

1 *Original Research*

2 Immunomodulatory activity of *Ganoderma lucidum* immunomodulatory
3 protein *via* PI3K/Akt and MAPK signaling pathways in macrophage
4 RAW264.7 cells

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18 *Running title:* Immunomodulatory activity of *G. lucidum* FIP

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25

26 ABSTRACT

27 *Ganoderma lucidum*, a traditional edible and medicinal fungus, holds an important
28 status in health care systems in China and other Asian countries. Fungal
29 immunomodulatory protein (FIP), one of the active ingredients isolated from *G.*
30 *lucidum*, is a class of naturally occurring proteins and possesses potential biological
31 functions. This study was conducted to explore the molecular mechanism of its
32 immunomodulatory potency in immune responses of macrophages. *In vitro* assays of
33 biological activity indicated that rFIP-glu significantly activated macrophage
34 RAW264.7 cells, and possessed the ability of pro- and anti-inflammation the cells.
35 RNA sequencing analysis showed that macrophage activation involved Toll-like
36 receptors and mitogen-activated protein kinases pathways. Furthermore, qRT-PCR
37 indicated that phosphoinositide 3 kinase inhibitor LY294002 blocked the mRNA
38 levels of MCP-1, MEK1/2 inhibitor U0126 reduced the mRNA levels of TNF- α and
39 MCP-1, and JNK inhibitor SP600125 prevented the up-regulation of iNOS mRNA in
40 the rFIP-glu-induced cells. FIP-glu mediated these inflammatory effects not through a
41 general pathway, instead through a different pathway for different inflammatory
42 mediator. These data indicate the possibility that rFIP-glu has an important
43 immune-regulation function and thus has potential therapeutic uses.

44 KEYWORDS

45 *Ganoderma lucidum* immunomodulatory protein (FIP-glu); immunomodulatory; RNA
46 sequencing (RNA-seq); mitogen-activated protein kinases (MAPK); phosphoinositide
47 3 kinase (PI3K)

48 *Ganoderma lucidum*, a traditional Chinese medicinal mushroom, is a species in
49 the genus of *Ganoderma* with numerous pharmacological effects such as improving
50 immune function, antitumor, antioxidant, reducing cardiovascular and cerebrovascular
51 diseases and heart diseases caused by body oxidation (1). Among more than 400
52 different bioactive compounds isolated from *G. lucidum*, fungal immunomodulatory
53 protein (FIP) is an important bioactive component with immune regulating activity
54 and is one of the most promising active ingredients developed by modern
55 biotechnologies (2). FIP is a small protein with similar structure and
56 immune-regulatory activity to phytohemagglutinin and immunoglobulins. Since the
57 first FIP (designated as Lingzhi-8 or LZ-8) was isolated from *G. lucidum* mycelia,
58 dozens of FIPs have been isolated and identified from different fungus species in
59 recent years (3-6). FIPs have immunomodulatory functions and play an important role
60 in anti-tumor, anti-allergy, anti-transplant rejection, *etc.*, which implies a promising
61 application for medicinal use (7). For example, FIPs suppress tumors by inhibition of
62 telomerase activity *via* decrease of *hTERT* promoter activity and translocation of its
63 protein (8-10). FIP-gmi induce apoptosis *via* β -catenin inhibition in lung cancer cells
64 (11). FIP-fve has anti-inflammatory effects on OVA-induced airway inflammation and
65 reduces airway remodeling by suppressing IL-17 (12). In spite of a few studies about
66 anti-tumor (13, 14) and immunomodulatory effects (15-17), the mechanism of these
67 activities remain unclear. The relationship between the activation of these proteins,
68 downstream cytokine expression and physiological function represents an active line
69 of investigation.

70 Macrophages, belonging to a group of mononuclear phagocytes, play vital roles
71 in processes of the immune response and are strategically positioned throughout the
72 body tissues (18). They possess functions of phagocytosis, antigen presentation and
73 production of cytokines, thereby initiating immune response (19). Following
74 activation, macrophages can release a wide array of pro- or anti-inflammatory
75 cytokines, which further activate fellow immune cells (20). Depending on these
76 signals, macrophages have been typed classically activated (pro-inflammation, M1)
77 and alternatively activated (anti-inflammation, M2) (21). Classically activated
78 macrophages are elicited in response to pro-inflammatory cytokines and
79 pathogen-associated molecular patterns (PAMPs), such as Interferon- γ (IFN- γ) and
80 lipopolysaccharide (LPS) to promote pathogen killing and chronic inflammation. (22,
81 23). These macrophages produce cytotoxic and inflammatory molecules nitric oxide
82 (NO) and reactive oxygen species (ROS), pro-inflammatory cytokines tumor necrosis
83 factor (TNF- α), interleukin (IL)-1 β and IL-6, chemokine monocyte chemoattractant
84 protein-1 (MCP-1, or C-C motif ligand 2 (CCL-2)), *etc.* (24). However, excessive
85 inflammatory mediators can be implicated in a number of chronic diseases, such as
86 arthritis, colitis and asthma (25). M2 macrophages, which are typed in response to
87 anti-inflammatory cytokines, parasitic infections and damage-associated molecular
88 patterns (DAMPs), such as IL-4 and IL-13, play an important role in inhibition of
89 chronic and acute inflammatory response and in tissue repair (23). M2 macrophages
90 are able to secrete high amounts of anti-inflammatory cytokines, such as IL-10 and
91 TGF- β (26).

92 Macrophages can be activated to an inflammation-promoting phenotype through
93 members of the Toll-like receptor (TLR) family such as TLR4 (20, 27, 28). Activated
94 TLRs induce activation of specific intracellular pathways including phosphoinositide
95 3 kinases (PI3K/Akt), mitogen activated protein kinases (MAPKs) and nuclear factor
96 kappa B (NF- κ B) (21, 29, 30). PI3K/Akt signaling pathway participates in
97 macrophage polarization (31-34), while MAPKs, including extracellular
98 signal-related kinase (ERK)-1/2, p38 and c-Jun NH₂-terminal kinase (JNK), and
99 NF- κ B are classic inflammation related signals and induce the expression of
100 pro-inflammatory mediators (35-38).

101 Here, we report that rFIP-glu produced in *Pichia pastoris* has the ability to induce
102 macrophage activation and produce pro- and anti-inflammatory mediators, which may
103 be through PI3K and MAPK pathways.

104

105 RESULTS

106 **Production of rFIP-glu in *Pichia pastoris*.** An expression vector pPIC9K
107 was used for achieving rFIP-glu. To facilitate purification, a His-tag was added at the
108 C-terminal of rFIP-glu (Fig. 1A). Following confirmation by sequencing and
109 linearization by *Sac I*, a recombination plasmid containing nucleotide sequences of
110 FIP-glu and His-tag was transformed into *Pichia pastoris* GS115 cells. The
111 transformants successfully secreted recombination proteins into the media compared
112 with the negative control (GS115 transformed with or without pPIC9K plasmid
113 incubated with or without MeOH) after induced by MeOH for 72 h (Fig. 1B). Western

114 blot analysis further confirmed that the secreted protein was rFIP-glu using anti-6×His
115 tag (Fig. 1C) and anti-rFIP-glu (Fig. 1D).

116

117 **Toxicity of rFIP-glu against RAW264.7 cells.** To investigate the activation
118 effect of rFIP-glu on the RAW264.7 cells, firstly we determined whether this
119 recombinant fungal protein possessed toxicity and measured its noncytotoxic range.
120 As shown in Fig. 2, the proliferation of RAW265.7 cells treated with 1 and 2 µg/mL
121 of rFIP-glu significantly increased ($p \leq 0.0001$), relative to the control group. A
122 culture of RAW264.7 cells incubated with 4 µg/mL of rFIP-glu resulted in no effect
123 on cell viability and more than 90% of cells with 8 µg/mL were viable ($p \leq 0.01$). The
124 viability of RAW264.7 cells with more than 8 µg/mL showed a rapid decrease ($p \leq$
125 0.0001). Based on these results, subsequent assays were performed at 4 µg/mL or no
126 more than 8 µg/mL. Additionally, rFIP-glu obviously influenced the morphology of
127 RAW264.7 macrophages with or without stimulation of LPS (Fig. S1).

128

129 **rFIP-glu improves phagocytosis of RAW264.7 cells.** Next, phagocytic
130 activities of RAW264.7 cells treated with rFIP-glu were examined by neutral red
131 uptake assay. As shown in Fig. 3, when the cells were treated with noncytotoxic
132 concentration of rFIP-glu ranged from 1 to 8 µg/mL, the phagocytosis increased and
133 then decreased. The phagocytosis of macrophage RAW264.7 cells were significantly
134 improved ($p \leq 0.05$) at 2 µg/mL of rFIP-glu, but suppressed ($p > 0.05$) at 8 µg/mL.
135 These indicate that rFIP-glu has the ability to enhance phagocytic activity of RAW

136 264.7 cells when the concentration is no higher than 8 $\mu\text{g}/\text{mL}$.

137

138 **rFIP-glu regulates pro- and anti-inflammatory genes at**

139 **transcriptional level in RAW264.7 cells.** To further evaluate the

140 immunostimulatory effects of rFIP-glu, we investigated whether rFIP-glu had the

141 ability to induce mRNA levels of relevant genes contributing to the function of

142 macrophages. These genes were determined by qRT-PCR after cells were treated with

143 rFIP-glu (1, 2, 4 and 8 $\mu\text{g}/\text{mL}$) for 6 h (Fig. 4). Compared to control, the

144 rFIP-glu-treated group showed a robust increase in the mRNA level of TNF- α (Fig.

145 4A; $p \leq 0.01$ at 1 $\mu\text{g}/\text{mL}$; $p \leq 0.001$ at 2, 4 and 8 $\mu\text{g}/\text{mL}$). Similarly, rFIP-glu also

146 significantly promoted the mRNA expression of Arginase II in a

147 concentration-dependent manner (Fig. 4B; $p \leq 0.001$ at 1 $\mu\text{g}/\text{mL}$; $p \leq 0.0001$ at 2, 4

148 and 8 $\mu\text{g}/\text{mL}$). The production of NO was measured firstly, but none was detected at 1

149 to 8 $\mu\text{g}/\text{mL}$ of rFIP-glu (Data not shown). Alternatively, we investigated the mRNA

150 expression of iNOS and found that it also dramatically increased in a

151 concentration-dependent manner (Fig. 4C; $p \leq 0.0001$ at 4 and 8 $\mu\text{g}/\text{mL}$). The mRNA

152 level of MCP-1 (CCL-2) was also increased and peaked at 2 $\mu\text{g}/\text{mL}$ ($p \leq 0.0001$), and

153 then decreased to no change at 8 $\mu\text{g}/\text{mL}$ compared with control (Fig. 4D). rFIP-glu

154 treatment concentration-dependently inhibited the mRNA expression levels of IL-10

155 (Fig. 4E; $p \leq 0.0001$) in RAW264.7 cells. These results exhibit that rFIP-glu

156 stimulates the immune responses by inducing pro-inflammatory mediators. In parallel,

157 rFIP-glu inhibited the mRNA expression level of CXCL-10 (Fig. 4F; $p \leq 0.01$ at 1

158 $\mu\text{g/mL}$; $p \leq 0.0001$ at 2, 4 and 8 $\mu\text{g/mL}$). This result exhibits that rFIP-glu induces
159 anti-inflammatory phenotype of macrophages. Additionally, there was little or no
160 effect on IL-6 at transcriptional level (Fig. 4G) and the mRNA expression of IL-1 β
161 was not detected (Data not shown). Taken together, rFIP-glu re-polarizes
162 macrophages by regulating of pro- and anti-inflammatory genes expression at
163 transcriptional level in RAW264.7 cells.

164

165 **rFIP-glu regulates LPS-induced pro- and anti-inflammatory**
166 **mediators at transcriptional level in RAW264.7 cells.** In order to further
167 determine that rFIP-glu induces or suppresses mRNA expression levels of pro- and
168 anti-inflammatory genes, RAW264.7 cells were stimulated with 1 $\mu\text{g/mL}$ LPS in the
169 presence or absence of increasing concentration of rFIP-glu for 6 h, and then
170 qRT-PCR analysis was performed. Compared with the normal control group, LPS
171 treatment (1 $\mu\text{g/mL}$) significantly increased the mRNA expression of IL-1 β , IL-6,
172 IL-10, TNF- α , MCP-1 (CCL-2), CXCL-10 and Arginase II and production of NO (Fig.
173 5). rFIP-glu treatment (1, 2, 4 and 8 $\mu\text{g/mL}$) significantly promoted the mRNA levels
174 of TNF- α (Fig. 5A; $p \leq 0.0001$), MCP-1 (CCL-2) (Fig. 5B; $p \leq 0.0001$) and Arginase
175 II (Fig. 5C; $p \leq 0.0001$) and concentration-dependently inhibited IL-10 expression at
176 transcriptional level (Fig. 5D; $p \leq 0.001$ at 2 $\mu\text{g/mL}$; $p \leq 0.0001$ at 4 and 8 $\mu\text{g/mL}$) in
177 LPS-stimulated RAW 264.7 cells. These results suggest that rFIP-glu promotes
178 inflammation in LPS-induced RAW264.7. On the other hand, rFIP-glu could
179 suppressed LPS-induced mRNA expression levels of IL-1 β (Fig. 5E; $p \leq 0.01$ at 2

180 $\mu\text{g}/\text{mL}$; $p \leq 0.0001$ at 4 and 8 $\mu\text{g}/\text{mL}$), IL-6 (Fig. 5F; $p \leq 0.01$ at 4 $\mu\text{g}/\text{mL}$; $p \leq 0.0001$
181 at 8 $\mu\text{g}/\text{mL}$) and CXCL-10 (Fig. 5G; $p \leq 0.01$ at 4 $\mu\text{g}/\text{mL}$; $p \leq 0.0001$ at 8 $\mu\text{g}/\text{mL}$) and
182 LPS-induced production of NO (Fig. 5H; $p \leq 0.01$ at 2 $\mu\text{g}/\text{mL}$; $p \leq 0.0001$ at 4 and 8
183 $\mu\text{g}/\text{mL}$) in a concentration-dependent manner. The results indicate that rFIP-glu
184 suppresses the LPS-induced expression of these inflammatory mediators at the
185 transcriptional level. Thus, rFIP-glu regulates pro- and anti-inflammatory genes
186 expression at transcriptional level in LPS-stimulated RAW264.7 cells.

187

188 **RNA sequencing results.** To give further insights into the molecular
189 mechanisms involved in the activity of rFIP-glu on macrophage RAW264.7 cells,
190 RNA-seq was performed at the sequencing core facility of Shanghai Institute of
191 Immunology. RAW264.7 cells were exposed to non-toxic rFIP-glu doses (4 $\mu\text{g}/\text{mL}$)
192 for 6 h (Fig. 6). There were approximately 50,000 (coding and non-coding) genes
193 detected. To determine sample relationships, principle component analysis (PCA) (Fig.
194 6A) and hierarchical clustering analysis (Heatmap) (Fig. 6B) were performed and
195 demonstrated that two different groups, rFIP-glu treatment group and control (PBS)
196 group, can be distinguished and showed segregation. Using an FDR ≤ 0.001 and fold
197 change > 1 to determine differently expressed genes after rFIP-glu treatment, more
198 than 700 genes were differentially expressed and we observed 578 up-regulated genes
199 and 159 down-regulated gene (Fig. 6C). Next, we used the Gene Ontology (GO)
200 database to characterize the differentially expressed genes. Subsets of these genes
201 were found to be involved in cellular process, regulation of biological process,

202 metabolic process, response to stimulus, developmental process, signaling and
203 localization (Fig. 6D). These genes encoded proteins that perform immunological
204 functions including inflammatory response, response to oxygen-containing compound,
205 cellular response to organonitrogen compound, regulation of protein phosphorylation,
206 regulation of protein modification process and regulation of programmed cell death
207 (Fig. 6E). Moreover, to investigate the possible signaling pathways through which
208 RAW264.7 cells activated by rFIP-glu, Kyoto Encyclopedia of Genes and Genomes
209 (KEGG) pathway enrichment analysis was performed. Fig. 6F showed the top 20
210 significantly enriched canonical pathways. In order to verify the RNA-seq results, 10
211 differential expression genes which were up- or down-regulated showed in the
212 RNA-seq results were selected. The expression levels of these genes measured by
213 RT-qPCR showed the same tendency with RNA-seq (Fig. 6G).

214

215 **PI3K and MAPK signaling pathways are involved in rFIP-glu-induced**
216 **macrophage activation.** Obviously, results mentioned above had been shown that
217 rFIP-glu was capable to promote macrophage proliferation and phagocytosis and
218 induce the mRNA expression of inflammatory mediators such as TNF- α , MCP-1
219 (CCL-2) and iNOS. Analysis of RNA-seq indicated that Toll-like receptors pathway
220 was involved in macrophage activation by rFIP-glu (Fig. S2). Signaling pathway
221 inhibitor, PI3K inhibitor LY294002, was used to further confirm the mechanisms
222 involved in rFIP-glu-induced macrophage activation. mRNA levels of TNF- α , MCP-1
223 (CCL-2) and iNOS were measure by qRT-PCR. Results showed that PI3K inhibitor

224 LY294002 blocked the mRNA levels of MCP-1 (CCL-2) induced by rFIP-glu in
225 RAW264.7 cells (Fig. 7B; $p \leq 0.0001$), while the mRNA expression of TNF- α was not
226 changed (Fig. 7A). These findings suggest that the PI3K pathway is related to
227 rFIP-glu-induced macrophage activation.

228 RNA-seq data implied that MAPK signaling pathway was also involved in
229 macrophage activation by rFIP-glu (Fig. S3). Signaling pathway inhibitors, MEK1/2
230 inhibitor U0126, JNK inhibitor SP600125 and p38 inhibitor SB203580, were used to
231 further confirm the mechanisms involved in rFIP-glu-induced macrophage activation.
232 mRNA levels of TNF- α , MCP-1 (CCL-2) and iNOS were measure by qRT-PCR.
233 Results showed that, in rFIP-glu-induced RAW264.7, MEK1/2 inhibitor U0126
234 blocked the mRNA levels of TNF- α (Fig. 7C; $p \leq 0.0001$) and MCP-1 (CCL-2) (Fig.
235 7D; $p \leq 0.0001$) and JNK inhibitor SP600125 prevented the up-regulation of iNOS
236 mRNA (Fig. 7E; $p \leq 0.001$). These findings suggest that the MEK1/2 and JNK
237 pathways are indeed related to rFIP-glu-induced macrophage activation.

238

239 Discussion

240 *G. lucidum* is well known as an edible medicinal mushroom for thousands of
241 years in China. FIP-glu or LZ-8 is one of the active ingredients in *G. lucidum*. From
242 beginning of discovery, FIP-glu is named immunomodulatory protein because of a
243 certain degree of homology with the heavy chain variable region of several
244 immunoglobulins (39, 40). FIP-glu possesses a variety of physiological activities,
245 such as anti-anaphylaxis, proliferation stimulation of lymphocytes, anti-tumor and

246 immunosuppression (7), suggesting that this protein has great potential in
247 development of immuno-regulated drugs or foods. Our results showed that rFIP-glu is
248 a potent stimulator of macrophage proliferation and activation. rFIP-glu can regulate
249 the mRNA expression of pro- and anti-inflammatory mediators in macrophage
250 RAW264.7 cells in the presence or absence of LPS. rFIP-glu mediates macrophage
251 activation through PI3K and MAPK pathways based on RNA-seq analysis.

252 Macrophages play an important role in host-defense. Macrophages perform
253 phagocytosis against pathogens as the first step, which is used to initiate the innate
254 immune response, and then orchestrate the adaptive response (41). Thus, phagocytosis
255 is a key indicator of evaluating macrophage activation. In the present study, rFIP-glu
256 significantly improved the phagocytosis of macrophage RAW264.7 cells at 2 µg/mL,
257 suggesting that rFIP-glu have abilities to enhance phagocytic activity of RAW 264.7
258 cells. The phagocytosis of macrophages can be enhanced by many bioactive
259 substances, such as polysaccharides (42, 43), peptides (44) and proteins (45, 46),
260 alkaloids (47) and phospholipids (48). Phagocytosis is one of the important innate
261 immune responses. Following RNA-seq analysis showed that rFIP-glu-induced
262 phagocytosis of macrophage RAW264.7 cells involved Fcγ receptor-mediated
263 phagocytosis and most genes involved in this process were up-regulated (Fig. S4).
264 There are two general classes of Fcγ receptors (FcγRs), activating receptors that
265 activate effector functions and inhibitory receptors that inhibit these functions (41). In
266 general, activation and inhibitory FcγRs are co-expressed on the same cell (49). The
267 phagocytosis involves the simultaneous clustering of activating and inhibitory FcγRs

268 and is regulated by the ratio of activating to inhibitory Fc γ Rs (50). Moreover,
269 Fc γ R-mediated phagocytosis is accompanied by the release of inflammatory
270 mediators, and excessive magnitude of the Fc γ R response could lead to excessive
271 inflammation (50, 51). RNA-seq analysis exhibited down-regulation of an activating
272 receptor, Fc γ RI and up-regulation of an inhibitory receptor, Fc γ RIIb, when
273 RAW264.7 cells were treated with 4 μ g/mL of rFIP-glu although the enhancement of
274 phagocytosis was not significant. This suggests that rFIP-glu participates in the
275 regulation of the phagocytosis of macrophages and the release of inflammatory
276 mediators. Additionally, Fc γ RIIb has ability to suppress allergic responses (52-55).
277 This possibly is one of the mechanisms of rFIP-glu-mediated anti-allergy.

278 In response to an immune challenge, macrophages become activated and produce
279 cytotoxic and inflammatory mediators, such as NO, ROS, TNF- α and IL-6, that
280 contribute to nonspecific immunity (56). Our results implied that rFIP-glu has the
281 predominant role in transcription of pro-inflammatory genes including TNF- α ,
282 MCP-1 (CCL-2), Arginase II and iNOS. Macrophages can be activated by
283 biologically active substances such as polysaccharides and proteins to produce the
284 pro-inflammatory molecules (24, 34, 57, 58). Similarly, most mushroom metabolites
285 also activate macrophages to produce various mediators, such as IL-1 β , TNF- α and
286 iNOS (59). PCP, an immunomodulatory protein from *Poria cocos*, can promote
287 TNF- α and IL-1 β production in RAW 264.7 cells (60). TNF- α are pro-inflammatory
288 cytokines and play an essential role in the immune response and inflammation (61).
289 MCP-1 (CCL-2) is a member of the CC chemokine family and involved in the

290 pathogenesis of multiple forms of inflammatory disorders as a mediator of acute and
291 chronic inflammation (62, 63). Arginase II, one of isoforms of arginase, is
292 up-regulated in M1 macrophages by pro-inflammatory stimuli and promotes
293 pro-inflammatory responses (64, 65). iNOS-dependent nitric oxide from activated
294 macrophages as a cytotoxic mediator can function in many diseases including cancer
295 (66). Interestingly, in rFIP-glu-treated macrophage RAW264.7 cells, the mRNA
296 expression of IL-6 was not changed, and that of IL-1 β was not detected due to less
297 transcripts possibly (Data not shown), although IL-1 β and IL-6 are important
298 pro-inflammatory cytokines as well. Moreover, the mRNA level of IL-10 was
299 suppressed by rFIP-glu. IL-10 is an anti-inflammation cytokine and is secreted by M2
300 macrophages to suppress the inflammation (26, 67). Studies show that an increase in
301 levels of M1 markers such as IL-1 β , MCP-1 (CCL-2), TNF- α and iNOS and a
302 decrease or little change in levels of M2 markers such as IL-10 will drive macrophage
303 M1 activation (68-71). The findings of the present investigation contributed to our
304 understanding that rFIP-glu promotes macrophage M1 polarization and initiates
305 pro-inflammatory responses. Unexpectedly, CXCL-10 were down-regulated at mRNA
306 levels in RAW264.7 cells induced by rFIP-glu. CXCL-10, belonging to the CXC
307 family of chemokines, is involved in systemic inflammation and can mediate the
308 recruitment of inflammatory cells (72, 73). Actually, CXCL-10 are expressed under
309 inflammatory conditions in M1 macrophages (74, 75) and their products are reduced
310 in M2 macrophages (76, 77). It seems that rFIP-glu induces M2 phenotypical
311 macrophages to suppress inflammation. To further confirm anti-inflammatory effects

312 of rFIP-glu, these related genes were detected in LPS-stimulated macrophage
313 RAW264.7 cells. Results showed that rFIP-glu indeed possessed anti-inflammation
314 activity through inhibiting LPS-induced mRNA levels of pro-inflammatory mediators
315 (IL-6, IL-1 β and CXCL-10) and the production of NO. A vast majority of bioactive
316 substances can attenuate LPS-induced inflammation by decreasing the mRNA levels
317 of pro-inflammatory mediators and increasing anti-inflammatory mediators.
318 Polysaccharides, SGP-1 and SGP-2 isolated from the rhizomes of *Smilax glabra*,
319 significantly suppressed the release of NO, TNF- α and IL-6 from LPS-induced RAW
320 264.7 cells (78). A prenylated flavonoid, 10-oxomornigrol F (OMF), can inhibit the
321 LPS-induced production of NO, TNF- α , IL-1 β and IL-6 in RAW264.7 cells (79). To
322 our surprise, rFIP-glu acted in strong synergy with LPS to induce the mRNA
323 expression levels of TNF- α , MCP-1 (CCL-2) and Arginase II. Meanwhile, mRNA
324 level of IL-10 was still suppressed by rFIP-glu in LPS stimulated RAW264.7 cells.
325 Another immunomodulatory protein, FIP-*apo* (APP) from *Auricularia polytricha*, also
326 accounts for synergistic effects with LPS by NO and TNF- α production (80). These
327 results mentioned above suggest that rFIP-glu can balance M1/M2 macrophages by
328 regulating pro- and anti-inflammatory mediators and exhibit immunomodulatory
329 activity. This phenomenon may confer macrophages an ability to quickly switch
330 between M1 or M2 associated functions allowing for appropriate responses to stimuli
331 and tissue environment (81). Re-polarization of macrophages is a key role and a
332 promising therapeutic option in many diseases (26, 82). For example, inflammatory
333 bowel diseases can be ameliorated by switching M1 macrophages to M2 (83, 84).

334 Conversion of M2 to M1 phenotype is a potential therapeutic intervention in
335 anti-tumor (85, 86).

336 Obviously, rFIP-glu has the ability to activate macrophages. The mechanisms
337 were further investigated. In this study, RNA-seq was used to investigate the
338 mechanisms of macrophage activation in rFIP-glu-treated RAW 264.7 cells. Our
339 results indicated that the macrophage activation induced by rFIP-glu involved
340 Toll-like receptors and MAPKs signaling pathways in macrophage RAW264.7 cells,
341 which is consistent with that PI3K/Akt, the downstream of Toll-like receptor, and
342 MAPK are involved in the activation of macrophages (34, 87-89). TLR4 is critical in
343 immune responses and involved mainly in inflammation responses (90). TLR4 can be
344 recognized and activated by many stimuli such as polysaccharides, and its expression
345 increases, and then activates PI3K/Akt and MAPKs pathways, with introduction of a
346 pool of inflammatory mediators (30, 34, 43, 87, 91). In addition, NF- κ B involves in
347 macrophage activation as well (24, 34, 92, 93). Similarly, RNA-seq analysis indicated
348 that NF- κ B pathway participated in rFIP-glu-mediated macrophage activation. More
349 evidences should be investigated in the future. Although rFIP-glu activated Toll-like
350 receptors, MAPKs and NF- κ B pathways, RNA-seq (Fig. S2) and qRT-PCR (Fig. S5)
351 confirmed that the mRNA expression level of TLR4 did not change. It suggests that
352 the mRNA expression of pro-inflammatory genes induced by rFIP-glu was not
353 through activating the TLR4 signaling pathway. RNA-seq analysis showed that TLR2
354 mRNA expression increased (Fig. S2), presuming TLR2 was a receptor of rFIP-glu. A
355 preliminary yeast two-hybrid experiment showed that rFIP-glu did not interact with

356 an extracellular part of TLR2 (Data not shown), suggesting TLR2 possibly was not a
357 receptor of rFIP-glu as well. It is noteworthy that some active substances can activate
358 all of these pathways (34, 57, 88), while some can only activate one or more (30, 87,
359 94). We next used specific PI3K/Akt and MAPKs pathway inhibitors to clarify
360 whether these signaling pathways were involved in macrophage activation induced by
361 rFIP-glu. Our results implied the involvement of PI3K in rFIP-glu mediated MCP-1
362 (CCL-2) mRNA production, MEK1/2 in TNF- α and MCP-1 (CCL-2), and JNK in
363 iNOS. Although the induction of phosphorylated MAPKs and PI3K/Akt receptors was
364 not evaluated by Western blot, the participation of them was confirmed by RNA-seq
365 as well as inhibition of the effects induced by pretreatment with signaling pathway
366 inhibitors. These results indicate that rFIP-glu may enter cells and act with MEK1/2,
367 JNK or PI3K indirectly or directly, and another hypothesis is that rFIP-glu interacts
368 with TLR2 within cells (Fig. 8). In addition, the synergistic activity of rFIP-glu and
369 LPS implied that rFIP-glu could enhance the expression of downstream mediators that
370 are generated by Toll-like receptors pathway (80). Heme oxygenase-1 (HO-1) is an
371 anti-inflammatory enzyme and attenuates the inflammatory response (95), which can
372 be regulated by nuclear factor erythroid 2-related factor 2 (Nrf2) in the inflammatory
373 response (96). The Induction of HO-1 can be through MAPK and PI3K signaling
374 pathways (94, 97, 98). In the present study, mRNA level of HO-1 was significantly
375 increased in rFIP-glu-induced RAW264.7 cells (Fig. S6). This result implies that the
376 anti-inflammation of rFIP-glu is possibly mediated by HO-1 in macrophage
377 RAW264.7 cells.

378

379 **MATERIALS AND METHODS**

380 **Reagents.** Neutral red staining solution was obtained from Sangon Biotech
381 (Shanghai, China). U0126 (MEK1/2 inhibitor), SP600125 (JNK inhibitor) and
382 SB203580 (p38 inhibitor) were purchased from Beyotime (Shanghai, China).
383 LY294002 (PI3K inhibitor) was purchased from Selleck Chemicals (Houston, TX,
384 USA). Anti-FIP-glu antiserum was raised in rabbits (99). Anti-6×His Tag mouse
385 monoclonal antibody, HRP-conjugated Goat Anti-Mouse IgG and HRP-conjugated
386 Goat Anti-Rabbit IgG were from Sangon Biotech (Shanghai, China).

387

388 **Production of rFIP-glu.** Production of recombinant FIP-glu (rFIP-glu) in *P.*
389 *pastoris* was performed according to the instruction provided by Pichia Expression
390 Kit (Invitrogen, USA). Briefly, a gene encoding FIP-glu and subcloned in pUC-57
391 vector was synthesized by Sangon Biotech (Shanghai) Co., Ltd. (China) based on
392 codon usage bias. Then, the gene was cloned into an expression cassette vector
393 pPIC9K. For convenience, a His-tag was added at 3' end of multiple clone sites of the
394 vector. After construction, the recombinant expression vector pPIC9K-glu-His
395 linearized by a restriction enzyme *Sac* I was transferred into *P. pastoris* GS115. After
396 confirmed by PCR (100) and sequencing, the transformant was induced by methanol
397 for producing rFIP-glu. The rFIP-glu was purified with nickel-nitrilotriacetic acid
398 (Ni-NTA) agarose resin (TaKaRa, Beijing, China). SDS-PAGE and Western blot
399 analysis were performed based on the methods of our lab (99, 101).

400

401 **Cell culture.** Macrophage RAW264.7 cells were purchased from the Cell Bank
402 of the Chinese Academy of Sciences (Shanghai, China), cultivated in DMEM medium
403 supplemented with antibiotics (100 U/mL penicillin and 100 mg/mL streptomycin)
404 and 10% FBS and incubated at 37 °C in a 5% CO₂ incubator. Cells were seeded at 2 ×
405 10⁵ cells per well in 24- or 96-well microplates and were incubated in 5% CO₂ at
406 37 °C.

407

408 **Cell viability.** Methylene blue uptake assay was performed to assess the effect
409 of rFIP-glu on the viability of macrophage RAW264.7 cells (102). Briefly, Raw264.7
410 cells were incubated for 24 h, and then were incubated with rFIP-glu at different
411 concentration (1, 2, 4 and 8 µg/mL), LPS (1 µg/mL) and Concanavalin A (ConA) (5
412 µg/mL) for 24 h. LPS and ConA were used as positive controls. The culture
413 supernatant was discarded and cells were stained by adding 50 µL of 0.6% methylene
414 blue to each well. Plates were incubated at 37 °C for 60 min, and then inverted to
415 drain the stain solution away. Wells were washed with phosphate buffered saline (PBS)
416 to remove unbound stain. Plates were air-dried for several minutes. Stained cells were
417 solubilized by adding 50 µL of Elution Buffer (Ethanol : PBS : Acetic acid = 50 : 49 :
418 1 (Volume)) for 20 min with a gentle shake. The absorbance value was measured at
419 570 nm using a microplate reader (BIO-TEK[®], USA) and the viability was expressed
420 as percentage versus control group.

421

422 **Phagocytosis assay.** Phagocytosis assay was measured by Neutral red uptake
423 assay (42). Briefly, Raw264.7 cells were incubated for 24 h, and then incubated with
424 rFIP-glu at different concentration (1, 2, 4 and 8 µg/mL) and ConA (5 µg/mL) for 24 h.
425 After the supernatant was discarded, 100 µL neutral red staining solution was added
426 into each well and the plates were continued to incubate for 30 min. The supernatant
427 was discarded and the cells were washed with PBS thrice to move free neutral red.
428 200 µL of cell lysis buffer (Ethanol : Acetic acid = 1 : 1 (Volume)) was added into
429 each well and the plates were shaken for 2 h at room temperature. The absorbance
430 value was measured at 540 nm using a microplate reader (BIO-TEK[®], USA) and the
431 phagocytosis was expressed as OD values.

432

433 **Measurement of NO.** Raw264.7 cells were incubated for 24 h, and then were
434 incubated with rFIP-glu at different concentration (1, 2, 4 and 8 µg/mL) and LPS (1
435 µg/mL) for 24 h. The supernatants were used to evaluate NO production using Griess
436 assay by a NO Assay kit (Beyotime, Shanghai, China). According to the
437 manufacturer's protocol, sodium nitrite (NaNO₂) was used to generate a standard
438 curve to calculate the NO concentration.

439

440 **RNA extraction, sequencing and bioinformatics analysis.** Macrophage
441 RAW264.7 cells were cultured with rFIP-glu (4 µg/mL) for 6 h. Cells were harvested
442 and total RNA was extracted using TaKaRa MiniBEST Universal RNA Extraction Kit
443 (Beijing, China). Sequencing library was generated using Illumina Truseq stranded

444 total RNA LT kit. On average 20 million Illumina paired-end reads (150 bp) were
445 generated for each sample. The reads were mapped to reference using Hisat and
446 differential expression analysis was performed using the R package DESeq2. In
447 addition, principle component analysis (PCA) was carried out on the genes
448 significantly expressed between all different groups. We combined results of two
449 Enrichment analysis tools. One was derived from GSEA 3.0 desktop by mapping all
450 genes to biological process of GO knowledge base and KEGG knowledge base. The
451 other was calculated by IPA (version 01-13) of which cutoff was $FDR \leq 0.001$ and
452 $\text{Log}_2\text{FoldChange} > 1$. The data were also analyzed on the free online platform of
453 Majorbio I-Sanger Cloud Platform (www.i-sanger.com).

454

455 **cDNA synthesis and Real-time quantitative PCR (RT-qPCR).** cDNA
456 was synthesized from 1 μg RNA using PrimeScript™ RT Master Mix (Perfect Real
457 Time) (TaKaRa, Beijing, China) according to the manufacturer's protocol. RT-qPCR
458 was performed using SYBR qPCR Master Mix (Vazyme, Nanjing, China) and Roche
459 LightCycler® 96 Application. For PCR, samples were heated to 95 °C for 1 min,
460 denatured at 95 °C for 20 s, annealed at 55 °C for 20 s, extended at 72 °C for 20 s, and
461 cycled 45 times. The primers in this study were listed in Table S1. All reactions were
462 performed in triplicate, and Ct values were normalized to β -actin. Relative expression
463 was calculated using the $2^{-\Delta\Delta\text{Ct}}$ method.

464

465 **Statistical analysis.** Graph Pad Prism 7 software was used to prepare graphs

466 and statistical analysis. Data are expressed as means \pm SD. The statistical analysis
467 used One-way ANOVA analysis. Significance was indicated as ns, $p > 0.05$; *, $p \leq$
468 0.05; **, $p \leq 0.01$; ***, $p \leq 0.001$; and ****, $p \leq 0.0001$.

469

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473

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823

824 ***Figure legends***

825 FIG 1 Production of rFIP-glu in *P. pastoris* GS115 cells. A, schematic map of the
826 recombinant expression vector pPIC9K-glu-His. B, rFIP-glu detected by
827 SDS-PAGE. C, Western blot analysis of rFIP-glu using anti-6×His tag. D,
828 Western blot analysis of rFIP-glu using anti-rFIP-glu. Lane M: protein molecular
829 mass marker. Lane 1, *P. pastoris* GS115 cells without being induced by MeOH.
830 Lane 2, *P. pastoris* GS115 cells induced by MeOH. Lane 3, *P. pastoris* GS115
831 cells containing expression vector pPIC9K without being induced by MeOH.
832 Lane 4, *P. pastoris* GS115 cells containing expression vector pPIC9K induced by
833 MeOH. Lane 5, *P. pastoris* GS115 cells containing expression vector
834 pPIC9K-glu-His without being induced by MeOH. Lane 6, *P. pastoris* GS115
835 cells containing expression vector pPIC9K-glu-His induced by MeOH.

836 FIG 2 Effect of rFIP-glu on the viability of RAW264.7 cells. RAW264.7 cells were
837 treated with different concentration of rFIP-glu (1, 2, 4, 8, 16 and 32 µg/mL) or
838 PBS (as control), Concanavalin A (ConA) and lipopolysaccharide (LPS) for 24 h.
839 The cells were measured by methylene blue uptake assay. Data were expressed
840 as means ± SD (n = 5). ns, $p > 0.05$; **, $p \leq 0.01$; ****, $p \leq 0.0001$ versus

841 control group.

842 FIG 3 Effects of rFIP-glu on RAW264.7 cells phagocytosis. RAW264.7 cells were
843 treated with different concentration of rFIP-glu (1, 2, 4 and 8 $\mu\text{g}/\text{mL}$). Control
844 cells were treated with PBS only and ConA cells as positive control were treated
845 with 5 $\mu\text{g}/\text{mL}$. The effects were assessed by neutral red uptake assay. Data were
846 expressed as means \pm SD (n = 3). *, $p \leq 0.05$ versus control group.

847 FIG 4 Effects of rFIP-glu on RAW264.7 cells. The cells were treated with different
848 concentration of rFIP-glu (1, 2, 4 and 8 $\mu\text{g}/\text{mL}$) for 6 h. The mRNA expression
849 of TNF- α (A), Arginase II (B), iNOS (C), MCP-1 (CCL-2) (D), IL-10 (E),
850 CXCL-10 (F) and IL-6 (G) was measured by qRT-PCR. Data were expressed as
851 means \pm SD (n = 3). ns, $p > 0.05$; **, $p \leq 0.01$; ***, $p \leq 0.001$; ****, $p \leq 0.0001$
852 versus control group.

853 FIG 5 Effects of rFIP-glu on LPS-induced RAW264.7 cells. Cells were treated with
854 different concentration of rFIP-glu (1, 2, 4 and 8 $\mu\text{g}/\text{mL}$) and LPS (1 $\mu\text{g}/\text{mL}$) and
855 incubated for 6 h. The mRNA expression of TNF- α (A), MCP-1 (CCL-2) (B),
856 Arginase II (C), IL-10 (D), IL-1 β (E), IL-6 (F) and CXCL-10 (G) was measured
857 by qRT-PCR. Data were expressed as means \pm SD (n = 3). #####, $p \leq 0.0001$
858 versus control group. ns, $p > 0.05$; **, $p \leq 0.01$; ***, $p \leq 0.001$; ****, $p \leq 0.0001$
859 versus LPS group. The content of NO (H) in cell supernatant was determined by
860 Griess assay. Values are means \pm SD (n = 5). #####, $p \leq 0.0001$ versus control
861 group. **, $p \leq 0.01$; ****, $p \leq 0.0001$ versus LPS group.

862 FIG 6 RNA-seq analysis of macrophage RAW264.7 cells. (A) Principle component

863 analysis of RAW264.7 cells treated with and without rFIP-glu. (B) Heatmap of
864 RAW264.7 cells treated with and without rFIP-glu. (C) Scatter plots of
865 differentially expressed genes between PBS- and rFIP-glu-treated macrophages.
866 Up-regulated genes are depicted in red and down-regulated gene in green (FDR
867 ≤ 0.001 , fold change > 1). (D) GO analysis of the differentially expressed genes.
868 (E) GO enrichment analysis of the differentially expressed genes. (F) KEGG
869 pathway enrichment analysis of the differentially expressed genes. (G)
870 Confirmation of RNA-seq results by qRT-PCR.

871 FIG 7 Effect of rFIP-glu on signaling pathways. RAW264.7 cells were pre-treated
872 with 50 μM of LY294002 for 30 min and then treated with 4 $\mu\text{g/ml}$ of rFIP-glu
873 for 6 h. The mRNA expression of MCP-1 (CCL-2) (A) and TNF- α (B) was
874 measured by qRT-PCR. RAW264.7 cells were pre-treated with 20 μM of U0126,
875 30 μM of SP600125 or 10 μM of SB203580 for 30 min and then treated with 4
876 $\mu\text{g/ml}$ of rFIP-glu for 6 h. The mRNA expression of TNF- α (D), MCP-1 (CCL-2)
877 (E) and iNOS (F) was measured by qRT-PCR. Data were expressed as means \pm
878 SD (n = 3). #####, $p \leq 0.0001$ versus control group. ***, $p \leq 0.001$; ****, $p \leq$
879 0.0001 versus rFIP-glu group.

880 FIG 8 Possible immunomodulatory signaling mechanism of rFIP-glu in RAW264.7
881 macrophages.

882

883 *Supplementary legends*

884 FIG S1 The effect of rFIP-glu on morphological changes of RAW264.7 cells.

885 RAW264.6 cells were incubated with LPS, rFIP-glu or both for 6 h. Cells were
886 subjected to microscopic analysis (200×). All experiments were performed in
887 duplicates. The data from one representative experiment out of two independent
888 experiments were shown. Bar is 50 μm. A, untreated cells. Untreated RAW 264.7
889 cells as control exhibited a round morphology. B, LPS-treated cells. LPS-treated
890 RAW 264.7 cells exhibited changes of morphology including pseudopodia
891 formation and cell spreading. C, rFIP-glu-treated cells. After stimulated by
892 rFIP-glu, the volume of RAW 264.7 cells increased and agglutination happened.
893 D, rFIP-glu and LPS-stimulated cells. rFIP-glu treatment reversed morphology
894 change in LPS-stimulated RAW 264.7 cells, with increase in volume and
895 agglutination.

896 FIG S2 Heatmap of Toll-like receptors pathway in RAW264.7 cells treated with and
897 without rFIP-glu. RAW264.7 cells were treated with 4 μg/mL of rFIP-glu for 6 h.

898 FIG S3 Heatmap of MAPK receptors pathway in RAW264.7 cells treated with and
899 without rFIP-glu. RAW264.7 cells were treated with 4 μg/mL of rFIP-glu for 6 h.

900 FIG S4 Heatmap of FcγR-mediated phagocytosis pathway in RAW264.7 cells treated
901 with and without rFIP-glu. RAW264.7 cells were treated with 4 μg/mL of
902 rFIP-glu for 6 h.

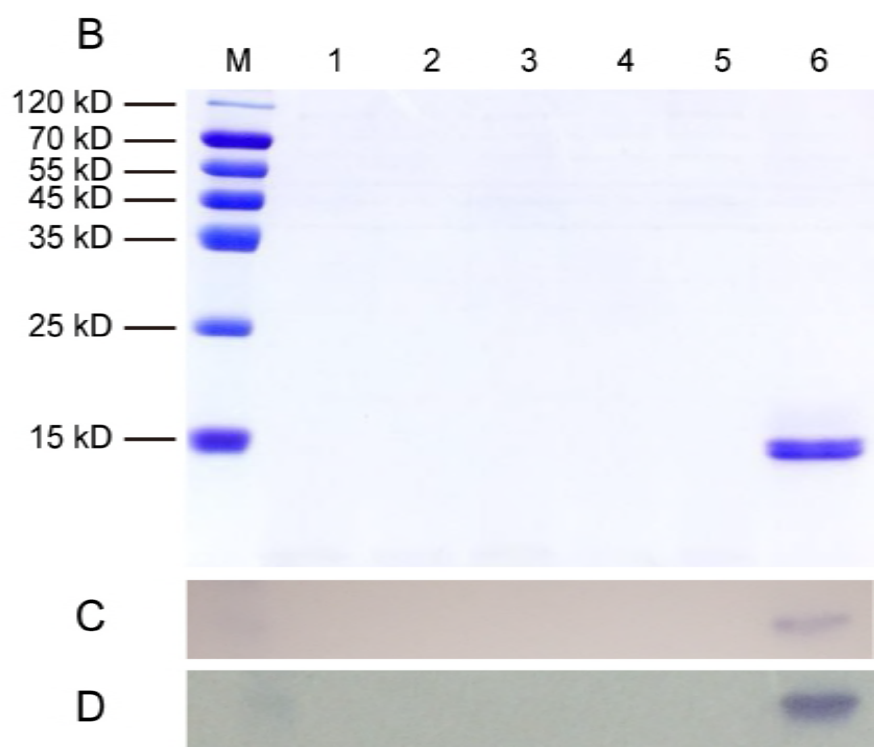
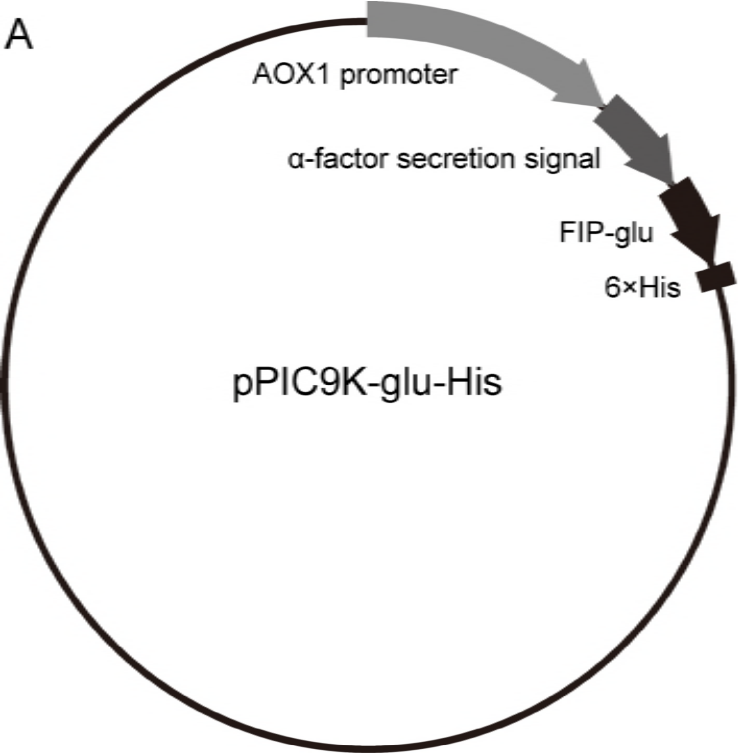
903 FIG S5 Effects of rFIP-glu on the mRNA level of TLR4 in RAW264.7 cells. The cells
904 were treated with 4 μg/mL of rFIP-glu for 6 h. The mRNA expression of TLR4
905 was measured by qRT-PCR.

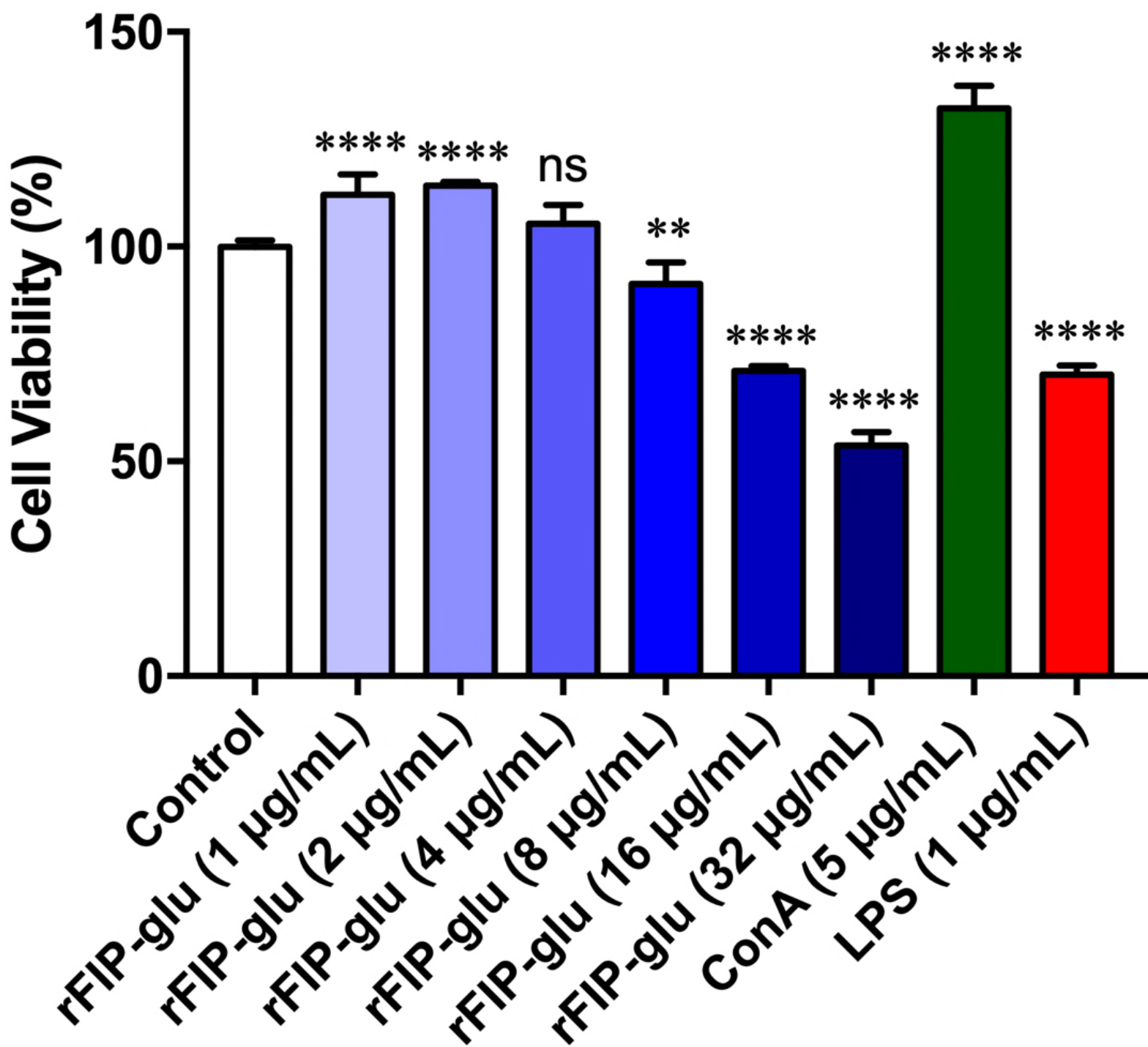
906 FIG S6 Effects of rFIP-glu on the mRNA level of HO-1 in RAW264.7 cells. The cells

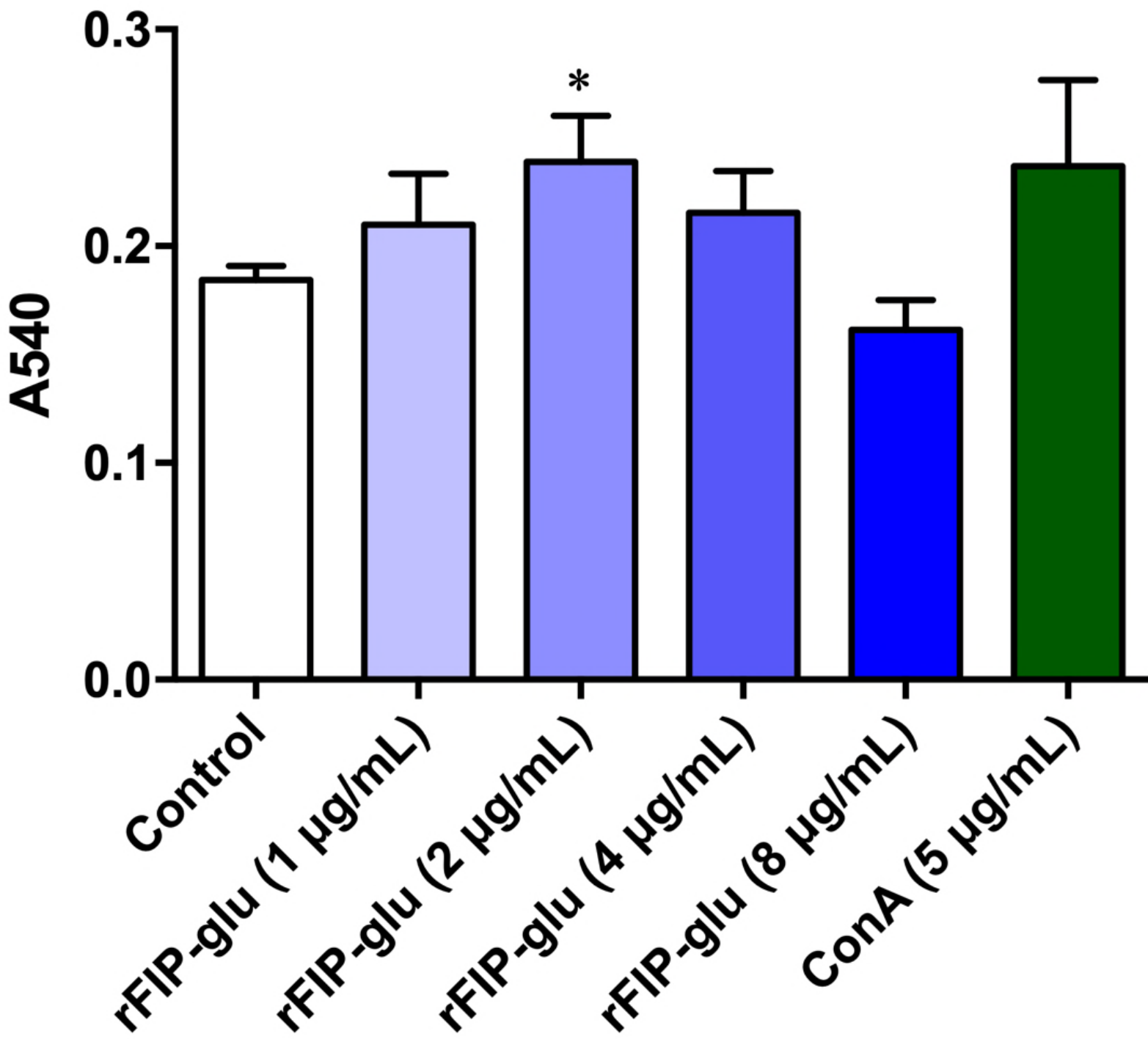
907 were treated with different concentrations of rFIP-glu (1, 2, 4 and 8 $\mu\text{g}/\text{mL}$) for 6
908 h. The mRNA expression of HO-1 was measured by qRT-PCR. Data were
909 expressed as means \pm SD (n = 3). ***, $p \leq 0.0001$ versus control group.

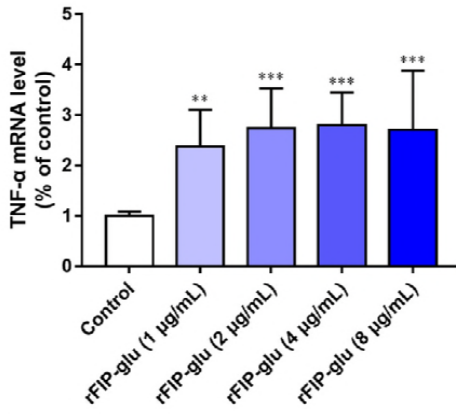
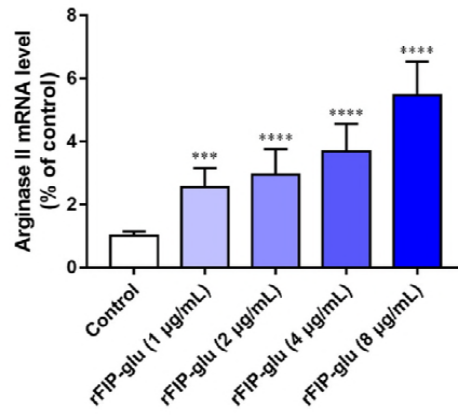
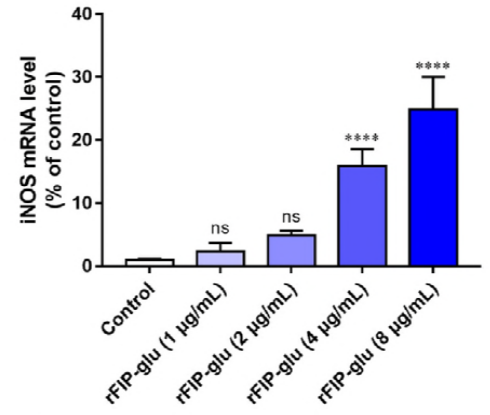
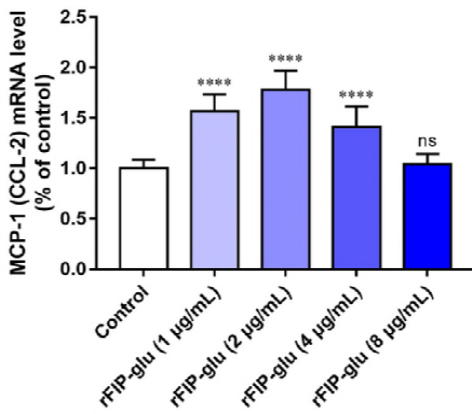
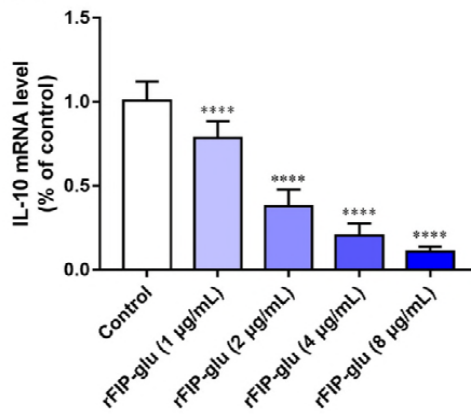
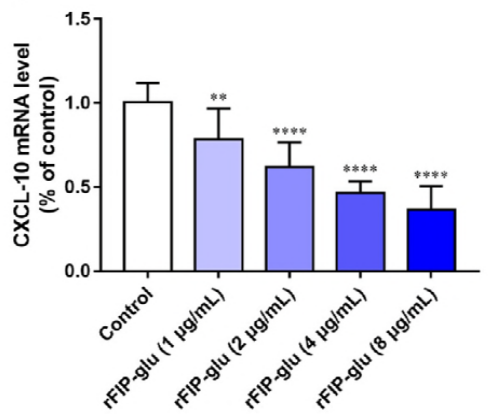
910 TABLE S1 Primers used in this study.

911







A**B****C****D****E****F****G**