

Table S1 Sequences with similar functions found in the NCBI database

Domain of function	Species	Genbank number
polypentadiene synthase	<i>Physcomitrium patens</i>	XP_024402925.1
	<i>Dunaliella salina</i>	APW83741.1
	<i>Dunaliella parva</i>	AMR55359.1
	<i>Clitopilus passeckerianus</i>	AVA16671.1
	<i>Saccharomyces boulardii</i>	KQC40560.1
	<i>Deinococcus wulumuqiensis R12</i>	AKA42980.1
	<i>Ceratodon purpureus</i>	KAG0565415.1
	<i>Sphagnum fallax</i>	KAH8960311.1
	<i>Sphagnum fallax</i>	KAH8966241.1
	<i>Sphagnum magellanicum</i>	KAH9531242.1
	<i>Sphagnum magellanicum</i>	KAH9560870.1
	<i>Marchantia polymorpha</i>	PTQ43161.1
	<i>Marchantia paleacea</i>	KAG6548034.1
	<i>Ceratodon purpureus</i>	KAG0609433.1
	<i>Amborella trichopoda</i>	ERN17565.1
phytylcopene desaturase	<i>Solanum lycopersicum</i>	NP_001234812.1
	<i>Citrullus lanatus</i>	AGT57744.1
	<i>Sphagnum magellanicum</i>	KAH9533365.1
	<i>Sphagnum fallax</i>	KAH8933817.1
	<i>Ceratodon purpureus</i>	KAG0582240.1

	<i>Ceratodon purpureus</i>	KAG0582034.1
	<i>Ceratodon purpureus</i>	KAG0621537.1
	<i>Ceratodon purpureus</i>	KAG0582241.1
	<i>Momordica charantia</i>	AAR86104.1
	<i>Quercus suber</i>	XP_023872284.1
	<i>Physcomitrium patens</i>	XP_024364025.1
	<i>Arabidopsis thaliana</i>	NP_001031895.1
	<i>Cucurbita pepo</i>	AFV33363.1
	<i>Dunaliella parva</i>	ARH02607.1
	<i>Dunaliella salina</i>	AAT46069.1
	<i>Selaginella moellendorffii</i>	XP_002982526.2
phytolycopene synthase	<i>Zea mays</i>	AAA99519.1
	<i>Oryza sativa</i>	AAD02489.1
	<i>Auxenochlorella protothecoides</i>	ADC32153.1
	<i>Arabidopsis thaliana</i>	AAK25906.1
	<i>Chlamydomonas reinhardtii</i>	AAT38476.1
	<i>Dunaliella salina</i>	ABB51091.1
	<i>Physcomitrium patens</i>	XP_024359580.1
	<i>Sphagnum magellanicum</i>	KAH9559659.1
	<i>Sphagnum fallax</i>	KAH8959222.1
	<i>Marchantia paleacea</i>	KAG6551553.1
	<i>Marchantia polymorpha</i>	OAE28876.1

<i>Dunaliella salina</i>	CAA75094.1
<i>Diospyros kaki</i>	ACY78343.1
<i>Plagiochasma appendiculatum</i>	AHA43672.1
<i>Selaginella moellendorffii</i>	XP_002988989.1

Supplementary Table 2. The primers sequences of genes

Gene name	Primer forward 5'-3'	Primer reversed 5'-3'
Nrf2	CAGTGCTCCTATGCGTGAA	GCGGCTTGAATGTTTGTC
HO-1	ACAGATGGCGTCACTTCG	TGAGGACCCACTGGAGGA
NQO1	AGGATGGGAGGTACTCGAATC	TGCTAGAGATGACTCGGAAGG
COX-2	GGTGCCTGGTCTGATGATG	TGCTGGTTTGGAAATAGTTGCT
P-38	GATACAAAGACGGGGCATCG	CACGATGTTGTTTCAGGTCCG
ERK	GCCTTCCAACCTCCTGCTGAAC	CGTACTCTGTCAAGAACCCTGTGTG
JNK	CGCCTTATGTGGTGACTCGCTAC	CTCCCATGATGCACCCAAGTAC
MMP-1	ATTCTACTGATATCGGGGCTTTGA	ATGTCCTTGGGGTATCCGTGTAG
MMP-2	ACCATGCGGAAGCCAAGATGTG	AGGGTCCAGGTCAGGTGTGTAAC
collagen type I	AGGGCAAAGATCCCTGAAGT	GGCAGAAAGCACAGCACTC
AP-1	CTTCTACGACGATGCCCTCAACG	GCCAGGTTCAAGGTCATGCTCTG
GAPDH	AGGTCGGTGTGAACGGATTTG	GGGGTCGTTGATGGCAACA

Supplementary Table 3. The optimized sequences of *pnCrtE*, *pnCrtB*, *pnCrtP*.

Gene name	Optimized sequences
<i>pnCrtE</i>	<p>ATGGGTAGCACCGTTATTGCACCGGGTTCTCAGTGTGTTGGC TTCAGCGTGGCGCGTCCGAACCTGACCACCTCTAAATCTGAA ACCCGTCAGCTGCAGCTGCGTACCCAGTTCTACGGTGTGCGT TGCGCGGGCCTGACCCGTAGCGCGACCAACCCGGTGGTTGTG GTTCTGCAGCCGATCCGTGCGCAGTCTGTTATCAGCGAAGTT GAAGGTAAAGCGACCCCGGAAGCCGTTTCTAAAAGCCTGCA GCTGTTTGAATTCGCAACCTACATGAAAGGCAAAGCGAACTC CGTGAACGTTGCGCTGGATAAAGCGGTGCCGATGCAGTACCC GGAACAGATCCACGAAGCGATGCGTTACAGCCTGCTGGCGA GCGGCAAACGTGTGCGTCCGGCGCTGTGCATTGCGGCGTGCG AACTGGTGGGTGGCACCGAAGCAATGGCAATGCCGGCGGCG TGCGCCATGGAAATGGTTCACACCATGAGCCTGATCCACGAC GACCTGCCATGCATGGATAACGACGATCTGCGCCGCGGCAA GCCGACCCTGCACAAACTGTACAATGATGGCATGGCGGTGCT GGCAGGCGACGCGCTGCTGTCCTTCGCTTTCGAACACATCGC GCGTAGCACCACCGGCGTGGCGGCGGACCGTGTCTGCGCGT TATCGCGCATCTGGGCAAGGCTGTCGGCTCTGAAGGCCTGGT TGCGGGCCAGATCGTTGACCTGGCGTCTGAAGGCGATCCGAG CGTTGGCCTGGACACCCTGGAGTACGTTACACCCATAAAAC</p>

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pnCrtB

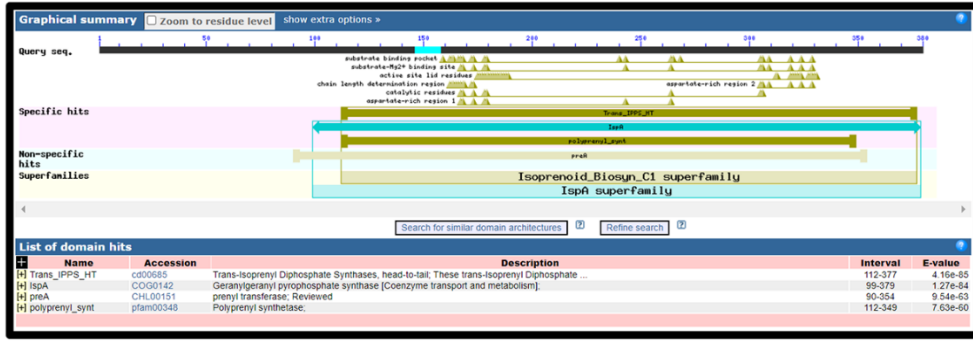
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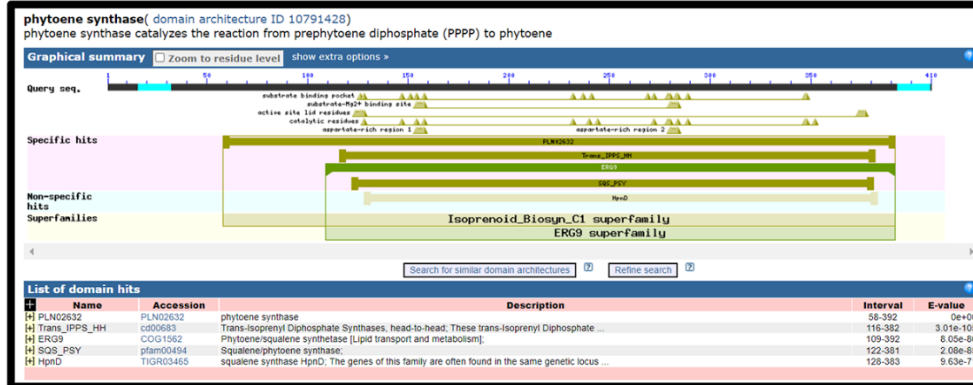
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A CrtE



B CrtB



C PDS

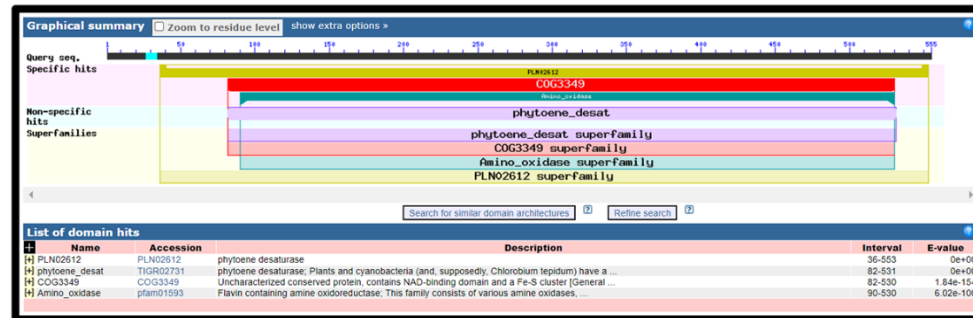


Fig S1. The amino acid functional domains from NCBI

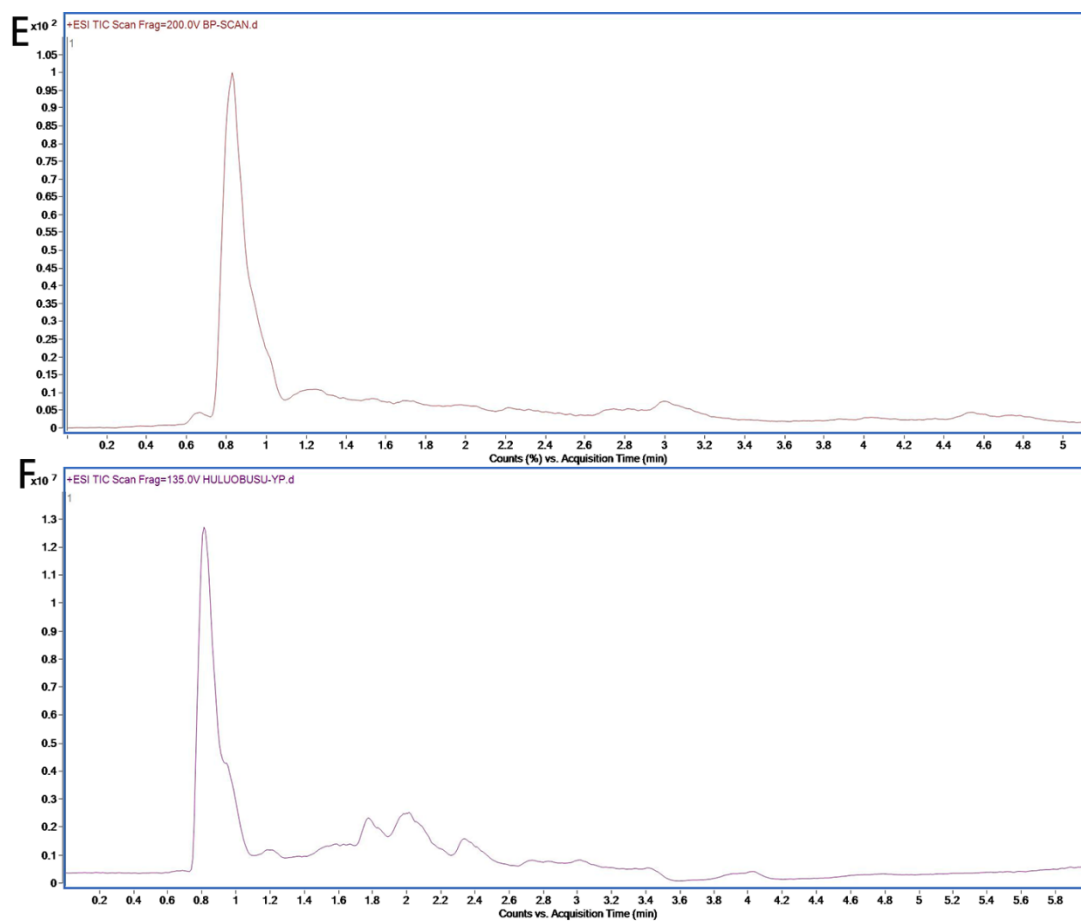


Fig S2. $^+$ ESI TIC scan ion peaks of ζ - carotene standard (A) and CE (B), respectively

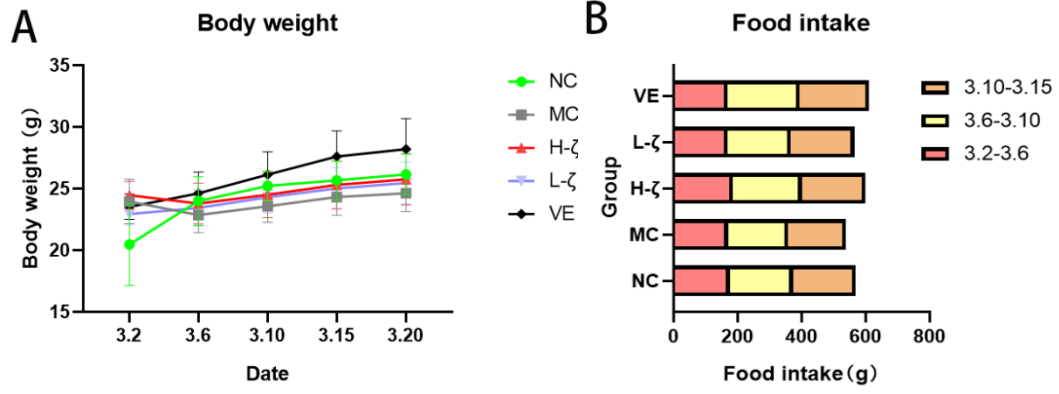


Fig S3. Changes in body weight(A) and feeding(B)

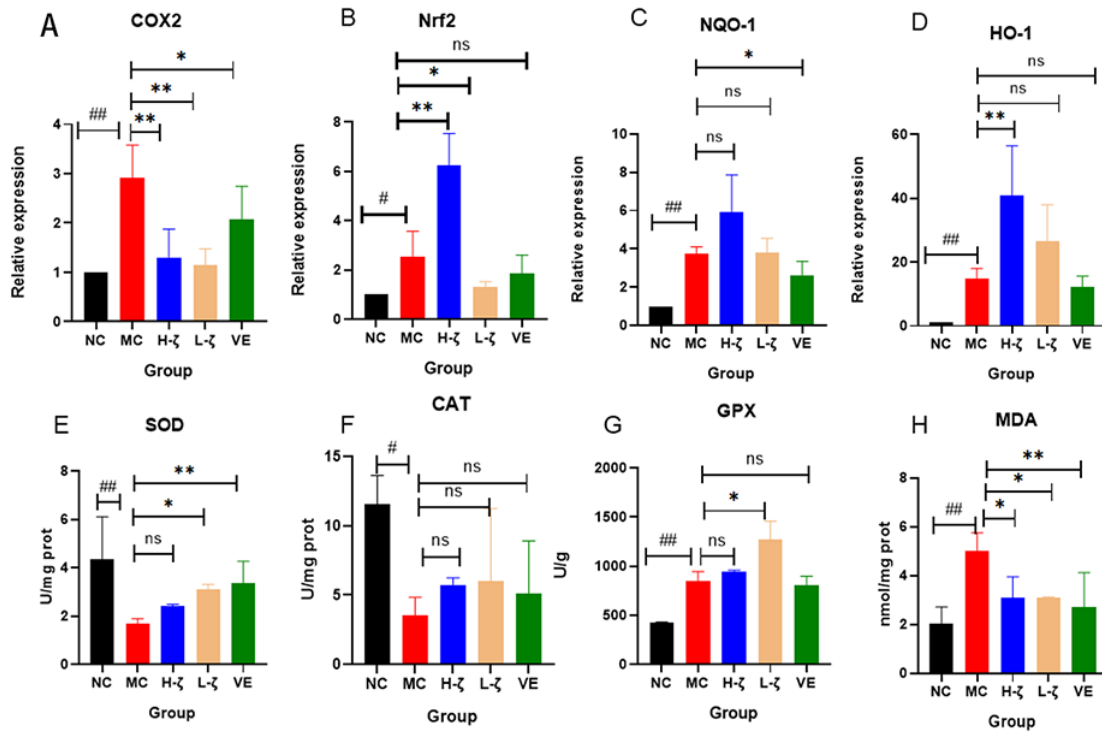


Fig S4. Nrf2/ARE antioxidant pathway, n=3. (# was MC vs NC P<0.05, ## was MC vs NC P<0.01, * was ζ or VE vs MC P<0.05, ** was ζ or VE vs MC P<0.01, ns was no significance).

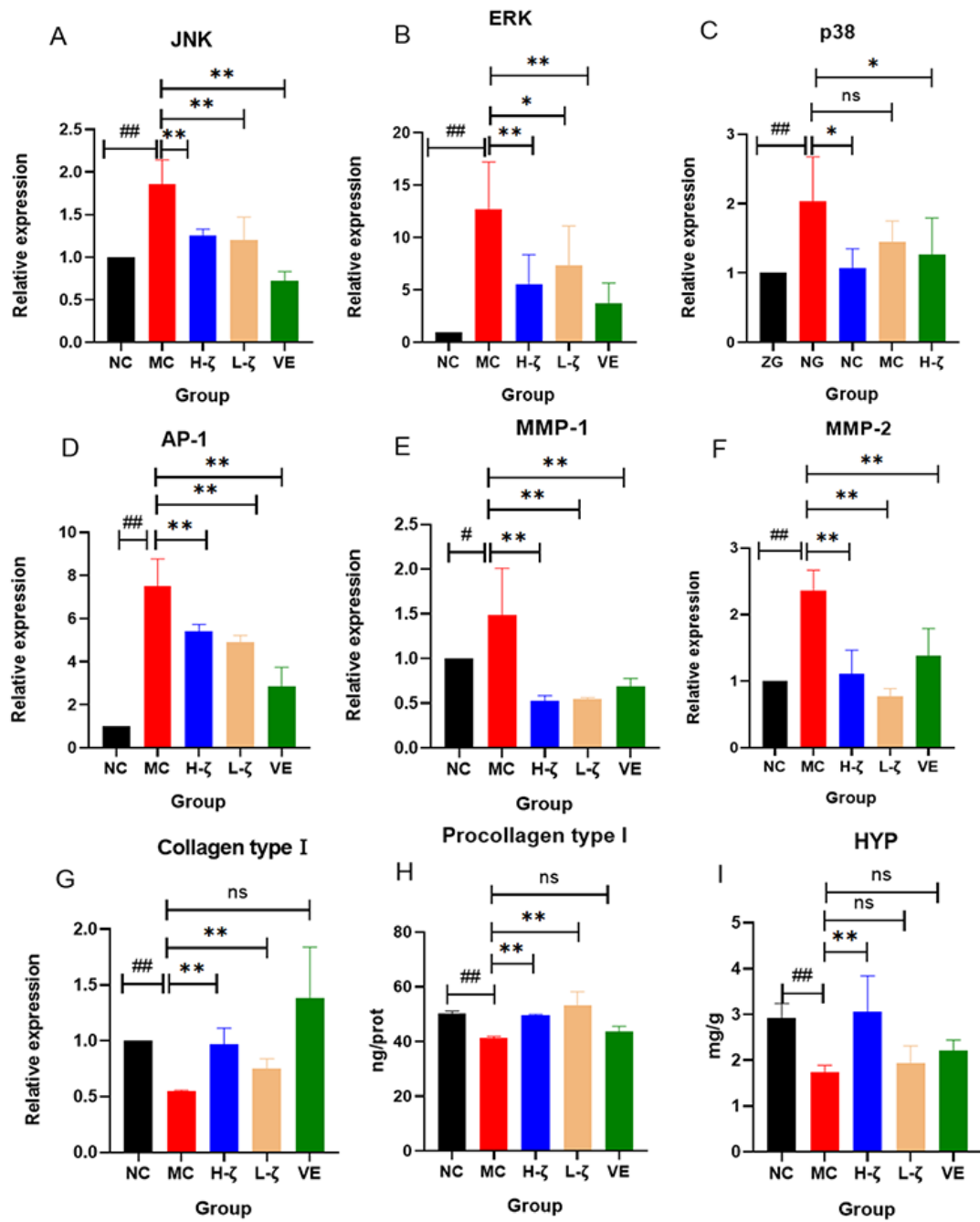


Fig S5. MAPK pathway (A-D) and collagen synthesis related factors (E-I), n=3. (# was MC vs NC P<0.05, ## was MC vs NC P<0.01, * was ζ or VE vs MC P<0.05 ** was ζ or VE vs MC P<0.01, ns was no significance).

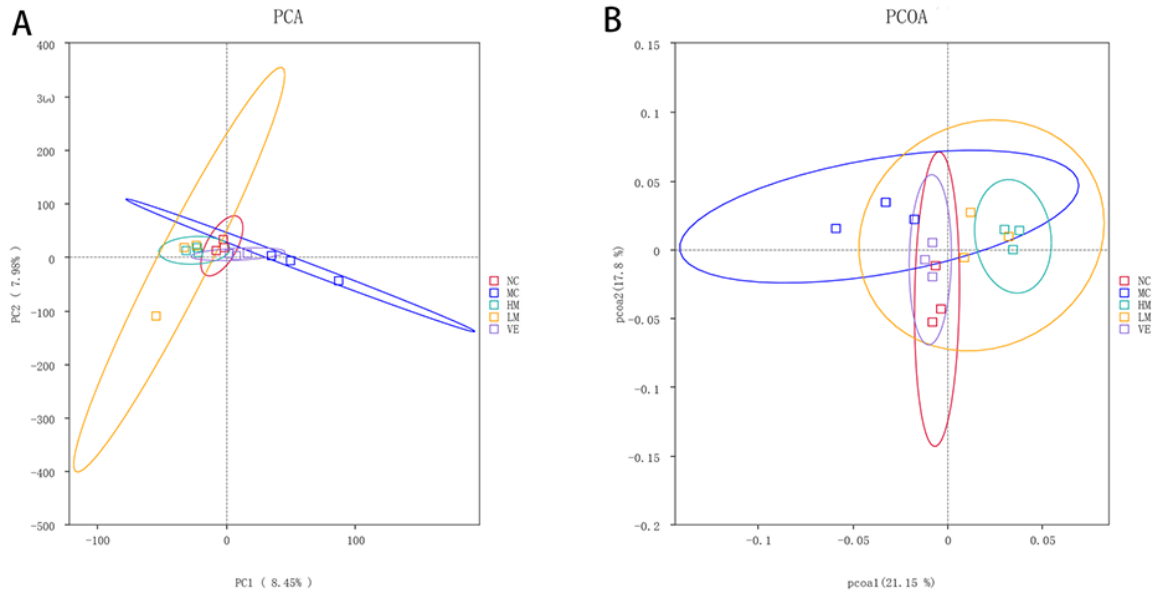


Fig S6. The beta diversity analysis of gut microbiota. (A was PCA and B was PCoA).

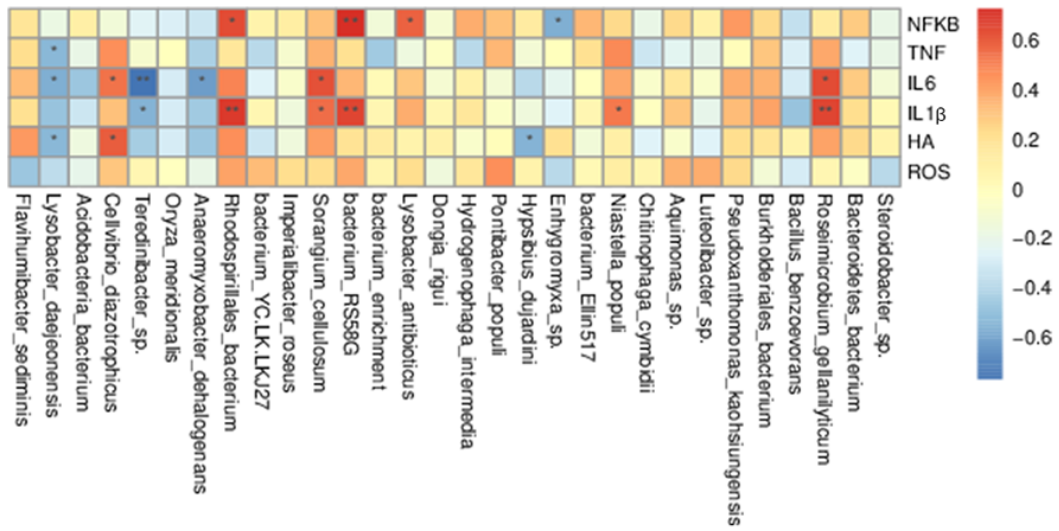


Fig S7. The Pearson correlation analysis of inflammatory factors at the species level