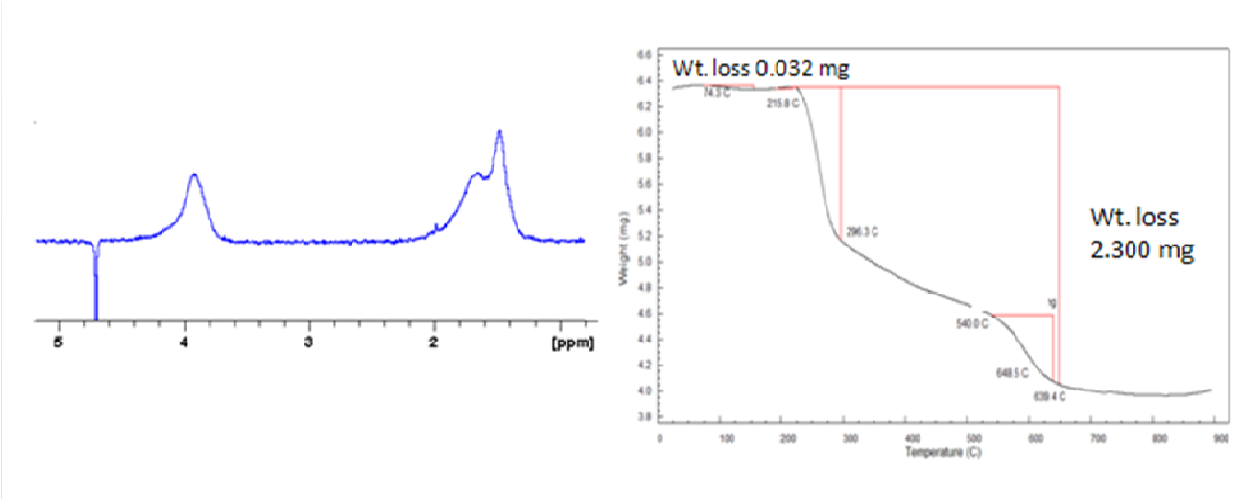
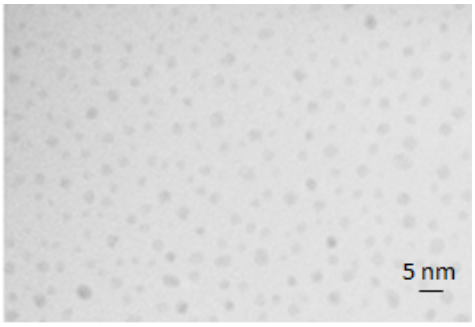
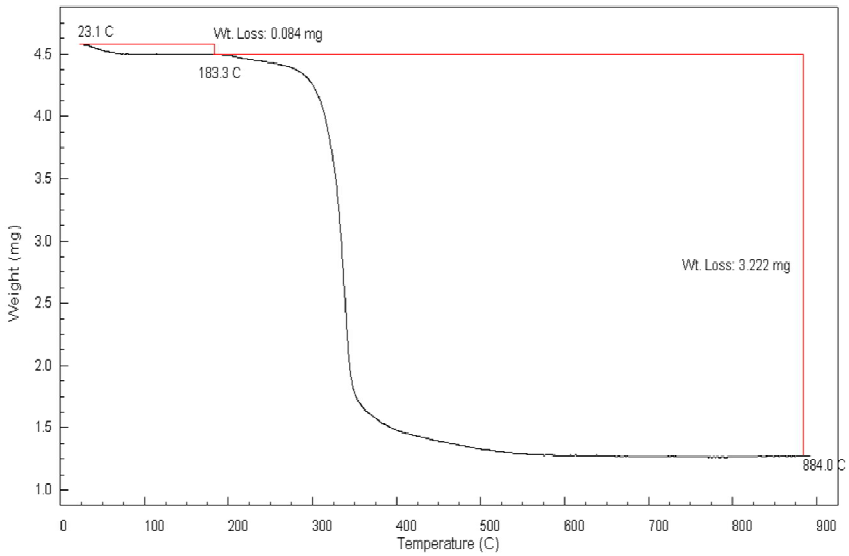
Supporting Information

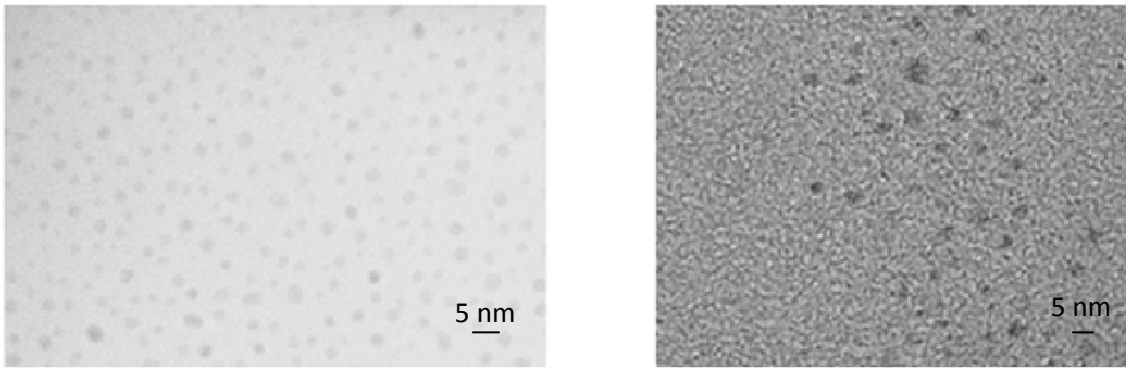




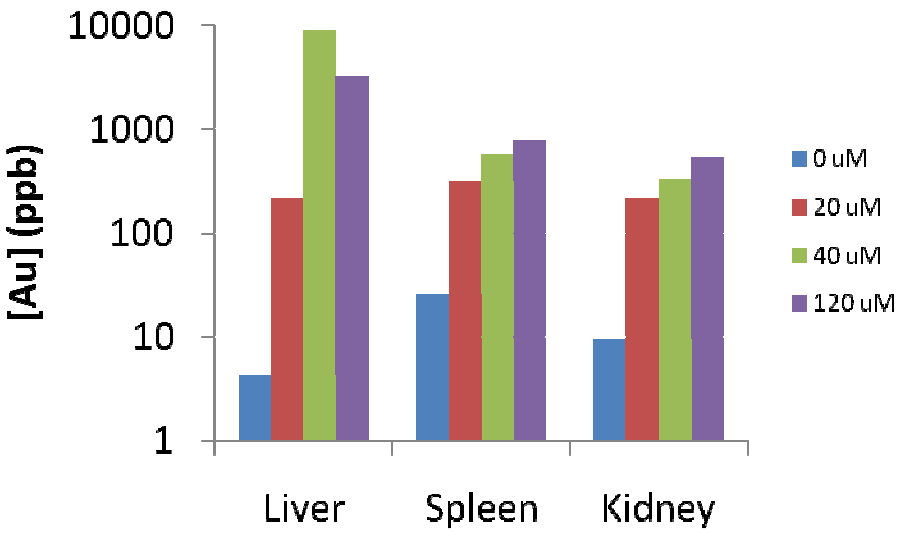
Supplemental 1. Characterization data for original TMPC. NMR shows characteristic peak broadening, while TGA gives an organic loss of 36%, within accepted literature values. TEM shows spherical cores with an average diameter of 2.5 ± 1.0 nm.

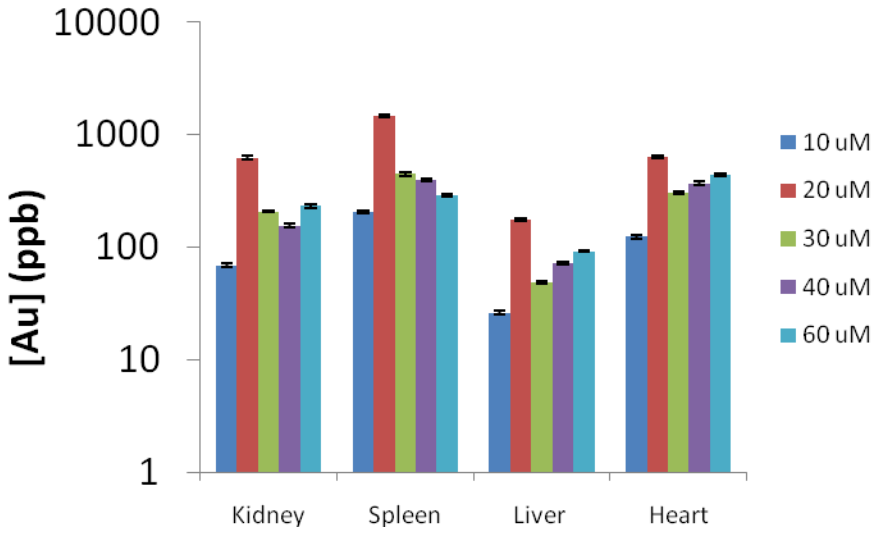


Supplemental 2. TGA analysis of PEG-ylated TMPC shows an organic loss of 3.306 mg of an original 4.5676 mg sample, for a total organic loss of 72%, which suggests the PEG ligands form a micellular composition around the nanoparticle, adding to the overall organic weight.



Supplemental 3. TEM comparison of TMPC (left) and PEG-ylated TMPC (right). No significant difference between core size/shape is noted after PEG-ylation. There appears to be no collapse to a polymeric structure after PEG-ylation. All average core values were assumed to have remained the same.





Supplemental 4 . Organ analysis for original TMPC study shows the highest concentration of particle was found within the liver and spleen. Most subjects were correlative with the exception of the 120 µM group, who were euthanized within 24 hours post-injection. It may be assumed the particle did not have enough time to complete its full circulation route in this timeframe. Organ analysis for gold content shows a positive correlation between gold concentration within the organ and injected concentration of PEG-ylated TMPC for both the liver and the heart (with the exception of 20 µM). A negative correlation is noted for the spleen, while the kidney is somewhat random due to different void times within the mice. The 20 µM groups' somewhat outlier behavior could be due to a lack of immunological recognition as noted for the larger concentrations, leading to a slower clearance rate. The 0 µM group was essentially zero and is not shown.

Time	Glucose				Ketone				Protein				Blood				Leukocytes			
	0	20	40	60	0	20	40	60	0	20	40	60	0	20	40	60	0	20	40	60
Baseline	-	-	-	-	-	-	-	-	'	'	''	'	-	-	-	-	-	-	-	-
30 min									+	+	++	+								
1 hour	-	-	X	-	-	-	X	-	+	+	X	+	-	-	X	-	-	-	X	-
1.5 hour	-	-	-	-	'	-	-	-	'	'	''	'	-	-	-	-	-	-	-	-
2 hour	-	-	-	-	-	+	-	-	+	+	++	+	-	-	-	-	-	-	-	-
2.5 hour	X	-	-	-	X	+	-	-	X	+	+	+	X	-	-	-	X	-	-	-
3 hours	-	-	-	-	-	-	-	-	+	++	+	+	-	-	-	-	-	-	-	-
4 hours	-	-	-	-	-	-	-	-	'	''	'	'''	-	-	-	-	-	-	-	-
8 hours	-	-	-	-	-	-	-	-	'	''	'	'	-	-	-	-	-	-	-	-
24 hours	-	X	X	X	+	X	X	X	+	X	X	X	-	X	X	X	-	X	X	X
2 weeks	-	-	-	-	-	-	-	-	'	''	''	'	-	-	-	-	-	-	-	-

Supplemental 5. MultiStix analyses for mice at all concentrations for PEG-ylated TMPC. No glucose, blood, or leukocytes were present in any sample at any concentration. Random ketone appearance at 2-3 hour period for 20 µM, which is quickly eliminated. Protein content was relatively consistent throughout the study, with only one high reading at 4 hours for 60 µM, which quickly returns to normal at 6 hours.

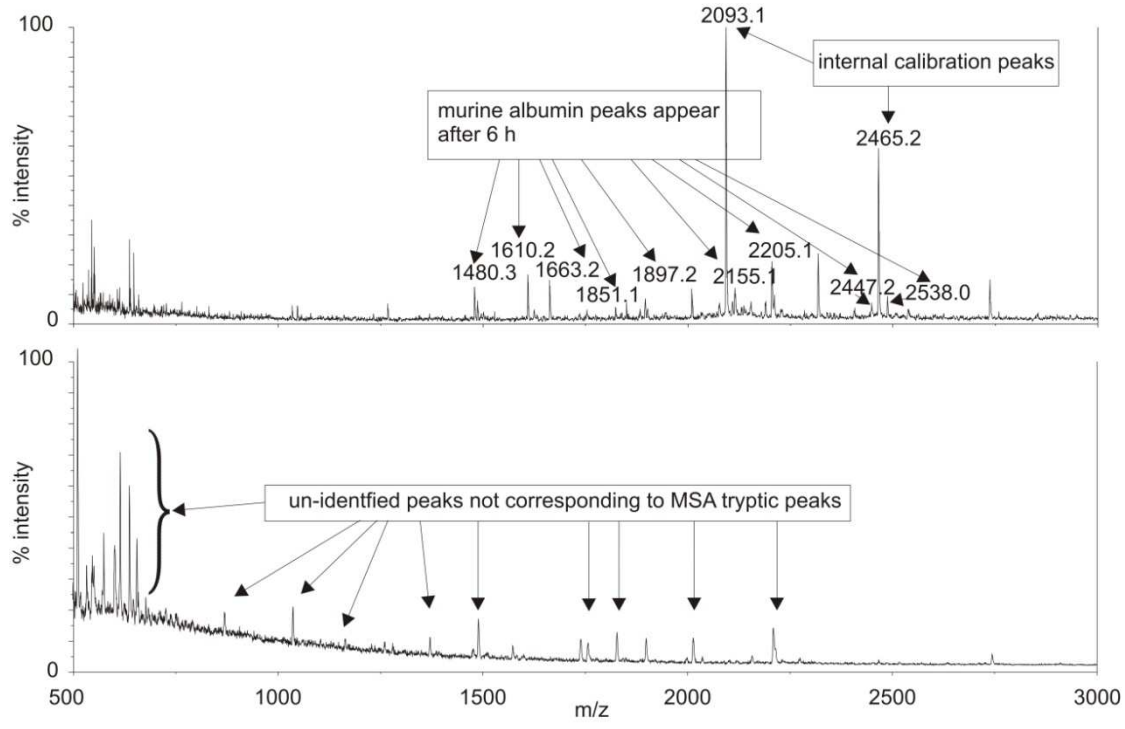


Figure 6. (top) MALDI-TOFMS for C-18 purified urine samples of mice injected with TMPC particles (top) Several peaks corresponding to digested murine serum albumin (MSA) are seen. (bottom) PEG-ylated particles. Several peaks not corresponding to digested MSA were seen.

MALDI-TOF MS Analysis

Peptide mass fingerprints were observed for MSA tryptic peptides six hours after injection with un-modified TMPCs, signifying renal damage. The relative peak areas of the peptide mass fingerprints were found to increase relative to ATCH clip internal standards over the remaining 24 hours of collection (data not shown). Although the peptide mass fingerprint assignments alone aren't adequate confirmation of the protein composition of the urinary samples, this analysis provides complementary confirmation of the extensive renal damage noted from histological examination of TMPCs.

Peptide mass fingerprinting analysis of urine attained from mice injected with PEG-ylated TMPCs revealed four possible MSA mass fingerprints (< 3000 m/z), three of which were not seen in the control (Tiopronin-injected urine samples with known kidney damage). Because these peaks do not match the fingerprints observed in the control kidney damage samples, it is speculated that these peaks may correspond to isobaric tryptic peptides of other proteins. Furthermore, a number peaks not corresponding to MSA were observed and searched against a peptide mass fingerprinting algorithm for potential identifications.