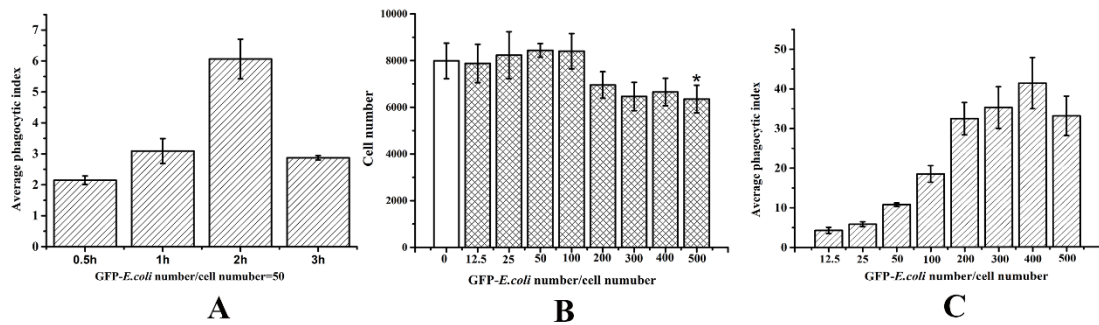
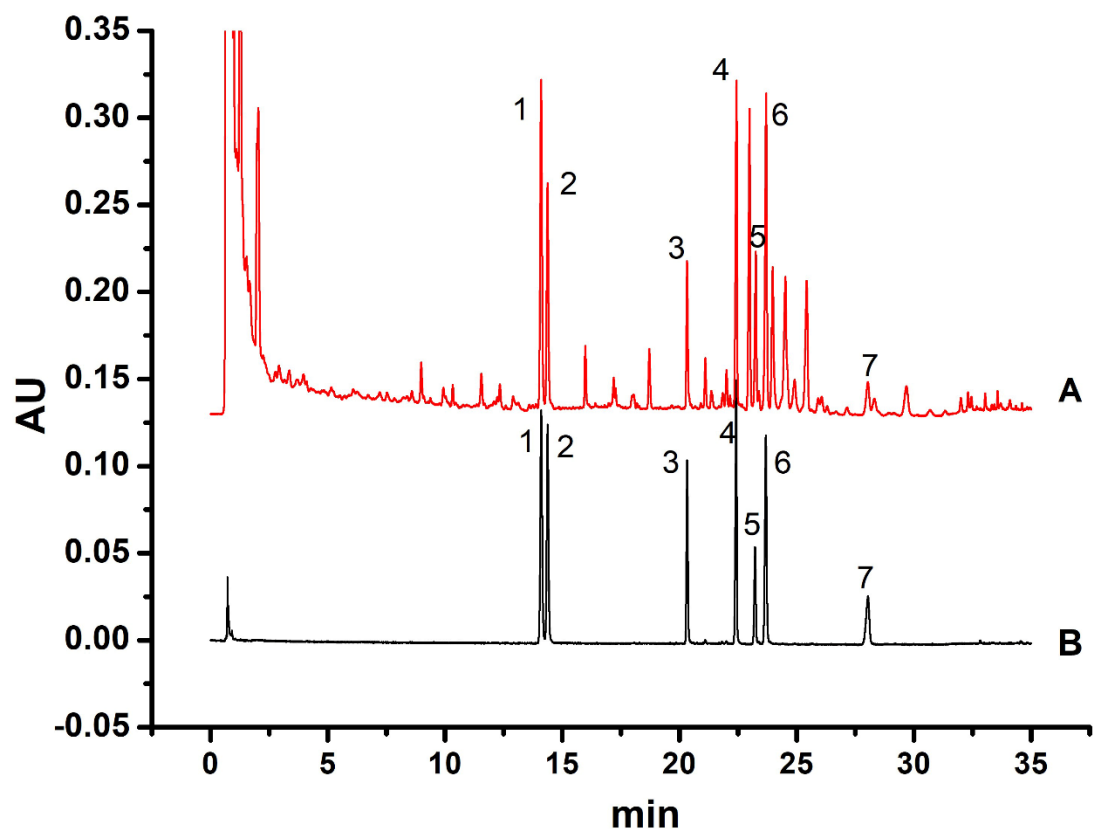


### Supplementary Materials:

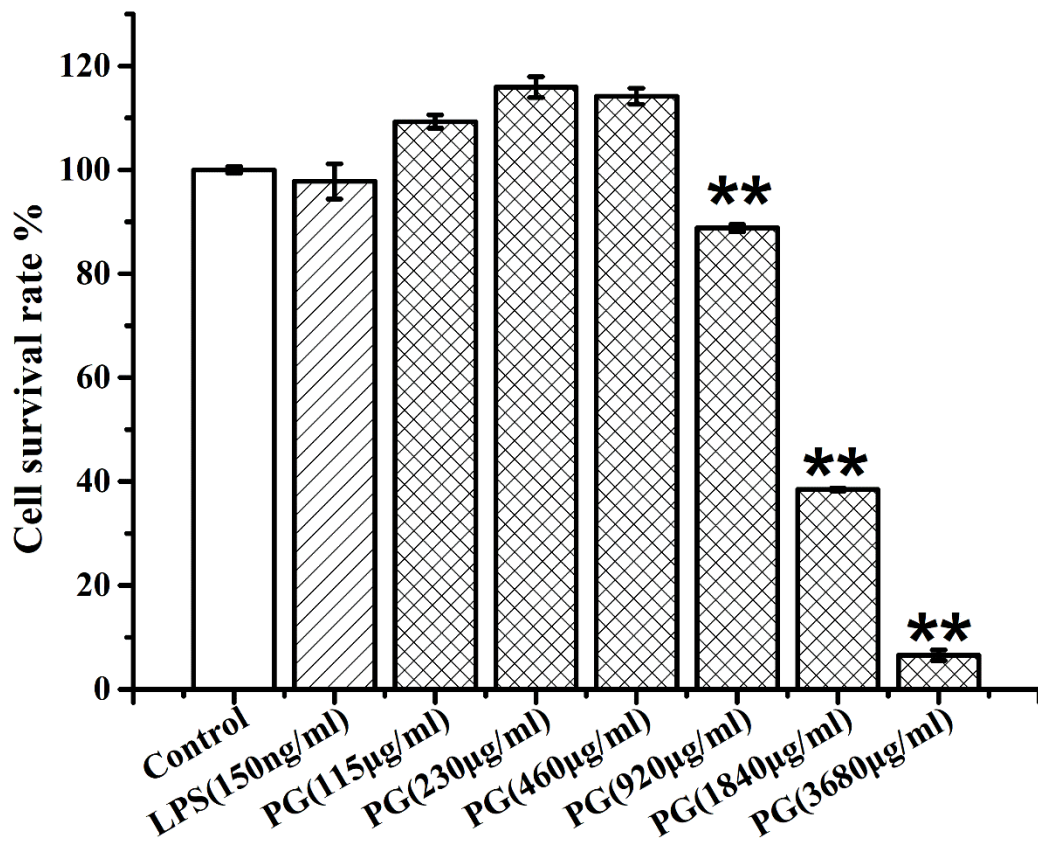
The influence of different incubation time (0.5, 1, 2, 3 h) was studied when the GFP-*E. coli* number/cell number was 50. The other conditions are the same as the content of **2.4 High content screening analyses of phagocytosis activity**. The average phagocytic index sustained increased in 0.5-2 h incubating but decreased at 3h, so we incubated for 2 h (Figure 1 A). Then we study influence of different GFP-*E. coli* number (GFP-*E. coli* number/cell number was from 12.5 to 500). As shown in Figure S1 B and C, The average phagocytic index increased when the GFP-*E. coli* number/cell number was from 12.5 to 400, while the cell number decreased when GFP-*E. coli* number/cell number was 200. Therefore, the GFP-*E. coli* number/cell number was determined to be 100 and incubation time was 2 h.



**FIGURE S1:** The study on methodology of phagocytosis activity. (A) The average phagocytic index of macrophage in different time incubating with GFP-*E. coli*. (B, C) The cell number and average phagocytic index when the GFP-*E. coli* number/cell number was from 12.5 to 400. \* $P < 0.05$  vs the group without GFP-*E. coli*.



**FIGURE S2:** UPLC ginsenoside profile of PG: (A) PG extract; (B) Standards. Detection at 203 nm wavelength. Peaks: (1) ginsenoside Rg1; (2) ginsenoside Re; (3) ginsenoside Rf; (4) ginsenosideRb1; (5) ginsenoside Rc; (6) ginsenoside Ro; (7) ginsenoside Rd.



**FIGURE S3:** Macrophage survival rate of co-treatment with PG extracts (115-3680 µg/ml) and the LPS (150 ng/ml), detected by CCK8 method. \*\* $P < 0.01$  vs control group.

**TABLE S1:** The information of potential biomarkers.

Metabolites	KEGG ID	Pathway
Data from the ESI- mode		
OPC6-CoA	C16331	alpha-Linolenic acid metabolism
trans-2-Enoyl-OPC6-CoA	C16332	alpha-Linolenic acid metabolism
PC(18:3(9Z,12Z,15Z)/15:0)	C00157	Glycerophospholipid metabolism
PS(18:0/20:4(8Z,11Z,14Z,17Z))	C02737	Glycerophospholipid metabolism
Phosphorylcholine	C00588	Glycerophospholipid metabolism
PE(18:0/16:1(9Z))	C00350	Glycerophospholipid metabolism
Glucosylceramide (d18:1/16:0)	C01190	Sphingolipid metabolism
Ceramide (d18:1/20:0)	C00195	Sphingolipid metabolism
2'-Deoxycytidine diphosphate (dCDP)	C00705	Pyrimidine metabolism
Xanthylic acid (XMP)	C00655	Purine metabolism
Deoxyadenosine monophosphate (dAMP)	C00360	Purine metabolism
3'-Phosphoadenylyl sulfate (PAPS)	C00053	Purine metabolism
Glutathione	C00051	Glutathione metabolism
Taurine	C00245	Taurine and hypotaurine metabolism
Inosine 5'-monophosphate (IMP)	C00130	Purine metabolism
(S)-3-Hydroxytetradecanoyl-CoA	C05260	Fatty acid degradation
(S)-3-Hydroxyhexadecanoyl-CoA	C05258	Fatty acid degradation
Data from the ESI+ mode		
Choline	C00114	Glycine, serine and threonine metabolism
Creatine	C00300	Glycine, serine and threonine metabolism
L-IsoLeucine	C00123	Valine, leucine and isoleucine biosynthesis

**TABLE S2:** Parameters of PCA and OPLS-DA models.

Model No.	Model type	Groups included	Component	R2X	R2Y (cum)	Q2Y (cum)
Data of ESI- mode						
M1	PCA	-	2	0.657	-	0.455
M2	OPLS-DA	PG-High & Control	1+1+0	0.837	0.999	0.985
Data of ESI+ mode						
M3	PCA	-	3	0.641	-	0.153
M4	OPLS-DA	PG-High & Control	1+3+0	0.891	1	0.982

**TABLE S3:** Results from pathway analysis of potential biomarkers with MetaboAnalyst 3.0.

Pathway name	Total	Hits	RAW p	FDR	Impact
Glycerophospholipid metabolism	30	5	4.83E-05	0.003964	0.32284
alpha-Linolenic acid metabolism	9	3	0.000223	0.009139	0
Purine metabolism	68	4	0.015644	0.4276	0.08939
Sphingolipid metabolism	21	2	0.03709	0.76034	0.32331
Fatty acid elongation in mitochondria	27	2	0.058781	0.87982	0.08606
Sulfur metabolism	5	1	0.072035	0.87982	0.3
Glycine, serine and threonine metabolism	31	2	0.075169	0.87982	0
Linoleic acid metabolism	6	1	0.085836	0.87982	0
Fatty acid metabolism	39	2	0.11165	0.9254	0.08739
Taurine and hypotaurine metabolism	8	1	0.11285	0.9254	0.42857
Valine, leucine and isoleucine biosynthesis	11	1	0.15196	1	0.33333
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	14	1	0.18942	1	0.0439
Glutathione metabolism	26	1	0.32409	1	0.36069
Arachidonic acid metabolism	36	1	0.41976	1	0
Valine, leucine and isoleucine degradation	38	1	0.43728	1	0
Pyrimidine metabolism	41	1	0.46262	1	0.0364
Arginine and proline metabolism	44	1	0.48687	1	0.01198
Primary bile acid biosynthesis	46	1	0.50245	1	0.02976
Aminoacyl-tRNA biosynthesis	69	1	0.65215	1	0
Steroid hormone biosynthesis	72	1	0.66817	1	0.02711

**TABLE S4:** The ADME indexes of PG's ingredients by network pharmacology analyses.

Molecule name	OB (%)	Caco-2	DL
Malonic acid	21.69	-0.23	0.01
Tridecanoic acid	22.32	1.04	0.05
Stigmasterol	43.83	1.44	0.76
beta-Elemene	25.63	1.84	0.06
3-Ethyl-3-methylheptane	37.33	1.81	0.02
beta-Sitosterol	36.91	1.32	0.75
Neohexane	37.81	1.77	0.01
Frutinone A	65.9	0.89	0.34
Humulene oxide	23.66	1.58	0.1
Kaempferol	41.88	0.26	0.24
Vulgarin	29.21	0.03	0.2
Mannose-b	43.04	-1.82	0.04
3-methylheptane	37.1	1.8	0.01
(2S,3S,4S,5S,6S)-3,4,5,6-tetrahydroxoxane-2-carboxylic acid(MAV)	56.17	-2.14	0.06
Ginsenoside Rb2	6.02	-3.92	0.04
Ginsenoside Re	4.27	-3.2	0.12
Ginsenoside Rc	8.16	-3.97	0.04
Ginsenoside Rg1	10.2	0.12	0.78
Ginsenoside Rg2	20.12	-0.04	0.82
<u>Ginsenoside Rb1</u>	6.24	-3.99	0.04

**TABLE S5:** The details of metabolic proteins through network pharmacology analyses.

UniProt ID	Protein name
P47712	Cytosolic phospholipase A2
Q15596	Nuclear receptor coactivator 2
P38936	Cyclin-dependent kinase inhibitor 1
P28161	Glutathione S-transferase Mu 2
P09211	Glutathione S-transferase P
P09488	Glutathione S-transferase Mu 1
P22303	Acetylcholinesterase
P06276	Cholinesterase
P11217	Glycogen phosphorylase, muscle form
P30520	Adenylosuccinate synthetase isozyme 2
Q9Y6K0	Choline/ethanolaminephosphotransferase 1

**TABLE S6: Proteins in M1 and M2 macrophage associated with potential biomarkers of PG.**

Protein ID	Gene Symbol	Description
M1		
P37238	Pparg	Peroxisome proliferator activated receptor gamma
M2		
P58681	Tlr7	Toll like receptor 7
Q61503	Nt5e	5'-Nucleotidase ecto
P70206	Plxna1	Plexin A1
P12025	Mdk	Midkine
P70207	Plxna2	Plexin A2
P07141	Csf1	Colony stimulating factor 1
Q62151	Ager	Advanced glycosylation end-product specific receptor
O88786	Il13ra2	Interleukin 13 receptor subunit alpha 2
P20109	Il13	Interleukin 13
P07214	Sparc	Secreted protein acidic and cysteine rich
P14901	Hmox1	Heme oxygenase 1
P16045	Lgals1	Galectin 1
P52633	Stat6	Signal transducer and activator of transcription 6
P13504	Il1r1	Interleukin 1 receptor type 1
P09803	Cdh1	Cadherin 1
P11835	Itgb2	Integrin subunit beta 2
P21981	Tgm2	Transglutaminase 2
ENSMUSG00000055170	Ifng	Interferon gamma
Q9WVH4	Foxo3	Forkhead box o3
P42227	Stat3	Signal transducer and activator of transcription 3
P42225	Stat1	Signal transducer and activator of transcription 1
P25799	Nfkb1	nuclear factor kappa B subunit 1
P11276	Fn1	Fibronectin 1
P35441	Thbs1	Thrombospondin 1
P26231	Ctnna1	Catenin alpha 1
Q61362	Chi3l1	Chitinase 3 like 1
ENSMUSG00000002603	Tgfb1	Transforming growth factor beta 1
Q02248	Ctnnb1	Catenin beta 1
Q9R1E0	Foxo1	Forkhead box o1
Q61221	Hif1a	Hypoxia inducible factor 1 subunit alpha
Both M1 and M2		
ENSMUSG00000000869	Il4	Interleukin 4
Q61176	Arg1	Arginase 1
ENSMUSG000000025746	Il6	Interleukin 6
P31041	Cd28	CD28 molecule

Q8K4B2	Irak3	Interleukin 1 receptor associated kinase 3
P06804	Tnf	Tumor necrosis factor
P29477	Nos2	Nitric oxide synthase 2

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