1	Yeast cell wall particle mediated nanotube-RNA delivery system loaded
2	with miR365 antagomir for post-traumatic osteoarthritis therapy via oral
3	route
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1	Gene binding ratio of RNA to AAT nanotubes						
2	Th	The miR365 antagomir/NPs nanomaterial was self-assembled with miR365 antagomir (RiboBio,					
3	Gu	Guangzhou, China) and AAT nanotubes with different volume ratios.					
4	1.	The fixed miRNA (1 µL, 25 uM miRNA) was incubated with different doses of AAT (0, 1, 2, 4, 6,					
5		8, 10 and 20 μ g, 1 mg/mL) to form the RNA/AAT complexes.					
6	2.	Then sonicate the RNA/AAT complexes with 100 amplitudes for 150 s with a sonicator (Q700,					
7		Qsonica, USA).					
8 9	3.	The binding ratio of miRNA to AAT was detected using 2% agarose gel assay.					
10	Ev	Evaluate the release and stability of AAT/RNA with different mass heparin sodium salt					
11	1.	Heparin sodium salt (40 mg/mL) was used to evaluate the release and stability of RNA/AAT.					
12	2.	Add 1 µL of miRNA (25 uM) into 10 µL RNase-free water and fully mixed.					
13	3.	Then 5 μL of AAT (1 $\mu g/\mu L)$ was added into the RNA mixture in the previous step and fully					
14		mixed.					
15	4.	Sonicate the RNA/AAT complexes with 100 amplitudes for 150 s.					
16	5.	The complexes solution with v/v ratio of 5:1 (AAT/miRNA) was incubated with different mass					
17		heparin sodium salt (0, 0.63, 1.25, 2.5, 5, 10, 20 mg/mL and naked miRNA as control) for 1 h at					
18		37 ℃.					
19	6.	The release of gene was detected using agarose gel assay as previously described.					
20							
21	Pro	eparation of YCWP					
22	S.c	S.cerevisiae SAF-Mannan, (SAF Agri, Milwaukee, WI) was used for yeast cell wall particle (YCWP)					
23	pre	preparation as described below:					
24	1.	YCWP were prepared by suspending S.cerevisiae SAF-Mannan (15 g) in 200 mL of water, and					
25		the pH was adjusted to 12.5 with 1 M NaOH and heating to 60 $^{\circ}\mathrm{C}$ for 1 h. During this period,					
26		shake the flask gently every 20 min (avoid violent vibration) to evenly disperse the yeast in the					
27		solution					

1	2.	The insoluble material containing the cell walls was recovered by centrifuging at 1700 $\times g$ for 5
2		min.

- 3 3. This material was then suspended in 200 mL of water, brought to pH 4 with HCl, and incubated at
 55 °C for 1 h. And shake the flask gently every 20 min.
- 5 4. Repeat step 2 and wash the insoluble material once with 200 mL of water, twice with 200 mL of
- 6 dehydrated isopropanol, and twice with 200 mL of acetone. After each washing step, centrifuge
- 7 the insoluble material at $1700 \times g$ for 5 min.
- 8 5. The resulting slurry was dried at room temperature to produce slightly off-white powder.
- 9

10 Preparation of fluorescently labeled gYCWP

- 11 YCWP was used for green fluorescence labeled gYCWP preparation as described below:
- 12 1. YCWP (1 g) was washed with 40 mL of sodium carbonate buffer (0.1 M, pH 9.2).
- 13 2. The YCWP was recovered by centrifuging at 1700 × g for 5 min and resuspended in 90 mL
 14 carbonate buffer.
- 15 3. 10 mL of 5-(4,6-dichlorotriazinyl) aminofluorescein (Invitrogen; 1 mg/mL in DMSO) was added
- 16 to the buffered YCWP suspension (10% v/v) and mixed at 25 °C in the dark for 16 h.
- 4. 50 mL of Tris buffer (2 mM) was added and incubated for 15 min at 25 °C.
- 18 5. The insoluble material washed with sterile pyrogen-free water for 4 times. Centrifuged the 19 insoluble material at $1700 \times g$ for 5 min at 4 °C.
- 20 6. The green gYCWP was then dehydrated with 40 mL of absolute ethanol and 40 mL of acetone
 21 onece respectively. After each washing step, centrifuge the gYCWP at 1700 × g for 5 min.
- 22 7. Dried the gYCWP in the dark at $25 \,^{\circ}$ C.

23

24 Tissue cells digestion

25 All tissues (from small intestine, lung, spleen, bone marrow, spermatophore, testis, kidney and liver)

- 26 need to be digested into a single cell suspension with different methods before cell lysis for RNA
- isolation. We used 2 mg/mL collagenase D (Roche) solution for lung, spleen and testis digestion and 2

1	mg/mL collagenase IV (Sigma) for liver, kidney, spermatophore and bone marrow digestion with the
2	steps as follows:

- Rinse the dirt and blood clots of the lung (and liver) with pre-cooling phosphate buffered saline
 (PBS).
- 5 2. Place isolated lung (and spleen, kidney, liver, testis) in the 6 cm petri-dish with sufficient
 6 collagenase solution to cover the bottom of the dish.
- 7 3. Inject 500 µL of collagenase solution per lung and liver (100 µL per spleen, testis and kidney)
 8 with a 0.5 mL syringe and then cut the tissue into 1-2 mm³ size pieces.
- 9 4. Digestion was achieved by adding 25 mL collagenase solution and incubation at 37 °C, 155 rpm
 10 for 60 min (all samples including spermatophore and bone marrow).
- 5. Digested cell suspension was filtered through a 70 µm sterile filter and cell was washed twicewith PBS.
- 13

14 The stability of YCWP in SGF and SIF

Simulated gastric fluid (SGF, which contains 0.2 g NaCl and 0.32 g pepsin in 100 mL water, and the pH was adjusted to 1.2 with HCl) and simulated intestinal fluid (SIF, which contains 0.68 g KH₂PO₄ and 1 g trypin in 100 mL water, and the pH was adjusted to 6.8 with HCl) were used to assess the stability of YCWP as described below: 10^5 YCWP was added into 500 µL of SGF and incubated for 4 hours at 37 °C. YCWP was recovered by centrifuging at $1700 \times g$ for 2 min. Then resuspended the YCWP with 500 µL SIF and incubated for 6 and 8 hours at 37 °C.

21

22 Detect the protective effect of NPs-YCWP on NPs in SGF

23 NPs-gYCWP with red labeled negative control RNA (Cy3 RNA) was used to detect the protective

effect of NPs-YCWP on NPs (Cy3RNA/NPs) at a pH 1.2 environment. 10⁵ YCWP was added into

25 500 μL of SGF, brought to pH 1.2 with HCl, and incubated in the dark for 4-8 h at 37 °C. Then

26 fluorescence was observed with fluorescence microscope.

1 NPs-YCWP can effectively release NPs in the SIF

NPs-YCWP that contained 10^4 YCWP was incubated with 50 µL SIF for 2-6 h at 37 °C. Then equal volume of heparin sodium salt (5 mg/mL) was added and incubated for 1 h at 37 °C. Centrifuge the mixture at $1700 \times g$ for 2 min and collect the supernatant liquid. The RNA intensity was measured using an agarose gel retardation assay.

6

7 Stability of NPs (RNA/AAT) in SIF

8 NPs were self assembled with RNA (2 µL of 25 µM negative control antagomir) and AAT (10 µg),

9 and incubated in 50 µL SIF for 4 or 8 h at 37 °C (naked RNA as control). Then added equal volume of

10 heparin sodium salt (5 mg/mL) and incubated for 1 h at 37 °C. The RNA intensity was measured using

- 11 an agarose gel retardation assay.
- 12



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Figure S1. Quantification of the agarose gel electrophoresis results. (A) Quantification of agarose
gel electrophoresis results of miR365 antagomir/NPs complexes at various v/v ratios (0, 1, 2, 4, 6, 8,
10 and 20). (B) Quantification of RNA release from miR365 antagomir/NPs by different mass heparin
sodium salt (0, 0.63, 1.25, 2.5, 5, 10, 20 mg/mL). The nk means naked miRNA control. Data were
expressed as mean ±SD. NS (no significance). *P < 0.05, ***P < 0.001 (n=3).



9

10 Figure S2. The eluate produced during the chemical treatment. S. cerevisiae SAF-Mannan was

- 11 used for YCWP preparation by alkaline-and-acid extraction and then treatment with isopropanol and
- 12 acetone. The eluate produced in each step during the chemical treatment was recorded.
- 13





Figure S3. Confocal microscope results of NPs-gYCWP. YCWP was fluorescently labeled with
aminofluorescein to construct green gYCWP. And AAT and Cy3 red labeled negative control RNA
(NgRNA) was used to construct NgRNA/NPs. Then NgRNA/NPs and gYCWP were fully mixed to
get NgRNA/NPs-gYCWP. Then gYCWP (A), NgRNA/NPs-gYCWP (B) and NgRNA-AAT-gYCWP
(C) were observed under confocal microscope.





Figure S4. Transmission electron microscope results of YCWP and NPs-YCWP. *S.cerevisiae*SAF-Mannan was used for YCWP preparation by alkaline and acid extracted and treatment with
alcohol and acetone to remove the genetic material of yeast itself. The NPs was self-assembled with
miR365 antagomir and AAT nanotubes. Charged NPs can be packaged into YCWP via electrostatic
self deposition. (A) YCWP. (B) NPs-YCWP.



Figure S5. *Ex vivo* semi-quantitative analysis of fluorescence biodistribution. (A) Fluorescence
intensity in each organ was determined using Living Image software from PerkinElmer IVIS. (B)
Mean fluorescence density in each organ. Data were expressed as mean ± SD (n=3).



Figure S6. F4/80 and IL-1β double immunofluorescence in distal femur and proximal tibia of
knee joint. Macrophages specific expression tag F4/80 and OA-related gene IL-1β was used to study
the function of macrophages in PTOA knee joint. Compared with the Exp group, more F4/80 (red)
and IL-1β (green) expression were detected both in distal femur (A) and proximal tibia (B). This is
representative data of four repeats (n=4). The arrow pointing part indicated that F4/80 or IL-1β
expression was high in this area.



Figure S7. Expression of Nr1D2, TNF-a and Arg-1 in different cells in vivo. After oral administration of miR365 antagomir/NPs-YCWP (10⁶/YCWP with 100 pmol miR365 antagomir) for 50 days, small intestine, lung, spleen, bone marrow, spermatophore, testis, kidney and liver were collected for gene expression quantification. CD11b MicroBeads were used for sorting macrophages $(M\phi)$ from small intestine, lung, spleen and bone marrow. (A) Nr1D2, (B) TNF- α , (C) Arg-1 and summed of TNF- α and Arg-1 (**D**) expression were quantified by RT-qPCR. For each gene expression detect, we logarithmized the data and compared them to the smallest expressed tissue cells. Data were expressed as mean \pm SD. NS (no significance), ND (Not detected). *P < 0.05, **P < 0.01, ***P < 0.01, * 0.001 versus control group (n=4).

Name Sequence (5' to 3') miR365 mature sequence UAAUGCCCCUAAAAAUCCUUAU NgmiRNA mature sequence UUUGUACUACACAAAAGUACUG miR365 antagomir AUAAGGAUUUUUAGGGGCAUUA NgmiRNA CAGUACUUUUGUGUAGUACAAA 18S forward primer CGGCTACCACATCCAAGGAA 18S reverse primer GCTGGAATTACCGCGGCT IL-1 β forward primer AACCTGCTGGTGTGTGACGTTC IL-1β reverse primer CAGCACGAGGCTTTTTTGTTGT IL-6 forward primer TCCAGTTGCCTTCTTGGGAC IL-6 reverse primer GTACTCCAGAAGACCAGAGG Nr1D2 forward primer AGTGGCATGGTTCTACTGTGT Nr1D2 reverse primer GCTCCTCCGAAAGAAACCCTT Line-1 forward primer TGAGTGGAACACAACTTCTGC Line-1 reverse primer CAGGCAAGCTCTCTTCTTGC $TNF\alpha$ forward primer ACCCTCACACTCAGATCATCTTC TNFα reverse primer TGGTGGTTTGCTACGACGT Arginase-1 forward primer CTCCAAGCCAAAGTCCTTAGAG Arginase-1 reverse primer AGGAGCTGTCATTAGGGACATC

2	Table S1.	The i	nformation	of miRNA	and	primers sequ	uences
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