baseline and 45 days post-gavage with saline or PC. (B)

4 Percentage of neutrophils. (C) Percentage of monocytes. (D) Percentage of abnormal lymphocytes. (E)

5 Platelet count. (F) Red blood cell count. (G) Lymphocyte ratio. For (A), whiskers indicate min to max.

6 For (B-G), data are presented as mean  $\pm$  SD. Data were processed by one-way ANOVA followed by

7 Tukey multiple-comparison post hoc tests. P<0.05 indicates significant differences between

8 treatments. The number of mice in each group is indicated in parentheses.

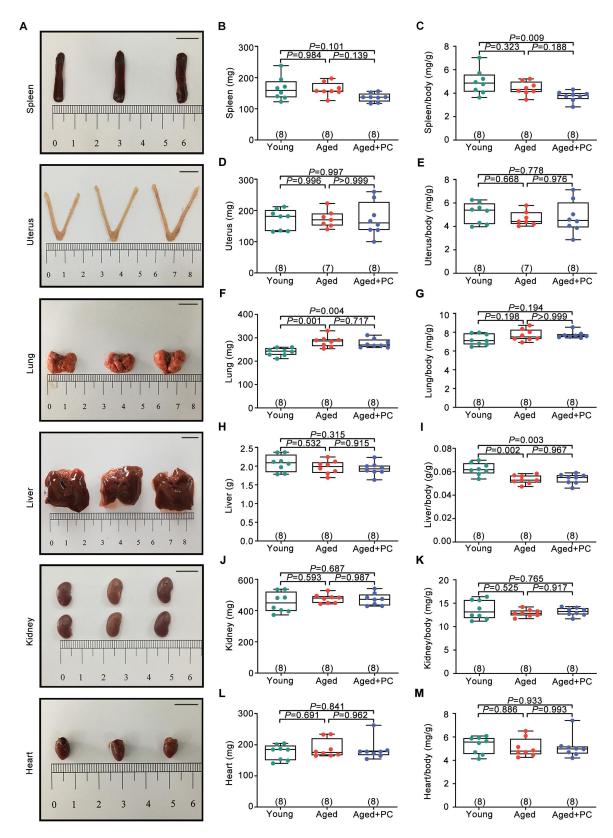
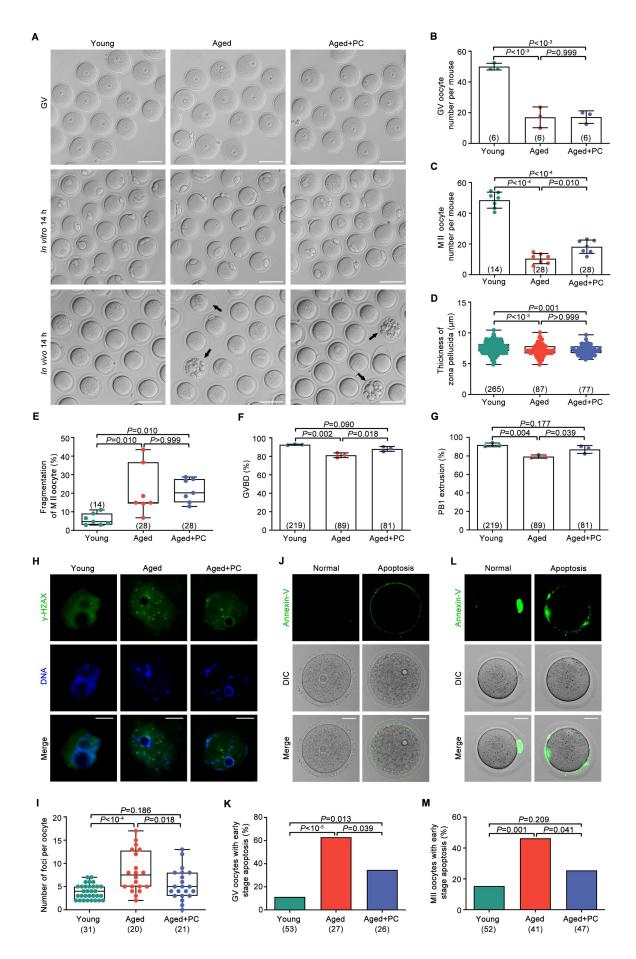




Fig. S2. PC has no effect on organ weight and relative organ weight in naturally aged mice. (A)
Organ views. No significant morphological differences were observed between treatments. Scale bar
= 1 cm. (B) Spleen weight. (C) Relative spleen weight. (D) Uterus weight. (E) Relative uterus weight.
(F) Lung weight. (G) Relative lung weight. (H) Liver weight. (I) Relative liver weight. (J) Kidney

- 14 weight. (K) Relative kidney weight. (L) Heart weight. (M) Relative heart weight. Whiskers indicate
- 15 min to max. Data are processed by one-way ANOVA followed by Tukey multiple-comparison post
- 16 hoc tests. P<0.05 indicates significant differences between treatments. The number of mice in each
- 17 group is indicated in parentheses.



- 19 Fig. S3. PC rescues oocyte quality and reduces early apoptosis in naturally aged mice. (A) 20 Oocyte morphology was assessed at the GV and MII stages in vitro or in vivo. Morphologically abnormal oocytes are indicated by black arrow. Scale =  $100 \mu m$ . (B) Number of GV oocytes. (C) 21 22 Number of MII oocytes. (D) Zona pellucida thickness of GV oocytes. (E) Percentage of MII oocytes 23 with fragmentation morphologies. (F) Percentage of oocytes undergoing GVBD. (G) Percentage of oocytes undergoing PB1 extrusion. (H) Diagram of DNA double-strand breaks in GV oocytes. Scale 24 bar = 20 μm. (I) Number of DNA double-stranded breaks in GV oocytes. (J) Representative images of 25 26 normal and early apoptotic GV oocytes. Early apoptosis is labeled by green fluorescence on the 27 oocyte membrane. Scale bar = 20 μm. (K) Percentage of apoptosis in GV oocytes. (L) Representative images of normal and early apoptotic MII oocytes. Early apoptosis is labeled by green fluorescence on 28 29 the oocyte membrane. Scale bar =  $20 \,\mu\text{m}$ . (M) Percentage of apoptotic MII oocytes. For (B, C, F, G),
- 30 data are presented as mean  $\pm$  SD. For (D, E, I), whiskers indicate min to max. Data were processed by
- 31 one-way ANOVA followed by Tukey multiple-comparison post hoc tests for (B-G, I), and chi-
- 32 squared tests for (K, M). *P*<0.05 indicates significant differences between treatments. The number of
- 33 mice or oocytes in each group is indicated in parentheses.

D Α Young vs. Aged Calcium signaling pathway Apelin signaling pathway Glycerophospholipids Phospholipase D signaling pathway Carboxylic acids and derivatives nma R-mediated phagocytosis Fatty Acyls Organooxygen compounds Fc ga Lysine degradation Count Steroids and steroid derivatives Thermogenesis 1.00
1.25
1.50
1.75
2.00 Glycerolipids Regulation of lipolysis in adipocytes Phenols Aldosterone synthesis and secretion Azepines Sphingolipid signaling pathway Vitamin B6 metabolism Benzene and substituted derivatives Benzoxazines EGFR tyrosine kinase inhibitor resistance pvalue Coumarins and derivatives Indoles and derivatives MAPK signaling pathway 0.02 0.04 0.06 0.08 ErbB signaling pathway Organonitrogen compounds Chemokine signaling pathway NF-kappa B signaling pathway Prenol lipids Purine nucleosides Pyridines and derivatives HIF-1 signaling pathway Axon regeneration VEGF signaling pathway Pyrimidine nucleosides Sphingolipids Tetrapyrroles and derivatives C-type lectin receptor signaling pathway Natural killer cell mediated cytotoxicity 15 10 5 0 Number of metabolites 0.06 0.07 0.08 0.09 0.10 0.11 Metabolite Ratio в Е Young vs. Aged+PC ABC transporters Carboxylic acids and derivatives Caffeine metabolism Fatty Acyls Vitamin B6 metabolism Prenol lipids Ubiquinone and other terpenoid-quinone biosynthesis Glycerophospholipids Phenylalanine metabolism Count Organooxygen compounds Cortisol synthesis and secretion • 1.00 • 1.25 • 1.50 • 1.75 Glycerolipids Cushing syndrome Imidazopyrimidines Steroid biosynthesis • Steroids and steroid derivatives Lysine degradation 2.00 Benzene and substituted derivatives Amino sugar and nucleotide sugar metabolism Furofurans pvalue Ether lipid metabolism . Indanes Sphingolipid metabolism 0.2 Indoles and derivatives Vitamin digestion and absorption 0.4 0.6 0.8 Lactones alpha-Linolenic acid metabolism Organonitrogen compounds . Steroid hormone biosynthesis Piperidines Tryptophan metabolism • Polypeptides Linoleic acid metabolism Pyridines and derivatives Choline metabolism in cancer Pyrimidine nucleosides Glycerophospholipid metabolism . 5 4 3 2 1 0 Number of metabolites 0.07 0.09 0.11 0.13 Metabolite Ratio С F Aged vs. Aged+PC Linoleic acid metabolism Glycerophospholipids ABC transporters Ŏ Fatty Acyls Carboxylic acids and derivatives Glycerophospholipid metabolism Aminoacyl-tRNA biosynthesis Steroids and steroid derivatives Mineral absorption Ō Count Benzene and substituted derivatives 1.0
1.5
2.0
2.5 Glycerolipids Protein digestion and absorption .... Prenol lipids
 Organonitrogen compounds Central carbon metabolism in cancer Fatty acid biosynthesis Organooxygen compounds Biosynthesis of amino acids 3.0 Imidazopyrimidines Pyrimidine nucleosides alpha-Linolenic acid metabolism Caffeine metabolism Azepines pvalue Cinnamic acids and derivatives Valine, leucine and isoleucine degradation 0.1 0.2 Epoxides Lipoic acid metabolism Indoles and derivatives Valine, leucine and isoleucine biosynthesis Isoquinolines and derivatives Phenol ethers 0.3 Shigellosis Ubiquinone and other terpenoid-quinone biosynthesis Phenols Polypeptides Phenylalanine metabolism Starch and sucrose metabolism 10 רי of r Metabolism of xenobiotics by cytochrome P450 5 υ etabolite: . Arginine and proline metabolism

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36 Fig. S4. HMDB classification and KEGG pathway enrichment analysis of differential metabolites. (A) HMDB classification of differential metabolites between the Young and Aged 37 groups. (B) HMDB classification of differential metabolites between the Young and Aged+PC groups. 38 39 (C) HMDB classification of differential metabolites between the Aged and Aged+PC groups. (D) 40 KEGG pathway enrichment analysis of differential metabolites between the Young and Aged groups. (E) KEGG pathway enrichment analysis of differential metabolites between the Young and Aged+PC 41 42 groups. (F) KEGG pathway enrichment analysis of differential metabolites between the Aged and 43 Aged+PC groups. Five mice per group were used for metabolomics analysis.

0.050

0.075

0.100

0.125

0.150

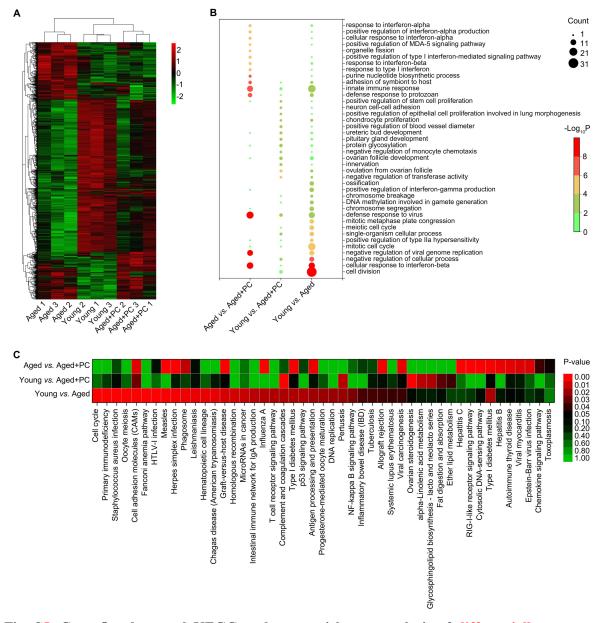
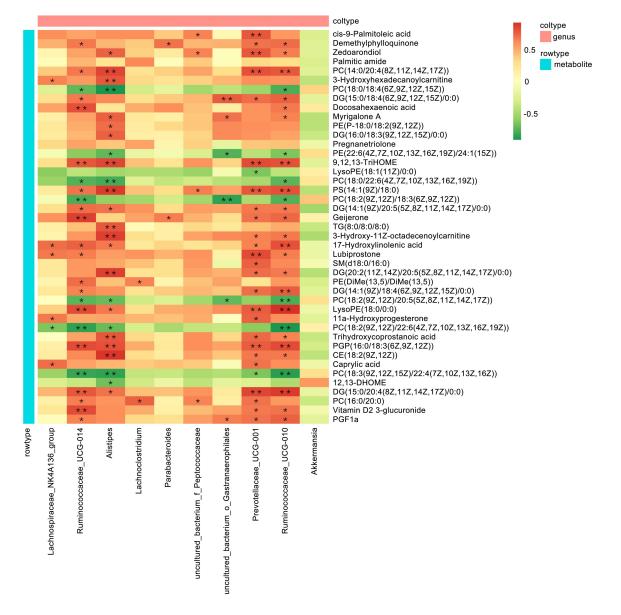


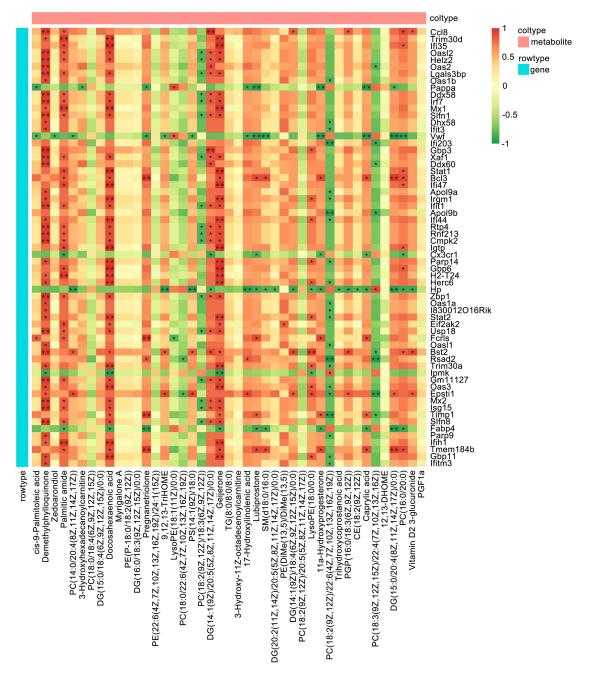
Fig. S5. Gene Ontology and KEGG pathway enrichment analysis of differentially expressed

- 46 genes (DEGs). (A) Cluster heat map of DEGs. (B) Gene Ontology enrichment analysis of the DEGs
- 47 in biological process. (C) Heatmap of differential KEGG pathways. Three mice per group were used
- 48 for RNA sequencing.

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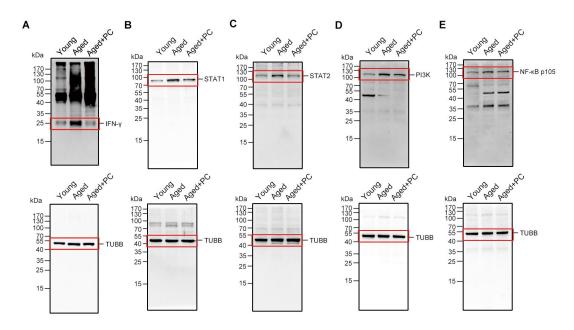


- 49
- 50 Fig. S6. Correlation heatmap of gut microbes and differential lipid metabolites in serum
- 51 between the Aged and Aged+PC groups. \*P<0.05 indicates significant correlation.





- Fig. S7. Correlation heatmap of differential lipid metabolites in serum and interferon-related genes of differentially expressed genes (DEGs) in ovary between the Aged and Aged+PC groups.
- 55 \**P*<0.05 indicates significant correlation.





57 Fig. S8. Raw western blot data. (A) Original western blot results for Fig. 6H. (B) Original western

58 blot results for Fig. 6J. (C) Original western blot results for Fig. 6L. (D) Original western blot results

59 for Fig. 6N. (E) Original western blot results for Fig. 6P.

Table S1 Sequences of primers for qRT-PCR

Gene	Forward	Reverse				
Gapdh	CGTCCCGTAGACAAAATGGT	TTGATGGCAACAATCTCCAC				
Gm4951	TGGGCTACTGAGCTTCTTCTT	GCCCTCACCTGATCTACCTG				
Ifi203	ACCATCCAGCAGTTCCTCAAA	TTTGGTACAGTTCCTCTCCTTGG				
Ifi44	AACTGACTGCTCGCAATAATGT	GTAACACAGCAATGCCTCTTGT				
Ifit3	TTCCCGGTTGACCTCACTCA	CTGAACTGCTCAGCCCAC				
Ifnar l	ACACTGCCCATTGACTCTCC	TTGGGTGCTACCCTCAGC				
Ifnar2	CTTCGTGTTTGGTAGTGATGGT	GGGGATGATTTCCAGCCGA				
Ifngr l	TACAGGTAAAGGTGTATTCGGGT	ACCGTGCATAGTCAGATTCTTTT				
Ifngr2	TCCTCGCCAGACTCGTTTTC	GTCTTGGGTCATTGCTGGAAG				
Igtp	CGCCTCATCAGCCCGTGGTCTAA	TGCCATTGCCAGAGTCCCCAGTC				
Isg15	CAATGGCCTGGGACCTAA	CGGCACACCAATCTTCTG				
Stat1	TCACAGTGGTTCGAGCTTCAG	GCAAACGAGACATCATAGGCA				
Stat2	TTCCGCTGTTCGCTATCTT	ATCTCCCACTGCGCCATT				
Zbp1	AAGAGTCCCCTGCGATTATTTG	TCTGGATGGCGTTTGAATTGG				

genus	Young	Aged	Aged+PC		
Alistipes	$0.00875 \pm 0.00299^{a}$	$0.05633 \pm 0.01948^{b}$	$0.01387 \pm 0.00499^{\rm a}$		
Ruminococcaceae_UCG-014	$0.00195\pm0.00087^{\rm a}$	$0.01810\pm0.00636^{b}$	$0.00162\pm0.00042^{\rm a}$		
Candidatus Saccharimonas	$0.00428 \pm 0.00122^{\rm a}$	$0.01377 \pm 0.00314^{b}$	$0.00635 \pm 0.00175^{\rm a}$		
uncultured_bacterium_f_Desulfovibrionaceae	$0.10170\pm 0.02028^{\rm a}$	$0.02219 \pm 0.00815^{b}$	$0.05036 \pm 0.03479^{ab}$		
uncultured_bacterium_f_Lachnospiraceae	$0.04398 \pm 0.01426^{a}$	$0.12882 \pm 0.03262^{b}$	$0.13756 \pm 0.07217^{ab}$		
Enterorhabdus	$0.00013 \pm 0.00008^{\rm a}$	$0.00124 \pm 0.00053^{b}$	$0.00199 \pm 0.00117^{ab}$		
Paraprevotella	$0.00228 \pm 0.00113^{\rm a}$	$0.00000 \pm 0.00000^{\rm b}$	$0.00055\pm0.00041^{ab}$		
Bilophila	$0.00049 \pm 0.00021^{\rm a}$	$0.00376 \pm 0.00162^{b}$	$0.00514 \pm 0.00439^{ab}$		
Lachnospiraceae UCG-006	$0.00075\pm0.00018^{\rm a}$	$0.00565 \pm 0.00250^{\rm b}$	$0.00443 \pm 0.00202^{ab}$		
Ruminococcaceae UCG-004	$0.00031 \pm 0.00013^{a}$	$0.00111 \pm 0.00039^{b}$	$0.00082 \pm 0.00032^{ab}$		
Parasutterella	$0.00753 \pm 0.00324^{\rm a}$	$0.00123 \pm 0.00044^{b}$	$0.00827 \pm 0.00426^{ab}$		
Lactobacillus	$0.01064\pm0.00263^{\rm a}$	$0.04872 \pm 0.01463^{\rm b}$	$0.05187 \pm 0.01871^{b}$		
Anaerotruncus	$0.00773 \pm 0.00295^{\rm a}$	$0.00092 \pm 0.00067^{b}$	$0.00000 \pm 0.00000^{\rm b}$		
Lachnospiraceae NK4A136 group	$0.12035 \pm 0.03162^{ab}$	$0.22365\pm0.05263^{\rm a}$	$0.07508 \pm 0.03558^{b}$		
Gordonibacter	$0.00040 \pm 0.00024^{ab}$	$0.00009\pm0.00009^{\rm a}$	$0.00000 \pm 0.00000^{\rm b}$		
Ruminococcaceae_UCG-013	$0.00027\pm0.00011^{a}$	$0.00148 \pm 0.00075^{ab}$	$0.00217\pm0.00053^{b}$		
Ruminiclostridium 9	$0.00425\pm0.00096^{\rm a}$	$0.01021\pm0.00312^{ab}$	$0.00814 \pm 0.00174^{b}$		
Ruminiclostridium 5	$0.00009 \pm 0.00009^{\rm a}$	$0.00091 \pm 0.00045^{ab}$	$0.00083 \pm 0.00038^{\rm b}$		
[Eubacterium] xylanophilum group	$0.00066 \pm 0.00035^{\rm a}$	$0.00036 \pm 0.00029^{ab}$	$0.00000 \pm 0.00000^{\rm b}$		
Alloprevotella	$0.02683 \pm 0.01076^{\rm a}$	$0.00785 \pm 0.00360^{ab}$	$0.00612\pm0.00229^{b}$		

Table S2 The relative abundance of gut microbes between groups of mice at the genus level

Data are represented as mean  $\pm$  SEM and statistical comparisons were made using *t*-tests by using Metastats. Without a common letter means statistically

significant differences between treatments (P < 0.05). Six mice for used for each treatment.

Description	Young group vs. Aged group			Young group vs. Aged+PC group			Aged group vs. Aged+PC group					
Description	setSize	NES	pvalue	qvalue	setSize	NES	pvalue	qvalue	setSize	NES	pvalue	qvalue
response to IFN-gamma	17	1.718	0.013	0.126	17	-0.581	0.956	0.907	17	-2.150	0.002	0.078
cellular response to IFN-alpha	12	1.764	0.008	0.105	12	0.698	0.867	0.890	12	-1.996	0.002	0.078
positive regulation of type I IFN- mediated signaling pathway	11	1.854	0.004	0.080	11	-1.737	0.009	0.146	11	-2.156	0.002	0.078
positive regulation of IFN-beta production	19	1.523	0.039	0.241	19	-0.853	0.680	0.828	19	-1.988	0.002	0.078
cellular response to IFN-beta	49	2.705	0.003	0.071	46	-1.017	0.427	0.730	49	-2.950	0.002	0.078
cellular response to IFN-gamma	56	2.138	0.003	0.071	52	0.891	0.669	0.824	57	-2.297	0.002	0.078
positive regulation of IFN-gamma production	31	1.886	0.002	0.071	31	1.207	0.215	0.586	30	-1.740	0.006	0.104
negative regulation of IFN-gamma production	14	1.744	0.009	0.106	14	1.471	0.056	0.343	16	-1.480	0.058	0.325

## Table S3 GSEA analysis of IFN-related GO items