

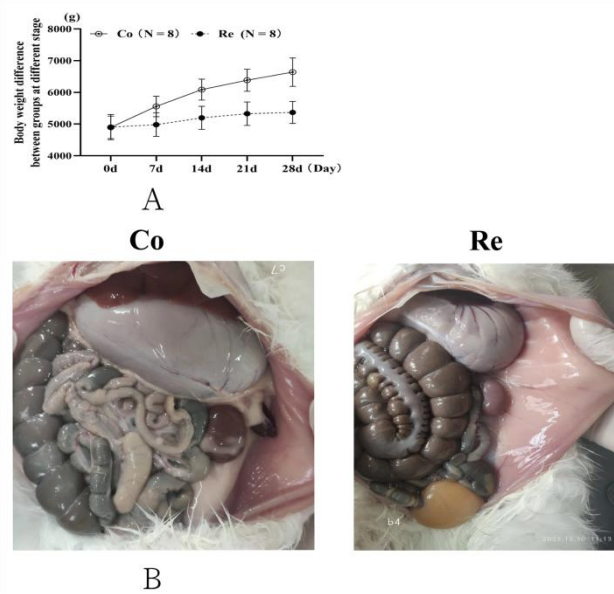


Fig. S1 The differences in body weight among different age and anatomical phenotypes between groups. In the figures, “Re” represents the rabbits in the short-term restricted diet group, and “Co” represents the rabbits in the control group.

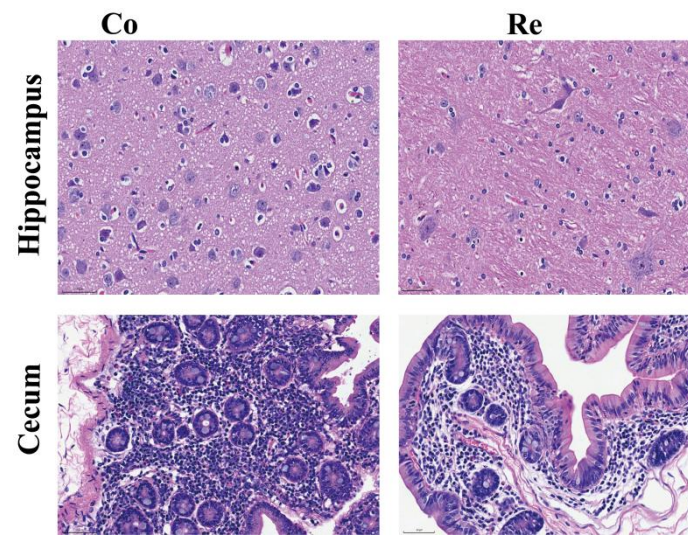


Fig. S2 Histopathological analysis of different tissues between groups using HE staining.

Table S1. Inter-group analysis of brain cortex tissues transcriptomes

Sample	RawReads (M)	RawBases (G)	CleanReads (M)	CleanBases (G)	ValidBases (%)	Q30 (%)	GC (%)	Gene number
Co1	103.14M	15.47G	101.85M	14.68G	94.89%	94.37%	51.71%	17236
Co2	104.69M	15.70G	103.35M	14.88G	94.78%	94.43%	51.60%	17238
Co3	104.40M	15.66G	103.16M	14.92G	95.30%	94.30%	52.43%	17240
Re1	102.31M	15.35G	101.01M	14.54G	94.77%	94.28%	51.81%	17139
Re2	102.52M	15.38G	101.28M	14.60G	94.97%	94.39%	51.97%	17318
Re6	93.64M	14.05G	88.38M	13.13G	93.45%	95.53%	53.04%	17366
Co1	103.14M	15.47G	101.85M	14.68G	94.89%	94.37%	51.71%	17236

Table S2.Analysis of inflammatory factor expression data in cerebral cortex between groups

Gene ID	BaseMean (Co)	BaseMean (Re)	FoldChange	log2FoldChange	p-value
CD40	67.3318	204.8189	3.0417	1.6049	0.0028
CD40LG	0.9605	17.5049	18.2957	4.1934	0.0316
TLR2	166.9688	518.7086	3.1068	1.6354	0.0421
IL1R1	713.5034	511.5318	0.7174	-0.4792	0.0405
IL12A	91.0988	171.7057	1.8855	0.9150	0.0114
TNFRSF13B	1.9210	44.7251	23.3785	4.5471	0.0016
SYK	212.5758	840.8361	3.9554	1.9838	0.0138
ICAM1	253.8384	560.0922	2.2057	1.1413	0.0063
TRAF1	533.1359	680.5946	1.2755	0.3511	0.0387
PIK3CD	276.1094	577.4385	2.0908	1.0640	0.0042
CD6	29.2105	101.1914	3.4650	1.7929	0.0432
CD247	19.0586	73.7994	3.8735	1.9536	0.0210
CD300A	25.2050	89.6010	3.5534	1.8292	0.0025
CD300LF	73.3597	242.5338	3.3052	1.7247	0.0060
CD101	65.1741	209.8434	3.2193	1.6868	0.0031
CD72	27.4579	87.1487	3.1744	1.6665	0.0261
CD8A	45.7609	114.0503	2.4910	1.3167	0.0453
TNFAIP8L2	318.1886	238.3205	398.0566	1.6695	0.7394
IL1R2	180.9232	80.6997	0.4458	-1.1655	0.0170
IL21R	44.0595	129.1776	2.9310	1.5514	0.0112
IL4R	178.2896	337.9210	1.8941	0.9215	0.0216
IL10RB	336.6758	530.2270	1.5742	0.6546	0.0310
IL-15L	23.1855	38.5249	1.6616	0.7326	0.2200
TNFAIP8L2	238.3205	398.0566	1.6695	0.7394	0.0375
TNFRSF13C	4.3427	44.5125	10.2231	3.3538	0.0153
TNFRSF17	33.0511	211.3333	6.3936	2.6766	0.0203
TNFSF13B	73.4054	628.6730	8.5652	3.0985	0.0266
BIRC3	263.2625	1595.8330	6.0619	2.5998	0.0267
BLNK	386.3488	832.6826	2.1552	1.1078	0.0037
LTB	17.6195	92.3196	5.2339	2.3879	0.0020
NLRC3	37.7738	161.9840	4.2881	2.1003	0.0077

Note: All data were recorded with an accuracy of 0.0001.

Table S3. Inflammatory factor-protein interaction information

Gene Node1	Gene Node2	Score	Gene Node1	Gene Node2	Score	Gene Node1	Gene Node2	Score
CD40	CD40LG	0.9990	CD40	IL21R	0.6790	IL1R1	IL4R	0.5050
TNFRSF17	TNLTG7A	0.9980	SYK	TLR2	0.6740	LTB	TRAF1	0.5010
CD247	SYK	0.9960	CD40	LTB	0.6570	CD8A	ICAM1	0.4890
TNFRSF13B	TNLTG7A	0.9950	ICAM1	IL1R1	0.6450	CD40	IL1R1	0.4880
IL1R1	IL1R2	0.9810	CD40LG	TNFRSF13B	0.6270	CD8A	CD6	0.4880
BIRC3	TRAF1	0.9680	CD40	SYK	0.6100	SYK	CD72	0.4870
PIK3CD	SYK	0.9640	CD40LG	TNFRSF17	0.6050	CD40LG	IL4R	0.4860
BLNK	SYK	0.9630	IL21R	IL4R	0.6040	IL4R	CD40LG	0.4860
CD247	CD8A	0.9500	CD40LG	LTB	0.5960	TNLTG7A	SYK	0.4730
CD40LG	TNLTG7A	0.9230	CD40LG	CD8A	0.5920	TNLTG7A	IL21R	0.4670
CD40	TRAF1	0.9180	IL1R2	TRAF1	0.5880	TRAF1	SYK	0.4490
CD40	TNLTG7A	0.8710	IL1R1	TLR2	0.5870	TNLTG7A	IL1R1	0.4450
CD40	TLR2	0.8390	CD40LG	TLR2	0.5800	CD8A	CD40	0.4380
CD40	ICAM1	0.8370	TLR2	TRAF1	0.5750	TRAF1	IL1R1	0.4350
TNFRSF13B	TNFRSF17	0.8080	BIRC3	CD40LG	0.5570	PIK3CD	BLNK	0.4330
CD247	CD6	0.7740	ICAM1	TRAF1	0.5450	LTB	BIRC3	0.4270
CD40LG	ICAM1	0.7550	BIRC3	CD40	0.5430	SYK	ICAM1	0.4260
CD40LG	TRAF1	0.7510	IL21R	TNFRSF13B	0.5340	IL4R	IL10RB	0.4250
LTB	TNLTG7A	0.7450	BIRC3	TNLTG7A	0.5240	TLR2	IL1R2	0.4180
ICAM1	TLR2	0.7270	BLNK	CD72	0.5200	TNLTG7A	CD8A	0.4130
CD40LG	IL21R	0.7190	CD40LG	SYK	0.5170	SYK	CD8A	0.4030
TNLTG7A	TRAF1	0.6860	CD40	CD72	0.5090	CD40	BLNK	0.4010

Note: Score represents the Pearson correlation coefficient between genes. All data were recorded with an accuracy of 0.0001.

Table S4. Comparison and analysis of transcriptome sequencing information in the cecum tissue between Co and Re

Sample	CleanReads (M)	CleanBases (G)	ValidBases (%)	Q30 (%)	GC (%)	Total reads	Gene Number
Co1	49.56	7.25	96.09	94.23	53.09	49564534	15953
Co2	50.08	7.3	95.9	94.09	52.54	50081640	15554
Co3	47.97	7.03	96.36	94.05	53.19	47968774	15851
Re1	50.04	7.35	96.72	94.22	53.4	50036248	15560
Re2	46.98	6.91	96.76	94.32	53.49	46975254	15597
Re3	46.88	6.89	96.72	93.99	53.08	46876124	15377

Table S5. Metagenomic sequence statistics between Co and Re groups

Sample	Raw Reads	Clean Reads	Clean Reads Percent	Total Size(bp)	Contigs Number	ORF Number	Total Size
Co1	76631258	75637306	98.70%	690724628	1666951	1479740	553268235
Co2	78098312	77068200	98.68%	661179519	1588690	1416668	530647437
Co3	79527984	78446824	98.64%	739006190	1846339	1620022	588563157
Co4	78949542	77956308	98.74%	766955697	1895510	1676427	614644836
Co5	100962404	99969410	99.02%	773695640	1798189	1631440	626198457
Co6	77696556	76751848	98.78%	662742606	1616172	1432619	530904732
Re1	99454918	98434712	98.97%	956230596	2425876	2115603	759161319
Re2	93682936	92756366	99.01%	908724125	2209700	1964305	728735598
Re3	96848764	96031660	99.16%	1006600967	2502159	2195495	800807868
Re4	85763238	84663872	98.72%	800639151	1952821	1729816	642038541
Re5	85919092	84747142	98.64%	781438596	1920705	1700812	626646894
Re6	81325614	80306774	98.75%	800395940	1932640	1722336	642553050

Table S6. Information on major components of commercial basal diets in this study

Main feed ingredients	Digestible Energy (kcal/kg)	Crude protein (≥%)	Crude fibre (≤%)	Crude ash (≤%)	Ca%	Total phosphorus (≥%)	NaCl%	Lysine (≥%)	Cystine and methionine (≥%)
Content	2491—3440	14	7.0-20.0	14	0.6-1.50	0.4	0.3-0.80	0.6	0.5