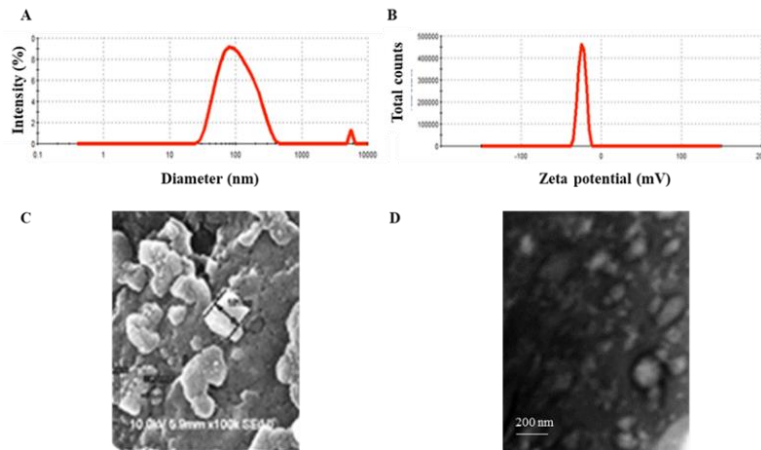


Supplementary table 1. Gene specific primers used in this study.

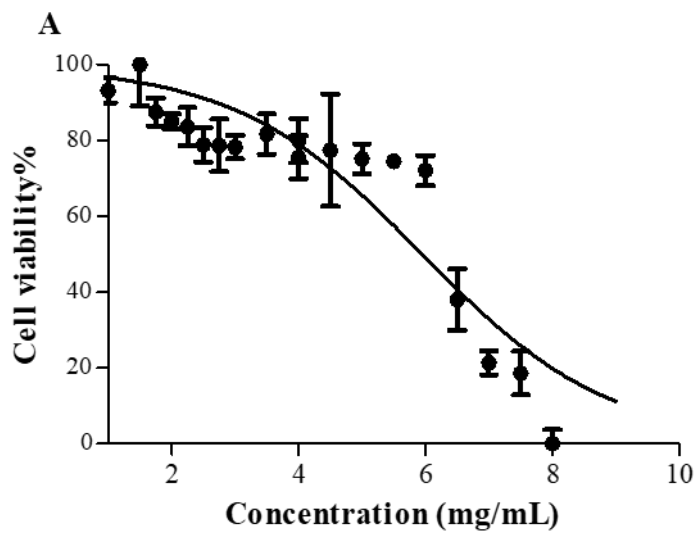
Gene name	Accession number	Primer name	Primer sequence (5'-3')
Zebrafish genes			
Toll like receptor 2 (<i>tlr2</i>)	NM_212812.1	tlr2-F tlr2-R	TCTCCGCTCTGGTTTCAC GGTCCCACAGTTGAGTATG
Toll like receptor 4b (<i>tlr4b</i>)	AY388400.1	tlr4b-F tlr4b-R	GGAATAATGGGCAGCCGTAAG AGCGACACCAACTATCAATG
Toll like receptor 5 (<i>tlr5b</i>)	BC163185.1	tlr5b-F tlr5b-R	GAAACATTCACCCCTGGCACA CTACAACCAGCACCACCAGAATG
<i>crel</i>	AY163837	crel-F crel-R	ACTACAGCTCCCAACAGCCTCAAA AAACTGGTAGCCCGTTGCTAGTGA
Interleukin-1 β (<i>il1β</i>)	AY340959.1	il1 β -F il1 β -R	TCAAACCCCAATCCACAGAG TCACTTCACGCTCTTGGATG
Tumor necrosis factor- α (<i>tnfa</i>)	AY427649	tnfa-F tnfa-R	AGAAGGAGAGTTGCCTTTACCGCT AACACCCTCCATACACCCGACTTT
Interleukin-6 (<i>il6</i>)	JN698962.1	il6-F il6-R	TCAACTTCTCCAGCGTGATG TCTTTCCCTCTTTTCTCCTG
Interleukin-10 (<i>il10</i>)	AY887900.1	il10-F il10-R	CCCTATGGATGTCACGTCATG CATATCCCGCTTGAGTTCCTG
Chemokine ligand 8a (<i>cxcl8a</i>)	XM_009306855.2	cxcl8a-R cxcl8a-R	CTTCCCTCCAAGCCACAC GATCCGGGCATTCATGG
Chemokine ligand 18b (<i>cxcl18b</i>)	NM_001115060	cxcl18b-F cxcl18b-R	CTGCTGCTGCCGTAGTTTA TCAACTTTGTGCGAGTTTGG
CC-chemokine (<i>ccl34a.4</i>)	BC162421.1	ccl34 a.4-F ccl34 a.4-R	TGCAGCTCAACCAGAAGATG CTTTGACGCATGGAGGATTT
Chemokines CCL-C24 (<i>ccl34b.4</i>)	NP_001108521	ccl34b.4-F ccl34b.4-R	TCGAGTTGGAGTAAACATGTG GTACCTTTCCTTCTCTGCGTAG
Defensin, beta-like1 (<i>defb11</i>)	NM_001081553.1	defb11-F defb11-R	CTGCTTGTCTTGTGCTACT GCAAACACACTCCTTGTCTG
Hepcidin (<i>hamp</i>)	NM_205583.2	hamp-F hamp-R	CATACAGCAGGTACAGGATGAG GAGGGTCTGTTAGTCTGTGTTT
Cathepsin D (<i>ctsd</i>)	NM_131710.2	ctsd-F ctsd-R	GAAACCCTCAGACGAACACTAAG GGGAAGCCCAGGTTGTATTT
Lysozyme-C (<i>lyz</i>)	AF402599	lyz-F lyz-R	AAGCAGGTTTAAGACCCACCGAGT AAGTCTGAACAGGCCACTTTGCAC
Alkaline phosphatase (<i>alp</i>)	JX847415.1	alp-F alp-R	GGTCGTACAACCTGTTATCCTC GAGCAAAGTCCCTCCAGTAATC
Mucin 2.1 (<i>muc2.1</i>)	NC_007136.7	muc 2.1-F muc 2.1-R	AATATGCCTTGCGGAACAAC GTGCTGAGGTTGCAGAATGA
Mucin 5.1 (<i>muc5.1</i>)	XM_009297795.1	muc 5.1-F muc 5.1-R	TGGCAACTTGGCTGATGATA TCGTACACCGACCAGTAGA
Mucin 5.2 (<i>muc5.2</i>)	XM_009297793.1	muc 5.2-F muc 5.2-R	GGTGTCTGTTCCGATCAATC TCATCCTTGTGCGCAATTGA
Mucin 5.3 (<i>muc5.3</i>)	ENSDARG0000089847	muc 5.3-F muc 5.3-R	GGGGAAAACACTACACCAGCAA TGTGAATTCTGTGCCAGAGC
Heat shock protein (<i>hsp70</i>)	AB062116.1	hsp70-F hsp70-R	CATGGTCTGGTGAAGATGAA GTCTGTGGACTCGTTGAAATA
Heat shock protein (<i>hsp90ab1</i>)	NM_131310.3	hsp90ab1-F hsp90ab1-R	GAAGAGGAGAAGGCAGAGAAAAG CGAGCCGACATCTTCAATCT
Transforming growth factor, β 1 (<i>tgfb1</i>)	XM_687246	tgfb1-F tgfb1-R	CCCAAGGAACCAGAAGTAGAAG GGATCTTCTATGGTGTGCTGAA
Matrix metalloproteinase 9 (<i>mmp9</i>)	AY151254	mmp9-F mmp9-R	TTTCCCTGATCGTGATAC GGGAAACCCTCCACGTATTT
Matrix metalloproteinase 13 (<i>mmp13</i>)	AF506756	mmp13-F mmp13-R	GAGAAGGTTTGGGCTCTCTATG TGAGTTGCTGTCTTCTGTAG
Tissue inhibitor of metalloproteinase 2 (<i>timp2b</i>)	BC056534	timp2b-F timp2b-R	GCGTTATGTGGAGTCAGTCTT CTCGATGTAGTCACACAGGTTTAT
Super oxide dismutase (<i>sod1</i>)	NM_131294.1	sod1-F sod1-R	AGGTGACTGGTGAATAACTGG GTCTCACACTATCGGTTGGC
Catalase (<i>cat</i>)	NM_130912.2	cat-F cat-R	CCAAGGTCTGGTCCCATAAAG GCTCAACCTCCGCGAAATA
β - actin	AF025305	β actin- F β actin- R	AATCTTGCGGTATCCACGAGACCA TCTCCTTCTGCATCCTGTCAGCAA

Mouse genes			
Toll-like receptor 4 (Tlr4)	NM_021297.3	Tlr4-F Tlr4-R	GCTTACACCACCTCTCAAAC ACAGCCACCAGATTCTTAAAC
Myeloid differentiation primary response gene 88 (Myd88)	NM_010851.3	Myd88-F Myd88-R	TCGATGCCTTTATCTGCTACTG GGTCGGACACACACAACTTA
Interleukin 6, transcript variant 1 (Il 6)	NM_031168.2	Il6-F Il6-R	CTTCCATCCAGTTGCCTTCT CTCCGACTTGTGAAGTGGTATAG
Interleukin 10 (Il 10)	NM_010548.2	Il10-F Il10-R	TTGAATTCCCTGGGTGAGAAAG TCCACTGCCTTGCTCTTATTT
Chemokine (C-X-C motif) ligand transcript variant 2 (Cxcl 12)	NM_013655.4	Cxcl12-F Cxcl12-R	CTCTGCATCAGTGACGGTAAA CACAGTTTGGAGTGTGAGGA
Chemokine (C-C motif) ligand 3 (Ccl 3)	NM_011337.2	Ccl3-F Ccl3-R	GAAGATTCCACGCCAATTCATC GATCTGCCGGTTTCTCTTAGTC
Defensin, alpha, 21 (Def 1)	NM_183253.3	Def1-F Def1-R	CCAGGGGAAGATGACCAGGCTG TGCAGCGACGATTCTACAAAGGC
Defensin, alpha, related sequence 2 (Def 2)	NM_007847.1	Def 2-F Def 2-R	GCATGGAATCTGGGTCAAGATAAC AGAAGGAAGAGCAATCAAGGCTAAG
Lysozyme 1 (Lyz 1)	NM_013590.4	Lyz1-F Lyz1-R	GAAGCACCGACTATGGGATATT GATCCCACAGGCATTCTTAGAT
Mucin 1 (Muc 1)	NM_013605.2	Muc1-F Muc1-R	GGCATTCCGGGCTCCTTCTT TGGAGTGGTAGTCGATGCTAAG
Catalase (Cat)	NM_009804.2	Cat-F Cat-R	GATGGTAACTGGGATCTTGTTGG GTGGGTTTCTCTTCTGGCTATG
Super oxide dismutase (Sod 1)	NM_131294.1	Sod1-F Sod1-R	AGGTGACTGGTAAAATTACTGG GTCTCACACTATCGGTTGGC
Superoxide dismutase 2; mitochondrial (Sod 2)	NM_013671.3	Sod2-F Sod2-R	AGCGTGACTTTGGGTCITTT AGCGACCTTGCTCCTTATTG
Glyceraldehyde-3-phosphate dehydrogenase (Gapdh)	NM_001289726.1	Gapdh-F Gapdh-R	AGGTCATCCCAGAGCTGAACG CACCTGTGCTGTAGCCGTAT

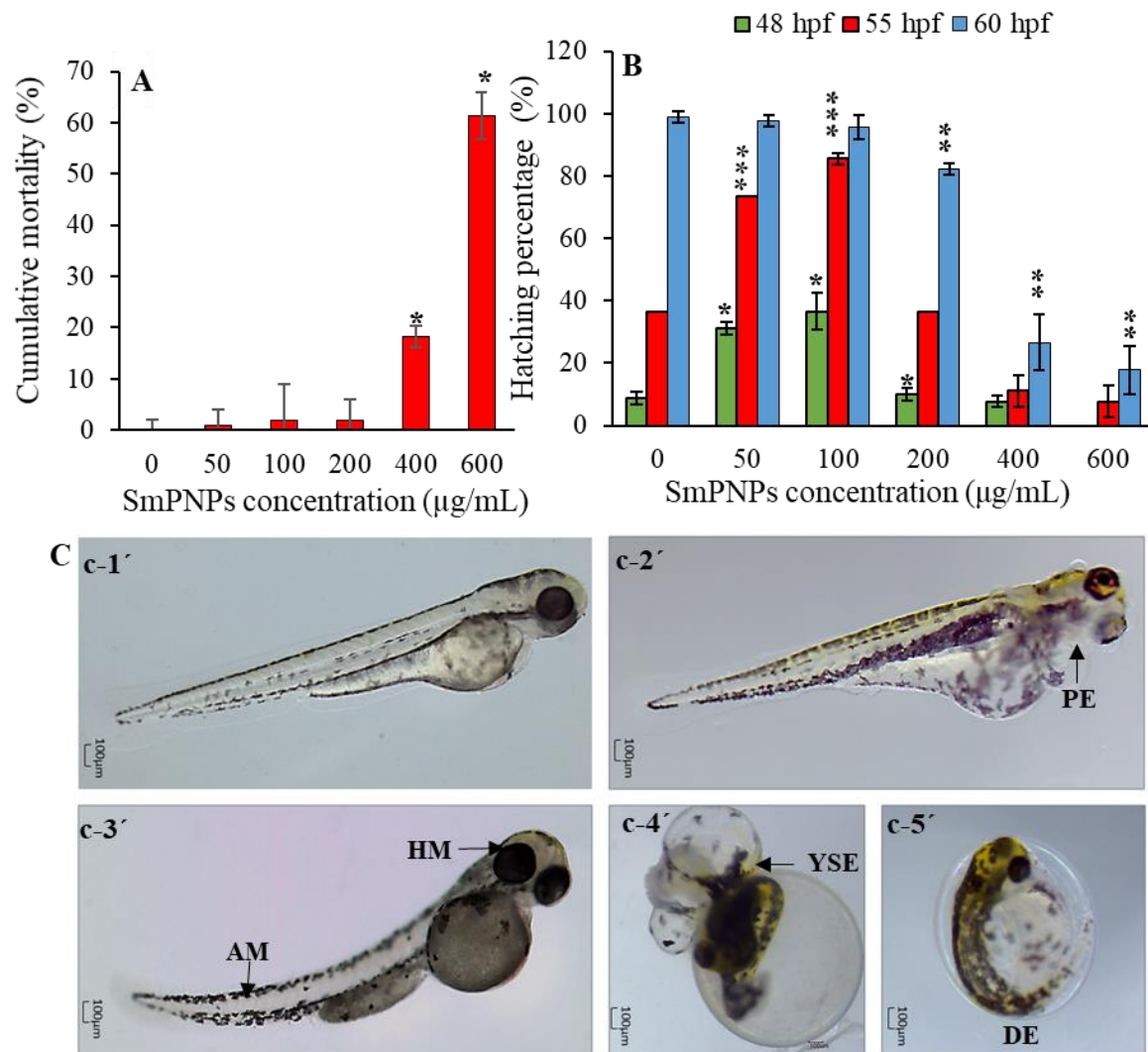
Supplementary figures



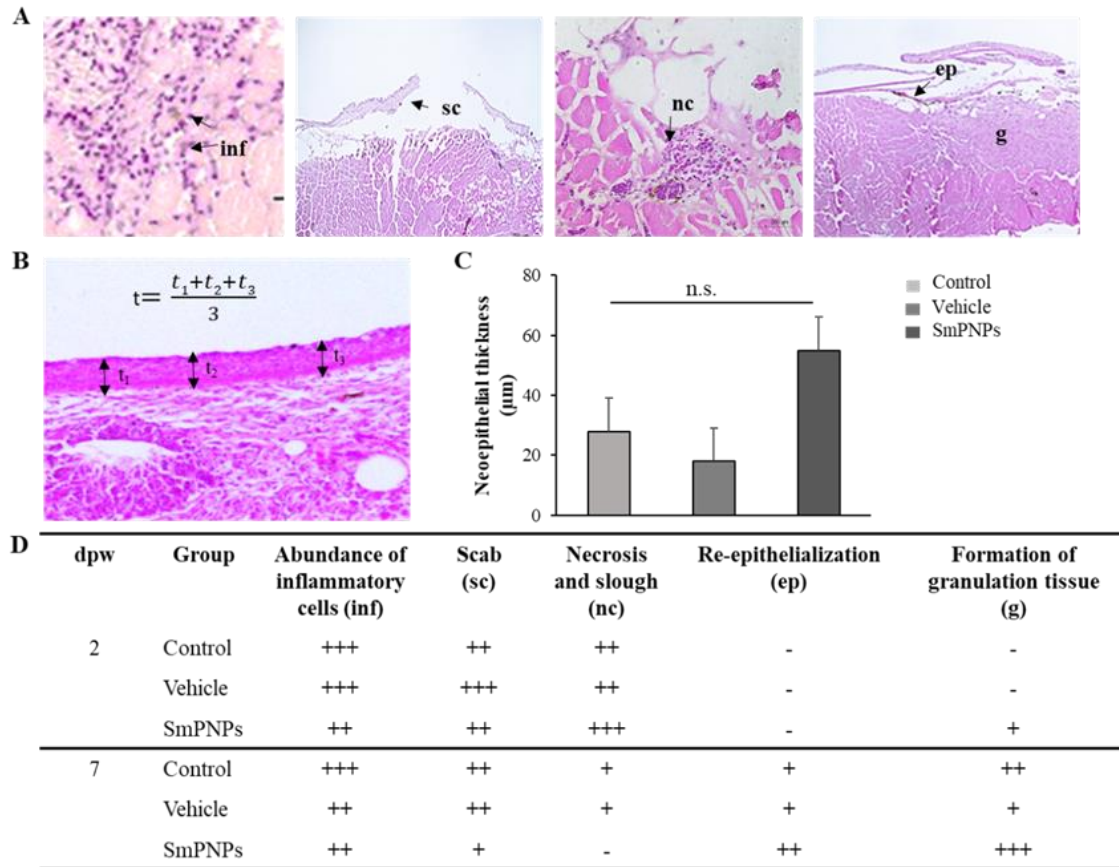
Sup. Fig. 1. Physicochemical properties of SmPNPs. A: size distribution, B: zeta potential. Morphology of SmPNPs under C: field-emission scanning electron microscopy (FE-SEM) and D: field-emission transmission electron microscopy (FE-TEM). FE-SEM and FE-TEM images show the irregular shape of SmPNPs.



Sup. Fig. 2. *In vitro* cytotoxicity assay of SmPNPs on Raw 264.7. SmPNPs were treated with different concentrations (1-8 mg/mL) of SmPNPs, and cell viability% was evaluated. Values were presented as means plus or minus standard error (\pm SE) of three independent experiments, and each carried out in triplicates.



Sup. Fig. 3. *In vivo* toxicity of SmPNPs exposed to zebrafish embryos. A: cumulative mortality, B: hatching rate, C: malformations of embryos induced by SmPNPs, c-1': control larva; c-2': pericardial oedema (PE); c-3': axial malformation (AE) and head malformation (HM); c-4': yolk sack oedema (YSE); c-5': dead embryo (DE). Data are expressed as means plus or minus standard error (\pm SE) from three independent experiments. Significant differences between experimental groups are denoted by asterisk (*) marks. (one-way and/or two-way ANOVA * $P < .05$, ** $P < .01$, *** $P < .001$).



Sup. Fig. 4. Quantitative analysis for major histological parameters in SmPNPs wound healing. A: representative images used for semi-quantitative analysis, B: quantitative analyzed criteria for neoepithelial thickness in healing wounds. C: graphs showing the nonepithelial thickness. The values are the mean \pm standard deviation (SD) (n=3). Unpaired two-tailed t-test was performed to find statistical significance ($*P < .05$). D: Selected histological indexes demonstrating the diminishing of abundance of inflammatory cells (inf), scab (sc), necrosis and slough (nc), re-epithelialization (ep) and formation of granulation tissue (g) on wound surface at 2 and 7 dpw. (Notes: +, slight; ++, moderate; +++, marked; -, absence).